MathIOmica

G. Mias Lab

Documentation: Functions and Examples

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ApplyBoxCoxTransform

`ApplyBoxCoxTransform[data]`
for a given *data* set, computes the Box–Cox transformation at the maximum likelihood λ parameter.

Details

- `ApplyBoxCoxTransform[data]` transforms the data (list, association or OmicsObject) by performing a Box-Cox transformation at the optimized parameter $\hat{\lambda}$, namely the value for a Box-Cox transformation parameter λ for which the log-likelihood that the transformation is normally distributed is maximized. The data must all be positive numbers.
- The objective is to transform a given input data set to be as normally distributed as possible, and thus, the function works by first calculating the transformation exponent $\hat{\lambda}$, at which the transformed data is as normally distributed as possible, and then outputting the Box-Cox transformation of the data at that parameter. The Box-Cox transformation is one possible procedure for standardizations of disparate data sets, along with other procedures (e.g. QuantileNormalization).
- The Box-Cox transformation is a rank-preserving transformation that takes as input a (not necessarily normally distributed) dataset $X = \{X_1, X_2, \ldots, X_N\}$, and finds a functional transformation of the data that 'best' makes it (approximately) normally distributed. To be more precise, it is a well known result from estimation theory that for a given dataset, if one wishes to infer what are the most likely parameters of a normal distribution that could have generated the data, then the optimal estimators of the mean μ and variance σ^2 are $\hat{\mu} = \frac{1}{N}\sum_i X_i$ and $\hat{\sigma}^2 = \frac{1}{N}\sum_i \left(X_i - \hat{\mu}\right)^2$, and the optimized log-likelihood is $\log(L(\hat{\mu}, \hat{\sigma}^2)) = \frac{-N}{2}(1 + \log(2\pi\hat{\sigma}^2))$.
- The Box-Cox power transform is a function of a transformation parameter λ and is defined as $X^{(\lambda)} = \log(X)$ for $\lambda = 0$ and $X^{(\lambda)} = \frac{X^\lambda - 1}{\lambda}$ for all other λ. Upon transforming the data in this fashion, the normal probability distribution $p(X) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(x-\mu)^2}{2\sigma^2}}$ rewritten in terms of $X^{(\lambda)}$ must pick up an extra Jacobian factor $J(\lambda)$ to conserve total probability, $p\left(X^{(\lambda)}\right) = \frac{J(\lambda)}{\sqrt{2\pi}\sigma^{(\lambda)}} e^{\frac{-\left(x^{(\lambda)} - \mu^{(\lambda)}\right)^2}{2\left(\sigma^{(\lambda)}\right)^2}}$.
- The value of this Jacobian factor is $J(\lambda) = \prod_i \left|\frac{dX_i^{(\lambda)}}{dX}\right| = \mathrm{GM}(X)^{N(\lambda-1)}$, where GM is the geometric mean of X, $GM(X) = (X_1 X_2 \ldots X_N)^{1/N}$. One consequence of this Jacobian factor is that the optimized log-likelihood of the normal distribution must now account for this Jacobian factor. Explicitly, $\log(L(\lambda, \hat{\mu}^{(\lambda)}, (\hat{\sigma}^{(\lambda)})^2)) = \frac{-N}{2}(1 + \log(2\pi(\hat{\sigma}^{(\lambda)})^2)) + \log(J(\lambda)) = \frac{-N}{2}(1 + \log(2\pi(\hat{\sigma}^{(\lambda)})^2)) + N(\lambda\text{-}1)\log(GM(X))$.
- Thus, to normalize a dataset $X = \{X_1, X_2, \ldots, X_N\}$ via a Box-Cox transformation, one must maximize $\log(L(\lambda, \hat{\mu}^{(\lambda)}, (\hat{\sigma}^{(\lambda)})^2))$ for the given X, and this gives one an optimized transformation exponent $\hat{\lambda}$.
- In the case of an Association or OmicsObject input the ApplyBoxCoxTransform returns the same object as its input with the new values of the data at the specified position. The selection of the position is performed using the options for the function that are internally passed to Applier and Returner.
- The following options can be given:

ComponentIndex	Missing[]	Selection of which component of a list to use in the association or OmicsObject input values.

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HorizontalSelection	False	Horizontal selection across components for a single level association with multi–list values.
ListIndex	Missing[]	Selection of which list to use in the association or OmicsObject input values.

Examples (8)

Basic Examples (5)

First we need to load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

Application to an OmicsObject (1)

Let's import the example protein data. These are located at:

```
In[1]:= proteinExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinExample"}
```

We can now get the data:

```
In[2]:= proteinExampleData = Get[proteinExampleFile];
```

Let' s query the first 5 proteins across all datasets for this OmicsObject:

```
In[3]:= proteinSubset = Query[All, 1 ;; 5]@proteinExampleData

Out[3]= <|7 → <|{A0AVT1, Protein} → {{0.937}, {17}},
    {A0FGR8, Protein} → {{1.073}, {24}}, {A0MZ66, Protein} → {{1.059}, {9}},
    {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}}|>,
  9 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}},
```

We perform a Box-Cox transformation. The function will calculate and display the progress across datasets, and also output the optimized $\hat{\lambda}$ parameter:

```
In[4]:= proteinExampleBoxCoxTransformed =
  ApplyBoxCoxTransform[proteinExampleData, ListIndex → 1, ComponentIndex → 1]
```

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```
Calculated Box-Cox parameter λ̂ = -0.152638
Calculated Box-Cox parameter λ̂ = -0.177086
Calculated Box-Cox parameter λ̂ = -0.421581
Calculated Box-Cox parameter λ̂ = -0.292287
Calculated Box-Cox parameter λ̂ = -0.432042
Calculated Box-Cox parameter λ̂ = 0.346673
Calculated Box-Cox parameter λ̂ = 0.368061
Calculated Box-Cox parameter λ̂ = 0.0834073
Calculated Box-Cox parameter λ̂ = 0.13413
Calculated Box-Cox parameter λ̂ = 0.166336
Calculated Box-Cox parameter λ̂ = 0.0866284
Calculated Box-Cox parameter λ̂ = -0.199247
Calculated Box-Cox parameter λ̂ = -0.221778
```

Out[4]=

```
<|7 → <|{A0AVT1, Protein} → {{-0.0653962}, {17.}}, {A0FGR8, Protein} → {{0.0700809}, {24.}},
    ··· 5222 ···, {Q9Y6X3, Protein} → Missing[KeyAbsent, {Q9Y6X3, Protein}]|>,
 9 → <|··· 1 ···|>, ··· 9 ···, 20 → <|··· 1 ···|>, 21 → <|··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

In[5]:=

```
Query[Key["20"]]@proteinExampleBoxCoxTransformed
```

Out[5]=

```
<|{A0AVT1, Protein} → {{-0.137674}, {16.}}, {A0FGR8, Protein} → {{-0.162752}, {22.}},
 ··· 5221 ···, {Q9Y6I9, Protein} → {{-0.269659}, {5.}}, {Q9Y6X3, Protein} → Missing[]|>
```

large output | show less | show more | show all | set size limit...

Let's plot the distribution of the set with Key "20" as an example:

In[6]:=

```
Query[(Key["20"]) /* Values /* Flatten /* Histogram, All, 1]@proteinExampleBoxCoxTransformed
```

Out[6]=

Application to Associations, Single List Values (1)

Let's generate some random data.

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In[1]:=
```
dataRandomAssociationExample =
 AssociationThread[Range[5] → RandomVariate[PoissonDistribution[10], {5, 100}]]
```

Out[1]=
```
<|1 → {8, 7, 15, 12, 13, 11, 12, 7, 6, 10, 18, 7, 9, 7, 8, 10, 14, 7, 8, 14, 13, 10, 14,
   7, 9, 6, 9, 12, 6, 13, 12, 14, 9, 14, 9, 11, 10, 10, 8, 8, 13, 12, 10, 8, 9, 11, 11, 4, 5, 12,
   8, 12, 19, 12, 6, 14, 17, 13, 11, 14, 9, 10, 6, 11, 14, 15, 13, 13, 8, 16, 19, 9, 8, 13, 10,
   14, 14, 13, 11, 11, 6, 10, 7, 16, 5, 11, 9, 12, 6, 8, 10, 10, 12, 15, 8, 13, 18, 4, 9, 11},
 2 → {12, 11, 11, 10, 12, 9, 16, 13, 10, 15, 17, 9, 13, 8, 13, 9, 10, 10, 6, 7, 10, 7, 12, 8,
   8, 13, 13, 9, 7, 12, 7, 10, 4, 7, 7, 12, 8, 5, 4, 11, 9, 9, 12, 14, 13, 12, 11, 8, 13,
   8, 7, 10, 6, 10, 9, 12, 4, 13, 3, 9, 5, 11, 9, 7, 5, 11, 15, 7, 14, 7, 8, 14, 9, 8, 7,
   12, 13, 7, 12, 7, 11, 11, 7, 2, 11, 13, 8, 9, 11, 10, 9, 6, 11, 16, 6, 13, 5, 6, 11, 9},
 3 → {9, 16, 17, 6, 3, 14, 10, 10, 9, 10, 9, 10, 4, 10, 11, 8, 11, 9, 10, 7, 6, 15, 11, 12, 8,
   16, 11, 8, 8, 8, 6, 9, 7, 13, 6, 14, 9, 11, 13, 18, 10, 8, 14, 3, 17, 9, 9, 4, 3, 6, 15,
   10, 10, 15, 7, 12, 10, 8, 9, 13, 7, 6, 14, 9, 13, 13, 8, 12, 14, 18, 8, 7, 6, 8, 10, 7,
   4, 11, 11, 17, 8, 8, 10, 13, 11, 6, 11, 18, 13, 10, 9, 8, 9, 13, 9, 13, 11, 11, 5, 8},
 4 → {9, 16, 15, 15, 9, 12, 10, 8, 9, 4, 4, 11, 12, 7, 11, 9, 16, 14, 11, 17, 13, 10, 10, 12, 7,
   18, 10, 11, 8, 12, 7, 5, 12, 7, 9, 6, 4, 6, 5, 11, 13, 9, 8, 16, 14, 15, 10, 7, 7, 11, 12,
   10, 14, 13, 14, 16, 8, 19, 9, 9, 7, 9, 11, 13, 15, 9, 13, 12, 7, 5, 8, 13, 13, 12, 9, 14,
   11, 10, 12, 16, 7, 5, 14, 8, 9, 10, 12, 15, 9, 10, 10, 12, 14, 10, 11, 17, 14, 16, 12, 14},
 5 → {14, 8, 13, 9, 5, 9, 8, 12, 6, 9, 15, 12, 8, 9, 2, 11, 13, 15, 12, 11, 9, 10, 11, 7, 9, 11,
   6, 10, 9, 7, 9, 9, 13, 9, 10, 14, 16, 3, 11, 8, 15, 7, 18, 10, 7, 14, 16, 11, 5, 12, 9, 14,
   10, 6, 10, 15, 7, 9, 5, 11, 10, 11, 8, 12, 14, 8, 10, 9, 12, 14, 7, 10, 13, 11, 13, 11,
   11, 13, 14, 9, 11, 10, 11, 6, 13, 11, 7, 7, 11, 10, 12, 10, 7, 16, 11, 11, 9, 10, 9, 9}|>
```

Let' s perform now a Box-Cox transformation. The function will calculate and display the progress across datasets, and also output the optimized $\hat{\lambda}$ for each set in order:

In[2]:=
```
dataRandomAssociationExampleBoxCoxTransformed = ApplyBoxCoxTransform[dataRandomAssociationExample]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.584431

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.964929

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.664137

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.844567

Calculated Box-Cox parameter $\hat{\lambda}$ = 1.0267

Out[2]=
```
<|1 → {4.0574, 3.62435, 6.61828, 5.59988, 5.95001, 5.2374, 5.59988, 3.62435, 3.16469,
   4.86093, 7.55482, 3.62435, 4.46847, 3.62435, 4.0574, 4.86093, 6.28911,
   3.62435, 4.0574, 6.28911, 5.95001, 4.86093, 6.28911, 3.62435, 4.46847,
   3.16469, 4.46847, 5.59988, 3.16469, 5.95001, 5.59988, 6.28911, 4.46847,
```

Application to an Association of Multi-List Values (1)

Let's generate some random data.

In[1]:=
```
dataRandomAssociationsExample = AssociationThread@
  (("Key" <> ToString[#]) & /@ Range[100] → RandomVariate[PoissonDistribution[10], {100, 2, 3}])
```

Out[1]=
```
<|Key1 → {{10, 9, 7}, {8, 7, 11}}, Key2 → {{14, 5, 12}, {10, 11, 4}},
 Key3 → {{12, 12, 5}, {8, 11, 12}}, Key4 → {{9, 15, 10}, {16, 11, 13}},
 Key5 → {{8, 13, 6}, {14, 7, 11}}, Key6 → {{8, 7, 11}, {5, 8, 8}},
 Key7 → {{9, 14, 9}, {13, 13, 7}}, Key8 → {{5, 9, 13}, {8, 14, 14}},
```

Let' s perform again a Box-Cox transformation. The function will calculate and display the progress across datasets, and also output the optimized $\hat{\lambda}$. As this is a single association, we set HorizontalSelection option to True to be able to select horizontally from the lists across Keys (see also Applier)

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In[2]:=
```
dataRandomAssociationsExampleTransformed = ApplyBoxCoxTransform[
  dataRandomAssociationsExample, ListIndex → 1, ComponentIndex → 1, HorizontalSelection → True]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.772531

Out[2]=
```
<|Key1 → {{6.37237, 9., 7.}, {8., 7., 11.}}, Key2 → {{8.64824, 5., 12.}, {10., 11., 4.}},
 Key3 → {{7.53199, 12., 5.}, {8., 11., 12.}}, Key4 → {{5.77306, 15., 10.}, {16., 11., 13.}},
 Key5 → {{5.15837, 13., 6.}, {14., 7., 11.}}, Key6 → {{5.15837, 7., 11.}, {5., 8., 8.}},
 Key7 → {{5.77306, 14., 9.}, {13., 13., 7.}}, Key8 → {{3.19363, 9., 13.}, {8., 14., 14.}},
 Key9 → {{5.77306, 12., 8.}, {12., 13., 9.}}, Key10 → {{7.53199, 8., 7.}, {8., 20., 10.}},
 Key11 → {{8.64824, 11., 11.}, {5., 5., 4.}}, Key12 → {{5.15837, 11., 10.}, {7., 9., 8.}},
 Key13 → {{6.95818, 14., 8.}, {12., 18., 9.}}, Key14 → {{9.19255, 7., 13.}, {11., 8., 6.}},
 Key15 → {{8.095, 5., 10.}, {9., 12., 7.}}, Key16 → {{6.37237, 6., 9.}, {6., 16., 13.}},
 Key17 → {{11.2937, 5., 8.}, {8., 10., 7.}}, Key18 → {{1.7302, 9., 13.}, {8., 10., 14.}},
 Key19 → {{5.77306, 7., 14.}, {8., 14., 8.}}, Key20 → {{5.15837, 11., 10.}, {11., 7., 10.}},
 Key21 → {{6.95818, 14., 13.}, {6., 15., 12.}}, Key22 → {{6.37237, 15., 7.}, {13., 9., 13.}},
 Key23 → {{2.48296, 8., 8.}, {11., 16., 7.}}, Key24 → {{6.95818, 7., 9.}, {7., 9., 10.}},
 Key25 → {{5.77306, 8., 9.}, {11., 15., 10.}}, Key26 → {{5.15837, 8., 10.}, {9., 7., 13.}},
 Key27 → {{5.77306, 10., 11.}, {11., 8., 11.}}, Key28 → {{8.64824, 13., 13.}, {12., 11., 11.}},
 Key29 → {{8.095, 8., 7.}, {7., 7., 15.}}, Key30 → {{2.48296, 16., 14.}, {9., 8., 9.}},
 Key31 → {{8.095, 11., 14.}, {19., 9., 10.}}, Key32 → {{6.95818, 11., 5.}, {8., 5., 8.}},
 Key33 → {{5.15837, 16., 14.}, {7., 15., 12.}}, Key34 → {{6.95818, 15., 8.}, {11., 6., 15.}},
 Key35 → {{9.72867, 8., 7.}, {5., 6., 9.}}, Key36 → {{6.95818, 16., 18.}, {11., 14., 9.}},
 Key37 → {{7.53199, 10., 11.}, {16., 6., 10.}}, Key38 → {{5.15837, 9., 6.}, {8., 4., 11.}},
 Key39 → {{6.37237, 10., 15.}, {1., 10., 9.}}, Key40 → {{4.5259, 12., 8.}, {17., 9., 6.}},
 Key41 → {{3.87245, 7., 9.}, {5., 7., 6.}}, Key42 → {{5.15837, 8., 8.}, {7., 8., 8.}},
 Key43 → {{7.53199, 13., 7.}, {9., 9., 7.}}, Key44 → {{4.5259, 7., 14.}, {7., 5., 7.}},
 Key45 → {{7.53199, 8., 14.}, {8., 6., 11.}}, Key46 → {{4.5259, 13., 7.}, {12., 10., 3.}},
 Key47 → {{9.72867, 9., 11.}, {7., 5., 9.}}, Key48 → {{5.77306, 12., 6.}, {9., 9., 10.}},
 Key49 → {{7.53199, 12., 10.}, {5., 10., 14.}}, Key50 → {{5.77306, 5., 7.}, {15., 10., 12.}},
 Key51 → {{9.72867, 9., 9.}, {12., 13., 6.}}, Key52 → {{5.77306, 6., 8.}, {7., 9., 5.}},
 Key53 → {{4.5259, 5., 8.}, {11., 9., 4.}}, Key54 → {{2.48296, 11., 10.}, {9., 8., 10.}},
 Key55 → {{6.37237, 9., 8.}, {12., 9., 7.}}, Key56 → {{6.37237, 9., 4.}, {13., 9., 15.}},
 Key57 → {{3.19363, 12., 12.}, {6., 10., 17.}}, Key58 → {{6.37237, 13., 12.}, {10., 10., 10.}},
 Key59 → {{7.53199, 5., 5.}, {6., 13., 8.}}, Key60 → {{6.37237, 6., 9.}, {11., 5., 7.}},
 Key61 → {{4.5259, 7., 10.}, {6., 10., 13.}}, Key62 → {{5.77306, 8., 8.}, {9., 12., 10.}},
 Key63 → {{6.95818, 13., 8.}, {15., 9., 13.}}, Key64 → {{4.5259, 15., 9.}, {8., 9., 12.}},
 Key65 → {{6.37237, 13., 7.}, {14., 12., 14.}}, Key66 → {{9.72867, 5., 8.}, {7., 11., 1.}},
 Key67 → {{4.5259, 10., 6.}, {12., 7., 11.}}, Key68 → {{6.37237, 8., 11.}, {16., 8., 11.}},
 Key69 → {{7.53199, 11., 5.}, {13., 6., 9.}}, Key70 → {{6.37237, 10., 8.}, {10., 9., 20.}},
 Key71 → {{7.53199, 12., 6.}, {7., 9., 18.}}, Key72 → {{5.77306, 9., 6.}, {9., 12., 8.}},
 Key73 → {{5.77306, 10., 9.}, {12., 11., 13.}}, Key74 → {{6.95818, 8., 7.}, {5., 8., 12.}},
 Key75 → {{5.77306, 14., 7.}, {8., 9., 6.}}, Key76 → {{7.53199, 11., 12.}, {13., 11., 17.}},
 Key77 → {{6.95818, 11., 8.}, {10., 9., 11.}}, Key78 → {{3.87245, 11., 11.}, {15., 11., 16.}},
 Key79 → {{5.77306, 13., 9.}, {13., 12., 11.}}, Key80 → {{5.77306, 11., 11.}, {10., 9., 9.}},
 Key81 → {{5.15837, 5., 12.}, {6., 12., 15.}}, Key82 → {{6.37237, 10., 14.}, {9., 8., 4.}},
 Key83 → {{6.37237, 7., 8.}, {10., 9., 15.}}, Key84 → {{3.87245, 7., 11.}, {8., 12., 13.}},
 Key85 → {{6.95818, 8., 8.}, {15., 17., 9.}}, Key86 → {{8.095, 8., 8.}, {12., 17., 9.}},
 Key87 → {{6.95818, 11., 5.}, {19., 16., 7.}}, Key88 → {{6.37237, 9., 9.}, {11., 11., 5.}},
 Key89 → {{6.37237, 13., 7.}, {11., 9., 10.}}, Key90 → {{7.53199, 8., 12.}, {6., 8., 9.}},
 Key91 → {{6.95818, 9., 7.}, {10., 11., 14.}}, Key92 → {{9.72867, 14., 6.}, {10., 10., 3.}},
 Key93 → {{8.64824, 11., 6.}, {8., 11., 10.}}, Key94 → {{3.87245, 3., 6.}, {12., 5., 6.}},
 Key95 → {{6.37237, 11., 8.}, {9., 12., 13.}}, Key96 → {{6.37237, 10., 11.}, {12., 14., 9.}},
 Key97 → {{8.095, 10., 7.}, {7., 10., 5.}}, Key98 → {{4.5259, 10., 11.}, {11., 12., 8.}},
 Key99 → {{5.77306, 9., 12.}, {8., 13., 9.}}, Key100 → {{5.15837, 17., 14.}, {10., 8., 11.}}|>
```

Application to a List (1)

We generate data from an exponential distribution that we can use.

In[1]:=
```
dataRandomExample=RandomVariate[ExponentialDistribution[10],1000];
```

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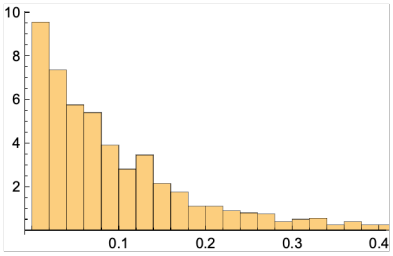
In[2]:=
```
Histogram[dataRandomExample, Automatic, "ProbabilityDensity"]
```

Out[2]=



The calculation below may take some time depending on the data length and complexity.

In[3]:=
```
dataRandomExampleBoxCox = ApplyBoxCoxTransform[dataRandomExample]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.264088

Out[3]=
```
{-3.29424, -2.33782, -1.96034, -2.15649, -0.965245, -2.29818, -2.52577, -2.27351, -1.40504, -2.25989,
 -1.84972, -2.13716, -1.62709, -2.2286, -0.780496, -2.04369, -2.75351, -2.22019, -2.00922, -2.16651,
 -1.48076, -2.22258, -1.63794, -1.68669, -2.34771, -1.38545, -2.29127, -1.91996, -1.388, -1.94332,
 -2.38873, -2.45712, -2.31933, -1.92297, -2.73741, -1.7254, -2.2417, -1.39799, -2.25816, -2.75397,
 -1.78148, -1.51497, -2.15711, -1.27831, -1.59235, -2.601, -2.94088, -1.6128, -2.19418, -1.9196,
 -2.3233, -1.45463, -1.45526, -3.07141, -1.11296, -1.91434, -2.61118, -1.95351, -2.02878, -1.70778,
 -2.82953, -1.87258, -2.73286, -1.65336, -3.06668, -1.95214, -1.41578, -2.36697, -1.63505, -1.98653,
 -2.10255, -1.43914, -2.21354, -2.40811, -2.08267, -1.11193, -2.07896, -1.99435, -0.932899, -2.08059,
 -1.43824, -1.77689, -1.56504, -2.90092, -2.77628, -2.50124, -2.1367, -1.89348, -1.55195, -2.64538,
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-3.17165, -2.2575, -1.83087, -2.55, -2.57833, -2.02544, -2.10768, -1.04209, -0.891715, -1.94085}
```

The transformed data Histogram looks like:

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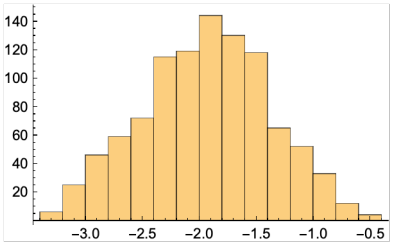
In[4]:=
```
Histogram[dataRandomExampleBoxCox]
```

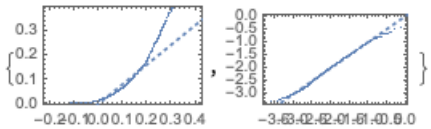
Out[4]=



Here is a Q-Q plot of the quantiles of the data before and after the transformation:

In[5]:=
```
{QuantilePlot[dataRandomExample], QuantilePlot[dataRandomExampleBoxCox]}
```

Out[5]=



Options (3)

ListIndex (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ListIndex allows selection of a list if the input data is an OmicsObject or other association with multi - list values. We generate below a random OmicsObject using also random data as metadata

In[2]:=
```
dataRandomOmicsObject = OmicsObjectCreator[{"Sample1", "Sample2", "Sample3"},
   ConstantArray[("Key" <> ToString[#]) & /@ Range[100], 3], RandomVariate[
    PoissonDistribution[10], {3, 100, 3}], RandomVariate[PoissonDistribution[10], {3, 100, 3}]];
```

Let's look at the first few keys to see the structure:

In[3]:=
```
Query[All, 1 ;; 5]@dataRandomOmicsObject
```

Out[3]=
```
<|Sample1 → <|Key1 → {{11, 10, 11}, {13, 7, 10}}, Key2 → {{14, 12, 8}, {11, 12, 13}},
    Key3 → {{6, 4, 12}, {10, 12, 11}}, Key4 → {{9, 14, 6}, {6, 11, 7}}, Key5 → {{3, 9, 9}, {7, 10, 10}}|>,
  Sample2 → <|Key1 → {{12, 10, 11}, {9, 16, 11}}, Key2 → {{8, 7, 11}, {8, 9, 6}},
    Key3 → {{12, 7, 11}, {11, 6, 12}}, Key4 → {{13, 8, 11}, {12, 9, 5}}, Key5 → {{8, 9, 8}, {8, 8, 7}}|>,
  Sample3 → <|Key1 → {{6, 8, 10}, {15, 9, 6}}, Key2 → {{16, 5, 14}, {12, 12, 10}},
    Key3 → {{11, 15, 14}, {13, 9, 5}}, Key4 → {{6, 7, 9}, {10, 13, 17}}, Key5 → {{10, 14, 13}, {7, 13, 9}}|>|>
```

We can perform the optimized Box Cox Transform on values from the first list, first component:

In[4]:=
```
ApplyBoxCoxTransform[dataRandomOmicsObject, ListIndex → 1, ComponentIndex → 1]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.841382

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.887658

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.321949

Out[4]=
```
<|Sample1 → <|Key1 → {{7.74898, 10., 11.}, {13., 7., 10.}}, Key2 → {{9.75957, 12., 8.}, {11., 12., 13.}},
    Key3 → {{4.17845, 4., 12.}, {10., 12., 11.}}, Key4 → {{6.36048, 14., 6.}, {6., 11., 7.}},
    Key5 → {{1.80683, 9., 9.}, {7., 10., 10.}}, Key6 → {{6.36048, 9., 8.}, {9., 6., 6.}},
```

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```
    Key7 → {{7.74898, 8., 11.}, {9., 8., 14.}}, Key8 → {{4.9217, 22., 7.}, {8., 13., 10.}},
    Key9 → {{7.06025, 15., 9.}, {11., 9., 13.}}, Key10 → {{8.42784, 8., 7.}, {15., 8., 8.}},
    Key11 → {{7.06025, 8., 10.}, {8., 8., 7.}}, Key12 → {{9.75957, 16., 15.}, {7., 4., 7.}},
    Key13 → {{10.4139, 8., 7.}, {14., 11., 10.}}, Key14 → {{9.09777, 7., 9.}, {16., 7., 6.}},
    Key15 → {{7.74898, 8., 14.}, {8., 10., 9.}}, Key16 → {{4.9217, 9., 12.}, {7., 4., 12.}},
    Key17 → {{7.74898, 11., 6.}, {7., 11., 8.}}, Key18 → {{6.36048, 11., 8.}, {10., 8., 13.}},
    Key19 → {{5.64824, 11., 11.}, {17., 10., 15.}}, Key20 → {{5.64824, 8., 5.}, {18., 11., 14.}},
    Key21 → {{6.36048, 5., 8.}, {4., 6., 5.}}, Key22 → {{7.06025, 9., 10.}, {13., 7., 7.}},
    Key23 → {{4.9217, 11., 15.}, {10., 10., 14.}}, Key24 → {{9.09777, 8., 11.}, {11., 13., 12.}},
    Key25 → {{11.7024, 8., 17.}, {15., 10., 11.}}, Key26 → {{8.42784, 11., 8.}, {14., 14., 12.}},
    Key27 → {{2.62714, 11., 11.}, {7., 15., 7.}}, Key28 → {{4.9217, 9., 11.}, {12., 7., 15.}},
    Key29 → {{4.9217, 12., 7.}, {11., 10., 6.}}, Key30 → {{5.64824, 7., 14.}, {11., 17., 7.}},
    Key31 → {{7.74898, 16., 14.}, {14., 11., 9.}}, Key32 → {{9.09777, 11., 10.}, {6., 9., 11.}},
    Key33 → {{7.06025, 7., 11.}, {8., 13., 18.}}, Key34 → {{5.64824, 15., 13.}, {10., 8., 10.}},
    Key35 → {{10.4139, 3., 10.}, {13., 16., 11.}}, Key36 → {{2.62714, 13., 7.}, {5., 12., 8.}},
    Key37 → {{7.06025, 12., 8.}, {6., 16., 11.}}, Key38 → {{6.36048, 11., 12.}, {16., 12., 17.}},
    Key39 → {{4.17845, 5., 12.}, {5., 5., 10.}}, Key40 → {{5.64824, 15., 12.}, {6., 14., 16.}},
    Key41 → {{7.74898, 14., 9.}, {14., 8., 13.}}, Key42 → {{9.75957, 6., 11.}, {18., 8., 12.}},
    Key43 → {{7.74898, 9., 12.}, {8., 6., 9.}}, Key44 → {{6.36048, 14., 13.}, {10., 8., 4.}},
    Key45 → {{5.64824, 13., 7.}, {12., 8., 9.}}, Key46 → {{8.42784, 5., 5.}, {9., 10., 14.}},
    Key47 → {{9.75957, 9., 6.}, {9., 10., 13.}}, Key48 → {{7.74898, 5., 10.}, {9., 16., 10.}},
    Key49 → {{4.17845, 12., 6.}, {10., 8., 13.}}, Key50 → {{7.74898, 10., 8.}, {6., 6., 8.}},
    Key51 → {{7.74898, 12., 4.}, {9., 10., 10.}}, Key52 → {{6.36048, 15., 10.}, {6., 8., 15.}},
    Key53 → {{5.64824, 2., 6.}, {8., 9., 7.}}, Key54 → {{5.64824, 6., 11.}, {5., 17., 11.}},
    Key55 → {{3.41519, 8., 14.}, {13., 13., 10.}}, Key56 → {{7.06025, 8., 11.}, {12., 6., 11.}},
    Key57 → {{4.17845, 11., 14.}, {11., 10., 9.}}, Key58 → {{9.09777, 9., 7.}, {13., 11., 9.}},
    Key59 → {{7.06025, 7., 13.}, {10., 10., 14.}}, Key60 → {{10.4139, 8., 13.}, {7., 9., 11.}},
    Key61 → {{6.36048, 6., 8.}, {7., 7., 15.}}, Key62 → {{4.9217, 9., 11.}, {11., 6., 9.}},
    Key63 → {{8.42784, 11., 10.}, {9., 11., 11.}}, Key64 → {{6.36048, 18., 8.}, {13., 12., 4.}},
    Key65 → {{8.42784, 15., 17.}, {10., 12., 16.}}, Key66 → {{6.36048, 13., 7.}, {12., 11., 4.}},
    Key67 → {{5.64824, 9., 9.}, {7., 15., 11.}}, Key68 → {{7.74898, 16., 6.}, {11., 11., 12.}},
    Key69 → {{6.36048, 13., 6.}, {9., 15., 14.}}, Key70 → {{8.42784, 10., 2.}, {12., 4., 5.}},
    Key71 → {{9.09777, 11., 8.}, {5., 9., 9.}}, Key72 → {{8.42784, 9., 9.}, {3., 7., 9.}},
    Key73 → {{4.9217, 8., 10.}, {11., 14., 12.}}, Key74 → {{7.74898, 9., 11.}, {8., 5., 8.}},
    Key75 → {{8.42784, 11., 7.}, {12., 13., 12.}}, Key76 → {{7.74898, 9., 8.}, {14., 10., 9.}},
    Key77 → {{8.42784, 5., 13.}, {9., 8., 9.}}, Key78 → {{6.36048, 16., 14.}, {6., 9., 6.}},
    Key79 → {{9.75957, 16., 13.}, {7., 7., 11.}}, Key80 → {{8.42784, 10., 10.}, {13., 11., 11.}},
    Key81 → {{11.7024, 11., 14.}, {13., 11., 16.}}, Key82 → {{4.17845, 9., 9.}, {5., 13., 18.}},
    Key83 → {{5.64824, 12., 8.}, {8., 7., 12.}}, Key84 → {{7.74898, 11., 5.}, {7., 12., 9.}},
    Key85 → {{7.74898, 7., 9.}, {9., 11., 11.}}, Key86 → {{9.75957, 9., 7.}, {11., 12., 14.}},
    Key87 → {{7.06025, 11., 8.}, {7., 9., 10.}}, Key88 → {{5.64824, 6., 9.}, {12., 13., 4.}},
    Key89 → {{6.36048, 7., 6.}, {7., 13., 11.}}, Key90 → {{7.74898, 9., 7.}, {7., 4., 10.}},
    Key91 → {{7.06025, 7., 9.}, {12., 11., 5.}}, Key92 → {{6.36048, 14., 7.}, {7., 10., 13.}},
    Key93 → {{6.36048, 15., 7.}, {9., 12., 9.}}, Key94 → {{5.64824, 10., 8.}, {12., 12., 8.}},
    Key95 → {{8.42784, 12., 9.}, {10., 15., 14.}}, Key96 → {{4.9217, 7., 12.}, {12., 15., 11.}},
    Key97 → {{4.17845, 12., 8.}, {6., 15., 8.}}, Key98 → {{4.17845, 8., 8.}, {8., 11., 9.}},
    Key99 → {{5.64824, 3., 6.}, {6., 8., 6.}}, Key100 → {{3.41519, 10., 12.}, {7., 6., 5.}}|>,
  Sample2 → <|Key1 → {{9.09926, 10., 11.}, {9., 16., 11.}}, Key2 → {{6.00837, 7., 11.}, {8., 9., 6.}},
    Key3 → {{9.09926, 7., 11.}, {11., 6., 12.}}, Key4 → {{9.85225, 8., 11.}, {12., 9., 5.}},
    Key5 → {{6.00837, 9., 8.}, {8., 8., 7.}}, Key6 → {{8.33919, 9., 14.}, {11., 11., 11.}},
    Key7 → {{7.5713, 14., 6.}, {7., 15., 11.}}, Key8 → {{6.79472, 9., 7.}, {7., 14., 6.}},
    Key9 → {{11.3393, 11., 17.}, {4., 7., 13.}}, Key10 → {{6.79472, 7., 16.}, {12., 11., 8.}},
    Key11 → {{5.21086, 8., 9.}, {9., 10., 4.}}, Key12 → {{9.09926, 12., 5.}, {6., 8., 8.}},
    Key13 → {{3.57455, 11., 12.}, {10., 9., 16.}}, Key14 → {{8.33919, 8., 9.}, {11., 7., 7.}},
    Key15 → {{12.8041, 9., 9.}, {3., 9., 13.}}, Key16 → {{11.3393, 10., 8.}, {5., 13., 10.}},
    Key17 → {{6.00837, 14., 7.}, {14., 13., 10.}}, Key18 → {{3.57455, 16., 11.}, {9., 10., 7.}},
    Key19 → {{4.4004, 15., 9.}, {9., 14., 8.}}, Key20 → {{5.21086, 13., 11.}, {11., 15., 8.}},
    Key21 → {{6.79472, 8., 9.}, {2., 15., 8.}}, Key22 → {{12.0743, 7., 13.}, {17., 11., 12.}},
    Key23 → {{2.7298, 9., 14.}, {13., 15., 6.}}, Key24 → {{5.21086, 10., 10.}, {15., 11., 11.}},
    Key25 → {{7.5713, 8., 11.}, {15., 11., 11.}}, Key26 → {{7.5713, 9., 16.}, {12., 12., 12.}},
    Key27 → {{4.4004, 6., 15.}, {13., 9., 9.}}, Key28 → {{12.8041, 9., 10.}, {5., 11., 12.}},
    Key29 → {{3.57455, 12., 9.}, {12., 6., 7.}}, Key30 → {{6.79472, 7., 14.}, {14., 8., 6.}},
    Key31 → {{7.5713, 13., 14.}, {8., 13., 12.}}, Key32 → {{8.33919, 8., 7.}, {6., 10., 7.}},
    Key33 → {{12.0743, 6., 8.}, {9., 16., 9.}}, Key34 → {{6.79472, 7., 7.}, {15., 11., 7.}},
    Key35 → {{9.85225, 10., 10.}, {11., 10., 13.}}, Key36 → {{6.79472, 5., 11.}, {10., 10., 7.}},
    Key37 → {{9.09926, 15., 16.}, {9., 11., 9.}}, Key38 → {{8.33919, 11., 10.}, {8., 14., 12.}},
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  Key39 → {{8.33919, 13., 14.}, {11., 15., 6.}}, Key40 → {{6.00837, 2., 13.}, {13., 11., 10.}},
  Key41 → {{9.09926, 9., 6.}, {18., 12., 11.}}, Key42 → {{8.33919, 9., 10.}, {9., 7., 12.}},
  Key43 → {{9.85225, 13., 17.}, {14., 4., 7.}}, Key44 → {{4.4004, 5., 11.}, {5., 5., 8.}},
  Key45 → {{6.79472, 11., 11.}, {10., 11., 11.}}, Key46 → {{11.3393, 13., 9.}, {10., 6., 7.}},
  Key47 → {{10.5987, 11., 8.}, {13., 10., 10.}}, Key48 → {{9.85225, 7., 16.}, {12., 13., 15.}},
  Key49 → {{10.5987, 9., 8.}, {9., 12., 14.}}, Key50 → {{5.21086, 10., 7.}, {7., 9., 7.}},
  Key51 → {{6.79472, 7., 6.}, {10., 12., 7.}}, Key52 → {{9.09926, 7., 12.}, {15., 8., 9.}},
  Key53 → {{5.21086, 13., 18.}, {11., 11., 13.}}, Key54 → {{3.57455, 9., 5.}, {14., 5., 11.}},
  Key55 → {{8.33919, 8., 18.}, {13., 11., 10.}}, Key56 → {{7.5713, 9., 17.}, {6., 7., 13.}},
  Key57 → {{1.86071, 7., 7.}, {7., 12., 8.}}, Key58 → {{7.5713, 6., 10.}, {9., 6., 7.}},
  Key59 → {{9.85225, 10., 10.}, {8., 11., 8.}}, Key60 → {{9.09926, 8., 13.}, {9., 9., 14.}},
  Key61 → {{6.79472, 8., 13.}, {11., 7., 10.}}, Key62 → {{7.5713, 9., 11.}, {15., 11., 6.}},
  Key63 → {{7.5713, 6., 5.}, {7., 8., 12.}}, Key64 → {{9.09926, 7., 13.}, {12., 5., 9.}},
  Key65 → {{7.5713, 7., 15.}, {8., 10., 7.}}, Key66 → {{5.21086, 10., 8.}, {11., 8., 13.}},
  Key67 → {{2.7298, 10., 11.}, {6., 8., 16.}}, Key68 → {{5.21086, 16., 9.}, {10., 10., 8.}},
  Key69 → {{8.33919, 6., 6.}, {11., 17., 10.}}, Key70 → {{6.79472, 9., 7.}, {14., 15., 8.}},
  Key71 → {{8.33919, 12., 9.}, {10., 18., 6.}}, Key72 → {{4.4004, 6., 8.}, {14., 9., 9.}},
  Key73 → {{6.00837, 7., 7.}, {12., 9., 15.}}, Key74 → {{9.09926, 10., 17.}, {19., 10., 9.}},
  Key75 → {{9.09926, 12., 9.}, {12., 10., 11.}}, Key76 → {{9.09926, 9., 12.}, {9., 12., 12.}},
  Key77 → {{3.57455, 4., 14.}, {6., 10., 12.}}, Key78 → {{7.5713, 9., 8.}, {12., 12., 11.}},
  Key79 → {{6.79472, 9., 11.}, {7., 20., 8.}}, Key80 → {{7.5713, 10., 9.}, {13., 10., 6.}},
  Key81 → {{7.5713, 14., 11.}, {7., 10., 7.}}, Key82 → {{7.5713, 8., 14.}, {8., 10., 8.}},
  Key83 → {{7.5713, 14., 10.}, {13., 15., 11.}}, Key84 → {{9.85225, 10., 6.}, {11., 6., 12.}},
  Key85 → {{7.5713, 12., 12.}, {10., 9., 11.}}, Key86 → {{12.8041, 6., 12.}, {10., 9., 8.}},
  Key87 → {{5.21086, 10., 4.}, {8., 8., 15.}}, Key88 → {{4.4004, 8., 11.}, {11., 7., 8.}},
  Key89 → {{3.57455, 14., 11.}, {14., 7., 8.}}, Key90 → {{9.85225, 9., 13.}, {8., 11., 7.}},
  Key91 → {{6.79472, 8., 4.}, {3., 9., 11.}}, Key92 → {{8.33919, 12., 6.}, {9., 6., 9.}},
  Key93 → {{8.33919, 10., 14.}, {7., 12., 11.}}, Key94 → {{9.09926, 10., 6.}, {10., 11., 10.}},
  Key95 → {{7.5713, 12., 9.}, {6., 8., 4.}}, Key96 → {{9.09926, 14., 15.}, {10., 8., 10.}},
  Key97 → {{7.5713, 9., 8.}, {15., 12., 13.}}, Key98 → {{8.33919, 8., 10.}, {5., 7., 9.}},
  Key99 → {{5.21086, 14., 9.}, {9., 8., 11.}}, Key100 → {{8.33919, 11., 7.}, {13., 10., 11.}}|>,
Sample3 → <|Key1 → {{2.42408, 8., 10.}, {15., 9., 6.}}, Key2 → {{4.47756, 5., 14.}, {12., 12., 10.}},
  Key3 → {{3.61576, 15., 14.}, {13., 9., 5.}}, Key4 → {{2.42408, 7., 9.}, {10., 13., 17.}},
  Key5 → {{3.41263, 14., 13.}, {7., 13., 9.}}, Key6 → {{3.61576, 6., 7.}, {6., 7., 9.}},
  Key7 → {{2.96075, 13., 8.}, {10., 7., 9.}}, Key8 → {{3.61576, 12., 9.}, {10., 9., 10.}},
  Key9 → {{3.80672, 14., 15.}, {12., 15., 11.}}, Key10 → {{3.80672, 8., 6.}, {9., 12., 4.}},
  Key11 → {{3.80672, 4., 9.}, {5., 11., 10.}}, Key12 → {{3.61576, 7., 8.}, {9., 7., 13.}},
  Key13 → {{2.96075, 13., 10.}, {7., 6., 8.}}, Key14 → {{3.19522, 5., 7.}, {7., 14., 8.}},
  Key15 → {{2.96075, 11., 11.}, {10., 10., 12.}}, Key16 → {{2.70546, 10., 9.}, {8., 9., 8.}},
  Key17 → {{3.98718, 10., 18.}, {6., 14., 5.}}, Key18 → {{2.10881, 11., 11.}, {10., 9., 10.}},
  Key19 → {{2.42408, 7., 9.}, {12., 12., 11.}}, Key20 → {{3.41263, 11., 15.}, {7., 7., 11.}},
  Key21 → {{4.32162, 12., 13.}, {7., 11., 12.}}, Key22 → {{3.41263, 5., 8.}, {6., 14., 19.}},
  Key23 → {{3.41263, 9., 16.}, {7., 11., 15.}}, Key24 → {{3.41263, 15., 13.}, {10., 12., 7.}},
  Key25 → {{3.61576, 13., 10.}, {4., 10., 5.}}, Key26 → {{3.19522, 17., 18.}, {9., 9., 7.}},
  Key27 → {{2.96075, 8., 11.}, {4., 12., 10.}}, Key28 → {{2.70546, 13., 8.}, {14., 10., 13.}},
  Key29 → {{3.41263, 6., 9.}, {9., 10., 14.}}, Key30 → {{3.98718, 9., 9.}, {7., 7., 10.}},
  Key31 → {{3.41263, 10., 9.}, {7., 11., 14.}}, Key32 → {{4.32162, 14., 13.}, {14., 11., 7.}},
  Key33 → {{3.41263, 8., 9.}, {13., 17., 9.}}, Key34 → {{3.61576, 8., 8.}, {7., 12., 6.}},
  Key35 → {{3.61576, 10., 7.}, {7., 13., 20.}}, Key36 → {{3.61576, 8., 8.}, {6., 16., 18.}},
  Key37 → {{4.32162, 8., 14.}, {8., 14., 15.}}, Key38 → {{2.70546, 10., 10.}, {7., 13., 12.}},
  Key39 → {{2.96075, 8., 11.}, {9., 7., 13.}}, Key40 → {{3.80672, 7., 8.}, {10., 11., 11.}},
  Key41 → {{3.98718, 9., 11.}, {11., 10., 5.}}, Key42 → {{3.19522, 6., 9.}, {7., 11., 12.}},
  Key43 → {{3.98718, 11., 13.}, {14., 9., 8.}}, Key44 → {{3.80672, 7., 13.}, {14., 12., 11.}},
  Key45 → {{3.41263, 12., 8.}, {13., 6., 12.}}, Key46 → {{3.80672, 6., 7.}, {16., 10., 14.}},
  Key47 → {{3.41263, 9., 12.}, {10., 14., 9.}}, Key48 → {{3.19522, 10., 10.}, {9., 6., 6.}},
  Key49 → {{3.80672, 9., 8.}, {7., 11., 7.}}, Key50 → {{3.19522, 13., 6.}, {10., 9., 10.}},
  Key51 → {{3.80672, 12., 12.}, {11., 7., 12.}}, Key52 → {{4.47756, 13., 11.}, {5., 12., 14.}},
  Key53 → {{2.96075, 5., 9.}, {14., 8., 18.}}, Key54 → {{3.41263, 8., 11.}, {14., 8., 19.}},
  Key55 → {{2.42408, 16., 12.}, {10., 6., 6.}}, Key56 → {{3.41263, 11., 8.}, {9., 9., 7.}},
  Key57 → {{2.96075, 6., 12.}, {8., 8., 6.}}, Key58 → {{1.74731, 9., 12.}, {12., 9., 6.}},
  Key59 → {{3.19522, 6., 11.}, {14., 7., 12.}}, Key60 → {{3.61576, 9., 12.}, {13., 12., 9.}},
  Key61 → {{2.96075, 10., 11.}, {14., 8., 9.}}, Key62 → {{3.19522, 13., 11.}, {10., 8., 10.}},
  Key63 → {{2.70546, 6., 7.}, {9., 6., 8.}}, Key64 → {{3.61576, 7., 8.}, {12., 4., 19.}},
  Key65 → {{2.96075, 14., 5.}, {9., 12., 10.}}, Key66 → {{4.90897, 11., 9.}, {5., 4., 9.}},
  Key67 → {{3.80672, 10., 11.}, {9., 10., 7.}}, Key68 → {{2.42408, 9., 15.}, {7., 7., 11.}},
  Key69 → {{2.42408, 11., 11.}, {15., 9., 7.}}, Key70 → {{3.19522, 11., 5.}, {11., 12., 6.}},
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Key71 → {{2.96075, 19., 9.}, {13., 8., 5.}}, Key72 → {{2.96075, 7., 12.}, {8., 8., 8.}},
Key73 → {{3.19522, 14., 5.}, {10., 7., 12.}}, Key74 → {{3.98718, 9., 5.}, {13., 12., 12.}},
Key75 → {{3.41263, 8., 11.}, {13., 7., 9.}}, Key76 → {{2.70546, 13., 12.}, {7., 7., 11.}},
Key77 → {{3.41263, 10., 12.}, {11., 8., 8.}}, Key78 → {{3.61576, 10., 12.}, {8., 10., 6.}},
Key79 → {{4.47756, 12., 11.}, {11., 11., 9.}}, Key80 → {{2.42408, 5., 12.}, {20., 6., 12.}},
Key81 → {{3.80672, 9., 6.}, {9., 16., 12.}}, Key82 → {{2.96075, 14., 8.}, {7., 8., 11.}},
Key83 → {{3.41263, 14., 6.}, {10., 7., 6.}}, Key84 → {{3.41263, 13., 8.}, {11., 8., 9.}},
Key85 → {{2.70546, 3., 9.}, {13., 13., 7.}}, Key86 → {{2.96075, 11., 7.}, {9., 8., 9.}},
Key87 → {{4.15845, 4., 10.}, {15., 11., 9.}}, Key88 → {{2.96075, 12., 6.}, {6., 9., 9.}},
Key89 → {{3.19522, 12., 13.}, {8., 14., 13.}}, Key90 → {{3.19522, 6., 9.}, {13., 15., 8.}},
Key91 → {{2.70546, 15., 10.}, {10., 7., 8.}}, Key92 → {{2.70546, 7., 9.}, {11., 12., 6.}},
Key93 → {{3.41263, 17., 17.}, {10., 6., 5.}}, Key94 → {{3.61576, 10., 9.}, {12., 7., 10.}},
Key95 → {{3.19522, 12., 9.}, {12., 8., 12.}}, Key96 → {{2.42408, 6., 10.}, {8., 8., 16.}},
Key97 → {{3.41263, 8., 14.}, {10., 5., 11.}}, Key98 → {{3.41263, 7., 7.}, {12., 13., 7.}},
Key99 → {{3.80672, 12., 17.}, {13., 10., 12.}}, Key100 → {{3.19522, 10., 10.}, {11., 11., 9.}} |> |>
```

We can perform the optimized Box Cox Transform on values from the second list, first component :

```
In[5]:= ApplyBoxCoxTransform[dataRandomOmicsObject, ListIndex → 2, ComponentIndex → 1]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.436521

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.92564

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.524358

```
Out[5]= <| Sample1 → <| Key1 → {{11., 10., 11.}, {4.72783, 7., 10.}}, Key2 → {{14., 12., 8.}, {4.23422, 12., 13.}},
Key3 → {{6., 4., 12.}, {3.96832, 12., 11.}}, Key4 → {{9., 14., 6.}, {2.71727, 11., 7.}},
Key5 → {{3., 9., 9.}, {3.06587, 10., 10.}}, Key6 → {{9., 9., 8.}, {3.68697, 6., 6.}},
Key7 → {{11., 8., 11.}, {3.68697, 8., 14.}}, Key8 → {{7., 22., 7.}, {3.38739, 13., 10.}},
Key9 → {{10., 15., 9.}, {4.23422, 9., 13.}}, Key10 → {{12., 8., 7.}, {5.18024, 8., 8.}},
Key11 → {{10., 8., 10.}, {3.38739, 8., 7.}}, Key12 → {{14., 16., 15.}, {3.06587, 4., 7.}},
Key13 → {{15., 8., 7.}, {4.95859, 11., 10.}}, Key14 → {{13., 7., 9.}, {5.39371, 7., 6.}},
Key15 → {{11., 8., 14.}, {3.38739, 10., 9.}}, Key16 → {{7., 9., 12.}, {3.06587, 4., 12.}},
Key17 → {{11., 11., 6.}, {3.06587, 11., 8.}}, Key18 → {{9., 11., 8.}, {3.96832, 8., 13.}},
Key19 → {{8., 11., 11.}, {5.59979, 10., 15.}}, Key20 → {{8., 8., 5.}, {5.79915, 11., 14.}},
Key21 → {{9., 5., 8.}, {1.90488, 6., 5.}}, Key22 → {{10., 9., 10.}, {4.72783, 7., 7.}},
Key23 → {{7., 11., 15.}, {3.96832, 10., 14.}}, Key24 → {{13., 8., 11.}, {4.23422, 13., 12.}},
Key25 → {{17., 8., 17.}, {5.18024, 10., 11.}}, Key26 → {{12., 11., 8.}, {4.95859, 14., 12.}},
Key27 → {{4., 11., 11.}, {3.06587, 15., 7.}}, Key28 → {{7., 9., 11.}, {4.48683, 7., 15.}},
Key29 → {{7., 12., 7.}, {4.23422, 10., 6.}}, Key30 → {{8., 7., 14.}, {4.23422, 17., 7.}},
Key31 → {{11., 16., 14.}, {4.95859, 11., 9.}}, Key32 → {{13., 11., 10.}, {2.71727, 9., 11.}},
Key33 → {{10., 7., 11.}, {3.38739, 13., 18.}}, Key34 → {{8., 15., 13.}, {3.96832, 8., 10.}},
Key35 → {{15., 3., 10.}, {4.72783, 16., 11.}}, Key36 → {{4., 13., 7.}, {2.33414, 12., 8.}},
Key37 → {{10., 12., 8.}, {2.71727, 16., 11.}}, Key38 → {{9., 11., 12.}, {5.39371, 12., 17.}},
Key39 → {{6., 5., 12.}, {2.33414, 5., 10.}}, Key40 → {{8., 15., 12.}, {2.71727, 14., 16.}},
Key41 → {{11., 14., 9.}, {4.95859, 8., 13.}}, Key42 → {{14., 6., 11.}, {5.79915, 8., 12.}},
Key43 → {{11., 9., 12.}, {3.38739, 6., 9.}}, Key44 → {{9., 14., 13.}, {3.96832, 8., 4.}},
Key45 → {{8., 13., 7.}, {4.48683, 8., 9.}}, Key46 → {{12., 5., 5.}, {3.68697, 10., 14.}},
Key47 → {{14., 9., 6.}, {3.68697, 10., 13.}}, Key48 → {{11., 5., 10.}, {3.68697, 16., 10.}},
Key49 → {{6., 12., 6.}, {3.96832, 8., 13.}}, Key50 → {{11., 10., 8.}, {2.71727, 6., 8.}},
Key51 → {{11., 12., 4.}, {3.68697, 10., 10.}}, Key52 → {{9., 15., 10.}, {2.71727, 8., 15.}},
Key53 → {{8., 2., 6.}, {3.38739, 9., 7.}}, Key54 → {{8., 6., 11.}, {2.33414, 17., 11.}},
Key55 → {{5., 8., 14.}, {4.72783, 13., 10.}}, Key56 → {{10., 8., 11.}, {4.48683, 6., 11.}},
Key57 → {{6., 11., 14.}, {4.23422, 10., 9.}}, Key58 → {{13., 9., 7.}, {4.72783, 11., 9.}},
Key59 → {{10., 7., 13.}, {3.96832, 10., 14.}}, Key60 → {{15., 8., 13.}, {3.06587, 9., 11.}},
Key61 → {{9., 6., 8.}, {3.06587, 7., 15.}}, Key62 → {{7., 9., 11.}, {4.23422, 6., 9.}},
Key63 → {{12., 11., 10.}, {3.68697, 11., 11.}}, Key64 → {{9., 18., 8.}, {4.72783, 12., 4.}},
Key65 → {{12., 15., 17.}, {3.96832, 12., 16.}}, Key66 → {{9., 13., 7.}, {4.48683, 11., 4.}},
Key67 → {{8., 9., 9.}, {3.06587, 15., 11.}}, Key68 → {{11., 16., 6.}, {4.23422, 11., 12.}},
Key69 → {{9., 13., 6.}, {3.68697, 15., 14.}}, Key70 → {{12., 10., 2.}, {4.48683, 4., 5.}},
Key71 → {{13., 11., 8.}, {2.33414, 9., 9.}}, Key72 → {{12., 9., 9.}, {1.40973, 7., 9.}},
Key73 → {{7., 8., 10.}, {4.23422, 14., 12.}}, Key74 → {{11., 9., 11.}, {3.38739, 5., 8.}},
Key75 → {{12., 11., 7.}, {4.48683, 13., 12.}}, Key76 → {{11., 9., 8.}, {4.95859, 10., 9.}},
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    Key77 → {{12., 5., 13.}, {3.68697, 8., 9.}}, Key78 → {{9., 16., 14.}, {2.71727, 9., 6.}},
    Key79 → {{14., 16., 13.}, {3.06587, 7., 11.}}, Key80 → {{12., 10., 10.}, {4.72783, 11., 11.}},
    Key81 → {{17., 11., 14.}, {4.72783, 11., 16.}}, Key82 → {{6., 9., 9.}, {2.33414, 13., 18.}},
    Key83 → {{8., 12., 8.}, {3.38739, 7., 12.}}, Key84 → {{11., 11., 5.}, {3.06587, 12., 9.}},
    Key85 → {{11., 7., 9.}, {3.68697, 11., 11.}}, Key86 → {{14., 9., 7.}, {4.23422, 12., 14.}},
    Key87 → {{10., 11., 8.}, {3.06587, 9., 10.}}, Key88 → {{8., 6., 9.}, {4.48683, 13., 4.}},
    Key89 → {{9., 7., 6.}, {3.06587, 13., 11.}}, Key90 → {{11., 9., 7.}, {3.06587, 4., 10.}},
    Key91 → {{10., 7., 9.}, {4.48683, 11., 5.}}, Key92 → {{9., 14., 7.}, {3.06587, 10., 13.}},
    Key93 → {{9., 15., 7.}, {3.68697, 12., 9.}}, Key94 → {{8., 10., 8.}, {4.48683, 12., 8.}},
    Key95 → {{12., 12., 9.}, {3.96832, 15., 14.}}, Key96 → {{7., 7., 12.}, {4.48683, 15., 11.}},
    Key97 → {{6., 12., 8.}, {2.71727, 15., 8.}}, Key98 → {{6., 8., 8.}, {3.38739, 11., 9.}},
    Key99 → {{8., 3., 6.}, {2.71727, 8., 6.}}, Key100 → {{5., 10., 12.}, {3.06587, 6., 5.}}|>,
  Sample2 → <|Key1 → {{12., 10., 11.}, {7.17706, 16., 11.}}, Key2 → {{8., 7., 11.}, {6.32414, 9., 6.}},
    Key3 → {{12., 7., 11.}, {8.86256, 6., 12.}}, Key4 → {{13., 8., 11.}, {9.69651, 9., 5.}},
    Key5 → {{8., 9., 8.}, {6.32414, 8., 7.}}, Key6 → {{11., 9., 14.}, {8.86256, 11., 11.}},
    Key7 → {{10., 14., 6.}, {5.46323, 15., 11.}}, Key8 → {{9., 9., 7.}, {5.46323, 14., 6.}},
    Key9 → {{15., 11., 17.}, {2.81773, 7., 13.}}, Key10 → {{9., 7., 16.}, {9.69651, 11., 8.}},
    Key11 → {{7., 8., 9.}, {7.17706, 10., 4.}}, Key12 → {{12., 12., 5.}, {4.5931, 8., 8.}},
    Key13 → {{5., 11., 12.}, {8.02295, 9., 16.}}, Key14 → {{11., 8., 9.}, {8.86256, 7., 7.}},
    Key15 → {{17., 9., 9.}, {1.90643, 9., 13.}}, Key16 → {{15., 10., 8.}, {3.71206, 13., 10.}},
    Key17 → {{8., 14., 7.}, {11.3494, 13., 10.}}, Key18 → {{5., 16., 11.}, {7.17706, 10., 7.}},
    Key19 → {{6., 15., 9.}, {7.17706, 14., 8.}}, Key20 → {{7., 13., 11.}, {8.86256, 15., 8.}},
    Key21 → {{9., 8., 9.}, {0.971789, 15., 8.}}, Key22 → {{16., 7., 13.}, {13.7965, 11., 12.}},
    Key23 → {{4., 9., 14.}, {10.5253, 15., 6.}}, Key24 → {{7., 10., 10.}, {12.169, 11., 11.}},
    Key25 → {{10., 8., 11.}, {12.169, 11., 11.}}, Key26 → {{10., 9., 16.}, {9.69651, 12., 12.}},
    Key27 → {{6., 6., 15.}, {10.5253, 9., 9.}}, Key28 → {{17., 9., 10.}, {3.71206, 11., 12.}},
    Key29 → {{5., 12., 9.}, {9.69651, 6., 7.}}, Key30 → {{9., 7., 14.}, {11.3494, 8., 6.}},
    Key31 → {{10., 13., 14.}, {6.32414, 13., 12.}}, Key32 → {{11., 8., 7.}, {4.5931, 10., 7.}},
    Key33 → {{16., 6., 8.}, {7.17706, 16., 9.}}, Key34 → {{9., 7., 7.}, {12.169, 11., 7.}},
    Key35 → {{13., 10., 10.}, {8.86256, 10., 13.}}, Key36 → {{9., 5., 11.}, {8.02295, 10., 7.}},
    Key37 → {{12., 15., 16.}, {7.17706, 11., 9.}}, Key38 → {{11., 11., 10.}, {6.32414, 14., 12.}},
    Key39 → {{11., 13., 14.}, {8.86256, 15., 6.}}, Key40 → {{8., 2., 13.}, {10.5253, 11., 10.}},
    Key41 → {{12., 9., 6.}, {14.6048, 12., 11.}}, Key42 → {{11., 9., 10.}, {7.17706, 7., 12.}},
    Key43 → {{13., 13., 17.}, {11.3494, 4., 7.}}, Key44 → {{6., 5., 11.}, {3.71206, 5., 8.}},
    Key45 → {{9., 11., 11.}, {8.02295, 11., 11.}}, Key46 → {{15., 13., 9.}, {8.02295, 6., 7.}},
    Key47 → {{14., 11., 8.}, {10.5253, 10., 10.}}, Key48 → {{13., 7., 16.}, {9.69651, 13., 15.}},
    Key49 → {{14., 9., 8.}, {7.17706, 12., 14.}}, Key50 → {{7., 10., 7.}, {5.46323, 9., 7.}},
    Key51 → {{9., 7., 6.}, {8.02295, 12., 7.}}, Key52 → {{12., 7., 12.}, {12.169, 8., 9.}},
    Key53 → {{7., 13., 18.}, {8.86256, 11., 13.}}, Key54 → {{5., 9., 5.}, {11.3494, 5., 11.}},
    Key55 → {{11., 8., 18.}, {10.5253, 11., 10.}}, Key56 → {{10., 9., 17.}, {4.5931, 7., 13.}},
    Key57 → {{3., 7., 7.}, {5.46323, 12., 8.}}, Key58 → {{10., 6., 10.}, {7.17706, 6., 7.}},
    Key59 → {{13., 10., 10.}, {6.32414, 11., 8.}}, Key60 → {{12., 8., 13.}, {7.17706, 9., 14.}},
    Key61 → {{9., 8., 13.}, {8.86256, 7., 10.}}, Key62 → {{10., 9., 11.}, {12.169, 11., 6.}},
    Key63 → {{10., 6., 5.}, {5.46323, 8., 12.}}, Key64 → {{12., 7., 13.}, {9.69651, 5., 9.}},
    Key65 → {{10., 7., 15.}, {6.32414, 10., 7.}}, Key66 → {{7., 10., 8.}, {8.86256, 8., 13.}},
    Key67 → {{4., 10., 11.}, {4.5931, 8., 16.}}, Key68 → {{7., 16., 9.}, {8.02295, 10., 8.}},
    Key69 → {{11., 6., 6.}, {8.86256, 17., 10.}}, Key70 → {{9., 9., 7.}, {11.3494, 15., 8.}},
    Key71 → {{11., 12., 9.}, {8.02295, 18., 6.}}, Key72 → {{6., 6., 8.}, {11.3494, 9., 9.}},
    Key73 → {{8., 7., 7.}, {9.69651, 9., 15.}}, Key74 → {{12., 10., 17.}, {15.4098, 10., 9.}},
    Key75 → {{12., 12., 9.}, {9.69651, 10., 11.}}, Key76 → {{12., 9., 12.}, {7.17706, 12., 12.}},
    Key77 → {{5., 4., 14.}, {4.5931, 10., 12.}}, Key78 → {{10., 9., 8.}, {9.69651, 12., 11.}},
    Key79 → {{9., 9., 11.}, {5.46323, 20., 8.}}, Key80 → {{10., 10., 9.}, {10.5253, 10., 6.}},
    Key81 → {{10., 14., 11.}, {5.46323, 10., 7.}}, Key82 → {{10., 8., 14.}, {6.32414, 10., 8.}},
    Key83 → {{10., 14., 10.}, {10.5253, 15., 11.}}, Key84 → {{13., 10., 6.}, {8.86256, 6., 12.}},
    Key85 → {{10., 12., 12.}, {8.02295, 9., 11.}}, Key86 → {{17., 6., 12.}, {8.02295, 9., 8.}},
    Key87 → {{7., 10., 4.}, {6.32414, 8., 15.}}, Key88 → {{6., 8., 11.}, {8.86256, 7., 8.}},
    Key89 → {{5., 14., 11.}, {11.3494, 7., 8.}}, Key90 → {{13., 9., 13.}, {6.32414, 11., 7.}},
    Key91 → {{9., 8., 4.}, {1.90643, 9., 11.}}, Key92 → {{11., 12., 6.}, {7.17706, 6., 9.}},
    Key93 → {{11., 10., 14.}, {5.46323, 12., 11.}}, Key94 → {{12., 10., 6.}, {8.02295, 11., 10.}},
    Key95 → {{10., 12., 9.}, {4.5931, 8., 4.}}, Key96 → {{12., 14., 15.}, {8.02295, 8., 10.}},
    Key97 → {{10., 9., 8.}, {12.169, 12., 13.}}, Key98 → {{11., 8., 10.}, {3.71206, 7., 9.}},
    Key99 → {{7., 14., 9.}, {7.17706, 8., 11.}}, Key100 → {{11., 11., 7.}, {10.5253, 10., 11.}}|>,
  Sample3 → <|Key1 → {{6., 8., 10.}, {5.98269, 9., 6.}}, Key2 → {{16., 5., 14.}, {5.11149, 12., 10.}},
    Key3 → {{11., 15., 14.}, {5.41234, 9., 5.}}, Key4 → {{6., 7., 9.}, {4.47158, 13., 17.}},
    Key5 → {{10., 14., 13.}, {3.38352, 13., 9.}}, Key6 → {{11., 6., 7.}, {2.97271, 7., 9.}},
    Key7 → {{8., 13., 8.}, {4.47158, 7., 9.}}, Key8 → {{11., 12., 9.}, {4.47158, 9., 10.}},
```

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```
Key9 → {{12., 14., 15.}, {5.11149, 15., 11.}}, Key10 → {{12., 8., 6.}, {4.12874, 12., 4.}},
Key11 → {{12., 4., 9.}, {2.52779, 11., 10.}}, Key12 → {{11., 7., 8.}, {4.12874, 7., 13.}},
Key13 → {{8., 13., 10.}, {3.38352, 6., 8.}}, Key14 → {{9., 5., 7.}, {3.38352, 14., 8.}},
Key15 → {{8., 11., 11.}, {4.47158, 10., 12.}}, Key16 → {{7., 10., 9.}, {3.76724, 9., 8.}},
Key17 → {{13., 10., 18.}, {2.97271, 14., 5.}}, Key18 → {{5., 11., 11.}, {4.47158, 9., 10.}},
Key19 → {{6., 7., 9.}, {5.11149, 12., 11.}}, Key20 → {{10., 11., 15.}, {3.38352, 7., 11.}},
Key21 → {{15., 12., 13.}, {3.38352, 11., 12.}}, Key22 → {{10., 5., 8.}, {2.97271, 14., 19.}},
Key23 → {{10., 9., 16.}, {3.38352, 11., 15.}}, Key24 → {{10., 15., 13.}, {4.47158, 12., 7.}},
Key25 → {{11., 13., 10.}, {2.03809, 10., 5.}}, Key26 → {{9., 17., 18.}, {4.12874, 9., 7.}},
Key27 → {{8., 8., 11.}, {2.03809, 12., 10.}}, Key28 → {{7., 13., 8.}, {5.70236, 10., 13.}},
Key29 → {{10., 6., 9.}, {4.12874, 10., 14.}}, Key30 → {{13., 9., 9.}, {3.38352, 7., 10.}},
Key31 → {{10., 10., 9.}, {3.38352, 11., 14.}}, Key32 → {{15., 14., 13.}, {5.70236, 11., 7.}},
Key33 → {{10., 8., 9.}, {5.41234, 17., 9.}}, Key34 → {{11., 8., 8.}, {3.38352, 12., 6.}},
Key35 → {{11., 10., 7.}, {3.38352, 13., 20.}}, Key36 → {{11., 8., 8.}, {2.97271, 16., 18.}},
Key37 → {{15., 8., 14.}, {3.76724, 14., 15.}}, Key38 → {{7., 10., 10.}, {3.38352, 13., 12.}},
Key39 → {{8., 8., 11.}, {4.12874, 7., 13.}}, Key40 → {{12., 7., 8.}, {4.47158, 11., 11.}},
Key41 → {{13., 9., 11.}, {4.79846, 10., 5.}}, Key42 → {{9., 6., 9.}, {3.38352, 11., 12.}},
Key43 → {{13., 11., 13.}, {5.70236, 9., 8.}}, Key44 → {{12., 7., 13.}, {5.70236, 12., 11.}},
Key45 → {{10., 12., 8.}, {5.41234, 6., 12.}}, Key46 → {{12., 6., 7.}, {6.25426, 10., 14.}},
Key47 → {{10., 9., 12.}, {4.47158, 14., 9.}}, Key48 → {{9., 10., 10.}, {4.12874, 6., 6.}},
Key49 → {{12., 9., 8.}, {3.38352, 11., 7.}}, Key50 → {{9., 13., 6.}, {4.47158, 9., 10.}},
Key51 → {{12., 12., 12.}, {4.79846, 7., 12.}}, Key52 → {{16., 13., 11.}, {2.52779, 12., 14.}},
Key53 → {{8., 5., 9.}, {5.70236, 8., 18.}}, Key54 → {{10., 8., 11.}, {5.70236, 8., 19.}},
Key55 → {{6., 16., 12.}, {4.47158, 6., 6.}}, Key56 → {{10., 11., 8.}, {4.12874, 9., 7.}},
Key57 → {{8., 6., 12.}, {3.76724, 8., 6.}}, Key58 → {{4., 9., 12.}, {5.11149, 9., 6.}},
Key59 → {{9., 6., 11.}, {5.70236, 7., 12.}}, Key60 → {{11., 9., 12.}, {5.41234, 12., 9.}},
Key61 → {{8., 10., 11.}, {5.70236, 8., 9.}}, Key62 → {{9., 13., 11.}, {4.47158, 8., 10.}},
Key63 → {{7., 6., 7.}, {4.12874, 6., 8.}}, Key64 → {{11., 7., 8.}, {5.11149, 4., 19.}},
Key65 → {{8., 14., 5.}, {4.12874, 12., 10.}}, Key66 → {{19., 11., 9.}, {2.52779, 4., 9.}},
Key67 → {{12., 10., 11.}, {4.12874, 10., 7.}}, Key68 → {{6., 9., 15.}, {3.38352, 7., 11.}},
Key69 → {{6., 11., 11.}, {5.98269, 9., 7.}}, Key70 → {{9., 11., 5.}, {4.79846, 12., 6.}},
Key71 → {{8., 19., 9.}, {5.41234, 8., 5.}}, Key72 → {{8., 7., 12.}, {3.76724, 8., 8.}},
Key73 → {{9., 14., 5.}, {4.47158, 7., 12.}}, Key74 → {{13., 9., 5.}, {5.41234, 12., 12.}},
Key75 → {{10., 8., 11.}, {5.41234, 7., 9.}}, Key76 → {{7., 13., 12.}, {3.38352, 7., 11.}},
Key77 → {{10., 10., 12.}, {4.79846, 8., 8.}}, Key78 → {{11., 10., 12.}, {3.76724, 10., 6.}},
Key79 → {{16., 12., 11.}, {4.79846, 11., 9.}}, Key80 → {{6., 5., 12.}, {7.26731, 6., 12.}},
Key81 → {{12., 9., 6.}, {4.12874, 16., 12.}}, Key82 → {{8., 14., 8.}, {3.38352, 8., 11.}},
Key83 → {{10., 14., 6.}, {4.47158, 7., 6.}}, Key84 → {{10., 13., 8.}, {4.79846, 8., 9.}},
Key85 → {{7., 3., 9.}, {5.41234, 13., 7.}}, Key86 → {{8., 11., 7.}, {4.12874, 8., 9.}},
Key87 → {{14., 4., 10.}, {5.98269, 11., 9.}}, Key88 → {{8., 12., 6.}, {2.97271, 9., 9.}},
Key89 → {{9., 12., 13.}, {3.76724, 14., 13.}}, Key90 → {{9., 6., 9.}, {5.41234, 15., 8.}},
Key91 → {{7., 15., 10.}, {4.47158, 7., 8.}}, Key92 → {{7., 7., 9.}, {4.79846, 12., 6.}},
Key93 → {{10., 17., 17.}, {4.47158, 6., 5.}}, Key94 → {{11., 10., 9.}, {5.11149, 7., 10.}},
Key95 → {{9., 12., 9.}, {5.11149, 8., 12.}}, Key96 → {{6., 6., 10.}, {3.76724, 8., 16.}},
Key97 → {{10., 8., 14.}, {4.47158, 5., 11.}}, Key98 → {{10., 7., 7.}, {5.11149, 13., 7.}},
Key99 → {{12., 12., 17.}, {5.41234, 10., 12.}}, Key100 → {{9., 10., 10.}, {4.79846, 11., 9.}} |> |>
```

ComponentIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

ComponentIndex allows selection of a component of a list if the input data is an OmicsObject or other association with multi - list values. For an example, we first generate a random OmicsObject using also random data as metadata

```
In[2]:= dataRandomOmicsObject = OmicsObjectCreator[{"Sample1", "Sample2", "Sample3"},
    ConstantArray[("Key" <> ToString[#]) & /@ Range[100], 3], RandomVariate[
     PoissonDistribution[10], {3, 100, 3}], RandomVariate[PoissonDistribution[10], {3, 100, 3}]];
```

Let's look at the first few keys to see the structure:

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```
In[3]:= Query[All, 1 ;; 5]@dataRandomOmicsObject
```

```
Out[3]= <|Sample1 → <|Key1 → {{11, 17, 9}, {9, 10, 7}}, Key2 → {{11, 5, 16}, {8, 9, 9}},
    Key3 → {{9, 7, 12}, {9, 14, 10}}, Key4 → {{12, 14, 11}, {14, 11, 11}}, Key5 → {{10, 11, 5}, {12, 10, 7}}|>,
  Sample2 → <|Key1 → {{15, 1, 9}, {15, 13, 10}}, Key2 → {{3, 7, 7}, {12, 12, 7}},
    Key3 → {{10, 8, 20}, {9, 13, 15}}, Key4 → {{11, 15, 5}, {10, 9, 7}}, Key5 → {{9, 11, 8}, {11, 9, 9}}|>,
  Sample3 → <|Key1 → {{9, 13, 4}, {8, 13, 11}}, Key2 → {{6, 13, 7}, {10, 6, 12}},
    Key3 → {{8, 6, 9}, {12, 11, 12}}, Key4 → {{15, 9, 11}, {5, 13, 11}}, Key5 → {{8, 13, 11}, {14, 14, 11}}|>|>
```

We can perform the optimized Box Cox Transform on values from the first list, first component:

```
In[4]:= ApplyBoxCoxTransform[dataRandomOmicsObject, ListIndex → 1, ComponentIndex → 1]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.660596

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.747296

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.933401

```
Out[4]= <|Sample1 → <|Key1 → {{5.86532, 17., 9.}, {9., 10., 7.}}, Key2 → {{5.86532, 5., 16.}, {8., 9., 9.}},
    Key3 → {{4.94919, 7., 12.}, {9., 14., 10.}}, Key4 → {{6.30189, 14., 11.}, {14., 11., 11.}},
    Key5 → {{5.41504, 11., 5.}, {12., 10., 7.}}, Key6 → {{3.43055, 8., 10.}, {8., 9., 10.}},
    Key7 → {{6.72627, 14., 10.}, {9., 10., 16.}}, Key8 → {{3.96056, 9., 9.}, {13., 7., 7.}},
    Key9 → {{4.46539, 12., 6.}, {10., 13., 11.}}, Key10 → {{6.72627, 7., 14.}, {14., 1., 8.}},
    Key11 → {{1.61408, 8., 8.}, {14., 11., 10.}}, Key12 → {{7.93771, 13., 9.}, {13., 5., 11.}},
    Key13 → {{2.86951, 5., 12.}, {10., 13., 10.}}, Key14 → {{7.54323, 10., 11.}, {13., 9., 15.}},
    Key15 → {{0.879108, 4., 12.}, {7., 11., 10.}}, Key16 → {{6.30189, 7., 14.}, {8., 13., 9.}},
    Key17 → {{3.43055, 14., 17.}, {6., 15., 7.}}, Key18 → {{7.13971, 15., 11.}, {10., 6., 12.}},
    Key19 → {{4.94919, 8., 10.}, {13., 13., 17.}}, Key20 → {{5.86532, 2., 8.}, {13., 8., 7.}},
    Key21 → {{6.72627, 12., 5.}, {13., 9., 13.}}, Key22 → {{7.13971, 10., 5.}, {10., 11., 15.}},
    Key23 → {{8.32391, 11., 19.}, {14., 6., 16.}}, Key24 → {{6.30189, 17., 9.}, {9., 6., 6.}},
    Key25 → {{5.86532, 10., 12.}, {10., 4., 11.}}, Key26 → {{6.30189, 8., 8.}, {5., 7., 7.}},
    Key27 → {{4.94919, 12., 9.}, {12., 14., 9.}}, Key28 → {{4.46539, 9., 5.}, {11., 8., 4.}},
    Key29 → {{4.94919, 14., 4.}, {9., 5., 12.}}, Key30 → {{5.86532, 10., 11.}, {14., 8., 8.}},
    Key31 → {{6.72627, 13., 12.}, {4., 5., 16.}}, Key32 → {{7.54323, 9., 11.}, {7., 13., 1.}},
    Key33 → {{6.72627, 12., 13.}, {9., 9., 10.}}, Key34 → {{4.46539, 7., 2.}, {11., 11., 10.}},
    Key35 → {{6.72627, 9., 10.}, {9., 12., 9.}}, Key36 → {{2.86951, 13., 7.}, {21., 11., 8.}},
    Key37 → {{4.94919, 15., 10.}, {9., 12., 13.}}, Key38 → {{5.86532, 12., 15.}, {10., 10., 11.}},
    Key39 → {{3.96056, 11., 8.}, {8., 7., 11.}}, Key40 → {{5.41504, 17., 8.}, {8., 8., 7.}},
    Key41 → {{7.93771, 14., 14.}, {12., 18., 8.}}, Key42 → {{5.41504, 12., 11.}, {9., 8., 9.}},
    Key43 → {{4.46539, 17., 8.}, {9., 12., 8.}}, Key44 → {{6.30189, 8., 11.}, {5., 11., 6.}},
    Key45 → {{4.46539, 4., 12.}, {12., 13., 13.}}, Key46 → {{5.41504, 11., 4.}, {17., 6., 13.}},
    Key47 → {{6.30189, 8., 10.}, {11., 9., 12.}}, Key48 → {{2.86951, 8., 4.}, {6., 6., 15.}},
    Key49 → {{4.94919, 11., 11.}, {11., 8., 16.}}, Key50 → {{2.86951, 11., 15.}, {14., 10., 11.}},
    Key51 → {{3.96056, 9., 6.}, {15., 10., 5.}}, Key52 → {{2.26875, 11., 8.}, {12., 17., 8.}},
    Key53 → {{4.46539, 12., 6.}, {8., 14., 12.}}, Key54 → {{4.94919, 10., 6.}, {11., 8., 10.}},
    Key55 → {{8.32391, 9., 16.}, {9., 8., 8.}}, Key56 → {{5.41504, 6., 10.}, {14., 5., 8.}},
    Key57 → {{4.94919, 9., 11.}, {7., 12., 9.}}, Key58 → {{7.54323, 7., 11.}, {9., 7., 10.}},
    Key59 → {{6.72627, 12., 4.}, {12., 14., 18.}}, Key60 → {{3.43055, 8., 4.}, {14., 14., 11.}},
    Key61 → {{5.41504, 6., 7.}, {6., 11., 12.}}, Key62 → {{3.96056, 12., 10.}, {15., 15., 13.}},
    Key63 → {{4.46539, 7., 8.}, {8., 10., 12.}}, Key64 → {{6.72627, 6., 6.}, {8., 8., 19.}},
    Key65 → {{8.70247, 8., 8.}, {9., 6., 8.}}, Key66 → {{2.26875, 9., 10.}, {9., 8., 13.}},
    Key67 → {{3.96056, 7., 3.}, {14., 13., 10.}}, Key68 → {{3.96056, 10., 9.}, {11., 12., 13.}},
    Key69 → {{3.96056, 15., 4.}, {9., 10., 3.}}, Key70 → {{2.86951, 6., 9.}, {7., 8., 9.}},
    Key71 → {{3.96056, 8., 11.}, {8., 15., 7.}}, Key72 → {{3.96056, 9., 6.}, {10., 11., 8.}},
    Key73 → {{3.43055, 6., 13.}, {11., 7., 10.}}, Key74 → {{4.94919, 8., 11.}, {12., 9., 5.}},
    Key75 → {{4.94919, 11., 11.}, {15., 8., 7.}}, Key76 → {{4.94919, 13., 8.}, {10., 11., 15.}},
    Key77 → {{3.96056, 12., 10.}, {8., 8., 12.}}, Key78 → {{2.26875, 9., 10.}, {10., 8., 7.}},
    Key79 → {{4.46539, 10., 11.}, {4., 9., 5.}}, Key80 → {{6.30189, 9., 13.}, {16., 4., 12.}},
    Key81 → {{7.13971, 5., 16.}, {9., 9., 15.}}, Key82 → {{3.96056, 8., 6.}, {6., 7., 11.}},
    Key83 → {{5.41504, 8., 14.}, {14., 9., 6.}}, Key84 → {{4.94919, 15., 11.}, {10., 6., 5.}},
    Key85 → {{4.46539, 13., 7.}, {10., 5., 11.}}, Key86 → {{4.46539, 12., 5.}, {13., 6., 10.}},
    Key87 → {{3.96056, 11., 9.}, {8., 7., 12.}}, Key88 → {{8.70247, 11., 5.}, {7., 8., 9.}},
    Key89 → {{3.43055, 9., 12.}, {12., 14., 12.}}, Key90 → {{3.96056, 7., 9.}, {14., 8., 8.}},
```

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```
  Key91 → {{0.879108, 10., 13.}, {9., 10., 10.}}, Key92 → {{6.72627, 10., 11.}, {8., 5., 10.}},
  Key93 → {{3.96056, 11., 11.}, {11., 8., 13.}}, Key94 → {{2.26875, 7., 9.}, {10., 6., 11.}},
  Key95 → {{3.96056, 9., 10.}, {7., 11., 9.}}, Key96 → {{4.46539, 10., 8.}, {14., 20., 12.}},
  Key97 → {{5.41504, 6., 10.}, {5., 10., 12.}}, Key98 → {{4.94919, 12., 9.}, {11., 13., 14.}},
  Key99 → {{3.43055, 10., 6.}, {14., 9., 10.}}, Key100 → {{6.72627, 10., 7.}, {10., 13., 9.}}|>,
Sample2 → <|Key1 → {{8.78686, 1., 9.}, {15., 13., 10.}}, Key2 → {{1.70313, 7., 7.}, {12., 12., 7.}},
  Key3 → {{6.14015, 8., 20.}, {9., 13., 15.}}, Key4 → {{6.69222, 15., 5.}, {10., 9., 7.}},
  Key5 → {{5.57393, 11., 8.}, {11., 9., 9.}}, Key6 → {{4.39041, 10., 12.}, {6., 5., 10.}},
  Key7 → {{3.11681, 14., 8.}, {10., 10., 7.}}, Key8 → {{4.99154, 10., 7.}, {12., 7., 9.}},
  Key9 → {{6.14015, 14., 14.}, {15., 10., 11.}}, Key10 → {{2.43256, 16., 13.}, {8., 5., 9.}},
  Key11 → {{7.23174, 7., 7.}, {9., 10., 14.}}, Key12 → {{3.76709, 11., 10.}, {6., 11., 8.}},
  Key13 → {{4.39041, 8., 10.}, {7., 11., 14.}}, Key14 → {{4.99154, 7., 9.}, {10., 10., 13.}},
  Key15 → {{1.70313, 7., 14.}, {8., 5., 13.}}, Key16 → {{4.99154, 3., 10.}, {9., 10., 9.}},
  Key17 → {{3.76709, 12., 12.}, {10., 8., 7.}}, Key18 → {{7.23174, 12., 7.}, {8., 11., 13.}},
  Key19 → {{9.28715, 7., 7.}, {5., 15., 16.}}, Key20 → {{5.57393, 8., 9.}, {7., 7., 13.}},
  Key21 → {{8.78686, 9., 13.}, {16., 12., 12.}}, Key22 → {{7.75999, 13., 7.}, {7., 11., 12.}},
  Key23 → {{4.99154, 6., 13.}, {13., 10., 12.}}, Key24 → {{4.39041, 4., 9.}, {5., 11., 10.}},
  Key25 → {{8.78686, 9., 5.}, {5., 11., 10.}}, Key26 → {{3.11681, 12., 9.}, {10., 8., 6.}},
  Key27 → {{8.27806, 5., 5.}, {6., 6., 8.}}, Key28 → {{7.23174, 11., 7.}, {10., 3., 10.}},
  Key29 → {{6.14015, 9., 6.}, {12., 5., 8.}}, Key30 → {{4.39041, 12., 14.}, {8., 11., 7.}},
  Key31 → {{7.75999, 13., 9.}, {14., 5., 6.}}, Key32 → {{6.14015, 7., 6.}, {10., 11., 5.}},
  Key33 → {{6.69222, 8., 8.}, {15., 11., 9.}}, Key34 → {{4.39041, 10., 14.}, {9., 13., 16.}},
  Key35 → {{5.57393, 9., 9.}, {12., 11., 8.}}, Key36 → {{4.99154, 7., 9.}, {7., 8., 11.}},
  Key37 → {{4.99154, 13., 12.}, {13., 10., 5.}}, Key38 → {{5.57393, 8., 8.}, {10., 7., 10.}},
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  Key41 → {{7.23174, 13., 8.}, {9., 4., 11.}}, Key42 → {{7.23174, 10., 5.}, {9., 8., 5.}},
  Key43 → {{6.14015, 13., 10.}, {6., 9., 9.}}, Key44 → {{6.69222, 7., 8.}, {10., 10., 12.}},
  Key45 → {{4.99154, 12., 8.}, {7., 9., 13.}}, Key46 → {{4.39041, 13., 11.}, {15., 5., 10.}},
  Key47 → {{3.76709, 15., 8.}, {8., 7., 9.}}, Key48 → {{3.11681, 10., 15.}, {6., 12., 7.}},
  Key49 → {{6.14015, 6., 7.}, {10., 9., 9.}}, Key50 → {{4.99154, 12., 11.}, {6., 9., 8.}},
  Key51 → {{6.14015, 16., 12.}, {12., 9., 11.}}, Key52 → {{5.57393, 12., 14.}, {8., 13., 16.}},
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  Key55 → {{3.11681, 10., 8.}, {10., 8., 6.}}, Key56 → {{4.39041, 8., 8.}, {6., 9., 12.}},
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  Key61 → {{3.76709, 5., 9.}, {9., 7., 12.}}, Key62 → {{6.14015, 10., 13.}, {5., 10., 5.}},
  Key63 → {{5.57393, 17., 10.}, {16., 10., 12.}}, Key64 → {{4.99154, 11., 6.}, {12., 9., 11.}},
  Key65 → {{2.43256, 11., 12.}, {8., 10., 12.}}, Key66 → {{4.39041, 10., 5.}, {8., 12., 12.}},
  Key67 → {{4.39041, 13., 10.}, {12., 10., 9.}}, Key68 → {{5.57393, 10., 7.}, {8., 10., 11.}},
  Key69 → {{9.7796, 14., 13.}, {9., 8., 10.}}, Key70 → {{6.69222, 5., 9.}, {11., 12., 9.}},
  Key71 → {{7.23174, 10., 10.}, {11., 10., 9.}}, Key72 → {{4.39041, 7., 13.}, {10., 8., 3.}},
  Key73 → {{7.23174, 19., 7.}, {7., 14., 5.}}, Key74 → {{2.43256, 11., 12.}, {6., 10., 7.}},
  Key75 → {{7.75999, 8., 12.}, {10., 12., 9.}}, Key76 → {{3.76709, 12., 3.}, {11., 8., 8.}},
  Key77 → {{5.57393, 10., 5.}, {8., 12., 16.}}, Key78 → {{6.69222, 12., 12.}, {15., 8., 8.}},
  Key79 → {{6.14015, 4., 8.}, {6., 10., 6.}}, Key80 → {{6.69222, 10., 5.}, {13., 13., 12.}},
  Key81 → {{7.75999, 10., 4.}, {15., 9., 13.}}, Key82 → {{4.99154, 13., 8.}, {11., 13., 12.}},
  Key83 → {{6.69222, 11., 11.}, {7., 12., 11.}}, Key84 → {{4.39041, 16., 6.}, {10., 12., 12.}},
  Key85 → {{7.23174, 8., 15.}, {6., 8., 13.}}, Key86 → {{6.69222, 9., 15.}, {15., 10., 8.}},
  Key87 → {{7.23174, 14., 9.}, {7., 8., 13.}}, Key88 → {{6.14015, 13., 5.}, {9., 10., 15.}},
  Key89 → {{6.69222, 13., 9.}, {8., 8., 10.}}, Key90 → {{7.75999, 9., 6.}, {11., 13., 12.}},
  Key91 → {{5.57393, 12., 8.}, {6., 12., 12.}}, Key92 → {{4.39041, 8., 8.}, {11., 9., 13.}},
  Key93 → {{5.57393, 10., 12.}, {15., 10., 6.}}, Key94 → {{9.28715, 8., 10.}, {12., 13., 11.}},
  Key95 → {{7.75999, 9., 9.}, {10., 9., 11.}}, Key96 → {{6.69222, 8., 12.}, {10., 6., 6.}},
  Key97 → {{4.39041, 10., 10.}, {7., 9., 8.}}, Key98 → {{8.78686, 8., 11.}, {12., 8., 10.}},
  Key99 → {{3.76709, 9., 6.}, {10., 8., 10.}}, Key100 → {{8.78686, 12., 6.}, {7., 14., 8.}}|>,
Sample3 → <|Key1 → {{7.25823, 13., 4.}, {8., 13., 11.}}, Key2 → {{4.63369, 13., 7.}, {10., 6., 12.}},
  Key3 → {{6.39102, 6., 9.}, {12., 11., 12.}}, Key4 → {{12.3469, 9., 11.}, {5., 13., 11.}},
  Key5 → {{6.39102, 13., 11.}, {14., 14., 11.}}, Key6 → {{6.39102, 14., 11.}, {8., 12., 12.}},
  Key7 → {{5.51655, 10., 18.}, {6., 10., 12.}}, Key8 → {{8.11902, 15., 9.}, {16., 15., 10.}},
  Key9 → {{13.1801, 11., 8.}, {15., 9., 16.}}, Key10 → {{5.51655, 8., 9.}, {8., 10., 12.}},
  Key11 → {{9.82399, 10., 12.}, {9., 16., 12.}}, Key12 → {{6.39102, 12., 10.}, {8., 11., 6.}},
  Key13 → {{5.51655, 14., 8.}, {12., 5., 10.}}, Key14 → {{12.3469, 11., 10.}, {9., 9., 10.}},
  Key15 → {{5.51655, 14., 8.}, {7., 7., 11.}}, Key16 → {{8.97409, 9., 14.}, {7., 6., 13.}},
  Key17 → {{7.25823, 12., 7.}, {13., 7., 10.}}, Key18 → {{8.97409, 11., 8.}, {9., 12., 11.}},
  Key19 → {{6.39102, 8., 5.}, {12., 7., 5.}}, Key20 → {{3.74093, 7., 10.}, {10., 9., 11.}},
  Key21 → {{3.74093, 10., 4.}, {8., 10., 14.}}, Key22 → {{7.25823, 13., 10.}, {10., 8., 11.}},
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Key23 → {{9.82399, 13., 9.}, {7., 9., 12.}}, Key24 → {{9.82399, 6., 11.}, {9., 15., 14.}},
Key25 → {{6.39102, 11., 9.}, {7., 8., 11.}}, Key26 → {{11.5101, 10., 10.}, {10., 11., 9.}},
Key27 → {{7.25823, 12., 13.}, {14., 13., 12.}}, Key28 → {{7.25823, 13., 14.}, {15., 9., 11.}},
Key29 → {{9.82399, 12., 3.}, {11., 9., 16.}}, Key30 → {{4.63369, 10., 14.}, {10., 13., 11.}},
Key31 → {{2.83612, 9., 13.}, {9., 8., 13.}}, Key32 → {{8.97409, 8., 9.}, {20., 9., 5.}},
Key33 → {{8.11902, 5., 12.}, {15., 14., 9.}}, Key34 → {{11.5101, 12., 7.}, {9., 16., 12.}},
Key35 → {{9.82399, 11., 10.}, {7., 9., 9.}}, Key36 → {{6.39102, 12., 15.}, {16., 11., 6.}},
Key37 → {{8.97409, 7., 5.}, {9., 13., 10.}}, Key38 → {{9.82399, 11., 10.}, {10., 14., 9.}},
Key39 → {{8.11902, 7., 15.}, {11., 12., 12.}}, Key40 → {{11.5101, 17., 10.}, {9., 10., 12.}},
Key41 → {{8.11902, 10., 7.}, {14., 14., 9.}}, Key42 → {{8.11902, 6., 6.}, {14., 13., 10.}},
Key43 → {{11.5101, 18., 7.}, {17., 14., 6.}}, Key44 → {{7.25823, 8., 9.}, {13., 9., 10.}},
Key45 → {{3.74093, 13., 12.}, {16., 6., 9.}}, Key46 → {{8.11902, 10., 10.}, {13., 10., 9.}},
Key47 → {{10.6692, 9., 9.}, {6., 6., 8.}}, Key48 → {{8.11902, 9., 18.}, {7., 9., 9.}},
Key49 → {{14.0098, 11., 13.}, {12., 12., 9.}}, Key50 → {{11.5101, 11., 6.}, {9., 12., 13.}},
Key51 → {{8.97409, 7., 7.}, {7., 12., 7.}}, Key52 → {{7.25823, 6., 11.}, {8., 7., 5.}},
Key53 → {{11.5101, 12., 7.}, {6., 9., 15.}}, Key54 → {{11.5101, 7., 6.}, {8., 12., 6.}},
Key55 → {{11.5101, 19., 12.}, {7., 10., 13.}}, Key56 → {{6.39102, 9., 8.}, {3., 11., 10.}},
Key57 → {{3.74093, 9., 6.}, {5., 11., 8.}}, Key58 → {{8.97409, 6., 14.}, {9., 10., 13.}},
Key59 → {{4.63369, 8., 3.}, {5., 6., 11.}}, Key60 → {{8.97409, 14., 7.}, {9., 4., 12.}},
Key61 → {{10.6692, 7., 9.}, {5., 9., 5.}}, Key62 → {{8.11902, 11., 9.}, {11., 18., 8.}},
Key63 → {{9.82399, 8., 9.}, {12., 4., 11.}}, Key64 → {{11.5101, 11., 5.}, {11., 13., 9.}},
Key65 → {{10.6692, 7., 16.}, {11., 10., 7.}}, Key66 → {{11.5101, 11., 8.}, {8., 11., 10.}},
Key67 → {{3.74093, 6., 5.}, {6., 8., 9.}}, Key68 → {{4.63369, 13., 10.}, {7., 10., 17.}},
Key69 → {{9.82399, 11., 9.}, {11., 12., 8.}}, Key70 → {{8.97409, 6., 12.}, {14., 12., 8.}},
Key71 → {{8.11902, 9., 10.}, {10., 9., 6.}}, Key72 → {{6.39102, 2., 12.}, {5., 12., 13.}},
Key73 → {{3.74093, 6., 8.}, {2., 14., 9.}}, Key74 → {{2.83612, 11., 7.}, {8., 6., 9.}},
Key75 → {{6.39102, 7., 8.}, {5., 16., 11.}}, Key76 → {{5.51655, 10., 9.}, {9., 8., 10.}},
Key77 → {{10.6692, 10., 8.}, {10., 9., 9.}}, Key78 → {{11.5101, 9., 12.}, {9., 12., 5.}},
Key79 → {{9.82399, 13., 14.}, {11., 6., 13.}}, Key80 → {{11.5101, 10., 15.}, {13., 6., 10.}},
Key81 → {{8.97409, 11., 5.}, {13., 10., 8.}}, Key82 → {{8.11902, 18., 14.}, {9., 9., 10.}},
Key83 → {{14.0098, 15., 13.}, {13., 7., 14.}}, Key84 → {{7.25823, 9., 11.}, {13., 9., 9.}},
Key85 → {{8.97409, 6., 12.}, {8., 15., 9.}}, Key86 → {{10.6692, 6., 13.}, {16., 9., 5.}},
Key87 → {{11.5101, 9., 11.}, {10., 10., 2.}}, Key88 → {{6.39102, 13., 10.}, {10., 6., 13.}},
Key89 → {{7.25823, 7., 3.}, {8., 15., 11.}}, Key90 → {{13.1801, 11., 9.}, {9., 9., 11.}},
Key91 → {{3.74093, 3., 16.}, {7., 9., 12.}}, Key92 → {{9.82399, 10., 12.}, {6., 13., 12.}},
Key93 → {{2.83612, 17., 12.}, {11., 12., 12.}}, Key94 → {{9.82399, 7., 8.}, {13., 18., 15.}},
Key95 → {{10.6692, 10., 9.}, {13., 15., 12.}}, Key96 → {{4.63369, 10., 10.}, {15., 8., 5.}},
Key97 → {{8.11902, 10., 11.}, {10., 17., 5.}}, Key98 → {{7.25823, 16., 7.}, {12., 8., 15.}},
Key99 → {{3.74093, 7., 19.}, {10., 13., 8.}}, Key100 → {{8.97409, 5., 10.}, {8., 7., 9.}}|>|>
```

We can perform the optimized Box Cox Transform on values from the first list, second component :

```
In[5]:= ApplyBoxCoxTransform[dataRandomOmicsObject, ListIndex → 1, ComponentIndex → 2]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.800252

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.986297

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.720851

```
Out[5]= <|Sample1 → <|Key1 → {{11., 10.813, 9.}, {9., 10., 7.}}, Key2 → {{11., 3.28068, 16.}, {8., 9., 9.}},
Key3 → {{9., 4.68053, 12.}, {9., 14., 10.}}, Key4 → {{12., 9.07716, 11.}, {14., 11., 11.}},
Key5 → {{10., 7.26471, 5.}, {12., 10., 7.}}, Key6 → {{6., 5.34931, 10.}, {8., 9., 10.}},
Key7 → {{13., 9.07716, 10.}, {9., 10., 16.}}, Key8 → {{7., 6.00155, 9.}, {13., 7., 7.}},
Key9 → {{8., 7.87869, 6.}, {10., 13., 11.}}, Key10 → {{13., 4.68053, 14.}, {14., 1., 8.}},
Key11 → {{3., 5.34931, 8.}, {14., 11., 10.}}, Key12 → {{16., 8.48253, 9.}, {13., 5., 11.}},
Key13 → {{5., 3.28068, 12.}, {10., 13., 10.}}, Key14 → {{15., 6.63945, 11.}, {13., 9., 15.}},
Key15 → {{2., 2.53981, 12.}, {7., 11., 10.}}, Key16 → {{12., 4.68053, 14.}, {8., 13., 9.}},
Key17 → {{6., 9.07716, 17.}, {6., 15., 7.}}, Key18 → {{14., 9.66335, 11.}, {10., 6., 12.}},
Key19 → {{9., 5.34931, 10.}, {13., 13., 17.}}, Key20 → {{11., 0.926465, 8.}, {13., 8., 7.}},
Key21 → {{13., 7.87869, 5.}, {13., 9., 13.}}, Key22 → {{14., 6.63945, 5.}, {10., 11., 15.}},
Key23 → {{17., 7.26471, 19.}, {14., 6., 16.}}, Key24 → {{12., 10.813, 9.}, {9., 6., 6.}},
Key25 → {{11., 6.63945, 12.}, {10., 4., 11.}}, Key26 → {{12., 5.34931, 8.}, {5., 7., 7.}},
Key27 → {{9., 7.87869, 9.}, {12., 14., 9.}}, Key28 → {{8., 6.00155, 5.}, {11., 8., 4.}},
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  Key29 → {{9., 9.07716, 4.}, {9., 5., 12.}}, Key30 → {{11., 6.63945, 11.}, {14., 8., 8.}},
  Key31 → {{13., 8.48253, 12.}, {4., 5., 16.}}, Key32 → {{15., 6.00155, 11.}, {7., 13., 1.}},
  Key33 → {{13., 7.87869, 13.}, {9., 9., 10.}}, Key34 → {{8., 4.68053, 2.}, {11., 11., 10.}},
  Key35 → {{13., 6.00155, 10.}, {9., 12., 9.}}, Key36 → {{5., 8.48253, 7.}, {21., 11., 8.}},
  Key37 → {{9., 9.66335, 10.}, {9., 12., 13.}}, Key38 → {{11., 7.87869, 15.}, {10., 10., 11.}},
  Key39 → {{7., 7.26471, 8.}, {8., 7., 11.}}, Key40 → {{10., 10.813, 8.}, {8., 8., 7.}},
  Key41 → {{16., 9.07716, 14.}, {12., 18., 8.}}, Key42 → {{10., 7.87869, 11.}, {9., 8., 9.}},
  Key43 → {{8., 10.813, 8.}, {9., 12., 8.}}, Key44 → {{12., 5.34931, 11.}, {5., 11., 6.}},
  Key45 → {{8., 2.53981, 12.}, {12., 13., 13.}}, Key46 → {{10., 7.26471, 4.}, {17., 6., 13.}},
  Key47 → {{12., 5.34931, 10.}, {11., 9., 12.}}, Key48 → {{5., 5.34931, 4.}, {6., 6., 15.}},
  Key49 → {{9., 7.26471, 11.}, {11., 8., 16.}}, Key50 → {{5., 7.26471, 15.}, {14., 10., 11.}},
  Key51 → {{7., 6.00155, 6.}, {15., 10., 5.}}, Key52 → {{4., 7.26471, 8.}, {12., 17., 8.}},
  Key53 → {{8., 7.87869, 6.}, {8., 14., 12.}}, Key54 → {{9., 6.63945, 6.}, {11., 8., 10.}},
  Key55 → {{17., 6.00155, 16.}, {9., 8., 8.}}, Key56 → {{10., 3.99231, 10.}, {14., 5., 8.}},
  Key57 → {{9., 6.00155, 11.}, {7., 12., 9.}}, Key58 → {{15., 4.68053, 11.}, {9., 7., 10.}},
  Key59 → {{13., 7.87869, 4.}, {12., 14., 18.}}, Key60 → {{6., 5.34931, 4.}, {14., 14., 11.}},
  Key61 → {{10., 3.99231, 7.}, {6., 11., 12.}}, Key62 → {{7., 7.87869, 10.}, {15., 15., 13.}},
  Key63 → {{8., 4.68053, 8.}, {8., 10., 12.}}, Key64 → {{13., 3.99231, 6.}, {8., 8., 19.}},
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  Key69 → {{7., 9.66335, 4.}, {9., 10., 3.}}, Key70 → {{5., 3.99231, 9.}, {7., 8., 9.}},
  Key71 → {{7., 5.34931, 11.}, {8., 15., 7.}}, Key72 → {{7., 6.00155, 6.}, {10., 11., 8.}},
  Key73 → {{6., 3.99231, 13.}, {11., 7., 10.}}, Key74 → {{9., 5.34931, 11.}, {12., 9., 5.}},
  Key75 → {{9., 7.26471, 11.}, {15., 8., 7.}}, Key76 → {{9., 8.48253, 8.}, {10., 11., 15.}},
  Key77 → {{7., 7.87869, 10.}, {8., 8., 12.}}, Key78 → {{4., 6.00155, 10.}, {10., 8., 7.}},
  Key79 → {{8., 6.63945, 11.}, {4., 9., 5.}}, Key80 → {{12., 6.00155, 13.}, {16., 4., 12.}},
  Key81 → {{14., 3.28068, 16.}, {9., 9., 15.}}, Key82 → {{7., 5.34931, 6.}, {6., 7., 11.}},
  Key83 → {{10., 5.34931, 14.}, {14., 9., 6.}}, Key84 → {{9., 9.66335, 11.}, {10., 6., 5.}},
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  Key87 → {{7., 7.26471, 9.}, {8., 7., 12.}}, Key88 → {{18., 7.26471, 5.}, {7., 8., 9.}},
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  Key91 → {{2., 6.63945, 13.}, {9., 10., 10.}}, Key92 → {{13., 6.63945, 11.}, {8., 5., 10.}},
  Key93 → {{7., 7.26471, 11.}, {11., 8., 13.}}, Key94 → {{4., 4.68053, 9.}, {10., 6., 11.}},
  Key95 → {{7., 6.00155, 10.}, {7., 11., 9.}}, Key96 → {{8., 6.63945, 8.}, {14., 20., 12.}},
  Key97 → {{10., 3.99231, 10.}, {5., 10., 12.}}, Key98 → {{9., 7.87869, 9.}, {11., 13., 14.}},
  Key99 → {{6., 6.63945, 6.}, {14., 9., 10.}}, Key100 → {{13., 6.63945, 7.}, {10., 13., 9.}}|>,
Sample2 → <|Key1 → {{15., 0., 9.}, {15., 13., 10.}}, Key2 → {{3., 5.89661, 7.}, {12., 12., 7.}},
  Key3 → {{10., 6.86939, 20.}, {9., 13., 15.}}, Key4 → {{11., 13.6405, 5.}, {10., 9., 7.}},
  Key5 → {{9., 9.77842, 8.}, {11., 9., 9.}}, Key6 → {{7., 8.81012, 12.}, {6., 5., 10.}},
  Key7 → {{5., 12.6765, 8.}, {10., 10., 7.}}, Key8 → {{8., 8.81012, 7.}, {12., 7., 9.}},
  Key9 → {{10., 12.6765, 14.}, {15., 10., 11.}}, Key10 → {{4., 14.6036, 13.}, {8., 5., 9.}},
  Key11 → {{12., 5.89661, 7.}, {9., 10., 14.}}, Key12 → {{6., 9.77842, 10.}, {6., 11., 8.}},
  Key13 → {{7., 6.86939, 10.}, {7., 11., 14.}}, Key14 → {{8., 5.89661, 9.}, {10., 10., 13.}},
  Key15 → {{3., 5.89661, 14.}, {8., 5., 13.}}, Key16 → {{8., 1.98234, 10.}, {9., 10., 9.}},
  Key17 → {{6., 10.7455, 12.}, {10., 8., 7.}}, Key18 → {{12., 10.7455, 7.}, {8., 11., 13.}},
  Key19 → {{16., 5.89661, 7.}, {5., 15., 16.}}, Key20 → {{9., 6.86939, 9.}, {7., 7., 13.}},
  Key21 → {{15., 7.8405, 13.}, {16., 12., 12.}}, Key22 → {{13., 11.7115, 7.}, {7., 11., 12.}},
  Key23 → {{8., 4.92192, 13.}, {13., 10., 12.}}, Key24 → {{7., 2.96537, 9.}, {5., 11., 10.}},
  Key25 → {{15., 7.8405, 5.}, {5., 11., 10.}}, Key26 → {{5., 10.7455, 9.}, {10., 8., 6.}},
  Key27 → {{14., 3.94499, 5.}, {6., 6., 8.}}, Key28 → {{12., 9.77842, 7.}, {10., 3., 10.}},
  Key29 → {{10., 7.8405, 6.}, {12., 5., 8.}}, Key30 → {{7., 10.7455, 14.}, {8., 11., 7.}},
  Key31 → {{13., 11.7115, 9.}, {14., 5., 6.}}, Key32 → {{10., 5.89661, 6.}, {10., 11., 5.}},
  Key33 → {{11., 6.86939, 8.}, {15., 11., 9.}}, Key34 → {{7., 8.81012, 14.}, {9., 13., 16.}},
  Key35 → {{9., 7.8405, 9.}, {12., 11., 8.}}, Key36 → {{8., 5.89661, 9.}, {7., 8., 11.}},
  Key37 → {{8., 11.7115, 12.}, {13., 10., 5.}}, Key38 → {{9., 6.86939, 8.}, {10., 7., 10.}},
  Key39 → {{16., 7.8405, 10.}, {15., 11., 14.}}, Key40 → {{11., 13.6405, 3.}, {12., 7., 12.}},
  Key41 → {{12., 11.7115, 8.}, {9., 4., 11.}}, Key42 → {{12., 8.81012, 5.}, {9., 8., 5.}},
  Key43 → {{10., 11.7115, 10.}, {6., 9., 9.}}, Key44 → {{11., 5.89661, 8.}, {10., 10., 12.}},
  Key45 → {{8., 10.7455, 8.}, {7., 9., 13.}}, Key46 → {{7., 11.7115, 11.}, {15., 5., 10.}},
  Key47 → {{6., 13.6405, 8.}, {8., 7., 9.}}, Key48 → {{5., 8.81012, 15.}, {6., 12., 7.}},
  Key49 → {{10., 4.92192, 7.}, {10., 9., 9.}}, Key50 → {{8., 10.7455, 11.}, {6., 9., 8.}},
  Key51 → {{10., 14.6036, 12.}, {12., 9., 11.}}, Key52 → {{9., 10.7455, 14.}, {8., 13., 16.}},
  Key53 → {{8., 6.86939, 19.}, {14., 8., 11.}}, Key54 → {{13., 7.8405, 10.}, {12., 11., 12.}},
  Key55 → {{5., 8.81012, 8.}, {10., 8., 6.}}, Key56 → {{7., 6.86939, 8.}, {6., 9., 12.}},
  Key57 → {{11., 7.8405, 8.}, {11., 11., 3.}}, Key58 → {{15., 5.89661, 9.}, {11., 6., 13.}},
  Key59 → {{9., 8.81012, 9.}, {7., 6., 12.}}, Key60 → {{12., 2.96537, 9.}, {13., 9., 10.}},
```

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```
  Key61 → {{6., 3.94499, 9.}, {9., 7., 12.}}, Key62 → {{10., 8.81012, 13.}, {5., 10., 5.}},
  Key63 → {{9., 15.5659, 10.}, {16., 10., 12.}}, Key64 → {{8., 9.77842, 6.}, {12., 9., 11.}},
  Key65 → {{4., 9.77842, 12.}, {8., 10., 12.}}, Key66 → {{7., 8.81012, 5.}, {8., 12., 12.}},
  Key67 → {{7., 11.7115, 10.}, {12., 10., 9.}}, Key68 → {{9., 8.81012, 7.}, {8., 10., 11.}},
  Key69 → {{17., 12.6765, 13.}, {9., 8., 10.}}, Key70 → {{11., 3.94499, 9.}, {11., 12., 9.}},
  Key71 → {{12., 8.81012, 10.}, {11., 10., 9.}}, Key72 → {{7., 5.89661, 13.}, {10., 8., 3.}},
  Key73 → {{12., 17.4883, 7.}, {7., 14., 5.}}, Key74 → {{4., 9.77842, 12.}, {6., 10., 7.}},
  Key75 → {{13., 6.86939, 12.}, {10., 12., 9.}}, Key76 → {{6., 10.7455, 3.}, {11., 8., 8.}},
  Key77 → {{9., 8.81012, 5.}, {8., 12., 16.}}, Key78 → {{11., 10.7455, 12.}, {15., 8., 8.}},
  Key79 → {{10., 2.96537, 8.}, {6., 10., 6.}}, Key80 → {{11., 8.81012, 5.}, {13., 13., 12.}},
  Key81 → {{13., 8.81012, 4.}, {15., 9., 13.}}, Key82 → {{8., 11.7115, 8.}, {11., 13., 12.}},
  Key83 → {{11., 9.77842, 11.}, {7., 12., 11.}}, Key84 → {{7., 14.6036, 6.}, {10., 12., 12.}},
  Key85 → {{12., 6.86939, 15.}, {6., 8., 13.}}, Key86 → {{11., 7.8405, 15.}, {15., 10., 8.}},
  Key87 → {{12., 12.6765, 9.}, {7., 8., 13.}}, Key88 → {{10., 11.7115, 5.}, {9., 10., 15.}},
  Key89 → {{11., 11.7115, 9.}, {8., 8., 10.}}, Key90 → {{13., 7.8405, 6.}, {11., 13., 12.}},
  Key91 → {{9., 10.7455, 8.}, {6., 12., 12.}}, Key92 → {{7., 6.86939, 8.}, {11., 9., 13.}},
  Key93 → {{9., 8.81012, 12.}, {15., 10., 6.}}, Key94 → {{16., 6.86939, 10.}, {12., 13., 11.}},
  Key95 → {{13., 7.8405, 9.}, {10., 9., 11.}}, Key96 → {{11., 6.86939, 12.}, {10., 6., 6.}},
  Key97 → {{7., 8.81012, 10.}, {7., 9., 8.}}, Key98 → {{15., 6.86939, 11.}, {12., 8., 10.}},
  Key99 → {{6., 7.8405, 6.}, {10., 8., 10.}}, Key100 → {{15., 10.7455, 6.}, {7., 14., 8.}}|>,
Sample3 → <|Key1 → {{9., 7.42611, 4.}, {8., 13., 11.}}, Key2 → {{6., 7.42611, 7.}, {10., 6., 12.}},
  Key3 → {{8., 3.66036, 9.}, {12., 11., 12.}}, Key4 → {{15., 5.37391, 11.}, {5., 13., 11.}},
  Key5 → {{8., 7.42611, 11.}, {14., 14., 11.}}, Key6 → {{8., 7.90973, 11.}, {8., 12., 12.}},
  Key7 → {{7., 5.90742, 18.}, {6., 10., 12.}}, Key8 → {{10., 8.3838, 9.}, {16., 15., 10.}},
  Key9 → {{16., 6.42621, 8.}, {15., 9., 16.}}, Key10 → {{7., 4.82355, 9.}, {8., 10., 12.}},
  Key11 → {{12., 5.90742, 12.}, {9., 16., 12.}}, Key12 → {{8., 6.93199, 10.}, {8., 11., 6.}},
  Key13 → {{7., 7.90973, 8.}, {12., 5., 10.}}, Key14 → {{15., 6.42621, 10.}, {9., 9., 10.}},
  Key15 → {{7., 7.90973, 8.}, {7., 7., 11.}}, Key16 → {{11., 5.37391, 14.}, {7., 6., 13.}},
  Key17 → {{9., 6.93199, 7.}, {13., 7., 10.}}, Key18 → {{11., 6.42621, 8.}, {9., 12., 11.}},
  Key19 → {{8., 4.82355, 5.}, {12., 7., 5.}}, Key20 → {{5., 4.2536, 10.}, {10., 9., 11.}},
  Key21 → {{5., 5.90742, 4.}, {8., 10., 14.}}, Key22 → {{9., 7.42611, 10.}, {10., 8., 11.}},
  Key23 → {{12., 7.42611, 9.}, {7., 9., 12.}}, Key24 → {{12., 3.66036, 11.}, {9., 15., 14.}},
  Key25 → {{8., 6.42621, 9.}, {7., 8., 11.}}, Key26 → {{14., 5.90742, 10.}, {10., 11., 9.}},
  Key27 → {{9., 6.93199, 13.}, {14., 13., 12.}}, Key28 → {{9., 7.42611, 14.}, {15., 9., 11.}},
  Key29 → {{12., 6.93199, 3.}, {11., 9., 16.}}, Key30 → {{6., 5.90742, 14.}, {10., 13., 11.}},
  Key31 → {{4., 5.37391, 13.}, {9., 8., 13.}}, Key32 → {{11., 4.82355, 9.}, {20., 9., 5.}},
  Key33 → {{10., 3.03871, 12.}, {15., 14., 9.}}, Key34 → {{14., 6.93199, 7.}, {9., 16., 12.}},
  Key35 → {{12., 6.42621, 10.}, {7., 9., 9.}}, Key36 → {{8., 6.93199, 15.}, {16., 11., 6.}},
  Key37 → {{11., 4.2536, 5.}, {9., 13., 10.}}, Key38 → {{12., 6.42621, 10.}, {10., 14., 9.}},
  Key39 → {{10., 4.2536, 15.}, {11., 12., 12.}}, Key40 → {{14., 9.30637, 10.}, {9., 10., 12.}},
  Key41 → {{10., 5.90742, 7.}, {14., 14., 9.}}, Key42 → {{10., 3.66036, 6.}, {14., 13., 10.}},
  Key43 → {{14., 9.75618, 7.}, {17., 14., 6.}}, Key44 → {{9., 4.82355, 9.}, {13., 9., 10.}},
  Key45 → {{5., 7.42611, 12.}, {16., 6., 9.}}, Key46 → {{10., 5.90742, 10.}, {13., 10., 9.}},
  Key47 → {{13., 5.37391, 9.}, {6., 6., 8.}}, Key48 → {{10., 5.37391, 18.}, {7., 9., 9.}},
  Key49 → {{17., 6.42621, 13.}, {12., 12., 9.}}, Key50 → {{14., 6.42621, 6.}, {9., 12., 13.}},
  Key51 → {{11., 4.2536, 7.}, {7., 12., 7.}}, Key52 → {{9., 3.66036, 11.}, {8., 7., 5.}},
  Key53 → {{14., 6.93199, 7.}, {6., 9., 15.}}, Key54 → {{14., 4.2536, 6.}, {8., 12., 6.}},
  Key55 → {{14., 10.1991, 12.}, {7., 10., 13.}}, Key56 → {{8., 5.37391, 8.}, {3., 11., 10.}},
  Key57 → {{5., 5.37391, 6.}, {5., 11., 8.}}, Key58 → {{11., 3.66036, 14.}, {9., 10., 13.}},
  Key59 → {{6., 4.82355, 3.}, {5., 6., 11.}}, Key60 → {{11., 7.90973, 7.}, {9., 4., 12.}},
  Key61 → {{13., 4.2536, 9.}, {5., 9., 5.}}, Key62 → {{10., 6.42621, 9.}, {11., 18., 8.}},
  Key63 → {{12., 4.82355, 9.}, {12., 4., 11.}}, Key64 → {{14., 6.42621, 5.}, {11., 13., 9.}},
  Key65 → {{13., 4.2536, 16.}, {11., 10., 7.}}, Key66 → {{14., 6.42621, 8.}, {8., 11., 10.}},
  Key67 → {{5., 3.66036, 5.}, {6., 8., 9.}}, Key68 → {{6., 7.42611, 10.}, {7., 10., 17.}},
  Key69 → {{12., 6.42621, 9.}, {11., 12., 8.}}, Key70 → {{11., 3.66036, 12.}, {14., 12., 8.}},
  Key71 → {{10., 5.37391, 10.}, {10., 9., 6.}}, Key72 → {{8., 0.899151, 12.}, {5., 12., 13.}},
  Key73 → {{5., 3.66036, 8.}, {2., 14., 9.}}, Key74 → {{4., 6.42621, 7.}, {8., 6., 9.}},
  Key75 → {{8., 4.2536, 8.}, {5., 16., 11.}}, Key76 → {{7., 5.90742, 9.}, {9., 8., 10.}},
  Key77 → {{13., 5.90742, 8.}, {10., 9., 9.}}, Key78 → {{14., 5.37391, 12.}, {9., 12., 5.}},
  Key79 → {{12., 7.42611, 14.}, {11., 6., 13.}}, Key80 → {{14., 5.90742, 15.}, {13., 6., 10.}},
  Key81 → {{11., 6.42621, 5.}, {13., 10., 8.}}, Key82 → {{10., 9.75618, 14.}, {9., 9., 10.}},
  Key83 → {{17., 8.3838, 13.}, {13., 7., 14.}}, Key84 → {{9., 5.37391, 11.}, {13., 9., 9.}},
  Key85 → {{11., 3.66036, 12.}, {8., 15., 9.}}, Key86 → {{13., 3.66036, 13.}, {16., 9., 5.}},
  Key87 → {{14., 5.37391, 11.}, {10., 10., 2.}}, Key88 → {{8., 7.42611, 10.}, {10., 6., 13.}},
  Key89 → {{9., 4.2536, 3.}, {8., 15., 11.}}, Key90 → {{16., 6.42621, 9.}, {9., 9., 11.}},
  Key91 → {{5., 1.67533, 16.}, {7., 9., 12.}}, Key92 → {{12., 5.90742, 12.}, {6., 13., 12.}},
```

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```
Key93 → {{4., 9.30637, 12.}, {11., 12., 12.}}, Key94 → {{12., 4.2536, 8.}, {13., 18., 15.}},
Key95 → {{13., 5.90742, 9.}, {13., 15., 12.}}, Key96 → {{6., 5.90742, 10.}, {15., 8., 5.}},
Key97 → {{10., 5.90742, 11.}, {10., 17., 5.}}, Key98 → {{9., 8.84911, 7.}, {12., 8., 15.}},
Key99 → {{5., 4.2536, 19.}, {10., 13., 8.}}, Key100 → {{11., 3.03871, 10.}, {8., 7., 9.}}|>|>
```

HorizontalSelection (1)

```
In[1]:= Needs["MathIOmica`"]
```

For input data that is an association with multi-list values we need to set HorizontalSelection to True to be able to select across the keys the right list and component. Let's generate some random data first:

```
In[2]:= dataRandomAssociationsExample = AssociationThread@
  (("Key" <> ToString[#]) & /@ Range[100] → RandomVariate[PoissonDistribution[10], {100, 2, 3}])
```

```
Out[2]= <|Key1 → {{6, 10, 11}, {5, 8, 10}}, Key2 → {{6, 15, 8}, {8, 9, 10}},
 Key3 → {{9, 11, 5}, {13, 13, 4}}, Key4 → {{14, 10, 12}, {9, 11, 8}}, Key5 → {{8, 3, 14}, {17, 8, 8}},
 Key6 → {{10, 13, 9}, {12, 11, 14}}, Key7 → {{14, 12, 10}, {9, 14, 7}}, Key8 → {{8, 10, 8}, {10, 15, 9}},
 Key9 → {{11, 6, 9}, {8, 15, 11}}, Key10 → {{10, 9, 10}, {9, 5, 10}}, Key11 → {{11, 14, 10}, {5, 11, 9}},
 Key12 → {{13, 6, 5}, {11, 14, 8}}, Key13 → {{7, 11, 9}, {13, 7, 11}}, Key14 → {{9, 8, 7}, {10, 13, 9}},
 Key15 → {{11, 8, 10}, {15, 6, 6}}, Key16 → {{9, 6, 10}, {7, 11, 7}}, Key17 → {{5, 11, 12}, {9, 15, 14}},
 Key18 → {{13, 7, 6}, {12, 8, 10}}, Key19 → {{16, 12, 14}, {15, 10, 4}},
 Key20 → {{8, 8, 2}, {9, 10, 16}}, Key21 → {{13, 16, 12}, {10, 8, 5}}, Key22 → {{13, 11, 11}, {9, 4, 14}},
 Key23 → {{8, 5, 6}, {12, 9, 5}}, Key24 → {{13, 15, 11}, {8, 6, 13}}, Key25 → {{7, 11, 7}, {11, 7, 15}},
 Key26 → {{7, 10, 9}, {10, 11, 6}}, Key27 → {{7, 11, 9}, {8, 18, 10}}, Key28 → {{14, 5, 8}, {7, 9, 5}},
 Key29 → {{9, 11, 11}, {9, 12, 7}}, Key30 → {{16, 7, 6}, {4, 10, 8}}, Key31 → {{11, 13, 14}, {13, 10, 8}},
 Key32 → {{13, 14, 12}, {12, 5, 6}}, Key33 → {{14, 4, 10}, {6, 9, 12}}, Key34 → {{7, 9, 9}, {15, 13, 7}},
 Key35 → {{11, 6, 9}, {12, 4, 9}}, Key36 → {{11, 13, 7}, {8, 6, 14}}, Key37 → {{9, 8, 12}, {10, 11, 11}},
 Key38 → {{11, 11, 9}, {8, 10, 11}}, Key39 → {{9, 13, 9}, {15, 9, 8}}, Key40 → {{13, 13, 13}, {9, 11, 17}},
 Key41 → {{10, 8, 12}, {10, 7, 11}}, Key42 → {{10, 6, 9}, {10, 11, 6}}, Key43 → {{8, 10, 10}, {8, 10, 10}},
 Key44 → {{6, 8, 8}, {14, 15, 10}}, Key45 → {{10, 10, 9}, {10, 6, 7}}, Key46 → {{15, 9, 6}, {13, 10, 9}},
 Key47 → {{5, 7, 9}, {8, 9, 12}}, Key48 → {{15, 8, 6}, {6, 8, 6}}, Key49 → {{16, 8, 10}, {3, 12, 11}},
 Key50 → {{12, 5, 12}, {10, 8, 12}}, Key51 → {{7, 13, 7}, {10, 7, 5}}, Key52 → {{9, 11, 13}, {12, 10, 13}},
 Key53 → {{10, 11, 16}, {13, 13, 10}}, Key54 → {{8, 8, 16}, {12, 8, 12}}, Key55 → {{11, 12, 8}, {16, 8, 8}},
 Key56 → {{8, 12, 14}, {13, 10, 15}}, Key57 → {{12, 12, 9}, {12, 6, 13}}, Key58 → {{13, 11, 9}, {6, 9, 12}},
 Key59 → {{6, 5, 10}, {7, 11, 4}}, Key60 → {{6, 12, 10}, {8, 8, 6}}, Key61 → {{8, 15, 10}, {7, 7, 4}},
 Key62 → {{16, 15, 9}, {8, 12, 11}}, Key63 → {{8, 8, 10}, {12, 11, 12}}, Key64 → {{8, 10, 15}, {11, 10, 6}},
 Key65 → {{7, 11, 10}, {12, 10, 6}}, Key66 → {{6, 13, 9}, {13, 12, 14}}, Key67 → {{12, 7, 8}, {11, 10, 5}},
 Key68 → {{11, 13, 7}, {9, 14, 11}}, Key69 → {{10, 7, 9}, {6, 12, 11}}, Key70 → {{8, 7, 7}, {7, 8, 8}},
 Key71 → {{6, 11, 7}, {12, 7, 8}}, Key72 → {{10, 8, 14}, {14, 5, 13}}, Key73 → {{10, 5, 13}, {8, 4, 9}},
 Key74 → {{14, 11, 4}, {8, 8, 5}}, Key75 → {{11, 12, 13}, {6, 15, 9}}, Key76 → {{8, 12, 10}, {5, 7, 9}},
 Key77 → {{10, 13, 9}, {15, 6, 9}}, Key78 → {{11, 12, 12}, {11, 10, 9}}, Key79 → {{11, 13, 6}, {7, 12, 7}},
 Key80 → {{10, 5, 14}, {10, 8, 5}}, Key81 → {{8, 7, 12}, {12, 11, 9}}, Key82 → {{8, 7, 12}, {14, 12, 14}},
 Key83 → {{12, 13, 18}, {12, 15, 13}}, Key84 → {{13, 15, 4}, {10, 16, 5}}, Key85 → {{13, 13, 7}, {8, 7, 8}},
 Key86 → {{9, 13, 14}, {8, 12, 9}}, Key87 → {{11, 8, 7}, {7, 10, 10}}, Key88 → {{7, 8, 12}, {9, 7, 8}},
 Key89 → {{9, 17, 10}, {14, 10, 18}}, Key90 → {{7, 9, 9}, {10, 11, 6}}, Key91 → {{8, 9, 8}, {7, 10, 9}},
 Key92 → {{4, 18, 7}, {10, 6, 12}}, Key93 → {{12, 10, 13}, {7, 6, 8}}, Key94 → {{10, 14, 18}, {6, 7, 10}},
 Key95 → {{10, 9, 13}, {13, 16, 10}}, Key96 → {{6, 13, 4}, {8, 8, 14}}, Key97 → {{12, 7, 10}, {6, 6, 8}},
 Key98 → {{11, 8, 13}, {14, 6, 5}}, Key99 → {{9, 21, 11}, {15, 10, 4}}, Key100 → {{8, 8, 8}, {12, 8, 8}}|>
```

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In[3]:=
```
ApplyBoxCoxTransform[dataRandomAssociationsExample,
 ListIndex → 1, ComponentIndex → 1, HorizontalSelection → True]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = 0.505933

Out[3]=
```
<|Key1 → {{2.91673, 10., 11.}, {5., 8., 10.}}, Key2 → {{2.91673, 15., 8.}, {8., 9., 10.}},
 Key3 → {{4.0309, 11., 5.}, {13., 13., 4.}}, Key4 → {{5.53572, 10., 12.}, {9., 11., 8.}},
 Key5 → {{3.68337, 3., 14.}, {17., 8., 8.}}, Key6 → {{4.35982, 13., 9.}, {12., 11., 14.}},
 Key7 → {{5.53572, 12., 10.}, {9., 14., 7.}}, Key8 → {{3.68337, 10., 8.}, {10., 15., 9.}},
 Key9 → {{4.67285, 6., 9.}, {8., 15., 11.}}, Key10 → {{4.35982, 9., 10.}, {9., 5., 10.}},
 Key11 → {{4.67285, 14., 10.}, {5., 11., 9.}}, Key12 → {{5.25927, 6., 5.}, {11., 14., 8.}},
 Key13 → {{3.31363, 11., 9.}, {13., 7., 11.}}, Key14 → {{4.0309, 8., 7.}, {10., 13., 9.}},
 Key15 → {{4.67285, 8., 10.}, {15., 6., 6.}}, Key16 → {{4.0309, 6., 10.}, {7., 11., 7.}},
 Key17 → {{2.48555, 11., 12.}, {9., 15., 14.}}, Key18 → {{5.25927, 7., 6.}, {12., 8., 10.}},
 Key19 → {{6.06077, 12., 14.}, {15., 10., 4.}}, Key20 → {{3.68337, 8., 2.}, {9., 10., 16.}},
 Key21 → {{5.25927, 16., 12.}, {10., 8., 5.}}, Key22 → {{5.25927, 11., 11.}, {9., 4., 14.}},
 Key23 → {{3.68337, 5., 6.}, {12., 9., 5.}}, Key24 → {{5.25927, 15., 11.}, {8., 6., 13.}},
 Key25 → {{3.31363, 11., 7.}, {11., 7., 15.}}, Key26 → {{3.31363, 10., 9.}, {10., 11., 6.}},
 Key27 → {{3.31363, 11., 9.}, {8., 18., 10.}}, Key28 → {{5.53572, 5., 8.}, {7., 9., 5.}},
 Key29 → {{4.0309, 11., 11.}, {9., 12., 7.}}, Key30 → {{6.06077, 7., 6.}, {4., 10., 8.}},
 Key31 → {{4.67285, 13., 14.}, {13., 10., 8.}}, Key32 → {{5.25927, 14., 12.}, {12., 5., 6.}},
 Key33 → {{5.53572, 4., 10.}, {6., 9., 12.}}, Key34 → {{3.31363, 9., 9.}, {15., 13., 7.}},
 Key35 → {{4.67285, 6., 9.}, {12., 4., 9.}}, Key36 → {{4.67285, 13., 7.}, {8., 6., 14.}},
 Key37 → {{4.0309, 8., 12.}, {10., 11., 11.}}, Key38 → {{4.67285, 11., 9.}, {8., 10., 11.}},
 Key39 → {{4.0309, 13., 9.}, {15., 9., 8.}}, Key40 → {{5.25927, 13., 13.}, {9., 11., 17.}},
 Key41 → {{4.35982, 8., 12.}, {10., 7., 11.}}, Key42 → {{4.35982, 6., 9.}, {10., 11., 6.}},
 Key43 → {{3.68337, 10., 10.}, {8., 10., 10.}}, Key44 → {{2.91673, 8., 8.}, {14., 15., 10.}},
 Key45 → {{4.35982, 10., 9.}, {10., 6., 7.}}, Key46 → {{5.80257, 9., 6.}, {13., 10., 9.}},
 Key47 → {{2.48555, 7., 9.}, {8., 9., 12.}}, Key48 → {{5.80257, 8., 6.}, {6., 8., 6.}},
 Key49 → {{6.06077, 8., 10.}, {3., 12., 11.}}, Key50 → {{4.9721, 5., 12.}, {10., 8., 12.}},
 Key51 → {{3.31363, 13., 7.}, {10., 7., 5.}}, Key52 → {{4.0309, 11., 13.}, {12., 10., 13.}},
 Key53 → {{4.35982, 11., 16.}, {13., 13., 10.}}, Key54 → {{3.68337, 8., 16.}, {12., 8., 12.}},
 Key55 → {{4.67285, 12., 8.}, {16., 8., 8.}}, Key56 → {{3.68337, 12., 14.}, {13., 10., 15.}},
 Key57 → {{4.9721, 12., 9.}, {12., 6., 13.}}, Key58 → {{5.25927, 11., 9.}, {6., 9., 12.}},
 Key59 → {{2.91673, 5., 10.}, {7., 11., 4.}}, Key60 → {{2.91673, 12., 10.}, {8., 8., 6.}},
 Key61 → {{3.68337, 15., 10.}, {7., 7., 4.}}, Key62 → {{6.06077, 15., 9.}, {8., 12., 11.}},
 Key63 → {{3.68337, 8., 10.}, {12., 11., 12.}}, Key64 → {{3.68337, 10., 15.}, {11., 10., 6.}},
 Key65 → {{3.31363, 11., 10.}, {12., 10., 6.}}, Key66 → {{2.91673, 13., 9.}, {13., 12., 14.}},
 Key67 → {{4.9721, 7., 8.}, {11., 10., 5.}}, Key68 → {{4.67285, 13., 7.}, {9., 14., 11.}},
 Key69 → {{4.35982, 7., 9.}, {6., 12., 11.}}, Key70 → {{3.68337, 7., 7.}, {7., 8., 8.}},
 Key71 → {{2.91673, 11., 7.}, {12., 7., 8.}}, Key72 → {{4.35982, 8., 14.}, {14., 5., 13.}},
 Key73 → {{4.35982, 5., 13.}, {8., 4., 9.}}, Key74 → {{5.53572, 11., 4.}, {8., 8., 5.}},
 Key75 → {{4.67285, 12., 13.}, {6., 15., 9.}}, Key76 → {{3.68337, 12., 10.}, {5., 7., 9.}},
 Key77 → {{4.35982, 13., 9.}, {15., 6., 9.}}, Key78 → {{4.67285, 12., 12.}, {11., 10., 9.}},
 Key79 → {{4.67285, 13., 6.}, {7., 12., 7.}}, Key80 → {{4.35982, 5., 14.}, {10., 8., 5.}},
 Key81 → {{3.68337, 7., 12.}, {12., 11., 9.}}, Key82 → {{3.68337, 7., 12.}, {14., 12., 14.}},
 Key83 → {{4.9721, 13., 18.}, {12., 15., 13.}}, Key84 → {{5.25927, 15., 4.}, {10., 16., 5.}},
 Key85 → {{5.25927, 13., 7.}, {8., 7., 8.}}, Key86 → {{4.0309, 13., 14.}, {8., 12., 9.}},
 Key87 → {{4.67285, 8., 7.}, {7., 10., 10.}}, Key88 → {{3.31363, 8., 12.}, {9., 7., 8.}},
 Key89 → {{4.0309, 17., 10.}, {14., 10., 18.}}, Key90 → {{3.31363, 9., 9.}, {10., 11., 6.}},
 Key91 → {{3.68337, 9., 8.}, {7., 10., 9.}}, Key92 → {{2.00919, 18., 7.}, {10., 6., 12.}},
 Key93 → {{4.9721, 10., 13.}, {7., 6., 8.}}, Key94 → {{4.35982, 14., 18.}, {6., 7., 10.}},
 Key95 → {{4.35982, 9., 13.}, {13., 16., 10.}}, Key96 → {{2.91673, 13., 4.}, {8., 8., 14.}},
 Key97 → {{4.9721, 7., 10.}, {6., 6., 8.}}, Key98 → {{4.67285, 8., 13.}, {14., 6., 5.}},
 Key99 → {{4.0309, 21., 11.}, {15., 10., 4.}}, Key100 → {{3.68337, 8., 8.}, {12., 8., 8.}}|>
```

See Also

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Applier ▪ **ApplyBoxCoxTransformExtended** ▪ **BoxCoxTransform** ▪ **BoxCoxTransformExtended** ▪ **OmicsObject** ▪ **QuantileNormalization** ▪ **StandardizeExtended**

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- MathIOmica Guide

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- MathIOmicaGuide
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ApplyBoxCoxTransformExtended

`ApplyBoxCoxTransformExtended[data]`
for a given *data* set, computes the Box–Cox transformation at the maximum likelihood λ parameter.

Details

- `ApplyBoxCoxTransformExtended[data]` transforms the data (list, association or OmicsObject) by performing a two parameter (extended) Box-Cox transformation at the optimized parameter set $\hat{\lambda}=\{\hat{\lambda}_1, \hat{\lambda}_2\}$ namely the values for a two parameter Box-Cox transformation parameters λ_1, λ_2 for which the log-likelihood that the transformation is normally distributed is maximized. The two parameter transformation allows for negative values for the data. The objective is to transform a given input data set to be as normally distributed as possible, and thus, the function works by first calculating the transformation parameters $\hat{\lambda}_1, \hat{\lambda}_2$, at which the transformed data is as normally distributed as possible, and then outputting the Box-Cox transformation of the data at these parameters. The two parameter Box-Cox transformation is one possible procedure for standardizations of disparate data sets, along with other procedures (e.g. ApplyBoxCoxTransform, QuantileNormalization).
The Box-Cox transformation is a rank-preserving transformation that takes as input a (not necessarily normally distributed) dataset $X=\{X_1, X_2, \ldots, X_N\}$, and finds a functional transformation of the data that 'best' makes it (approximately) normally distributed. To be more precise, it is a well known result from estimation theory that for a given dataset, if one wishes to infer what are the most likely parameters of a normal distribution that could have generated the data, then the optimal estimators of the mean μ and variance σ^2 are $\hat{\mu}=\frac{1}{N}\sum_i X_i$ and $\hat{\sigma}^2=\frac{1}{N}\sum_i\left(X_i-\hat{\mu}\right)^2$, and the optimized log-likelihood is $\log(L(\hat{\mu},\hat{\sigma}^2))=\frac{-N}{2}(1+\log(2\pi\hat{\sigma}^2))$.

- The two parameter Box-Cox power transform is a function of two transformation parameter set $\lambda=\{\lambda_1, \lambda_2\}$ and is defined as
$X^{(\lambda)}=\log(X+\lambda_2)$ for $\lambda_1=0$ and $X^{(\lambda)}=\frac{(X+\lambda_2)^{\lambda_1}-1}{\lambda_1}$ for non – zero λ_1. Upon transforming the data in this fashion, the normal probability distribution $p(X)=\frac{1}{\sqrt{2\pi}\sigma}e^{-\frac{(x-\mu)^2}{2\sigma^2}}$ rewritten in terms of $X^{(\lambda)}$ must pick up an extra Jacobian factor $J(\lambda)$ to conserve total probability, $p\left(X^{(\lambda)}\right)=\frac{J(\lambda)}{\sqrt{2\pi}\sigma^{(\lambda)}}e^{\frac{-\left(x^{(\lambda)}-\mu^{(\lambda)}\right)^2}{2\left(\sigma^{(\lambda)}\right)^2}}$.
The value of this Jacobian factor is $J(\lambda)=\prod_i\left|\frac{dX_i^{(\lambda)}}{dX}\right|$. Explicitly, $\log(L(\lambda,\hat{\mu}^{(\lambda)},(\hat{\sigma}^{(\lambda)})^2))=\frac{-N}{2}(1+\log(2\pi(\hat{\sigma}^{(\lambda)})^2))+\log(J(\lambda))=\frac{-N}{2}(1+\log(2\pi(\hat{\sigma}^{(\lambda)})^2))+(\lambda_1-1)\sum_i\log(X_i+\lambda_2)$.
Thus, to normalize a dataset $X=\{X_1, X_2, \ldots, X_N\}$ via a Box-Cox transformation, one must maximize $\log(L(\lambda,\hat{\mu}^{(\lambda)},(\hat{\sigma}^{(\lambda)})^2))$ for the given X, and this gives one the optimized transformation exponent $\hat{\lambda}_1$ and shift parameter $\hat{\lambda}_2$.
In the case of an Association or OmicsObject input the ApplyBoxCoxTransform returns the same object as its input with the new values of the data at the specified position. The selection of the position is performed using the options for the function that are internally passed to Applier and Returner.
The following options can be given:

ComponentIndex	Missing[]	Selection of which component of a list to use in the association or OmicsObject input values.
HorizontalSelection	False	Horizontal selection across components for a single level association with multi–list values.
ListIndex	Missing[]	Selection of which list to use in the association or OmicsObject input values.

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SearchMaxFactor	1	Scaling factor to extend the search range maximum in the optimization to be more than the data range search maximum r_{max} (defined as $r_{max} = \text{Max}[\text{Abs}[inputDataMaximum], \text{Abs}[inputDataMinimum]]$)

Examples (9)

Basic Examples (5)

First we need to load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

Application to an OmicsObject (1)

Let's import the example protein data. These are located at:

```
In[1]:= proteinExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinExample"}
```

We can now get the data:

```
In[2]:= proteinExampleData = Get[proteinExampleFile];
```

Let' s query the first 5 proteins across all datasets for this OmicsObject:

```
In[3]:= proteinSubset = Query[All, 1 ;; 5]@proteinExampleData

Out[3]= <|7 → <|{A0AVT1, Protein} → {{0.937}, {17}},
    {A0FGR8, Protein} → {{1.073}, {24}}, {A0MZ66, Protein} → {{1.059}, {9}},
    {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}}|>,
  9 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}},
```

We perform a Box-Cox transformation. The function will calculate and display the progress across datasets, and also output the optimized $\hat{\lambda}$ parameter set:

```
In[4]:= proteinExampleBoxCoxTransformedExtended =
         ApplyBoxCoxTransformExtended[proteinExampleData, ListIndex → 1, ComponentIndex → 1]
```

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```
Calculated Box-Cox parameter λ̂ = {-7.39307, 5.651}
Calculated Box-Cox parameter λ̂ = {-4.63235, 4.146}
Calculated Box-Cox parameter λ̂ = {-5.8265, 3.432}
Calculated Box-Cox parameter λ̂ = {-8.25084, 6.906}
Calculated Box-Cox parameter λ̂ = {-6.027, 3.997}
Calculated Box-Cox parameter λ̂ = {-2.69152, 4.543}
Calculated Box-Cox parameter λ̂ = {-0.31183, 0.958071}
Calculated Box-Cox parameter λ̂ = {-2.82949, 3.80047}
Calculated Box-Cox parameter λ̂ = {-3.29425, 3.727}
Calculated Box-Cox parameter λ̂ = {-5.03963, 6.44}
Calculated Box-Cox parameter λ̂ = {-6.61127, 8.256}
Calculated Box-Cox parameter λ̂ = {-7.56888, 6.281}
Calculated Box-Cox parameter λ̂ = {-7.84288, 6.665}
```

Out[4]=

```
<|7 → <|{A0AVT1, Protein} → {{0.135262}, {17.}}, {A0FGR8, Protein} → {{0.135262}, {24.}},
   ··· 5221 ···, {Q9Y6I9, Protein} → Missing[], {Q9Y6X3, Protein} → Missing[]|>,
 9 → <| ··· 1 ··· |>, ··· 9 ···, 20 → <| ··· 1 ··· |>, 21 → <| ··· 1 ··· |>|>
```

large output | show less | show more | show all | set size limit...

In[5]:=

```
Query[Key["20"]]@proteinExampleBoxCoxTransformedExtended
```

Out[5]=

```
<|{A0AVT1, Protein} → {{0.13212}, {16.}}, {A0FGR8, Protein} → {{0.13212}, {22.}},
 ··· 5221 ···, {Q9Y6I9, Protein} → {{0.13212}, {5.}}, {Q9Y6X3, Protein} → Missing[]|>
```

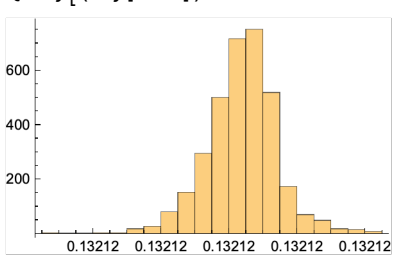
large output | show less | show more | show all | set size limit...

Let's plot the distribution of the set with Key "20" as an example:

In[6]:=

```
Query[(Key["20"]) /* Values /* Flatten /* Histogram, All, 1]@proteinExampleBoxCoxTransformedExtended
```

Out[6]=



Application to Associations, Single List Values (1)

Let's generate some random data.

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In[1]:=
```
dataRandomAssociationExample =
 AssociationThread[Range[5] → RandomVariate[PoissonDistribution[10], {5, 100}]]
```

Out[1]=
```
<|1 → {9, 9, 7, 12, 12, 7, 6, 11, 5, 12, 14, 13, 11, 11, 12, 16, 8, 8, 9, 10, 13, 10, 12,
   13, 5, 12, 12, 15, 9, 14, 11, 12, 7, 3, 11, 16, 9, 10, 17, 6, 10, 11, 11, 9, 11, 8, 11, 15,
   5, 12, 15, 9, 12, 12, 9, 13, 16, 17, 10, 15, 8, 5, 8, 5, 15, 11, 8, 15, 10, 9, 10, 11, 6, 8,
   5, 4, 8, 10, 12, 8, 11, 14, 7, 15, 8, 17, 14, 10, 7, 18, 9, 9, 17, 16, 6, 19, 14, 14, 7, 8},
 2 → {9, 11, 7, 5, 11, 5, 9, 5, 11, 14, 11, 7, 13, 13, 3, 7, 8, 11, 6, 9, 10, 13, 11, 17, 9, 12,
   9, 6, 12, 6, 5, 8, 10, 7, 6, 10, 8, 13, 10, 13, 5, 10, 14, 8, 4, 13, 10, 14, 6, 6, 8, 16,
   9, 6, 9, 10, 7, 8, 14, 14, 6, 10, 10, 6, 10, 9, 11, 11, 11, 13, 12, 12, 10, 14, 7, 7,
   11, 14, 11, 5, 12, 13, 10, 8, 11, 6, 10, 10, 16, 8, 15, 5, 10, 9, 11, 14, 6, 10, 7, 8},
 3 → {5, 11, 8, 11, 5, 3, 11, 11, 9, 13, 9, 10, 10, 11, 14, 11, 11, 9, 5, 9, 8, 9, 11, 9, 10, 5,
   9, 15, 5, 9, 18, 10, 10, 10, 10, 4, 12, 8, 11, 8, 12, 10, 15, 9, 8, 8, 11, 7, 7, 10, 5,
   6, 10, 13, 13, 13, 10, 8, 11, 11, 6, 9, 13, 13, 6, 16, 7, 17, 9, 9, 4, 13, 7, 12, 10, 11,
   10, 9, 8, 14, 12, 11, 12, 8, 17, 13, 9, 16, 14, 13, 9, 11, 12, 12, 8, 11, 14, 17, 6, 9},
 4 → {7, 4, 5, 11, 7, 7, 18, 9, 19, 7, 12, 9, 12, 9, 5, 6, 13, 10, 11, 9, 10, 8, 9, 11, 19, 13,
   8, 7, 10, 17, 5, 8, 8, 10, 10, 7, 13, 6, 13, 9, 10, 11, 8, 11, 14, 14, 11, 10, 17, 10,
   8, 10, 11, 6, 14, 10, 8, 10, 12, 5, 9, 6, 10, 9, 9, 12, 9, 11, 15, 11, 8, 11, 6, 17, 8,
   9, 10, 7, 11, 11, 8, 12, 6, 7, 11, 10, 8, 15, 7, 13, 10, 8, 14, 8, 9, 9, 7, 10, 6, 6},
 5 → {11, 9, 8, 5, 8, 13, 12, 8, 16, 9, 8, 10, 9, 7, 13, 6, 18, 10, 5, 16, 9, 11, 6, 12, 11, 4,
   12, 11, 8, 7, 11, 17, 11, 11, 9, 9, 12, 14, 7, 8, 6, 10, 8, 9, 10, 7, 9, 8, 8, 9, 13,
   12, 11, 5, 7, 7, 10, 10, 5, 10, 9, 16, 4, 7, 5, 7, 9, 15, 6, 14, 8, 7, 7, 12, 11, 17,
   8, 9, 10, 5, 11, 5, 7, 12, 6, 10, 9, 13, 9, 13, 10, 10, 11, 8, 12, 11, 16, 10, 7, 11}|>
```

Let' s perform now a Box-Cox transformation. The function will calculate and display the progress across datasets, and also output the optimized $\hat{\lambda}$ for each set in order:

In[2]:=
```
dataRandomAssociationExampleBoxCoxTransformedExtended =
 ApplyBoxCoxTransformExtended[dataRandomAssociationExample]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.483813, -3.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.474996, -3.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.516866, -3.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.416067, -4.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.394766, -4.}

Out[2]=
```
<|1 → {2.85124, 2.85124, 1.97518, 3.91717, 3.91717, 1.97518, 1.44998, 3.5857,
   0.823531, 3.91717, 4.52728, 4.23011, 3.5857, 3.5857, 3.91717, 5.08237,
   2.436, 2.436, 2.85124, 3.23206, 4.23011, 3.23206, 3.91717, 4.23011,
   0.823531, 3.91717, 3.91717, 4.8108, 2.85124, 4.52728, 3.5857, 3.91717,
```

Application to an Association of Multi-List Values (1)

Let's generate some random data.

In[1]:=
```
dataRandomAssociationsExample = AssociationThread@
  (("Key" <> ToString[#]) & /@ Range[100] → RandomVariate[PoissonDistribution[10], {100, 2, 3}])
```

Out[1]=
```
<|Key1 → {{8, 6, 7}, {11, 6, 15}}, Key2 → {{15, 8, 12}, {11, 9, 13}},
 Key3 → {{11, 16, 5}, {13, 9, 8}}, Key4 → {{12, 7, 15}, {9, 9, 7}},
 Key5 → {{17, 3, 7}, {8, 13, 9}}, Key6 → {{22, 15, 6}, {19, 14, 8}},
 Key7 → {{4, 13, 13}, {9, 6, 11}}, Key8 → {{10, 10, 7}, {9, 15, 5}},
```

Let' s perform again a Box-Cox transformation. The function will calculate and display the progress across datasets, and also output the optimized $\hat{\lambda}$ parameter set. As this is a single association, we set HorizontalSelection option to True to be able to select horizontally from

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the lists across Keys (see also Applier)

In[2]:=
```
dataRandomAssociationsExampleTransformedExteded = ApplyBoxCoxTransformExtended[
  dataRandomAssociationsExample, ListIndex → 1, ComponentIndex → 1, HorizontalSelection → True]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = {-0.0462923, 12.2121}

Out[2]=
```
<|Key1 → {{2.80647, 6., 7.}, {11., 6., 15.}},
 Key2 → {{3.06344, 8., 12.}, {11., 9., 13.}},
 Key3 → {{2.9265, 16., 5.}, {13., 9., 8.}},
 Key4 → {{2.96292, 7., 15.}, {9., 9., 7.}}, Key5 → {{3.1242, 3., 7.}, {8., 13., 9.}},
```

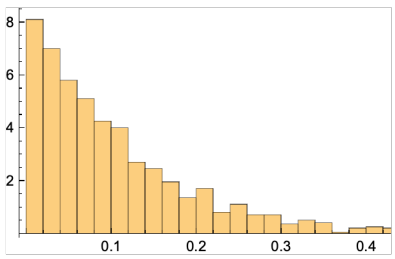
Application to a List (1)

We generate data from an exponential distribution that we can use.

In[1]:=
```
dataRandomExample=RandomVariate[ExponentialDistribution[10],1000];
```

In[2]:=
```
Histogram[dataRandomExample, Automatic, "ProbabilityDensity"]
```

Out[2]=



The calculation below may take some time depending on the data length and complexity.

In[3]:=
```
dataRandomExampleBoxCoxExtended = ApplyBoxCoxTransformExtended[dataRandomExample]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.298346, -0.0000434025}

Out[3]=
```
{-2.70404, -2.54095, -1.9422, -2.5082, -2.16529, -2.62848, -1.47427, -1.5534, -1.27724, -1.77338, -2.45513,
 -2.49761, -1.66321, -1.77204, -2.32092, -1.21809, -1.36693, -2.28422, -3.0316, -1.99376, -1.97305,
 -1.68225, -1.39514, -1.79012, -1.9753, -2.24413, -2.18685, -2.33718, -1.75308, -1.2394, -1.82694,
 -1.63595, -1.43369, -1.74809, -2.095, -1.80192, -1.22599, -1.56927, -1.3736, -1.7179, -2.00862,
 -1.5823, -2.11234, -2.74515, -1.4827, -2.70674, -0.833481, -1.66988, -2.1007, -2.24339, -2.56896,
 -2.20357, -1.47491, -2.09507, -1.08964, -1.76466, -2.24201, -0.905917, -1.28339, -1.7758, -1.13073,
 -2.09369, -1.49569, -2.18988, -1.90174, -1.38557, -1.84899, -2.52882, -3.05945, -2.10936, -2.23791,
 -1.25851, -1.57517, -1.34632, -1.96545, -1.16034, -0.961575, -1.47332, -1.14964, -1.32886, -1.45052,
 -2.09821, -1.47388, -1.45054, -2.03985, -1.74921, -1.80972, -2.18234, -1.625, -1.74903, -1.96611,
 -1.27148, -1.89922, -1.18618, -2.06474, -2.2649, -1.58369, -2.34983, -1.99027, -2.78274, -1.82736,
 -1.64636, -2.08263, -1.82302, -2.1375, -1.90727, -2.46733, -1.90228, -2.29784, -1.81097, -2.10056,
 -2.23906, -1.03404, -2.40743, -2.34982, -1.20409, -1.98275, -0.73497, -1.95313, -1.91256, -1.77993,
 -1.44972, -1.57363, -1.97255, -1.42528, -1.69473, -1.04078, -2.06595, -1.12617, -2.31319, -1.5099,
 -0.95604, -1.6328, -0.907855, -1.09033, -2.34772, -1.85369, -2.0677, -1.93259, -1.1534, -1.51873,
 -2.45488, -2.60695, -1.31454, -1.42732, -1.42714, -1.66884, -1.84488, -1.32246, -1.71912, -1.43261,
 -1.51221, -1.34305, -2.49341, -2.46205, -1.84664, -1.31035, -2.28844, -2.15341, -1.58931, -2.40829,
 -1.58077, -1.37235, -1.2396, -1.80787, -1.67121, -1.50279, -1.5635, -2.97131, -1.47333, -2.50654,
 -2.11793, -1.74967, -1.32221, -1.20247, -1.54167, -2.64677, -2.24287, -1.75847, -1.6369, -2.27326,
 -1.89644, -1.77851, -2.22535, -2.0553, -2.04737, -1.29378, -1.62166, -1.73299, -1.43048, -1.38953,
 -1.7558, -1.60029, -2.67615, -1.63719, -2.03569, -1.81084, -1.59069, -2.0447, -1.14499, -1.57569,
 -1.44239, -1.59083, -0.790805, -1.65477, -1.2181, -1.6324, -2.03154, -2.4066, -2.16072, -1.16524,
 -1.77155, -1.13894, -1.3174, -2.30555, -1.14616, -1.09735, -1.21246, -1.1092, -1.94819, -1.70817,
 -1.12407, -2.07581, -1.93461, -1.99639, -1.64763, -1.67799, -2.39556, -2.14078, -2.32207, -2.07986,
 -1.0811, -1.66793, -1.2361, -2.02986, -1.42631, -1.01429, -2.10298, -2.79338, -1.01581, -1.86491,
 -1.66177, -1.9163, -1.07945, -1.25359, -1.77748, -2.41329, -1.86067, -2.25904, -1.96386, -2.48368,
 -1.48377, -1.40079, -1.6336, -1.15851, -1.85175, -2.10754, -1.59994, -2.32387, -0.960073, -0.738731,
 -1.4203, -1.27306, -1.39744, -2.03094, -1.34355, -2.19272, -1.90603, -1.7534, -2.10997, -1.67995,
```

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-3.35181, -1.41477, -1.45831, -1.67366, -1.9714, -1.66325, -1.74641, -1.77139, -1.81866, -1.79172,
-1.35907, -1.85613, -1.63966, -1.71385, -2.13264, -1.81404, -1.55885, -2.24858, -1.88063, -1.81457,
-0.771463, -2.03211, -1.961, -2.4523, -1.78227, -2.13033, -2.063, -2.53381, -0.978717, -1.59118,
-1.86798, -1.87353, -1.40971, -1.84425, -2.52714, -2.3428, -2.33621, -1.58558, -1.83647, -1.4359,
-2.25352, -1.29382, -2.20939, -1.2809, -1.77512, -1.54833, -1.69008, -2.11719, -1.96723, -2.10686,
-2.04387, -2.57541, -2.2271, -2.01877, -1.56828, -1.47113, -1.11515, -1.32889, -1.78561, -1.91121,
-2.29788, -1.86369, -2.20375, -2.35333, -2.08881, -1.17975, -1.61819, -2.21861, -2.06449, -1.6517,
-1.92381, -0.678124, -1.41496, -1.61289, -2.09017, -1.57482, -1.4547, -1.25568, -1.57674, -1.24657,
-1.9465, -1.12676, -1.5514, -1.90559, -1.9317, -1.44904, -1.3698, -2.40329, -1.37949, -1.13317,
-0.685664, -2.05269, -1.4749, -1.22681, -2.01435, -1.68771, -2.52566, -1.5227, -1.5321, -1.8224,
-1.66545, -2.52141, -1.98125, -2.60279, -2.69133, -1.06297, -2.2393, -1.40585, -1.94296, -2.67113,
-2.00144, -2.39364, -2.00871, -1.22606, -2.14213, -1.05128, -2.26735, -2.60491, -2.58386, -1.64609,
-1.90729, -2.05513, -1.29184, -2.33233, -1.91412, -1.8815, -1.2492, -1.97654, -0.440025, -1.73383,
-1.22523, -0.912263, -1.73364, -2.30366, -1.89932, -1.7565, -1.14764, -1.79699, -1.95858, -1.25992,
-1.6707, -2.36879, -2.62881, -1.80352, -1.82522, -1.15502, -1.21252, -1.3765, -1.61077, -2.78109,
-1.35544, -2.71704, -1.5466, -1.61578, -2.16294, -0.946669, -2.737, -0.80319, -1.76584, -1.59586,
-2.15074, -2.51069, -1.05861, -1.46375, -2.60025, -1.1105, -1.91454, -1.9794, -1.92178, -1.25828,
-2.09404, -1.71439, -2.02072, -1.59247, -2.33816, -1.46122, -1.98201, -1.80152, -1.28023, -2.27959,
-1.01516, -2.76887, -2.17572, -2.15219, -2.00601, -2.28292, -2.40644, -1.73446, -2.75678, -1.26317,
-1.37664, -1.58311, -1.7446, -2.36435, -1.50045, -2.07139, -2.51307, -1.83653, -2.33499, -1.38028,
-1.19646, -2.23409, -1.89006, -2.21398, -2.06236, -0.952178, -0.760686, -1.86021, -2.38158, -2.25518,
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-1.22187, -1.51186, -3.0036, -2.33534, -2.63095, -2.14093, -2.92088, -1.55147, -1.86256, -1.22289,
-2.99769, -2.23531, -1.84349, -1.50418, -0.881021, -2.07189, -1.52901, -2.4179, -1.17651, -2.31777,
-2.24832, -2.71079, -1.71937, -1.47463, -2.48971, -2.51211, -2.70556, -2.25016, -2.82486, -1.54906,
-2.32065, -1.68705, -1.68182, -0.879855, -1.03262, -1.57771, -2.02967, -2.131, -1.38428, -2.32053,
-1.68532, -2.56225, -0.993183, -1.5543, -2.20823, -1.60822, -2.07349, -2.50267, -1.42659, -0.979431,
-1.90348, -1.32348, -2.28511, -2.02997, -2.2883, -1.3098, -1.84718, -1.80455, -1.79159, -2.24414,
-1.6638, -0.97807, -2.22765, -2.51919, -1.71155, -2.51752, -1.50789, -2.18096, -1.59144, -1.62535,
-2.38799, -2.00367, -1.28816, -2.2123, -2.03247, -1.12843, -1.67341, -0.942081, -1.40351, -2.44933,
-1.73692, -0.776005, -1.33999, -2.61554, -1.43655, -1.72215, -0.890532, -2.06088, -1.33479, -1.53841,
-1.67379, -1.52839, -1.38886, -1.81588, -1.40034, -1.54653, -0.82605, -1.17372, -2.3676, -2.24207,
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-1.90938, -1.23777, -1.42616, -1.74342, -1.62862, -1.89402, -1.82509, -1.98901, -1.72052, -2.13142,
-1.8531, -1.77464, -0.89438, -1.34064, -2.97943, -2.06088, -2.283, -1.62832, -1.98889, -2.65586,
-1.57692, -0.816506, -1.09137, -1.50223, -2.56562, -2.14279, -1.85969, -1.21982, -0.997932, -1.19049,
-1.77545, -1.91892, -2.41767, -1.0669, -1.98495, -2.75692, -1.99947, -1.9122, -2.11787, -2.34712,
-2.11958, -1.60121, -1.44922, -1.7386, -1.78575, -1.93061, -2.45043, -1.64819, -1.93971, -1.86094,
-1.83198, -2.026, -1.72394, -1.94674, -1.56997, -1.93548, -2.11941, -1.8931, -1.54631, -1.49744,
-1.59022, -2.31927, -1.71065, -1.60882, -1.81411, -2.74276, -2.08644, -1.81269, -2.46841, -1.69387,
-2.34891, -1.25863, -0.960703, -1.90691, -1.65528, -1.86853, -1.26913, -2.55408, -2.19073, -2.14271,
-1.95179, -2.11967, -1.61746, -2.17856, -1.23958, -1.64487, -2.16623, -1.76109, -2.14018, -2.06297,
-0.441246, -2.15547, -2.20464, -0.800321, -2.08032, -1.76872, -1.24881, -0.915599, -1.2872, -1.34963,
-2.25639, -1.82377, -2.21715, -2.03158, -1.75027, -2.39405, -2.31336, -1.27088, -2.18534, -1.86915,
-2.32538, -2.05908, -1.11411, -1.61291, -2.44744, -2.65577, -2.22272, -2.4586, -2.11412, -2.47001,
-2.14068, -0.777916, -1.53812, -0.669654, -1.50793, -1.87598, -0.964391, -2.10555, -2.39278,
-1.05449, -1.96871, -2.38336, -2.4133, -1.58055, -1.51965, -3.04546, -1.05269, -1.83735, -2.287,
-2.09541, -1.3774, -1.12975, -1.44417, -1.36358, -1.60813, -1.85438, -1.85637, -2.21794, -2.77029,
-1.74553, -2.16615, -1.81496, -1.75597, -2.82403, -1.36505, -1.32681, -2.97938, -2.33521, -2.56432,
-1.76948, -2.45043, -1.43149, -1.7841, -2.16523, -1.26282, -1.82131, -0.940498, -0.945186, -1.41468,
-2.92554, -1.39837, -2.59391, -1.80104, -1.35353, -2.38355, -1.85575, -1.02298, -0.75333, -1.79317,
-1.6578, -1.35671, -1.40185, -1.49097, -2.50991, -1.08256, -1.72938, -1.56363, -1.64879, -1.0488,
-2.23724, -1.98465, -2.88596, -1.96836, -1.88276, -2.35239, -2.43545, -1.45479, -2.69935, -2.12006,
-2.19666, -1.54292, -2.5629, -1.62741, -2.28399, -1.61377, -1.67015, -1.53652, -1.64696, -1.73425,
-1.89881, -1.80067, -1.48435, -1.93934, -2.27832, -1.48894, -2.04881, -2.19742, -1.26167, -1.23984,
-1.48905, -1.56409, -1.35492, -1.38578, -1.98521, -1.75598, -1.26906, -1.06515, -1.45635, -1.43559,
-2.09302, -1.55685, -1.43193, -1.71509, -1.96346, -1.92242, -1.60852, -1.62966, -2.4325, -1.55378,
-1.80318, -2.22488, -2.72336, -1.95861, -1.85809, -1.83786, -1.33509, -1.71173, -2.05733, -1.59936,
-1.74228, -1.43743, -1.37235, -1.62742, -1.99106, -1.7149, -2.10285, -1.57561, -1.44073, -2.31098,
-1.54796, -1.95836, -1.97152, -2.24802, -1.84927, -1.57045, -1.90213, -1.76732, -1.72587, -2.09018,
-1.60291, -2.74004, -2.30544, -1.92556, -1.98699, -1.48075, -2.79529, -1.35789, -1.31858, -1.99607,
-1.7618, -1.62378, -3.2908, -2.02436, -1.85305, -2.26355, -1.59708, -1.56971, -1.1867, -2.28602,
-2.882, -2.25193, -1.90356, -1.67332, -2.76532, -2.18753, -1.77137, -2.43501, -2.62122, -1.89444,
-2.49691, -2.1634, -2.0327, -1.48979, -2.03992, -1.9652, -2.08679, -1.60076, -1.01573, -1.33412,
-1.16998, -1.60089, -1.37451, -2.43892, -1.09681, -1.45387, -1.61877, -2.02215, -2.26208, -0.650191,
-1.06515, -1.84575, -2.63791, -1.12372, -2.07624, -2.43109, -2.76973, -1.79121, -1.77138, -1.29541,

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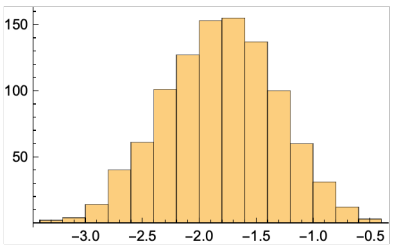
```
-2.89706, -2.69796, -1.28861, -1.6996, -1.22539, -2.42361, -2.29614, -1.17291, -2.01108, -1.66136,
-2.07761, -1.38814, -1.7404, -1.6951, -1.08354, -1.74944, -1.82922, -2.80731, -1.55836, -2.51488,
-2.43594, -1.97751, -1.99961, -1.85326, -2.29915, -1.44959, -2.10139, -2.54174, -0.883774, -1.69162,
-1.1397, -1.89253, -2.37164, -1.13885, -2.78909, -1.25303, -2.0739, -2.33299, -1.86426, -1.676,
-1.6409, -2.03989, -2.92442, -0.991386, -1.47603, -2.06533, -1.57763, -2.73867, -2.21645, -1.68501,
-1.41193, -0.975847, -1.56987, -2.03539, -1.25857, -2.97077, -2.06538, -1.54052, -1.85287, -1.7214,
-2.07194, -2.37422, -1.50071, -1.57469, -1.92558, -1.53248, -2.46412, -1.77839, -1.36227, -2.39417}
```

The transformed data Histogram looks like:

In[4]:=
```
Histogram[dataRandomExampleBoxCoxExtended]
```

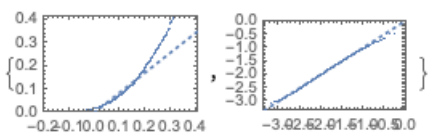
Out[4]=



Here is a Q-Q plot of the quantiles of the data before and after the transformation:

In[5]:=
```
{QuantilePlot[dataRandomExample], QuantilePlot[dataRandomExampleBoxCoxExtended]}
```

Out[5]=



Options (4)

ListIndex (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ListIndex allows selection of a list if the input data is an OmicsObject or other association with multi - list values. We generate below a random OmicsObject using also random data as metadata

In[2]:=
```
dataRandomOmicsObject = OmicsObjectCreator[{"Sample1", "Sample2", "Sample3"},
   ConstantArray[("Key" <> ToString[#]) & /@ Range[100], 3], RandomVariate[
    PoissonDistribution[10], {3, 100, 3}], RandomVariate[PoissonDistribution[10], {3, 100, 3}]];
```

Let's look at the first few keys to see the structure:

In[3]:=
```
Query[All, 1 ;; 5]@dataRandomOmicsObject
```

Out[3]=
```
<|Sample1 → <|Key1 → {{8, 7, 11}, {11, 8, 13}}, Key2 → {{10, 8, 11}, {7, 16, 13}},
   Key3 → {{10, 11, 14}, {10, 9, 12}}, Key4 → {{8, 13, 9}, {9, 12, 12}}, Key5 → {{8, 7, 9}, {12, 11, 9}}|>,
 Sample2 → <|Key1 → {{9, 10, 12}, {6, 11, 14}}, Key2 → {{10, 10, 14}, {12, 10, 13}},
   Key3 → {{16, 7, 12}, {14, 14, 4}}, Key4 → {{8, 12, 10}, {7, 15, 9}}, Key5 → {{10, 4, 7}, {9, 9, 13}}|>,
 Sample3 → <|Key1 → {{6, 12, 9}, {8, 10, 14}}, Key2 → {{8, 10, 8}, {8, 6, 11}},
   Key3 → {{13, 7, 14}, {10, 5, 10}}, Key4 → {{11, 8, 11}, {10, 12, 10}}, Key5 → {{12, 12, 10}, {13, 8, 12}}|>|>
```

We can perform the optimized Box Cox Transform on values from the first list, first

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component:

In[4]:=
```
ApplyBoxCoxTransformExtended[dataRandomOmicsObject, ListIndex → 1, ComponentIndex → 1]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = {-1.48904, 23.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {-0.398217, 20.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.452377, -4.}

Out[4]=
```
<|Sample1 → <|Key1 → {{0.667533, 7., 11.}, {11., 8., 13.}}, Key2 → {{0.667892, 8., 11.}, {7., 16., 13.}},
  Key3 → {{0.667892, 11., 14.}, {10., 9., 12.}}, Key4 → {{0.667533, 13., 9.}, {9., 12., 12.}},
  Key5 → {{0.667533, 7., 9.}, {12., 11., 9.}}, Key6 → {{0.668201, 12., 4.}, {5., 3., 9.}},
  Key7 → {{0.668201, 7., 9.}, {11., 14., 10.}}, Key8 → {{0.667719, 11., 10.}, {11., 9., 11.}},
  Key9 → {{0.668339, 9., 11.}, {4., 12., 6.}}, Key10 → {{0.668589, 11., 10.}, {14., 9., 3.}},
  Key11 → {{0.667892, 9., 14.}, {8., 12., 10.}}, Key12 → {{0.668052, 8., 7.}, {16., 16., 9.}},
  Key13 → {{0.667719, 8., 15.}, {10., 5., 5.}}, Key14 → {{0.667719, 9., 14.}, {9., 7., 12.}},
  Key15 → {{0.667892, 9., 9.}, {7., 7., 9.}}, Key16 → {{0.667533, 17., 13.}, {18., 8., 11.}},
  Key17 → {{0.668052, 6., 16.}, {10., 8., 14.}}, Key18 → {{0.667719, 11., 10.}, {8., 9., 13.}},
  Key19 → {{0.667719, 6., 10.}, {13., 7., 13.}}, Key20 → {{0.668052, 12., 16.}, {13., 5., 5.}},
  Key21 → {{0.668201, 12., 8.}, {5., 11., 5.}}, Key22 → {{0.667111, 12., 8.}, {6., 8., 10.}},
  Key23 → {{0.668469, 13., 8.}, {9., 10., 13.}}, Key24 → {{0.667533, 6., 10.}, {6., 4., 8.}},
  Key25 → {{0.668201, 17., 6.}, {11., 20., 6.}}, Key26 → {{0.667111, 10., 6.}, {10., 10., 8.}},
  Key27 → {{0.668052, 11., 12.}, {4., 12., 12.}}, Key28 → {{0.666323, 14., 8.}, {12., 9., 12.}},
  Key29 → {{0.667719, 7., 10.}, {7., 13., 11.}}, Key30 → {{0.668201, 8., 14.}, {16., 13., 17.}},
  Key31 → {{0.668339, 8., 14.}, {8., 7., 8.}}, Key32 → {{0.667719, 8., 7.}, {7., 9., 11.}},
  Key33 → {{0.667719, 6., 8.}, {10., 16., 6.}}, Key34 → {{0.667331, 8., 7.}, {10., 8., 10.}},
  Key35 → {{0.667719, 14., 14.}, {10., 7., 8.}}, Key36 → {{0.667719, 10., 8.}, {11., 5., 7.}},
  Key37 → {{0.669328, 17., 12.}, {15., 9., 9.}}, Key38 → {{0.667331, 9., 14.}, {5., 15., 9.}},
  Key39 → {{0.668589, 16., 10.}, {11., 10., 11.}}, Key40 → {{0.668052, 8., 13.}, {8., 10., 10.}},
  Key41 → {{0.668589, 9., 9.}, {11., 7., 11.}}, Key42 → {{0.667533, 9., 5.}, {12., 17., 17.}},
  Key43 → {{0.667533, 6., 11.}, {11., 8., 5.}}, Key44 → {{0.667719, 10., 8.}, {10., 9., 9.}},
  Key45 → {{0.668052, 9., 11.}, {9., 14., 5.}}, Key46 → {{0.668469, 7., 8.}, {15., 8., 9.}},
  Key47 → {{0.667719, 8., 5.}, {10., 7., 12.}}, Key48 → {{0.667331, 6., 6.}, {10., 12., 11.}},
  Key49 → {{0.667719, 7., 7.}, {10., 11., 10.}}, Key50 → {{0.668339, 9., 10.}, {12., 11., 8.}},
  Key51 → {{0.667719, 9., 19.}, {12., 5., 13.}}, Key52 → {{0.668201, 16., 11.}, {8., 15., 7.}},
  Key53 → {{0.667719, 8., 15.}, {16., 9., 7.}}, Key54 → {{0.667331, 10., 12.}, {7., 11., 9.}},
  Key55 → {{0.668201, 10., 13.}, {9., 12., 6.}}, Key56 → {{0.667892, 11., 10.}, {10., 7., 15.}},
  Key57 → {{0.667111, 12., 14.}, {6., 8., 9.}}, Key58 → {{0.668201, 7., 8.}, {13., 8., 6.}},
  Key59 → {{0.668469, 9., 8.}, {11., 11., 12.}}, Key60 → {{0.668469, 7., 7.}, {9., 12., 5.}},
  Key61 → {{0.667892, 10., 7.}, {5., 11., 11.}}, Key62 → {{0.667533, 6., 5.}, {15., 13., 11.}},
  Key63 → {{0.667892, 13., 10.}, {14., 8., 14.}}, Key64 → {{0.667331, 8., 7.}, {13., 10., 19.}},
  Key65 → {{0.668339, 9., 5.}, {5., 11., 6.}}, Key66 → {{0.669175, 12., 8.}, {7., 13., 8.}},
  Key67 → {{0.667533, 15., 8.}, {9., 5., 10.}}, Key68 → {{0.667892, 10., 7.}, {13., 5., 13.}},
  Key69 → {{0.667331, 7., 9.}, {10., 12., 7.}}, Key70 → {{0.667719, 12., 9.}, {16., 7., 11.}},
  Key71 → {{0.668469, 15., 7.}, {9., 13., 8.}}, Key72 → {{0.667719, 7., 14.}, {9., 6., 3.}},
  Key73 → {{0.668339, 11., 8.}, {9., 9., 16.}}, Key74 → {{0.667533, 10., 11.}, {18., 11., 6.}},
  Key75 → {{0.668469, 9., 11.}, {10., 9., 6.}}, Key76 → {{0.667892, 13., 9.}, {9., 4., 11.}},
  Key77 → {{0.668469, 10., 4.}, {7., 11., 12.}}, Key78 → {{0.668339, 7., 8.}, {12., 7., 12.}},
  Key79 → {{0.667719, 13., 12.}, {11., 6., 9.}}, Key80 → {{0.668052, 6., 9.}, {16., 10., 12.}},
  Key81 → {{0.668201, 13., 8.}, {12., 13., 14.}}, Key82 → {{0.668052, 2., 12.}, {12., 7., 11.}},
  Key83 → {{0.667331, 8., 17.}, {12., 19., 12.}}, Key84 → {{0.667111, 10., 8.}, {15., 11., 7.}},
  Key85 → {{0.667719, 14., 15.}, {12., 14., 11.}}, Key86 → {{0.667719, 14., 4.}, {11., 7., 11.}},
  Key87 → {{0.667111, 11., 20.}, {6., 4., 9.}}, Key88 → {{0.666872, 13., 13.}, {9., 16., 11.}},
  Key89 → {{0.668052, 10., 8.}, {5., 11., 13.}}, Key90 → {{0.667111, 6., 14.}, {9., 13., 11.}},
  Key91 → {{0.668589, 9., 14.}, {13., 12., 8.}}, Key92 → {{0.667892, 7., 13.}, {6., 7., 13.}},
  Key93 → {{0.667331, 7., 5.}, {14., 5., 14.}}, Key94 → {{0.667892, 14., 14.}, {12., 11., 5.}},
  Key95 → {{0.668339, 12., 9.}, {14., 8., 5.}}, Key96 → {{0.668201, 7., 13.}, {11., 10., 15.}},
  Key97 → {{0.666872, 12., 4.}, {14., 10., 13.}}, Key98 → {{0.668469, 10., 13.}, {6., 14., 8.}},
  Key99 → {{0.667533, 7., 6.}, {9., 7., 6.}}, Key100 → {{0.668052, 13., 7.}, {14., 10., 13.}}|>,
 Sample2 → <|Key1 → {{1.85425, 10., 12.}, {6., 11., 14.}}, Key2 → {{1.86306, 10., 14.}, {12., 10., 13.}},
  Key3 → {{1.90845, 7., 12.}, {14., 14., 4.}}, Key4 → {{1.845, 12., 10.}, {7., 15., 9.}},
  Key5 → {{1.86306, 4., 7.}, {9., 9., 13.}}, Key6 → {{1.86306, 12., 11.}, {12., 9., 10.}},
  Key7 → {{1.85425, 12., 12.}, {11., 11., 7.}}, Key8 → {{1.8872, 10., 12.}, {8., 6., 12.}},
  Key9 → {{1.83529, 12., 8.}, {12., 7., 11.}}, Key10 → {{1.83529, 10., 8.}, {6., 4., 10.}},
  Key11 → {{1.85425, 11., 10.}, {8., 5., 10.}}, Key12 → {{1.87147, 10., 12.}, {10., 9., 9.}},
```

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```
  Key13 → {{1.82505, 13., 9.}, {15., 19., 11.}}, Key14 → {{1.85425, 6., 11.}, {5., 10., 10.}},
  Key15 → {{1.85425, 12., 8.}, {15., 15., 9.}}, Key16 → {{1.8795, 10., 7.}, {14., 8., 16.}},
  Key17 → {{1.845, 10., 12.}, {9., 8., 9.}}, Key18 → {{1.85425, 19., 5.}, {8., 11., 10.}},
  Key19 → {{1.8795, 12., 7.}, {6., 9., 14.}}, Key20 → {{1.845, 8., 8.}, {12., 7., 8.}},
  Key21 → {{1.83529, 10., 9.}, {15., 6., 11.}}, Key22 → {{1.80283, 8., 15.}, {10., 11., 9.}},
  Key23 → {{1.86306, 10., 8.}, {9., 9., 12.}}, Key24 → {{1.8872, 9., 7.}, {10., 5., 9.}},
  Key25 → {{1.80283, 12., 6.}, {8., 9., 9.}}, Key26 → {{1.92129, 14., 15.}, {7., 11., 13.}},
  Key27 → {{1.8872, 5., 9.}, {10., 8., 10.}}, Key28 → {{1.8872, 16., 14.}, {11., 13., 14.}},
  Key29 → {{1.83529, 7., 7.}, {13., 12., 16.}}, Key30 → {{1.85425, 14., 15.}, {10., 11., 12.}},
  Key31 → {{1.85425, 9., 12.}, {15., 9., 15.}}, Key32 → {{1.845, 12., 13.}, {6., 10., 14.}},
  Key33 → {{1.845, 12., 11.}, {10., 12., 13.}}, Key34 → {{1.845, 5., 8.}, {16., 6., 9.}},
  Key35 → {{1.86306, 10., 9.}, {11., 15., 11.}}, Key36 → {{1.87147, 7., 10.}, {13., 14., 14.}},
  Key37 → {{1.83529, 10., 8.}, {11., 14., 7.}}, Key38 → {{1.87147, 9., 5.}, {11., 15., 15.}},
  Key39 → {{1.8795, 11., 7.}, {5., 11., 10.}}, Key40 → {{1.87147, 11., 11.}, {11., 6., 16.}},
  Key41 → {{1.87147, 13., 11.}, {15., 9., 12.}}, Key42 → {{1.86306, 9., 9.}, {16., 9., 7.}},
  Key43 → {{1.85425, 8., 8.}, {10., 9., 15.}}, Key44 → {{1.85425, 12., 9.}, {4., 14., 9.}},
  Key45 → {{1.8795, 11., 8.}, {13., 8., 14.}}, Key46 → {{1.90845, 9., 10.}, {12., 8., 10.}},
  Key47 → {{1.82505, 14., 11.}, {11., 8., 13.}}, Key48 → {{1.86306, 15., 10.}, {12., 10., 9.}},
  Key49 → {{1.85425, 15., 7.}, {7., 10., 8.}}, Key50 → {{1.85425, 7., 9.}, {5., 8., 7.}},
  Key51 → {{1.81425, 14., 15.}, {11., 7., 9.}}, Key52 → {{1.86306, 9., 6.}, {12., 7., 7.}},
  Key53 → {{1.8872, 7., 12.}, {7., 10., 10.}}, Key54 → {{1.83529, 7., 8.}, {8., 12., 6.}},
  Key55 → {{1.845, 7., 14.}, {6., 6., 11.}}, Key56 → {{1.8872, 5., 9.}, {12., 12., 3.}},
  Key57 → {{1.87147, 13., 6.}, {4., 17., 10.}}, Key58 → {{1.845, 7., 10.}, {8., 9., 9.}},
  Key59 → {{1.87147, 10., 9.}, {13., 8., 13.}}, Key60 → {{1.86306, 10., 17.}, {9., 14., 10.}},
  Key61 → {{1.86306, 6., 9.}, {12., 7., 13.}}, Key62 → {{1.83529, 8., 18.}, {6., 9., 20.}},
  Key63 → {{1.87147, 14., 14.}, {9., 5., 9.}}, Key64 → {{1.8795, 10., 12.}, {4., 9., 9.}},
  Key65 → {{1.845, 10., 12.}, {14., 16., 12.}}, Key66 → {{1.87147, 7., 11.}, {14., 11., 12.}},
  Key67 → {{1.86306, 10., 13.}, {13., 16., 14.}}, Key68 → {{1.8872, 10., 14.}, {4., 10., 7.}},
  Key69 → {{1.82505, 15., 10.}, {9., 17., 9.}}, Key70 → {{1.85425, 12., 10.}, {7., 11., 6.}},
  Key71 → {{1.82505, 11., 10.}, {12., 8., 8.}}, Key72 → {{1.85425, 12., 21.}, {11., 12., 12.}},
  Key73 → {{1.8872, 10., 8.}, {9., 17., 9.}}, Key74 → {{1.8795, 8., 14.}, {6., 7., 11.}},
  Key75 → {{1.87147, 10., 12.}, {13., 11., 8.}}, Key76 → {{1.8795, 10., 5.}, {17., 5., 11.}},
  Key77 → {{1.86306, 12., 7.}, {7., 11., 9.}}, Key78 → {{1.8795, 7., 10.}, {6., 11., 8.}},
  Key79 → {{1.93321, 13., 8.}, {10., 14., 8.}}, Key80 → {{1.85425, 10., 10.}, {4., 9., 9.}},
  Key81 → {{1.80283, 11., 10.}, {6., 11., 9.}}, Key82 → {{1.81425, 7., 9.}, {11., 12., 6.}},
  Key83 → {{1.87147, 13., 15.}, {18., 12., 10.}}, Key84 → {{1.8795, 12., 12.}, {7., 7., 13.}},
  Key85 → {{1.86306, 8., 13.}, {11., 8., 15.}}, Key86 → {{1.89457, 10., 13.}, {7., 10., 7.}},
  Key87 → {{1.85425, 17., 12.}, {7., 11., 8.}}, Key88 → {{1.81425, 5., 9.}, {15., 17., 5.}},
  Key89 → {{1.90165, 8., 9.}, {15., 9., 10.}}, Key90 → {{1.86306, 10., 17.}, {13., 7., 8.}},
  Key91 → {{1.87147, 8., 7.}, {13., 13., 10.}}, Key92 → {{1.8872, 7., 9.}, {8., 9., 12.}},
  Key93 → {{1.845, 10., 7.}, {13., 11., 7.}}, Key94 → {{1.85425, 8., 12.}, {15., 10., 11.}},
  Key95 → {{1.90845, 10., 9.}, {5., 7., 10.}}, Key96 → {{1.845, 11., 10.}, {16., 6., 9.}},
  Key97 → {{1.87147, 14., 10.}, {9., 18., 10.}}, Key98 → {{1.85425, 10., 7.}, {10., 13., 10.}},
  Key99 → {{1.87147, 11., 9.}, {11., 9., 8.}}, Key100 → {{1.8872, 10., 11.}, {11., 9., 7.}}|>,
Sample3 → ⟨|Key1 → {{0.814128, 12., 9.}, {8., 10., 14.}}, Key2 → {{1.92809, 10., 8.}, {8., 6., 11.}},
  Key3 → {{3.76224, 7., 14.}, {10., 5., 10.}}, Key4 → {{3.12038, 8., 11.}, {10., 12., 10.}},
  Key5 → {{3.45232, 12., 10.}, {13., 8., 12.}}, Key6 → {{1.92809, 8., 11.}, {9., 7., 7.}},
  Key7 → {{4.05381, 13., 11.}, {8., 10., 6.}}, Key8 → {{1.42306, 12., 12.}, {14., 11., 11.}},
  Key9 → {{2.36768, 8., 10.}, {9., 13., 8.}}, Key10 → {{3.45232, 9., 8.}, {11., 11., 7.}},
  Key11 → {{3.45232, 5., 13.}, {8., 12., 11.}}, Key12 → {{2.7613, 5., 11.}, {5., 5., 9.}},
  Key13 → {{1.92809, 8., 7.}, {14., 6., 10.}}, Key14 → {{0.814128, 17., 11.}, {10., 13., 11.}},
  Key15 → {{2.7613, 10., 11.}, {15., 13., 14.}}, Key16 → {{4.32981, 8., 5.}, {10., 14., 15.}},
  Key17 → {{4.59239, 14., 7.}, {15., 12., 4.}}, Key18 → {{1.42306, 8., 12.}, {11., 7., 8.}},
  Key19 → {{3.76224, 11., 5.}, {7., 12., 8.}}, Key20 → {{2.7613, 10., 6.}, {8., 11., 10.}},
  Key21 → {{2.7613, 10., 11.}, {11., 7., 8.}}, Key22 → {{2.7613, 10., 8.}, {11., 7., 8.}},
  Key23 → {{3.12038, 11., 12.}, {5., 11., 9.}}, Key24 → {{1.42306, 8., 6.}, {9., 8., 6.}},
  Key25 → {{3.76224, 11., 7.}, {6., 12., 9.}}, Key26 → {{3.45232, 10., 10.}, {12., 14., 9.}},
  Key27 → {{4.59239, 9., 8.}, {10., 10., 13.}}, Key28 → {{9.8168×10^-16, 15., 5.}, {7., 8., 15.}},
  Key29 → {{4.05381, 7., 10.}, {7., 13., 10.}}, Key30 → {{2.36768, 11., 9.}, {10., 12., 7.}},
  Key31 → {{2.36768, 9., 18.}, {11., 13., 11.}}, Key32 → {{2.36768, 10., 4.}, {8., 6., 14.}},
  Key33 → {{3.45232, 9., 7.}, {15., 13., 13.}}, Key34 → {{2.36768, 10., 13.}, {8., 11., 7.}},
  Key35 → {{5.08372, 8., 9.}, {12., 8., 5.}}, Key36 → {{2.36768, 9., 12.}, {8., 12., 8.}},
  Key37 → {{9.8168×10^-16, 7., 10.}, {7., 10., 12.}}, Key38 → {{3.76224, 6., 8.}, {6., 9., 9.}},
  Key39 → {{2.7613, 11., 6.}, {14., 8., 9.}}, Key40 → {{1.42306, 11., 8.}, {10., 16., 12.}},
  Key41 → {{1.92809, 13., 14.}, {10., 10., 10.}}, Key42 → {{1.92809, 5., 11.}, {12., 9., 10.}},
```

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Key43 → {{1.42306, 7., 13.}, {12., 10., 13.}}, Key44 → {{2.7613, 5., 6.}, {9., 12., 7.}},
Key45 → {{4.32981, 15., 10.}, {16., 9., 7.}}, Key46 → {{3.76224, 6., 8.}, {10., 12., 11.}},
Key47 → {{1.42306, 10., 22.}, {6., 13., 16.}}, Key48 → {{2.7613, 16., 12.}, {13., 9., 8.}},
Key49 → {{4.32981, 11., 12.}, {9., 11., 9.}}, Key50 → {{1.92809, 11., 12.}, {9., 10., 9.}},
Key51 → {{2.36768, 10., 13.}, {16., 10., 12.}}, Key52 → {{4.32981, 8., 10.}, {13., 6., 13.}},
Key53 → {{3.12038, 15., 6.}, {9., 10., 15.}}, Key54 → {{3.45232, 11., 9.}, {10., 10., 10.}},
Key55 → {{1.92809, 5., 8.}, {16., 9., 15.}}, Key56 → {{2.36768, 9., 19.}, {11., 10., 8.}},
Key57 → {{1.92809, 8., 11.}, {11., 5., 12.}}, Key58 → {{2.7613, 8., 12.}, {13., 16., 11.}},
Key59 → {{4.59239, 7., 11.}, {10., 17., 14.}}, Key60 → {{4.84323, 12., 8.}, {11., 13., 9.}},
Key61 → {{3.12038, 8., 6.}, {11., 10., 10.}}, Key62 → {{4.05381, 12., 8.}, {16., 6., 13.}},
Key63 → {{2.7613, 15., 7.}, {9., 8., 11.}}, Key64 → {{0.814128, 14., 11.}, {14., 10., 15.}},
Key65 → {{5.08372, 10., 6.}, {13., 11., 13.}}, Key66 → {{3.45232, 14., 13.}, {11., 10., 8.}},
Key67 → {{2.36768, 14., 3.}, {10., 8., 16.}}, Key68 → {{4.05381, 14., 16.}, {10., 4., 14.}},
Key69 → {{1.42306, 8., 17.}, {16., 8., 11.}}, Key70 → {{2.7613, 14., 9.}, {11., 3., 6.}},
Key71 → {{3.45232, 13., 9.}, {7., 8., 11.}}, Key72 → {{9.8168×10^-16, 11., 7.}, {10., 8., 7.}},
Key73 → {{4.05381, 15., 9.}, {12., 5., 6.}}, Key74 → {{3.76224, 12., 13.}, {6., 5., 5.}},
Key75 → {{2.7613, 11., 16.}, {9., 11., 7.}}, Key76 → {{2.7613, 5., 5.}, {11., 4., 11.}},
Key77 → {{3.45232, 12., 9.}, {11., 15., 10.}}, Key78 → {{4.32981, 17., 12.}, {13., 11., 17.}},
Key79 → {{-2.21055, 9., 12.}, {6., 9., 10.}}, Key80 → {{2.36768, 12., 8.}, {14., 11., 9.}},
Key81 → {{1.92809, 7., 9.}, {9., 6., 6.}}, Key82 → {{3.45232, 7., 8.}, {6., 5., 7.}},
Key83 → {{1.42306, 7., 10.}, {6., 12., 7.}}, Key84 → {{3.76224, 7., 17.}, {11., 10., 8.}},
Key85 → {{1.92809, 16., 6.}, {6., 11., 8.}}, Key86 → {{0.814128, 10., 12.}, {11., 5., 11.}},
Key87 → {{2.36768, 8., 10.}, {6., 6., 13.}}, Key88 → {{3.76224, 11., 10.}, {12., 8., 8.}},
Key89 → {{0.814128, 3., 10.}, {10., 7., 6.}}, Key90 → {{1.92809, 10., 5.}, {20., 7., 8.}},
Key91 → {{1.92809, 8., 11.}, {11., 9., 11.}}, Key92 → {{2.36768, 6., 18.}, {6., 5., 4.}},
Key93 → {{3.45232, 10., 6.}, {8., 10., 14.}}, Key94 → {{1.92809, 11., 10.}, {11., 9., 11.}},
Key95 → {{1.92809, 10., 9.}, {10., 5., 8.}}, Key96 → {{1.92809, 9., 8.}, {9., 13., 8.}},
Key97 → {{2.36768, 13., 5.}, {12., 9., 11.}}, Key98 → {{2.7613, 8., 13.}, {11., 12., 12.}},
Key99 → {{3.45232, 4., 7.}, {11., 9., 12.}}, Key100 → {{4.05381, 11., 9.}, {11., 8., 6.}}|>|>
```

We can perform the optimized Box Cox Transform on values from the second list, first component :

```
In[5]:= ApplyBoxCoxTransformExtended[dataRandomOmicsObject, ListIndex → 2, ComponentIndex → 1]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.417023, -4.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.32333, -4.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.39933, -5.}

```
Out[5]= <|Sample1 → <|Key1 → {{8., 7., 11.}, {3.00045, 8., 13.}}, Key2 → {{10., 8., 11.}, {1.39355, 16., 13.}},
Key3 → {{10., 11., 14.}, {2.66434, 9., 12.}}, Key4 → {{8., 13., 9.}, {2.29371, 12., 12.}},
Key5 → {{8., 7., 9.}, {3.3096, 11., 9.}}, Key6 → {{12., 12., 4.}, {1.0649×10^-15, 3., 9.}},
Key7 → {{12., 7., 9.}, {3.00045, 14., 10.}}, Key8 → {{9., 11., 10.}, {3.00045, 9., 11.}},
Key9 → {{13., 9., 11.}, {-2.39795, 12., 6.}}, Key10 → {{15., 11., 10.}, {3.86621, 9., 3.}},
Key11 → {{10., 9., 14.}, {1.87682, 12., 10.}}, Key12 → {{11., 8., 7.}, {4.36107, 16., 9.}},
Key13 → {{9., 8., 15.}, {2.66434, 5., 5.}}, Key14 → {{9., 9., 14.}, {2.29371, 7., 12.}},
Key15 → {{10., 9., 9.}, {1.39355, 7., 9.}}, Key16 → {{8., 17., 13.}, {4.80984, 8., 11.}},
Key17 → {{11., 6., 16.}, {2.66434, 8., 14.}}, Key18 → {{9., 11., 10.}, {1.87682, 9., 13.}},
Key19 → {{9., 6., 10.}, {3.59694, 7., 13.}}, Key20 → {{11., 12., 16.}, {3.59694, 5., 5.}},
Key21 → {{12., 12., 8.}, {1.0649×10^-15, 11., 5.}}, Key22 → {{6., 12., 8.}, {0.80372, 8., 10.}},
Key23 → {{14., 13., 8.}, {2.29371, 10., 13.}}, Key24 → {{8., 6., 10.}, {0.80372, 4., 8.}},
Key25 → {{12., 17., 6.}, {3.00045, 20., 6.}}, Key26 → {{6., 10., 6.}, {2.66434, 10., 8.}},
Key27 → {{11., 11., 12.}, {-2.39795, 12., 12.}}, Key28 → {{3., 14., 8.}, {3.3096, 9., 12.}},
Key29 → {{9., 7., 10.}, {1.39355, 13., 11.}}, Key30 → {{12., 8., 14.}, {4.36107, 13., 17.}},
Key31 → {{13., 8., 14.}, {1.87682, 7., 8.}}, Key32 → {{9., 8., 7.}, {1.39355, 9., 11.}},
Key33 → {{9., 6., 8.}, {2.66434, 16., 6.}}, Key34 → {{7., 8., 7.}, {2.66434, 8., 10.}},
Key35 → {{9., 14., 14.}, {2.66434, 7., 8.}}, Key36 → {{9., 10., 8.}, {3.00045, 5., 7.}},
Key37 → {{23., 17., 12.}, {4.12021, 9., 9.}}, Key38 → {{7., 9., 14.}, {1.0649×10^-15, 15., 9.}},
Key39 → {{15., 16., 10.}, {3.00045, 10., 11.}}, Key40 → {{11., 8., 13.}, {1.87682, 10., 10.}},
Key41 → {{15., 9., 9.}, {3.00045, 7., 11.}}, Key42 → {{8., 9., 5.}, {3.3096, 17., 17.}},
Key43 → {{8., 6., 11.}, {3.00045, 8., 5.}}, Key44 → {{9., 10., 8.}, {2.66434, 9., 9.}},
Key45 → {{11., 9., 11.}, {2.29371, 14., 5.}}, Key46 → {{14., 7., 8.}, {4.12021, 8., 9.}},
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  Key47 → {{9., 8., 5.}, {2.66434, 7., 12.}}, Key48 → {{7., 6., 6.}, {2.66434, 12., 11.}},
  Key49 → {{9., 7., 7.}, {2.66434, 11., 10.}}, Key50 → {{13., 9., 10.}, {3.3096, 11., 8.}},
  Key51 → {{9., 9., 19.}, {3.3096, 5., 13.}}, Key52 → {{12., 16., 11.}, {1.87682, 15., 7.}},
  Key53 → {{9., 8., 15.}, {4.36107, 9., 7.}}, Key54 → {{7., 10., 12.}, {1.39355, 11., 9.}},
  Key55 → {{12., 10., 13.}, {2.29371, 12., 6.}}, Key56 → {{10., 11., 10.}, {2.66434, 7., 15.}},
  Key57 → {{6., 12., 14.}, {0.80372, 8., 9.}}, Key58 → {{12., 7., 8.}, {3.59694, 8., 6.}},
  Key59 → {{14., 9., 8.}, {3.00045, 11., 12.}}, Key60 → {{14., 7., 7.}, {2.29371, 12., 5.}},
  Key61 → {{10., 10., 7.}, {1.0649×10^-15, 11., 11.}}, Key62 → {{8., 6., 5.}, {4.12021, 13., 11.}},
  Key63 → {{10., 13., 10.}, {3.86621, 8., 14.}}, Key64 → {{7., 8., 7.}, {3.59694, 10., 19.}},
  Key65 → {{13., 9., 5.}, {1.0649×10^-15, 11., 6.}}, Key66 → {{21., 12., 8.}, {1.39355, 13., 8.}},
  Key67 → {{8., 15., 8.}, {2.29371, 5., 10.}}, Key68 → {{10., 10., 7.}, {3.59694, 5., 13.}},
  Key69 → {{7., 7., 9.}, {2.66434, 12., 7.}}, Key70 → {{9., 12., 9.}, {4.36107, 7., 11.}},
  Key71 → {{14., 15., 7.}, {2.29371, 13., 8.}}, Key72 → {{9., 7., 14.}, {2.29371, 6., 3.}},
  Key73 → {{13., 11., 8.}, {2.29371, 9., 16.}}, Key74 → {{8., 10., 11.}, {4.80984, 11., 6.}},
  Key75 → {{14., 9., 11.}, {2.66434, 9., 6.}}, Key76 → {{10., 13., 9.}, {2.29371, 4., 11.}},
  Key77 → {{14., 10., 4.}, {1.39355, 11., 12.}}, Key78 → {{13., 7., 8.}, {3.3096, 7., 12.}},
  Key79 → {{9., 13., 12.}, {3.00045, 6., 9.}}, Key80 → {{11., 6., 9.}, {4.36107, 10., 12.}},
  Key81 → {{12., 13., 8.}, {3.3096, 13., 14.}}, Key82 → {{11., 2., 12.}, {3.3096, 7., 11.}},
  Key83 → {{7., 8., 17.}, {3.3096, 19., 12.}}, Key84 → {{6., 10., 8.}, {4.12021, 11., 7.}},
  Key85 → {{9., 14., 15.}, {3.3096, 14., 11.}}, Key86 → {{9., 14., 4.}, {3.00045, 7., 11.}},
  Key87 → {{6., 11., 20.}, {0.80372, 4., 9.}}, Key88 → {{5., 13., 13.}, {2.29371, 16., 11.}},
  Key89 → {{11., 10., 8.}, {1.0649×10^-15, 11., 13.}}, Key90 → {{6., 6., 14.}, {2.29371, 13., 11.}},
  Key91 → {{15., 9., 14.}, {3.59694, 12., 8.}}, Key92 → {{10., 7., 13.}, {0.80372, 7., 13.}},
  Key93 → {{7., 7., 5.}, {3.86621, 5., 14.}}, Key94 → {{10., 14., 14.}, {3.3096, 11., 5.}},
  Key95 → {{13., 12., 9.}, {3.86621, 8., 5.}}, Key96 → {{12., 7., 13.}, {3.00045, 10., 15.}},
  Key97 → {{5., 12., 4.}, {3.86621, 10., 13.}}, Key98 → {{14., 10., 13.}, {0.80372, 14., 8.}},
  Key99 → {{8., 7., 6.}, {2.29371, 7., 6.}}, Key100 → {{11., 13., 7.}, {3.86621, 10., 13.}}|〉,
Sample2 → 〈|Key1 → {{9., 10., 12.}, {0.776962, 11., 14.}}, Key2 → {{10., 10., 14.}, {2.96547, 10., 13.}},
  Key3 → {{16., 7., 12.}, {3.41873, 14., 4.}}, Key4 → {{8., 12., 10.}, {1.31904, 15., 9.}},
  Key5 → {{10., 4., 7.}, {2.11136, 9., 13.}}, Key6 → {{10., 12., 11.}, {2.96547, 9., 10.}},
  Key7 → {{9., 12., 12.}, {2.70948, 11., 7.}}, Key8 → {{13., 10., 12.}, {1.74911, 6., 12.}},
  Key9 → {{7., 12., 8.}, {2.96547, 7., 11.}}, Key10 → {{7., 10., 8.}, {0.776962, 4., 10.}},
  Key11 → {{9., 11., 10.}, {1.74911, 5., 10.}}, Key12 → {{11., 10., 12.}, {2.42737, 9., 9.}},
  Key13 → {{6., 13., 9.}, {3.62252, 19., 11.}}, Key14 → {{9., 6., 11.}, {6.86744×10^-16, 10., 10.}},
  Key15 → {{9., 12., 8.}, {3.62252, 15., 9.}}, Key16 → {{12., 10., 7.}, {3.41873, 8., 16.}},
  Key17 → {{8., 10., 12.}, {2.11136, 8., 9.}}, Key18 → {{9., 19., 5.}, {1.74911, 11., 10.}},
  Key19 → {{12., 12., 7.}, {0.776962, 9., 14.}}, Key20 → {{8., 8., 8.}, {2.96547, 7., 8.}},
  Key21 → {{7., 10., 9.}, {3.62252, 6., 11.}}, Key22 → {{4., 8., 15.}, {2.42737, 11., 9.}},
  Key23 → {{10., 10., 8.}, {2.11136, 9., 12.}}, Key24 → {{13., 9., 7.}, {2.42737, 5., 9.}},
  Key25 → {{4., 12., 6.}, {1.74911, 9., 9.}}, Key26 → {{18., 14., 15.}, {1.31904, 11., 13.}},
  Key27 → {{13., 5., 9.}, {2.42737, 8., 10.}}, Key28 → {{13., 16., 14.}, {2.70948, 13., 14.}},
  Key29 → {{7., 7., 7.}, {3.20064, 12., 16.}}, Key30 → {{9., 14., 15.}, {2.42737, 11., 12.}},
  Key31 → {{9., 9., 12.}, {3.62252, 9., 15.}}, Key32 → {{8., 12., 13.}, {0.776962, 10., 14.}},
  Key33 → {{8., 12., 11.}, {2.42737, 12., 13.}}, Key34 → {{8., 5., 8.}, {3.81412, 6., 9.}},
  Key35 → {{10., 10., 9.}, {2.70948, 15., 11.}}, Key36 → {{11., 7., 10.}, {3.20064, 14., 14.}},
  Key37 → {{7., 10., 8.}, {2.70948, 14., 7.}}, Key38 → {{11., 9., 5.}, {2.70948, 15., 15.}},
  Key39 → {{12., 11., 7.}, {6.86744×10^-16, 11., 10.}}, Key40 → {{11., 11., 11.}, {2.70948, 6., 16.}},
  Key41 → {{11., 13., 11.}, {3.62252, 9., 12.}}, Key42 → {{10., 9., 9.}, {3.81412, 9., 7.}},
  Key43 → {{9., 8., 8.}, {2.42737, 9., 15.}}, Key44 → {{9., 12., 9.}, {-3.09278, 14., 9.}},
  Key45 → {{12., 11., 8.}, {3.20064, 8., 14.}}, Key46 → {{16., 9., 10.}, {2.96547, 8., 10.}},
  Key47 → {{6., 14., 11.}, {2.70948, 8., 13.}}, Key48 → {{10., 15., 10.}, {2.96547, 10., 9.}},
  Key49 → {{9., 15., 7.}, {1.31904, 10., 8.}}, Key50 → {{9., 7., 9.}, {6.86744×10^-16, 8., 7.}},
  Key51 → {{5., 14., 15.}, {2.70948, 7., 9.}}, Key52 → {{10., 9., 6.}, {2.96547, 7., 7.}},
  Key53 → {{13., 7., 12.}, {1.31904, 10., 10.}}, Key54 → {{7., 7., 8.}, {1.74911, 12., 6.}},
  Key55 → {{8., 7., 14.}, {0.776962, 6., 11.}}, Key56 → {{13., 5., 9.}, {2.96547, 12., 3.}},
  Key57 → {{11., 13., 6.}, {-3.09278, 17., 10.}}, Key58 → {{8., 7., 10.}, {1.74911, 9., 9.}},
  Key59 → {{11., 10., 9.}, {3.20064, 8., 13.}}, Key60 → {{10., 10., 17.}, {2.11136, 14., 10.}},
  Key61 → {{10., 6., 9.}, {2.96547, 7., 13.}}, Key62 → {{7., 8., 18.}, {0.776962, 9., 20.}},
  Key63 → {{11., 14., 14.}, {2.11136, 5., 9.}}, Key64 → {{12., 10., 12.}, {-3.09278, 9., 9.}},
  Key65 → {{8., 10., 12.}, {3.41873, 16., 12.}}, Key66 → {{11., 7., 11.}, {3.41873, 11., 12.}},
  Key67 → {{10., 10., 13.}, {3.20064, 16., 14.}}, Key68 → {{13., 10., 14.}, {-3.09278, 10., 7.}},
  Key69 → {{6., 15., 10.}, {2.11136, 17., 9.}}, Key70 → {{9., 12., 10.}, {1.31904, 11., 6.}},
  Key71 → {{6., 11., 10.}, {2.96547, 8., 8.}}, Key72 → {{9., 12., 21.}, {2.70948, 12., 12.}},
  Key73 → {{13., 10., 8.}, {2.11136, 17., 9.}}, Key74 → {{12., 8., 14.}, {0.776962, 7., 11.}},
```

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```
  Key75 → {{11., 10., 12.}, {3.20064, 11., 8.}}, Key76 → {{12., 10., 5.}, {3.99521, 5., 11.}},
  Key77 → {{10., 12., 7.}, {1.31904, 11., 9.}}, Key78 → {{12., 7., 10.}, {0.776962, 11., 8.}},
  Key79 → {{20., 13., 8.}, {2.42737, 14., 8.}}, Key80 → {{9., 10., 10.}, {-3.09278, 9., 9.}},
  Key81 → {{4., 11., 10.}, {0.776962, 11., 9.}}, Key82 → {{5., 7., 9.}, {2.70948, 12., 6.}},
  Key83 → {{11., 13., 15.}, {4.1671, 12., 10.}}, Key84 → {{12., 12., 12.}, {1.31904, 7., 13.}},
  Key85 → {{10., 8., 13.}, {2.70948, 8., 15.}}, Key86 → {{14., 10., 13.}, {1.31904, 10., 7.}},
  Key87 → {{9., 17., 12.}, {1.31904, 11., 8.}}, Key88 → {{5., 5., 9.}, {3.62252, 17., 5.}},
  Key89 → {{15., 8., 9.}, {3.62252, 9., 10.}}, Key90 → {{10., 10., 17.}, {3.20064, 7., 8.}},
  Key91 → {{11., 8., 7.}, {3.20064, 13., 10.}}, Key92 → {{13., 7., 9.}, {1.74911, 9., 12.}},
  Key93 → {{8., 10., 7.}, {3.20064, 11., 7.}}, Key94 → {{9., 8., 12.}, {3.62252, 10., 11.}},
  Key95 → {{16., 10., 9.}, {6.86744×10^-16, 7., 10.}}, Key96 → {{8., 11., 10.}, {3.81412, 6., 9.}},
  Key97 → {{11., 14., 10.}, {2.11136, 18., 10.}}, Key98 → {{9., 10., 7.}, {2.42737, 13., 10.}},
  Key99 → {{11., 11., 9.}, {2.70948, 9., 8.}}, Key100 → {{13., 10., 11.}, {2.70948, 9., 7.}}|⟩,
Sample3 → ⟨|Key1 → {{6., 12., 9.}, {1.37907, 10., 14.}}, Key2 → {{8., 10., 8.}, {1.37907, 6., 11.}},
  Key3 → {{13., 7., 14.}, {2.25779, 5., 10.}}, Key4 → {{11., 8., 11.}, {2.25779, 12., 10.}},
  Key5 → {{12., 12., 10.}, {3.24092, 8., 12.}}, Key6 → {{8., 8., 11.}, {1.85181, 7., 7.}},
  Key7 → {{14., 13., 11.}, {1.37907, 10., 6.}}, Key8 → {{7., 12., 12.}, {3.5176, 11., 11.}},
  Key9 → {{9., 8., 10.}, {1.85181, 13., 8.}}, Key10 → {{12., 9., 8.}, {2.61742, 11., 7.}},
  Key11 → {{12., 5., 13.}, {1.37907, 12., 11.}}, Key12 → {{10., 5., 11.}, {-2.50419, 5., 9.}},
  Key13 → {{8., 8., 7.}, {3.5176, 6., 10.}}, Key14 → {{6., 17., 11.}, {2.25779, 13., 11.}},
  Key15 → {{10., 10., 11.}, {3.77636, 13., 14.}}, Key16 → {{15., 8., 5.}, {2.25779, 14., 15.}},
  Key17 → {{16., 14., 7.}, {3.77636, 12., 4.}}, Key18 → {{7., 8., 12.}, {2.61742, 7., 8.}},
  Key19 → {{13., 11., 5.}, {0.798576, 12., 8.}}, Key20 → {{10., 10., 6.}, {1.37907, 11., 10.}},
  Key21 → {{10., 10., 11.}, {2.61742, 7., 8.}}, Key22 → {{10., 10., 8.}, {2.61742, 7., 8.}},
  Key23 → {{11., 11., 12.}, {-2.50419, 11., 9.}}, Key24 → {{7., 8., 6.}, {1.85181, 8., 6.}},
  Key25 → {{13., 11., 7.}, {1.11209×10^-15, 12., 9.}}, Key26 → {{12., 10., 10.}, {2.9426, 14., 9.}},
  Key27 → {{16., 9., 8.}, {2.25779, 10., 13.}}, Key28 → {{5., 15., 5.}, {0.798576, 8., 15.}},
  Key29 → {{14., 7., 10.}, {0.798576, 13., 10.}}, Key30 → {{9., 11., 9.}, {2.25779, 12., 7.}},
  Key31 → {{9., 9., 18.}, {2.61742, 13., 11.}}, Key32 → {{9., 10., 4.}, {1.37907, 6., 14.}},
  Key33 → {{12., 9., 7.}, {3.77636, 13., 13.}}, Key34 → {{9., 10., 13.}, {1.37907, 11., 7.}},
  Key35 → {{18., 8., 9.}, {2.9426, 8., 5.}}, Key36 → {{9., 9., 12.}, {1.37907, 12., 8.}},
  Key37 → {{5., 7., 10.}, {0.798576, 10., 12.}}, Key38 → {{13., 6., 8.}, {1.11209×10^-15, 9., 9.}},
  Key39 → {{10., 11., 6.}, {3.5176, 8., 9.}}, Key40 → {{7., 11., 8.}, {2.25779, 16., 12.}},
  Key41 → {{8., 13., 14.}, {2.25779, 10., 10.}}, Key42 → {{8., 5., 11.}, {2.9426, 9., 10.}},
  Key43 → {{7., 7., 13.}, {2.9426, 10., 13.}}, Key44 → {{10., 5., 6.}, {1.85181, 12., 7.}},
  Key45 → {{15., 15., 10.}, {4.02001, 9., 7.}}, Key46 → {{13., 6., 8.}, {2.25779, 12., 11.}},
  Key47 → {{7., 10., 22.}, {1.11209×10^-15, 13., 16.}}, Key48 → {{10., 16., 12.}, {3.24092, 9., 8.}},
  Key49 → {{15., 11., 12.}, {1.85181, 11., 9.}}, Key50 → {{8., 11., 12.}, {1.85181, 10., 9.}},
  Key51 → {{9., 10., 13.}, {4.02001, 10., 12.}}, Key52 → {{15., 8., 10.}, {3.24092, 6., 13.}},
  Key53 → {{11., 15., 6.}, {1.85181, 10., 15.}}, Key54 → {{12., 11., 9.}, {2.25779, 10., 10.}},
  Key55 → {{8., 5., 8.}, {4.02001, 9., 15.}}, Key56 → {{9., 9., 19.}, {2.61742, 10., 8.}},
  Key57 → {{8., 8., 11.}, {2.61742, 5., 12.}}, Key58 → {{10., 8., 12.}, {3.24092, 16., 11.}},
  Key59 → {{16., 7., 11.}, {2.25779, 17., 14.}}, Key60 → {{17., 12., 8.}, {2.61742, 13., 9.}},
  Key61 → {{11., 8., 6.}, {2.61742, 10., 10.}}, Key62 → {{14., 12., 8.}, {4.02001, 6., 13.}},
  Key63 → {{10., 15., 7.}, {1.85181, 8., 11.}}, Key64 → {{6., 14., 11.}, {3.5176, 10., 15.}},
  Key65 → {{18., 10., 6.}, {3.24092, 11., 13.}}, Key66 → {{12., 14., 13.}, {2.61742, 10., 8.}},
  Key67 → {{9., 14., 3.}, {2.25779, 8., 16.}}, Key68 → {{14., 14., 16.}, {2.25779, 4., 14.}},
  Key69 → {{7., 8., 17.}, {4.02001, 8., 11.}}, Key70 → {{10., 14., 9.}, {2.61742, 3., 6.}},
  Key71 → {{12., 13., 9.}, {0.798576, 8., 11.}}, Key72 → {{5., 11., 7.}, {2.25779, 8., 7.}},
  Key73 → {{14., 15., 9.}, {2.9426, 5., 6.}}, Key74 → {{13., 12., 13.}, {1.11209×10^-15, 5., 5.}},
  Key75 → {{10., 11., 16.}, {1.85181, 11., 7.}}, Key76 → {{10., 5., 5.}, {2.61742, 4., 11.}},
  Key77 → {{12., 12., 9.}, {2.61742, 15., 10.}}, Key78 → {{15., 17., 12.}, {3.24092, 11., 17.}},
  Key79 → {{4., 9., 12.}, {1.11209×10^-15, 9., 10.}}, Key80 → {{9., 12., 8.}, {3.5176, 11., 9.}},
  Key81 → {{8., 7., 9.}, {1.85181, 6., 6.}}, Key82 → {{12., 7., 8.}, {1.11209×10^-15, 5., 7.}},
  Key83 → {{7., 7., 10.}, {1.11209×10^-15, 12., 7.}}, Key84 → {{13., 7., 17.}, {2.61742, 10., 8.}},
  Key85 → {{8., 16., 6.}, {1.11209×10^-15, 11., 8.}}, Key86 → {{6., 10., 12.}, {2.61742, 5., 11.}},
  Key87 → {{9., 8., 10.}, {1.11209×10^-15, 6., 13.}}, Key88 → {{13., 11., 10.}, {2.9426, 8., 8.}},
  Key89 → {{6., 3., 10.}, {2.25779, 7., 6.}}, Key90 → {{8., 10., 5.}, {4.88023, 7., 8.}},
  Key91 → {{8., 8., 11.}, {2.61742, 9., 11.}}, Key92 → {{9., 6., 18.}, {1.11209×10^-15, 5., 4.}},
  Key93 → {{12., 10., 6.}, {1.37907, 10., 14.}}, Key94 → {{8., 11., 10.}, {2.61742, 9., 11.}},
  Key95 → {{8., 10., 9.}, {2.25779, 5., 8.}}, Key96 → {{8., 9., 8.}, {1.85181, 13., 8.}},
  Key97 → {{9., 13., 5.}, {2.9426, 9., 11.}}, Key98 → {{10., 8., 13.}, {2.61742, 12., 12.}},
  Key99 → {{12., 4., 7.}, {2.61742, 9., 12.}}, Key100 → {{14., 11., 9.}, {2.61742, 8., 6.}}|⟩|⟩
```

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ComponentIndex (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ComponentIndex allows selection of a component of a list if the input data is an OmicsObject or other association with multi - list values. For an example, we first generate a random OmicsObject using also random data as metadata

In[2]:=
```
dataRandomOmicsObject = OmicsObjectCreator[{"Sample1", "Sample2", "Sample3"},
   ConstantArray[("Key" <> ToString[#]) & /@ Range[100], 3], RandomVariate[
    PoissonDistribution[10], {3, 100, 3}], RandomVariate[PoissonDistribution[10], {3, 100, 3}]];
```

Let's look at the first few keys to see the structure:

In[3]:=
```
Query[All, 1 ;; 5]@dataRandomOmicsObject
```

Out[3]=
```
<|Sample1 → <|Key1 → {{12, 13, 9}, {15, 6, 12}}, Key2 → {{10, 10, 10}, {11, 10, 10}},
   Key3 → {{17, 12, 12}, {9, 11, 11}}, Key4 → {{9, 4, 9}, {8, 10, 7}}, Key5 → {{18, 13, 10}, {8, 12, 8}}|>,
 Sample2 → <|Key1 → {{12, 5, 11}, {15, 8, 6}}, Key2 → {{6, 9, 8}, {10, 7, 11}},
   Key3 → {{12, 10, 10}, {7, 12, 9}}, Key4 → {{19, 16, 5}, {9, 5, 11}}, Key5 → {{12, 4, 10}, {4, 5, 9}}|>,
 Sample3 → <|Key1 → {{13, 9, 8}, {3, 7, 7}}, Key2 → {{5, 12, 15}, {16, 10, 9}},
   Key3 → {{6, 3, 11}, {10, 8, 19}}, Key4 → {{9, 11, 10}, {8, 9, 9}}, Key5 → {{13, 7, 13}, {17, 3, 8}}|>|>
```

We can perform the optimized Box Cox Transform on values from the first list, first component:

In[4]:=
```
ApplyBoxCoxTransformExtended[dataRandomOmicsObject, ListIndex → 1, ComponentIndex → 1]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.496841, -3.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.430211, -3.}

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.48755, -2.}

Out[4]=
```
⟨|Sample1 → ⟨|Key1 → {{3.98367, 13., 9.}, {15., 6., 12.}}, Key2 → {{3.2798, 10., 10.}, {11., 10., 10.}},
   Key3 → {{5.45566, 12., 12.}, {9., 11., 11.}}, Key4 → {{2.88959, 4., 9.}, {8., 10., 7.}},
   Key5 → {{5.7161, 13., 10.}, {8., 12., 8.}}, Key6 → {{2.46503, 11., 4.}, {5., 5., 7.}},
   Key7 → {{2.88959, 10., 9.}, {18., 13., 13.}}, Key8 → {{4.61234, 7., 9.}, {8., 8., 13.}},
   Key9 → {{3.98367, 11., 9.}, {7., 7., 11.}}, Key10 → {{3.2798, 7., 7.}, {12., 5., 8.}},
   Key11 → {{4.30593, 7., 10.}, {12., 17., 10.}}, Key12 → {{3.98367, 10., 12.}, {9., 9., 9.}},
   Key13 → {{3.98367, 12., 16.}, {13., 8., 12.}}, Key14 → {{4.90502, 11., 12.}, {8., 8., 7.}},
   Key15 → {{2.46503, 10., 9.}, {9., 6., 9.}}, Key16 → {{2.46503, 7., 11.}, {5., 9., 12.}},
   Key17 → {{2.46503, 13., 11.}, {7., 17., 12.}}, Key18 → {{3.98367, 18., 11.}, {7., 9., 8.}},
   Key19 → {{4.90502, 10., 18.}, {13., 13., 7.}}, Key20 → {{3.2798, 14., 5.}, {9., 10., 10.}},
   Key21 → {{2.46503, 6., 8.}, {10., 5., 8.}}, Key22 → {{1.99513, 5., 9.}, {9., 12., 15.}},
   Key23 → {{4.30593, 7., 7.}, {4., 13., 10.}}, Key24 → {{3.2798, 10., 11.}, {7., 10., 13.}},
   Key25 → {{3.98367, 8., 7.}, {9., 9., 9.}}, Key26 → {{8.93825×10^-16, 10., 9.}, {11., 11., 7.}},
   Key27 → {{4.30593, 9., 16.}, {11., 9., 10.}}, Key28 → {{4.61234, 6., 10.}, {8., 12., 12.}},
   Key29 → {{3.2798, 3., 12.}, {9., 4., 13.}}, Key30 → {{4.61234, 10., 13.}, {11., 10., 10.}},
   Key31 → {{1.99513, 4., 8.}, {12., 16., 3.}}, Key32 → {{-2.01271, 9., 9.}, {10., 7., 5.}},
   Key33 → {{1.46133, 11., 6.}, {6., 13., 7.}}, Key34 → {{8.93825×10^-16, 10., 14.}, {5., 7., 12.}},
   Key35 → {{3.64283, 12., 11.}, {7., 7., 7.}}, Key36 → {{1.46133, 7., 8.}, {9., 11., 9.}},
   Key37 → {{2.46503, 12., 12.}, {9., 12., 12.}}, Key38 → {{2.46503, 7., 6.}, {11., 8., 8.}},
   Key39 → {{1.46133, 12., 15.}, {12., 13., 10.}}, Key40 → {{1.99513, 10., 11.}, {13., 10., 14.}},
   Key41 → {{2.88959, 11., 9.}, {9., 8., 9.}}, Key42 → {{3.64283, 14., 12.}, {15., 9., 9.}},
   Key43 → {{2.88959, 9., 16.}, {8., 11., 11.}}, Key44 → {{3.98367, 8., 10.}, {3., 10., 16.}},
   Key45 → {{3.98367, 6., 9.}, {9., 8., 6.}}, Key46 → {{2.88959, 12., 16.}, {8., 6., 8.}},
   Key47 → {{2.46503, 15., 6.}, {8., 14., 11.}}, Key48 → {{2.88959, 9., 8.}, {12., 8., 9.}},
   Key49 → {{2.88959, 9., 12.}, {12., 13., 9.}}, Key50 → {{2.88959, 14., 6.}, {10., 5., 20.}},
   Key51 → {{2.88959, 11., 7.}, {9., 11., 12.}}, Key52 → {{1.46133, 10., 12.}, {5., 13., 5.}},
   Key53 → {{4.61234, 9., 15.}, {10., 10., 7.}}, Key54 → {{2.88959, 12., 6.}, {10., 6., 8.}},
```

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```
  Key55 → {{4.30593, 12., 12.}, {15., 6., 13.}}, Key56 → {{4.61234, 5., 9.}, {6., 8., 8.}},
  Key57 → {{4.61234, 7., 11.}, {6., 14., 7.}}, Key58 → {{2.88959, 11., 8.}, {5., 17., 11.}},
  Key59 → {{5.18568, 13., 6.}, {12., 13., 11.}}, Key60 → {{2.46503, 9., 8.}, {8., 8., 8.}},
  Key61 → {{4.90502, 11., 19.}, {3., 16., 13.}}, Key62 → {{1.46133, 10., 10.}, {8., 8., 11.}},
  Key63 → {{0.827469, 6., 11.}, {11., 13., 12.}}, Key64 → {{4.61234, 12., 12.}, {6., 3., 4.}},
  Key65 → {{4.61234, 10., 8.}, {9., 9., 5.}}, Key66 → {{2.46503, 13., 12.}, {9., 6., 7.}},
  Key67 → {{3.98367, 11., 12.}, {11., 12., 12.}}, Key68 → {{3.98367, 9., 6.}, {15., 10., 14.}},
  Key69 → {{3.2798, 9., 11.}, {10., 4., 10.}}, Key70 → {{4.61234, 10., 11.}, {6., 10., 4.}},
  Key71 → {{5.96795, 11., 8.}, {12., 11., 13.}}, Key72 → {{1.99513, 7., 10.}, {11., 14., 11.}},
  Key73 → {{2.46503, 8., 9.}, {8., 7., 6.}}, Key74 → {{3.64283, 13., 7.}, {10., 10., 17.}},
  Key75 → {{1.46133, 11., 9.}, {12., 7., 10.}}, Key76 → {{3.98367, 10., 15.}, {8., 16., 10.}},
  Key77 → {{2.88959, 10., 7.}, {13., 11., 14.}}, Key78 → {{2.88959, 11., 7.}, {10., 6., 12.}},
  Key79 → {{1.99513, 11., 14.}, {6., 11., 16.}}, Key80 → {{3.98367, 9., 9.}, {9., 12., 15.}},
  Key81 → {{3.64283, 13., 12.}, {13., 8., 10.}}, Key82 → {{2.46503, 11., 3.}, {9., 11., 19.}},
  Key83 → {{3.98367, 17., 5.}, {12., 12., 7.}}, Key84 → {{3.98367, 11., 7.}, {10., 8., 10.}},
  Key85 → {{3.98367, 4., 9.}, {6., 5., 11.}}, Key86 → {{4.61234, 10., 17.}, {15., 9., 5.}},
  Key87 → {{2.88959, 12., 7.}, {15., 9., 10.}}, Key88 → {{2.88959, 5., 5.}, {8., 15., 15.}},
  Key89 → {{2.88959, 7., 7.}, {13., 7., 10.}}, Key90 → {{2.46503, 18., 7.}, {16., 7., 9.}},
  Key91 → {{2.88959, 10., 11.}, {8., 7., 13.}}, Key92 → {{1.46133, 11., 15.}, {8., 12., 8.}},
  Key93 → {{4.30593, 8., 10.}, {10., 8., 5.}}, Key94 → {{3.2798, 10., 9.}, {11., 12., 9.}},
  Key95 → {{3.64283, 11., 10.}, {10., 8., 1.}}, Key96 → {{2.88959, 8., 9.}, {5., 11., 4.}},
  Key97 → {{4.90502, 8., 10.}, {10., 10., 10.}}, Key98 → {{2.88959, 12., 8.}, {6., 14., 7.}},
  Key99 → {{2.46503, 11., 11.}, {13., 9., 7.}}, Key100 → {{0.827469, 9., 10.}, {10., 12., 15.}} |⟩,
Sample2 → ⟨| Key1 → {{3.65753, 5., 11.}, {15., 8., 6.}}, Key2 → {{1.40446, 9., 8.}, {10., 7., 11.}},
  Key3 → {{3.65753, 10., 10.}, {7., 12., 9.}}, Key4 → {{5.33759, 16., 5.}, {9., 5., 11.}},
  Key5 → {{3.65753, 4., 10.}, {4., 5., 9.}}, Key6 → {{4.44564, 7., 6.}, {10., 13., 12.}},
  Key7 → {{1.40446, 6., 17.}, {7., 13., 11.}}, Key8 → {{1.89574, 10., 13.}, {11., 10., 10.}},
  Key9 → {{1.40446, 7., 13.}, {12., 13., 10.}}, Key10 → {{3.36196, 5., 10.}, {12., 12., 11.}},
  Key11 → {{2.7, 13., 8.}, {12., 5., 11.}}, Key12 → {{2.7, 7., 14.}, {7., 14., 7.}},
  Key13 → {{4.44564, 11., 12.}, {18., 11., 11.}}, Key14 → {{1.40446, 5., 11.}, {12., 13., 10.}},
  Key15 → {{1.03226×10^-15, 6., 13.}, {11., 15., 5.}}, Key16 → {{4.44564, 8., 8.}, {4., 16., 17.}},
  Key17 → {{2.7, 8., 13.}, {9., 14., 9.}}, Key18 → {{1.40446, 10., 5.}, {16., 10., 15.}},
  Key19 → {{3.93491, 12., 10.}, {10., 10., 9.}}, Key20 → {{1.89574, 12., 15.}, {9., 10., 8.}},
  Key21 → {{3.93491, 13., 7.}, {14., 13., 13.}}, Key22 → {{4.68283, 9., 9.}, {14., 12., 8.}},
  Key23 → {{2.7, 7., 11.}, {6., 12., 7.}}, Key24 → {{3.0445, 12., 11.}, {6., 9., 5.}},
  Key25 → {{2.7, 16., 7.}, {10., 8., 17.}}, Key26 → {{3.65753, 10., 6.}, {7., 6., 11.}},
  Key27 → {{3.93491, 9., 7.}, {10., 11., 8.}}, Key28 → {{2.32096, 6., 10.}, {10., 9., 7.}},
  Key29 → {{3.0445, 8., 8.}, {12., 6., 12.}}, Key30 → {{3.36196, 5., 13.}, {7., 11., 10.}},
  Key31 → {{2.32096, 11., 8.}, {7., 7., 11.}}, Key32 → {{1.89574, 7., 7.}, {13., 10., 12.}},
  Key33 → {{3.93491, 14., 11.}, {13., 7., 11.}}, Key34 → {{4.1969, 9., 9.}, {9., 7., 8.}},
  Key35 → {{4.1969, 14., 8.}, {9., 6., 11.}}, Key36 → {{1.89574, 10., 14.}, {15., 7., 13.}},
  Key37 → {{3.65753, 15., 6.}, {6., 9., 15.}}, Key38 → {{3.36196, 5., 14.}, {6., 7., 10.}},
  Key39 → {{2.32096, 7., 18.}, {6., 12., 6.}}, Key40 → {{1.89574, 9., 12.}, {8., 11., 11.}},
  Key41 → {{3.0445, 11., 8.}, {18., 14., 10.}}, Key42 → {{-2.32444, 18., 6.}, {15., 15., 12.}},
  Key43 → {{3.0445, 10., 9.}, {9., 15., 9.}}, Key44 → {{3.93491, 13., 12.}, {14., 10., 12.}},
  Key45 → {{2.32096, 3., 9.}, {7., 8., 9.}}, Key46 → {{2.32096, 12., 8.}, {13., 13., 23.}},
  Key47 → {{2.7, 12., 10.}, {8., 16., 6.}}, Key48 → {{-2.32444, 10., 5.}, {10., 4., 12.}},
  Key49 → {{3.36196, 7., 12.}, {6., 8., 4.}}, Key50 → {{2.7, 13., 15.}, {14., 11., 7.}},
  Key51 → {{0.807582, 15., 11.}, {13., 9., 4.}}, Key52 → {{0.807582, 17., 8.}, {6., 11., 9.}},
  Key53 → {{4.44564, 10., 16.}, {12., 15., 10.}}, Key54 → {{2.7, 17., 12.}, {9., 4., 7.}},
  Key55 → {{3.65753, 13., 10.}, {6., 12., 9.}}, Key56 → {{2.7, 6., 5.}, {11., 8., 7.}},
  Key57 → {{2.32096, 12., 16.}, {15., 13., 10.}}, Key58 → {{3.0445, 13., 7.}, {13., 12., 7.}},
  Key59 → {{4.68283, 13., 7.}, {7., 11., 10.}}, Key60 → {{3.36196, 10., 8.}, {15., 9., 11.}},
  Key61 → {{3.36196, 4., 6.}, {3., 14., 10.}}, Key62 → {{2.32096, 10., 9.}, {4., 15., 11.}},
  Key63 → {{2.32096, 11., 7.}, {10., 7., 13.}}, Key64 → {{1.03226×10^-15, 13., 11.}, {8., 14., 19.}},
  Key65 → {{3.0445, 13., 11.}, {12., 7., 14.}}, Key66 → {{3.36196, 10., 9.}, {7., 8., 15.}},
  Key67 → {{4.1969, 7., 5.}, {9., 10., 4.}}, Key68 → {{0.807582, 10., 7.}, {8., 7., 8.}},
  Key69 → {{3.65753, 4., 13.}, {13., 11., 5.}}, Key70 → {{1.03226×10^-15, 15., 12.}, {11., 5., 9.}},
  Key71 → {{3.0445, 13., 10.}, {6., 7., 7.}}, Key72 → {{1.40446, 7., 9.}, {16., 8., 16.}},
  Key73 → {{3.36196, 5., 8.}, {12., 7., 11.}}, Key74 → {{3.0445, 3., 9.}, {7., 12., 9.}},
  Key75 → {{3.0445, 3., 8.}, {10., 9., 14.}}, Key76 → {{4.68283, 11., 9.}, {4., 11., 8.}},
  Key77 → {{3.93491, 9., 12.}, {12., 11., 6.}}, Key78 → {{2.7, 18., 6.}, {11., 5., 11.}},
  Key79 → {{2.32096, 7., 10.}, {9., 15., 10.}}, Key80 → {{1.89574, 6., 13.}, {7., 11., 10.}},
  Key81 → {{1.03226×10^-15, 15., 12.}, {13., 12., 11.}}, Key82 → {{3.65753, 15., 5.}, {17., 12., 7.}},
  Key83 → {{3.36196, 9., 12.}, {8., 9., 6.}}, Key84 → {{2.7, 6., 10.}, {12., 7., 9.}},
```

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```
    Key85 → {{3.36196, 9., 15.}, {9., 10., 7.}}, Key86 → {{1.89574, 6., 13.}, {10., 11., 13.}},
    Key87 → {{2.7, 13., 17.}, {10., 13., 7.}}, Key88 → {{0.807582, 11., 11.}, {4., 9., 12.}},
    Key89 → {{1.89574, 8., 6.}, {8., 10., 9.}}, Key90 → {{3.93491, 10., 10.}, {13., 14., 8.}},
    Key91 → {{2.32096, 15., 15.}, {10., 14., 7.}}, Key92 → {{2.7, 8., 8.}, {8., 9., 6.}},
    Key93 → {{1.40446, 7., 7.}, {7., 12., 17.}}, Key94 → {{2.32096, 8., 12.}, {12., 11., 12.}},
    Key95 → {{3.65753, 8., 9.}, {12., 6., 8.}}, Key96 → {{2.7, 14., 11.}, {12., 14., 15.}},
    Key97 → {{2.32096, 9., 15.}, {7., 11., 9.}}, Key98 → {{3.93491, 12., 12.}, {7., 9., 7.}},
    Key99 → {{3.65753, 8., 13.}, {10., 6., 10.}}, Key100 → {{3.93491, 19., 13.}, {13., 8., 9.}}|⟩,
  Sample3 → ‹|Key1 → {{4.55148, 9., 8.}, {3., 7., 7.}}, Key2 → {{1.45323, 12., 15.}, {16., 10., 9.}},
    Key3 → {{1.98088, 3., 11.}, {10., 8., 19.}}, Key4 → {{3.24566, 11., 10.}, {8., 9., 9.}},
    Key5 → {{4.55148, 7., 13.}, {17., 3., 8.}}, Key6 → {{3.60197, 7., 8.}, {15., 6., 8.}},
    Key7 → {{5.11174, 6., 11.}, {11., 13., 10.}}, Key8 → {{3.60197, 11., 14.}, {15., 11., 6.}},
    Key9 → {{2.44428, 9., 12.}, {9., 15., 10.}}, Key10 → {{2.86217, 11., 8.}, {8., 13., 12.}},
    Key11 → {{2.44428, 12., 13.}, {5., 4., 14.}}, Key12 → {{3.9361, 14., 10.}, {10., 5., 8.}},
    Key13 → {{5.62933, 5., 13.}, {11., 12., 6.}}, Key14 → {{0.824658, 13., 10.}, {13., 12., 8.}},
    Key15 → {{3.24566, 12., 19.}, {7., 9., 21.}}, Key16 → {{3.24566, 15., 13.}, {3., 8., 5.}},
    Key17 → {{4.25169, 5., 6.}, {9., 9., 14.}}, Key18 → {{1.45323, 7., 11.}, {11., 8., 9.}},
    Key19 → {{3.60197, 8., 7.}, {11., 8., 7.}}, Key20 → {{5.37528, 10., 8.}, {8., 6., 5.}},
    Key21 → {{4.8376, 12., 12.}, {9., 13., 7.}}, Key22 → {{4.55148, 13., 7.}, {13., 6., 6.}},
    Key23 → {{2.86217, 12., 9.}, {6., 13., 6.}}, Key24 → {{4.8376, 13., 12.}, {8., 9., 8.}},
    Key25 → {{2.44428, 11., 13.}, {10., 12., 12.}}, Key26 → {{0.824658, 12., 10.}, {8., 9., 9.}},
    Key27 → {{4.55148, 10., 10.}, {9., 14., 12.}}, Key28 → {{3.24566, 11., 10.}, {6., 10., 11.}},
    Key29 → {{2.44428, 13., 13.}, {6., 8., 10.}}, Key30 → {{3.60197, 8., 9.}, {11., 15., 6.}},
    Key31 → {{2.86217, 8., 9.}, {10., 2., 12.}}, Key32 → {{4.25169, 7., 12.}, {13., 9., 16.}},
    Key33 → {{4.25169, 9., 3.}, {16., 10., 9.}}, Key34 → {{1.45323, 11., 12.}, {11., 12., 10.}},
    Key35 → {{3.60197, 8., 9.}, {13., 15., 8.}}, Key36 → {{2.86217, 11., 10.}, {8., 12., 11.}},
    Key37 → {{0.824658, 15., 13.}, {11., 6., 12.}}, Key38 → {{4.55148, 14., 12.}, {16., 10., 12.}},
    Key39 → {{3.9361, 14., 7.}, {14., 10., 12.}}, Key40 → {{4.55148, 11., 17.}, {8., 8., 8.}},
    Key41 → {{3.24566, 12., 10.}, {16., 14., 13.}}, Key42 → {{1.98088, 7., 10.}, {11., 8., 7.}},
    Key43 → {{1.98088, 13., 5.}, {18., 9., 22.}}, Key44 → {{5.11174, 7., 14.}, {9., 11., 11.}},
    Key45 → {{4.25169, 5., 8.}, {11., 11., 12.}}, Key46 → {{5.11174, 11., 8.}, {10., 9., 9.}},
    Key47 → {{1.98088, 8., 9.}, {10., 9., 13.}}, Key48 → {{1.45323, 9., 7.}, {13., 10., 9.}},
    Key49 → {{4.55148, 15., 10.}, {5., 11., 13.}}, Key50 → {{2.86217, 9., 21.}, {19., 12., 10.}},
    Key51 → {{3.60197, 19., 5.}, {11., 7., 9.}}, Key52 → {{1.98088, 6., 13.}, {11., 7., 7.}},
    Key53 → {{3.9361, 10., 16.}, {6., 15., 11.}}, Key54 → {{4.55148, 7., 12.}, {9., 7., 9.}},
    Key55 → {{3.9361, 12., 3.}, {4., 13., 6.}}, Key56 → {{4.25169, 5., 14.}, {10., 12., 6.}},
    Key57 → {{3.9361, 6., 8.}, {15., 6., 12.}}, Key58 → {{2.86217, 10., 5.}, {10., 9., 12.}},
    Key59 → {{2.86217, 12., 10.}, {12., 6., 11.}}, Key60 → {{2.44428, 9., 10.}, {15., 7., 15.}},
    Key61 → {{1.98088, 10., 6.}, {13., 12., 13.}}, Key62 → {{4.25169, 7., 7.}, {14., 12., 13.}},
    Key63 → {{1.45323, 9., 3.}, {12., 13., 14.}}, Key64 → {{4.8376, 12., 11.}, {9., 10., 8.}},
    Key65 → {{1.98088, 9., 6.}, {7., 8., 5.}}, Key66 → {{4.8376, 3., 8.}, {8., 9., 9.}},
    Key67 → {{5.37528, 8., 10.}, {10., 7., 8.}}, Key68 → {{4.55148, 7., 11.}, {10., 8., 8.}},
    Key69 → {{4.25169, 16., 13.}, {14., 14., 9.}}, Key70 → {{1.98088, 11., 11.}, {9., 6., 11.}},
    Key71 → {{3.24566, 7., 6.}, {11., 15., 11.}}, Key72 → {{3.60197, 10., 10.}, {15., 6., 12.}},
    Key73 → {{3.60197, 9., 10.}, {6., 16., 8.}}, Key74 → {{2.86217, 10., 10.}, {12., 12., 11.}},
    Key75 → {{2.44428, 9., 6.}, {9., 3., 14.}}, Key76 → {{2.86217, 7., 6.}, {6., 7., 8.}},
    Key77 → {{3.24566, 10., 6.}, {10., 10., 11.}}, Key78 → {{3.60197, 12., 9.}, {10., 10., 14.}},
    Key79 → {{2.44428, 9., 10.}, {3., 11., 12.}}, Key80 → {{3.60197, 10., 11.}, {14., 8., 14.}},
    Key81 → {{3.60197, 10., 6.}, {7., 9., 9.}}, Key82 → {{4.55148, 9., 11.}, {15., 12., 8.}},
    Key83 → {{3.9361, 14., 11.}, {8., 13., 4.}}, Key84 → {{1.98088, 17., 12.}, {8., 11., 6.}},
    Key85 → {{4.25169, 7., 8.}, {7., 10., 9.}}, Key86 → {{4.8376, 11., 7.}, {8., 5., 12.}},
    Key87 → {{3.24566, 7., 10.}, {12., 3., 8.}}, Key88 → {{3.24566, 7., 15.}, {11., 15., 9.}},
    Key89 → {{5.11174, 11., 8.}, {10., 12., 8.}}, Key90 → {{2.44428, 7., 10.}, {9., 11., 14.}},
    Key91 → {{3.60197, 13., 9.}, {8., 13., 13.}}, Key92 → {{1.45323, 8., 8.}, {6., 12., 10.}},
    Key93 → {{2.44428, 6., 6.}, {5., 9., 12.}}, Key94 → {{4.55148, 12., 3.}, {11., 10., 10.}},
    Key95 → {{2.86217, 9., 12.}, {5., 14., 5.}}, Key96 → {{1.98088, 10., 10.}, {7., 11., 9.}},
    Key97 → {{-2.05107, 7., 8.}, {6., 18., 6.}}, Key98 → {{3.24566, 12., 12.}, {17., 7., 7.}},
    Key99 → {{2.86217, 15., 5.}, {6., 12., 8.}}, Key100 → {{2.44428, 13., 11.}, {7., 10., 4.}}|› |⟩
```

We can perform the optimized Box Cox Transform on values from the first list, second component :

```
In[5]:= ApplyBoxCoxTransformExtended[dataRandomOmicsObject, ListIndex → 1, ComponentIndex → 2]
```

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```
Calculated Box-Cox parameter λ̂ = {0.780773, 18.}

Calculated Box-Cox parameter λ̂ = {0.37463, -3.}

Calculated Box-Cox parameter λ̂ = {0.459162, -3.}
```

Out[5]=

```
<|Sample1 → <|Key1 → {{12., 17.4213, 9.}, {15., 6., 12.}}, Key2 → {{10., 15.9926, 10.}, {11., 10., 10.}},
  Key3 → {{17., 16.9486, 12.}, {9., 11., 11.}}, Key4 → {{9., 13.028, 9.}, {8., 10., 7.}},
  Key5 → {{18., 17.4213, 10.}, {8., 12., 8.}}, Key6 → {{8., 16.4724, 4.}, {5., 5., 7.}},
  Key7 → {{9., 15.9926, 9.}, {18., 13., 13.}}, Key8 → {{14., 14.5298, 9.}, {8., 8., 13.}},
  Key9 → {{12., 16.4724, 9.}, {7., 7., 11.}}, Key10 → {{10., 14.5298, 7.}, {12., 5., 8.}},
  Key11 → {{13., 14.5298, 10.}, {12., 17., 10.}}, Key12 → {{12., 15.9926, 12.}, {9., 9., 9.}},
  Key13 → {{12., 16.9486, 16.}, {13., 8., 12.}}, Key14 → {{15., 16.4724, 12.}, {8., 8., 7.}},
  Key15 → {{8., 15.9926, 9.}, {9., 6., 9.}}, Key16 → {{8., 14.5298, 11.}, {5., 9., 12.}},
  Key17 → {{8., 17.4213, 11.}, {7., 17., 12.}}, Key18 → {{12., 19.7374, 11.}, {7., 9., 8.}},
  Key19 → {{15., 15.9926, 18.}, {13., 13., 7.}}, Key20 → {{10., 17.8907, 5.}, {9., 10., 10.}},
  Key21 → {{8., 14.0339, 8.}, {10., 5., 8.}}, Key22 → {{7., 13.5333, 9.}, {9., 12., 15.}},
  Key23 → {{13., 14.5298, 7.}, {4., 13., 10.}}, Key24 → {{10., 15.9926, 11.}, {7., 10., 13.}},
  Key25 → {{12., 15.0215, 7.}, {9., 9., 9.}}, Key26 → {{4., 15.9926, 9.}, {11., 11., 7.}},
  Key27 → {{13., 15.509, 16.}, {11., 9., 10.}}, Key28 → {{14., 14.0339, 10.}, {8., 12., 12.}},
  Key29 → {{10., 12.5176, 12.}, {9., 4., 13.}}, Key30 → {{14., 15.9926, 13.}, {11., 10., 10.}},
  Key31 → {{7., 13.028, 8.}, {12., 16., 3.}}, Key32 → {{3., 15.509, 9.}, {10., 7., 5.}},
  Key33 → {{6., 16.4724, 6.}, {6., 13., 7.}}, Key34 → {{4., 15.9926, 14.}, {5., 7., 12.}},
  Key35 → {{11., 16.9486, 11.}, {7., 7., 7.}}, Key36 → {{6., 14.5298, 8.}, {9., 11., 9.}},
  Key37 → {{8., 16.9486, 12.}, {9., 12., 12.}}, Key38 → {{8., 14.5298, 6.}, {11., 8., 8.}},
  Key39 → {{6., 16.9486, 15.}, {12., 13., 10.}}, Key40 → {{7., 15.9926, 11.}, {13., 10., 14.}},
  Key41 → {{9., 16.4724, 9.}, {9., 8., 9.}}, Key42 → {{11., 17.8907, 12.}, {15., 9., 9.}},
  Key43 → {{9., 15.509, 16.}, {8., 11., 11.}}, Key44 → {{12., 15.0215, 10.}, {3., 10., 16.}},
  Key45 → {{12., 14.0339, 9.}, {9., 8., 6.}}, Key46 → {{9., 16.9486, 16.}, {8., 6., 8.}},
  Key47 → {{8., 18.3569, 6.}, {8., 14., 11.}}, Key48 → {{9., 15.509, 8.}, {12., 8., 9.}},
  Key49 → {{9., 15.509, 12.}, {12., 13., 9.}}, Key50 → {{9., 17.8907, 6.}, {10., 5., 20.}},
  Key51 → {{9., 16.4724, 7.}, {9., 11., 12.}}, Key52 → {{6., 15.9926, 12.}, {5., 13., 5.}},
  Key53 → {{14., 15.509, 15.}, {10., 10., 7.}}, Key54 → {{9., 16.9486, 6.}, {10., 6., 8.}},
  Key55 → {{13., 16.9486, 12.}, {15., 6., 13.}}, Key56 → {{14., 13.5333, 9.}, {6., 8., 8.}},
  Key57 → {{14., 14.5298, 11.}, {6., 14., 7.}}, Key58 → {{9., 16.4724, 8.}, {5., 17., 11.}},
  Key59 → {{16., 17.4213, 6.}, {12., 13., 11.}}, Key60 → {{8., 15.509, 8.}, {8., 8., 8.}},
  Key61 → {{15., 16.4724, 19.}, {3., 16., 13.}}, Key62 → {{6., 15.9926, 10.}, {8., 8., 11.}},
  Key63 → {{5., 14.0339, 11.}, {11., 13., 12.}}, Key64 → {{14., 16.9486, 12.}, {6., 3., 4.}},
  Key65 → {{14., 15.9926, 8.}, {9., 9., 5.}}, Key66 → {{8., 17.4213, 12.}, {9., 6., 7.}},
  Key67 → {{12., 16.4724, 12.}, {11., 12., 12.}}, Key68 → {{12., 15.509, 6.}, {15., 10., 14.}},
  Key69 → {{10., 15.509, 11.}, {10., 4., 10.}}, Key70 → {{14., 15.9926, 11.}, {6., 10., 4.}},
  Key71 → {{19., 16.4724, 8.}, {12., 11., 13.}}, Key72 → {{7., 14.5298, 10.}, {11., 14., 11.}},
  Key73 → {{8., 15.0215, 9.}, {8., 7., 6.}}, Key74 → {{11., 17.4213, 7.}, {10., 10., 17.}},
  Key75 → {{6., 16.4724, 9.}, {12., 7., 10.}}, Key76 → {{12., 15.9926, 15.}, {8., 16., 10.}},
  Key77 → {{9., 15.9926, 7.}, {13., 11., 14.}}, Key78 → {{9., 16.4724, 7.}, {10., 6., 12.}},
  Key79 → {{7., 16.4724, 14.}, {6., 11., 16.}}, Key80 → {{12., 15.509, 9.}, {9., 12., 15.}},
  Key81 → {{11., 17.4213, 12.}, {13., 8., 10.}}, Key82 → {{8., 16.4724, 3.}, {9., 11., 19.}},
  Key83 → {{12., 19.2801, 5.}, {12., 12., 7.}}, Key84 → {{12., 16.4724, 7.}, {10., 8., 10.}},
  Key85 → {{12., 13.028, 9.}, {6., 5., 11.}}, Key86 → {{14., 15.9926, 17.}, {15., 9., 5.}},
  Key87 → {{9., 16.9486, 7.}, {15., 9., 10.}}, Key88 → {{9., 13.5333, 5.}, {8., 15., 15.}},
  Key89 → {{9., 14.5298, 7.}, {13., 7., 10.}}, Key90 → {{8., 19.7374, 7.}, {16., 7., 9.}},
  Key91 → {{9., 15.9926, 11.}, {8., 7., 13.}}, Key92 → {{6., 16.4724, 15.}, {8., 12., 8.}},
  Key93 → {{13., 15.0215, 10.}, {10., 8., 5.}}, Key94 → {{10., 15.9926, 9.}, {11., 12., 9.}},
  Key95 → {{11., 16.4724, 10.}, {10., 8., 1.}}, Key96 → {{9., 15.0215, 9.}, {5., 11., 4.}},
  Key97 → {{15., 15.0215, 10.}, {10., 10., 10.}}, Key98 → {{9., 16.9486, 8.}, {6., 14., 7.}},
  Key99 → {{8., 16.4724, 11.}, {13., 9., 7.}}, Key100 → {{5., 15.509, 10.}, {10., 12., 15.}}|>,
 Sample2 → <|Key1 → {{12., 0.791466, 11.}, {15., 8., 6.}}, Key2 → {{6., 2.55366, 8.}, {10., 7., 11.}},
  Key3 → {{12., 2.86416, 10.}, {7., 12., 9.}}, Key4 → {{19., 4.30843, 5.}, {9., 5., 11.}},
  Key5 → {{12., 5.92703×10^-16, 10.}, {4., 5., 9.}}, Key6 → {{15., 1.81761, 6.}, {10., 13., 12.}},
  Key7 → {{6., 1.35918, 17.}, {7., 13., 11.}}, Key8 → {{7., 2.86416, 13.}, {11., 10., 10.}},
  Key9 → {{6., 1.81761, 13.}, {12., 13., 10.}}, Key10 → {{11., 0.791466, 10.}, {12., 12., 11.}},
  Key11 → {{9., 3.65522, 8.}, {12., 5., 11.}}, Key12 → {{9., 1.81761, 14.}, {7., 14., 7.}},
  Key13 → {{15., 3.14801, 12.}, {18., 11., 11.}}, Key14 → {{6., 0.791466, 11.}, {12., 13., 10.}},
  Key15 → {{4., 1.35918, 13.}, {11., 15., 5.}}, Key16 → {{15., 2.20882, 8.}, {4., 16., 17.}},
  Key17 → {{9., 2.20882, 13.}, {9., 14., 9.}}, Key18 → {{6., 2.86416, 5.}, {16., 10., 15.}},
```

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```
  Key19 → {{13., 3.41045, 10.}, {10., 10., 9.}}, Key20 → {{7., 3.41045, 15.}, {9., 10., 8.}},
  Key21 → {{13., 3.65522, 7.}, {14., 13., 13.}}, Key22 → {{16., 2.55366, 9.}, {14., 12., 8.}},
  Key23 → {{9., 1.81761, 11.}, {6., 12., 7.}}, Key24 → {{10., 3.41045, 11.}, {6., 9., 5.}},
  Key25 → {{9., 4.30843, 7.}, {10., 8., 17.}}, Key26 → {{12., 2.86416, 6.}, {7., 6., 11.}},
  Key27 → {{13., 2.55366, 7.}, {10., 11., 8.}}, Key28 → {{8., 1.35918, 10.}, {10., 9., 7.}},
  Key29 → {{10., 2.20882, 8.}, {12., 6., 12.}}, Key30 → {{11., 0.791466, 13.}, {7., 11., 10.}},
  Key31 → {{8., 3.14801, 8.}, {7., 7., 11.}}, Key32 → {{7., 1.81761, 7.}, {13., 10., 12.}},
  Key33 → {{13., 3.88512, 11.}, {13., 7., 11.}}, Key34 → {{14., 2.55366, 9.}, {9., 7., 8.}},
  Key35 → {{14., 3.88512, 8.}, {9., 6., 11.}}, Key36 → {{7., 2.86416, 14.}, {15., 7., 13.}},
  Key37 → {{12., 4.1023, 6.}, {6., 9., 15.}}, Key38 → {{11., 0.791466, 14.}, {6., 7., 10.}},
  Key39 → {{8., 1.81761, 18.}, {6., 12., 6.}}, Key40 → {{7., 2.55366, 12.}, {8., 11., 11.}},
  Key41 → {{10., 3.14801, 8.}, {18., 14., 10.}}, Key42 → {{3., 4.69271, 6.}, {15., 15., 12.}},
  Key43 → {{10., 2.86416, 9.}, {9., 15., 9.}}, Key44 → {{13., 3.65522, 12.}, {14., 10., 12.}},
  Key45 → {{8., -2.66929, 9.}, {7., 8., 9.}}, Key46 → {{8., 3.41045, 8.}, {13., 13., 23.}},
  Key47 → {{9., 3.41045, 10.}, {8., 16., 6.}}, Key48 → {{3., 2.86416, 5.}, {10., 4., 12.}},
  Key49 → {{11., 1.81761, 12.}, {6., 8., 4.}}, Key50 → {{9., 3.65522, 15.}, {14., 11., 7.}},
  Key51 → {{5., 4.1023, 11.}, {13., 9., 4.}}, Key52 → {{5., 4.50487, 8.}, {6., 11., 9.}},
  Key53 → {{15., 2.86416, 16.}, {12., 15., 10.}}, Key54 → {{9., 4.50487, 12.}, {9., 4., 7.}},
  Key55 → {{12., 3.65522, 10.}, {6., 12., 9.}}, Key56 → {{9., 1.35918, 5.}, {11., 8., 7.}},
  Key57 → {{8., 3.41045, 16.}, {15., 13., 10.}}, Key58 → {{10., 3.65522, 7.}, {13., 12., 7.}},
  Key59 → {{16., 3.65522, 7.}, {7., 11., 10.}}, Key60 → {{11., 2.86416, 8.}, {15., 9., 11.}},
  Key61 → {{11., 5.92703×10^-16, 6.}, {3., 14., 10.}}, Key62 → {{8., 2.86416, 9.}, {4., 15., 11.}},
  Key63 → {{8., 3.14801, 7.}, {10., 7., 13.}}, Key64 → {{4., 3.65522, 11.}, {8., 14., 19.}},
  Key65 → {{10., 3.65522, 11.}, {12., 7., 14.}}, Key66 → {{11., 2.86416, 9.}, {7., 8., 15.}},
  Key67 → {{14., 1.81761, 5.}, {9., 10., 4.}}, Key68 → {{5., 2.86416, 7.}, {8., 7., 8.}},
  Key69 → {{12., 5.92703×10^-16, 13.}, {13., 11., 5.}}, Key70 → {{4., 4.1023, 12.}, {11., 5., 9.}},
  Key71 → {{10., 3.65522, 10.}, {6., 7., 7.}}, Key72 → {{6., 1.81761, 9.}, {16., 8., 16.}},
  Key73 → {{11., 0.791466, 8.}, {12., 7., 11.}}, Key74 → {{10., -2.66929, 9.}, {7., 12., 9.}},
  Key75 → {{10., -2.66929, 8.}, {10., 9., 14.}}, Key76 → {{16., 3.14801, 9.}, {4., 11., 8.}},
  Key77 → {{13., 2.55366, 12.}, {12., 11., 6.}}, Key78 → {{9., 4.69271, 6.}, {11., 5., 11.}},
  Key79 → {{8., 1.81761, 10.}, {9., 15., 10.}}, Key80 → {{7., 1.35918, 13.}, {7., 11., 10.}},
  Key81 → {{4., 4.1023, 12.}, {13., 12., 11.}}, Key82 → {{12., 4.1023, 5.}, {17., 12., 7.}},
  Key83 → {{11., 2.55366, 12.}, {8., 9., 6.}}, Key84 → {{9., 1.35918, 10.}, {12., 7., 9.}},
  Key85 → {{11., 2.55366, 15.}, {9., 10., 7.}}, Key86 → {{7., 1.35918, 13.}, {10., 11., 13.}},
  Key87 → {{9., 3.65522, 17.}, {10., 13., 7.}}, Key88 → {{5., 3.14801, 11.}, {4., 9., 12.}},
  Key89 → {{7., 2.20882, 6.}, {8., 10., 9.}}, Key90 → {{13., 2.86416, 10.}, {13., 14., 8.}},
  Key91 → {{8., 4.1023, 15.}, {10., 14., 7.}}, Key92 → {{9., 2.20882, 8.}, {8., 9., 6.}},
  Key93 → {{6., 1.81761, 7.}, {7., 12., 17.}}, Key94 → {{8., 2.20882, 12.}, {12., 11., 12.}},
  Key95 → {{12., 2.20882, 9.}, {12., 6., 8.}}, Key96 → {{9., 3.88512, 11.}, {12., 14., 15.}},
  Key97 → {{8., 2.55366, 15.}, {7., 11., 9.}}, Key98 → {{13., 3.41045, 12.}, {7., 9., 7.}},
  Key99 → {{12., 2.20882, 13.}, {10., 6., 10.}}, Key100 → {{13., 4.87288, 13.}, {13., 8., 9.}}|〉,
Sample3 → 〈|Key1 → {{13., 2.7804, 8.}, {3., 7., 7.}}, Key2 → {{5., 3.79503, 15.}, {16., 10., 9.}},
  Key3 → {{6., -2.17788, 11.}, {10., 8., 19.}}, Key4 → {{9., 3.48058, 10.}, {8., 9., 9.}},
  Key5 → {{13., 1.93814, 13.}, {17., 3., 8.}}, Key6 → {{10., 1.93814, 8.}, {15., 6., 8.}},
  Key7 → {{15., 1.42882, 11.}, {11., 13., 10.}}, Key8 → {{10., 3.48058, 14.}, {15., 11., 6.}},
  Key9 → {{7., 2.7804, 12.}, {9., 15., 10.}}, Key10 → {{8., 3.48058, 8.}, {8., 13., 12.}},
  Key11 → {{7., 3.79503, 13.}, {5., 4., 14.}}, Key12 → {{11., 4.37153, 10.}, {10., 5., 8.}},
  Key13 → {{17., 0.816146, 13.}, {11., 12., 6.}}, Key14 → {{4., 4.09109, 10.}, {13., 12., 8.}},
  Key15 → {{9., 3.79503, 19.}, {7., 9., 21.}}, Key16 → {{9., 4.63849, 13.}, {3., 8., 5.}},
  Key17 → {{12., 0.816146, 6.}, {9., 9., 14.}}, Key18 → {{5., 1.93814, 11.}, {11., 8., 9.}},
  Key19 → {{10., 2.38222, 7.}, {11., 8., 7.}}, Key20 → {{16., 3.14407, 8.}, {8., 6., 5.}},
  Key21 → {{14., 3.79503, 12.}, {9., 13., 7.}}, Key22 → {{13., 4.09109, 7.}, {13., 6., 6.}},
  Key23 → {{8., 3.79503, 9.}, {6., 13., 6.}}, Key24 → {{14., 4.09109, 12.}, {8., 9., 8.}},
  Key25 → {{7., 3.48058, 13.}, {10., 12., 12.}}, Key26 → {{4., 3.79503, 10.}, {8., 9., 9.}},
  Key27 → {{13., 3.14407, 10.}, {9., 14., 12.}}, Key28 → {{9., 3.48058, 10.}, {6., 10., 11.}},
  Key29 → {{7., 4.09109, 13.}, {6., 8., 10.}}, Key30 → {{10., 2.38222, 9.}, {11., 15., 6.}},
  Key31 → {{8., 2.38222, 9.}, {10., 2., 12.}}, Key32 → {{12., 1.93814, 12.}, {13., 9., 16.}},
  Key33 → {{12., 2.7804, 3.}, {16., 10., 9.}}, Key34 → {{5., 3.48058, 12.}, {11., 12., 10.}},
  Key35 → {{10., 2.38222, 9.}, {13., 15., 8.}}, Key36 → {{8., 3.48058, 10.}, {8., 12., 11.}},
  Key37 → {{4., 4.63849, 13.}, {11., 6., 12.}}, Key38 → {{13., 4.37153, 12.}, {16., 10., 12.}},
  Key39 → {{11., 4.37153, 7.}, {14., 10., 12.}}, Key40 → {{13., 3.48058, 17.}, {8., 8., 8.}},
  Key41 → {{9., 3.79503, 10.}, {16., 14., 13.}}, Key42 → {{6., 1.93814, 10.}, {11., 8., 7.}},
  Key43 → {{6., 4.09109, 5.}, {18., 9., 22.}}, Key44 → {{15., 1.93814, 14.}, {9., 11., 11.}},
  Key45 → {{12., 0.816146, 8.}, {11., 11., 12.}}, Key46 → {{15., 3.48058, 8.}, {10., 9., 9.}},
  Key47 → {{6., 2.38222, 9.}, {10., 9., 13.}}, Key48 → {{5., 2.7804, 7.}, {13., 10., 9.}},
```

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```
Key49 → {{13., 4.63849, 10.}, {5., 11., 13.}}, Key50 → {{8., 2.7804, 21.}, {19., 12., 10.}},
Key51 → {{10., 5.60105, 5.}, {11., 7., 9.}}, Key52 → {{6., 1.42882, 13.}, {11., 7., 7.}},
Key53 → {{11., 3.14407, 16.}, {6., 15., 11.}}, Key54 → {{13., 1.93814, 12.}, {9., 7., 9.}},
Key55 → {{11., 3.79503, 3.}, {4., 13., 6.}}, Key56 → {{12., 0.816146, 14.}, {10., 12., 6.}},
Key57 → {{11., 1.42882, 8.}, {15., 6., 12.}}, Key58 → {{8., 3.14407, 5.}, {10., 9., 12.}},
Key59 → {{8., 3.79503, 10.}, {12., 6., 11.}}, Key60 → {{7., 2.7804, 10.}, {15., 7., 15.}},
Key61 → {{6., 3.14407, 6.}, {13., 12., 13.}}, Key62 → {{12., 1.93814, 7.}, {14., 12., 13.}},
Key63 → {{5., 2.7804, 3.}, {12., 13., 14.}}, Key64 → {{14., 3.79503, 11.}, {9., 10., 8.}},
Key65 → {{6., 2.7804, 6.}, {7., 8., 5.}}, Key66 → {{14., -2.17788, 8.}, {8., 9., 9.}},
Key67 → {{16., 2.38222, 10.}, {10., 7., 8.}}, Key68 → {{13., 1.93814, 11.}, {10., 8., 8.}},
Key69 → {{12., 4.89367, 13.}, {14., 14., 9.}}, Key70 → {{6., 3.48058, 11.}, {9., 6., 11.}},
Key71 → {{9., 1.93814, 6.}, {11., 15., 11.}}, Key72 → {{10., 3.14407, 10.}, {15., 6., 12.}},
Key73 → {{10., 2.7804, 10.}, {6., 16., 8.}}, Key74 → {{8., 3.14407, 10.}, {12., 12., 11.}},
Key75 → {{7., 2.7804, 6.}, {9., 3., 14.}}, Key76 → {{8., 1.93814, 6.}, {6., 7., 8.}},
Key77 → {{9., 3.14407, 6.}, {10., 10., 11.}}, Key78 → {{10., 3.79503, 9.}, {10., 10., 14.}},
Key79 → {{7., 2.7804, 10.}, {3., 11., 12.}}, Key80 → {{10., 3.14407, 11.}, {14., 8., 14.}},
Key81 → {{10., 3.14407, 6.}, {7., 9., 9.}}, Key82 → {{13., 2.7804, 11.}, {15., 12., 8.}},
Key83 → {{11., 4.37153, 11.}, {8., 13., 4.}}, Key84 → {{6., 5.13843, 12.}, {8., 11., 6.}},
Key85 → {{12., 1.93814, 8.}, {7., 10., 9.}}, Key86 → {{14., 3.48058, 7.}, {8., 5., 12.}},
Key87 → {{9., 1.93814, 10.}, {12., 3., 8.}}, Key88 → {{9., 1.93814, 15.}, {11., 15., 9.}},
Key89 → {{15., 3.48058, 8.}, {10., 12., 8.}}, Key90 → {{7., 1.93814, 10.}, {9., 11., 14.}},
Key91 → {{10., 4.09109, 9.}, {8., 13., 13.}}, Key92 → {{5., 2.38222, 8.}, {6., 12., 10.}},
Key93 → {{7., 1.42882, 6.}, {5., 9., 12.}}, Key94 → {{13., 3.79503, 3.}, {11., 10., 10.}},
Key95 → {{8., 2.7804, 12.}, {5., 14., 5.}}, Key96 → {{6., 3.14407, 10.}, {7., 11., 9.}},
Key97 → {{2., 1.93814, 8.}, {6., 18., 6.}}, Key98 → {{9., 3.79503, 12.}, {17., 7., 7.}},
Key99 → {{8., 4.63849, 5.}, {6., 12., 8.}}, Key100 → {{7., 4.09109, 11.}, {7., 10., 4.}} ⋯ |⟩
```

HorizontalSelection (1)

```
In[1]:= Needs["MathIOmica`"]
```

For input data that is an association with multi-list values we need to set HorizontalSelection to True to be able to select across the keys the right list and component. Let's generate some random data first:

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In[2]:=
```
dataRandomAssociationsExample = AssociationThread@
  (("Key" <> ToString[#]) & /@ Range[100] → RandomVariate[PoissonDistribution[10], {100, 2, 3}])
```

Out[2]=
```
<|Key1 → {{9, 8, 11}, {11, 6, 11}}, Key2 → {{12, 10, 12}, {5, 14, 13}},
 Key3 → {{11, 15, 6}, {14, 15, 7}}, Key4 → {{13, 9, 11}, {20, 12, 12}}, Key5 → {{9, 10, 6}, {12, 3, 17}},
 Key6 → {{10, 13, 5}, {10, 13, 11}}, Key7 → {{15, 12, 16}, {5, 10, 10}}, Key8 → {{9, 11, 12}, {6, 9, 17}},
 Key9 → {{8, 16, 7}, {10, 16, 10}}, Key10 → {{7, 8, 10}, {10, 13, 8}}, Key11 → {{7, 11, 4}, {9, 7, 18}},
 Key12 → {{8, 6, 12}, {10, 9, 9}}, Key13 → {{15, 9, 10}, {8, 6, 7}}, Key14 → {{14, 12, 12}, {9, 14, 14}},
 Key15 → {{13, 17, 10}, {13, 5, 9}}, Key16 → {{10, 9, 9}, {9, 9, 13}}, Key17 → {{10, 15, 11}, {10, 8, 15}},
 Key18 → {{12, 10, 12}, {10, 12, 8}}, Key19 → {{11, 10, 12}, {12, 15, 4}},
 Key20 → {{10, 7, 13}, {21, 13, 8}}, Key21 → {{14, 14, 9}, {12, 7, 10}}, Key22 → {{9, 11, 10}, {8, 6, 11}},
 Key23 → {{12, 12, 9}, {5, 16, 13}}, Key24 → {{9, 11, 8}, {5, 6, 7}}, Key25 → {{4, 10, 12}, {6, 7, 7}},
 Key26 → {{16, 8, 9}, {7, 8, 12}}, Key27 → {{12, 10, 11}, {7, 14, 12}}, Key28 → {{6, 13, 10}, {9, 10, 6}},
 Key29 → {{9, 13, 13}, {11, 10, 8}}, Key30 → {{12, 15, 11}, {8, 13, 16}}, Key31 → {{15, 7, 7}, {12, 6, 5}},
 Key32 → {{12, 12, 16}, {12, 10, 14}}, Key33 → {{19, 10, 13}, {7, 8, 9}}, Key34 → {{6, 14, 14}, {22, 20, 9}},
 Key35 → {{10, 8, 8}, {10, 10, 11}}, Key36 → {{9, 15, 9}, {10, 5, 9}}, Key37 → {{8, 7, 14}, {9, 7, 6}},
 Key38 → {{16, 9, 18}, {12, 17, 10}}, Key39 → {{9, 11, 9}, {6, 12, 13}}, Key40 → {{9, 9, 13}, {9, 8, 15}},
 Key41 → {{12, 9, 9}, {9, 9, 8}}, Key42 → {{10, 14, 10}, {8, 12, 13}}, Key43 → {{5, 6, 10}, {11, 7, 10}},
 Key44 → {{14, 8, 12}, {10, 8, 10}}, Key45 → {{8, 11, 8}, {10, 8, 6}}, Key46 → {{13, 6, 9}, {10, 7, 9}},
 Key47 → {{4, 10, 3}, {11, 10, 6}}, Key48 → {{9, 15, 12}, {8, 10, 8}}, Key49 → {{9, 11, 9}, {10, 13, 9}},
 Key50 → {{11, 9, 8}, {6, 19, 4}}, Key51 → {{10, 13, 5}, {14, 17, 8}}, Key52 → {{9, 12, 7}, {8, 11, 8}},
 Key53 → {{11, 6, 12}, {8, 6, 12}}, Key54 → {{17, 11, 7}, {15, 9, 10}}, Key55 → {{10, 6, 8}, {7, 10, 9}},
 Key56 → {{14, 13, 10}, {9, 7, 7}}, Key57 → {{8, 8, 12}, {12, 6, 16}}, Key58 → {{11, 14, 9}, {8, 13, 13}},
 Key59 → {{3, 5, 9}, {10, 9, 12}}, Key60 → {{8, 12, 12}, {5, 6, 14}}, Key61 → {{19, 7, 12}, {10, 13, 9}},
 Key62 → {{12, 9, 5}, {14, 9, 8}}, Key63 → {{5, 11, 5}, {11, 16, 11}}, Key64 → {{6, 11, 6}, {10, 8, 6}},
 Key65 → {{9, 13, 14}, {9, 9, 4}}, Key66 → {{10, 4, 7}, {9, 17, 6}}, Key67 → {{14, 14, 11}, {5, 12, 9}},
 Key68 → {{7, 8, 10}, {9, 13, 8}}, Key69 → {{8, 11, 4}, {6, 12, 13}}, Key70 → {{8, 13, 7}, {16, 12, 14}},
 Key71 → {{12, 2, 9}, {13, 12, 9}}, Key72 → {{10, 13, 9}, {8, 10, 13}}, Key73 → {{13, 6, 8}, {12, 9, 10}},
 Key74 → {{9, 11, 7}, {10, 5, 13}}, Key75 → {{10, 11, 8}, {4, 5, 14}}, Key76 → {{15, 10, 11}, {6, 6, 11}},
 Key77 → {{7, 12, 7}, {8, 15, 7}}, Key78 → {{16, 11, 7}, {15, 11, 7}}, Key79 → {{15, 6, 12}, {10, 11, 12}},
 Key80 → {{19, 10, 12}, {17, 6, 9}}, Key81 → {{16, 7, 12}, {10, 5, 16}}, Key82 → {{8, 13, 9}, {6, 8, 5}},
 Key83 → {{9, 8, 16}, {7, 11, 13}}, Key84 → {{9, 10, 8}, {10, 4, 14}}, Key85 → {{11, 9, 13}, {14, 7, 11}},
 Key86 → {{10, 11, 8}, {7, 12, 9}}, Key87 → {{10, 14, 12}, {8, 10, 13}}, Key88 → {{11, 17, 6}, {15, 10, 7}},
 Key89 → {{16, 13, 6}, {7, 10, 7}}, Key90 → {{8, 19, 10}, {12, 9, 12}}, Key91 → {{11, 8, 8}, {12, 9, 6}},
 Key92 → {{14, 10, 11}, {10, 10, 6}}, Key93 → {{7, 7, 11}, {16, 10, 9}}, Key94 → {{10, 13, 8}, {8, 18, 7}},
 Key95 → {{11, 12, 12}, {8, 3, 7}}, Key96 → {{10, 11, 10}, {15, 4, 11}}, Key97 → {{11, 12, 7}, {13, 9, 10}},
 Key98 → {{13, 8, 9}, {11, 10, 12}}, Key99 → {{11, 6, 11}, {10, 6, 13}}, Key100 → {{15, 8, 0}, {8, 20, 9}}|>
```

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In[3]:=
```
ApplyBoxCoxTransformExtended[dataRandomAssociationsExample,
 ListIndex → 1, ComponentIndex → 1, HorizontalSelection → True]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = {-0.0438474, 19.}

Out[3]=
```
<|Key1 → {{3.10021, 8., 11.}, {11., 6., 11.}}, Key2 → {{3.18796, 10., 12.}, {5., 14., 13.}},
 Key3 → {{3.15973, 15., 6.}, {14., 15., 7.}}, Key4 → {{3.21525, 9., 11.}, {20., 12., 12.}},
 Key5 → {{3.10021, 10., 6.}, {12., 3., 17.}}, Key6 → {{3.13051, 13., 5.}, {10., 13., 11.}},
 Key7 → {{3.26726, 12., 16.}, {5., 10., 10.}}, Key8 → {{3.10021, 11., 12.}, {6., 9., 17.}},
 Key9 → {{3.06876, 16., 7.}, {10., 16., 10.}}, Key10 → {{3.03607, 8., 10.}, {10., 13., 8.}},
 Key11 → {{3.03607, 11., 4.}, {9., 7., 18.}}, Key12 → {{3.06876, 6., 12.}, {10., 9., 9.}},
 Key13 → {{3.26726, 9., 10.}, {8., 6., 7.}}, Key14 → {{3.24167, 12., 12.}, {9., 14., 14.}},
 Key15 → {{3.21525, 17., 10.}, {13., 5., 9.}}, Key16 → {{3.13051, 9., 9.}, {9., 9., 13.}},
 Key17 → {{3.13051, 15., 11.}, {10., 8., 15.}}, Key18 → {{3.18796, 10., 12.}, {10., 12., 8.}},
 Key19 → {{3.15973, 10., 12.}, {12., 15., 4.}}, Key20 → {{3.13051, 7., 13.}, {21., 13., 8.}},
 Key21 → {{3.24167, 14., 9.}, {12., 7., 10.}}, Key22 → {{3.10021, 11., 10.}, {8., 6., 11.}},
 Key23 → {{3.18796, 12., 9.}, {5., 16., 13.}}, Key24 → {{3.10021, 11., 8.}, {5., 6., 7.}},
 Key25 → {{2.9295, 10., 12.}, {6., 7., 7.}}, Key26 → {{3.29208, 8., 9.}, {7., 8., 12.}},
 Key27 → {{3.18796, 10., 11.}, {7., 14., 12.}}, Key28 → {{3.00204, 13., 10.}, {9., 10., 6.}},
 Key29 → {{3.10021, 13., 13.}, {11., 10., 8.}}, Key30 → {{3.18796, 15., 11.}, {8., 13., 16.}},
 Key31 → {{3.26726, 7., 7.}, {12., 6., 5.}}, Key32 → {{3.18796, 12., 16.}, {12., 10., 14.}},
 Key33 → {{3.36232, 10., 13.}, {7., 8., 9.}}, Key34 → {{3.00204, 14., 14.}, {22., 20., 9.}},
 Key35 → {{3.13051, 8., 8.}, {10., 10., 11.}}, Key36 → {{3.10021, 15., 9.}, {10., 5., 9.}},
 Key37 → {{3.06876, 7., 14.}, {9., 7., 6.}}, Key38 → {{3.29208, 9., 18.}, {12., 17., 10.}},
 Key39 → {{3.10021, 11., 9.}, {6., 12., 13.}}, Key40 → {{3.10021, 9., 13.}, {9., 8., 15.}},
 Key41 → {{3.18796, 9., 9.}, {9., 9., 8.}}, Key42 → {{3.13051, 14., 10.}, {8., 12., 13.}},
 Key43 → {{2.96656, 6., 10.}, {11., 7., 10.}}, Key44 → {{3.24167, 8., 12.}, {10., 8., 10.}},
 Key45 → {{3.06876, 11., 8.}, {10., 8., 6.}}, Key46 → {{3.21525, 6., 9.}, {10., 7., 9.}},
 Key47 → {{2.9295, 10., 3.}, {11., 10., 6.}}, Key48 → {{3.10021, 15., 12.}, {8., 10., 8.}},
 Key49 → {{3.10021, 11., 9.}, {10., 13., 9.}}, Key50 → {{3.15973, 9., 8.}, {6., 19., 4.}},
 Key51 → {{3.13051, 13., 5.}, {14., 17., 8.}}, Key52 → {{3.10021, 12., 7.}, {8., 11., 8.}},
 Key53 → {{3.15973, 6., 12.}, {8., 6., 12.}}, Key54 → {{3.31617, 11., 7.}, {15., 9., 10.}},
 Key55 → {{3.13051, 6., 8.}, {7., 10., 9.}}, Key56 → {{3.24167, 13., 10.}, {9., 7., 7.}},
 Key57 → {{3.06876, 8., 12.}, {12., 6., 16.}}, Key58 → {{3.15973, 14., 9.}, {8., 13., 13.}},
 Key59 → {{2.89072, 5., 9.}, {10., 9., 12.}}, Key60 → {{3.06876, 12., 12.}, {5., 6., 14.}},
 Key61 → {{3.36232, 7., 12.}, {10., 13., 9.}}, Key62 → {{3.18796, 9., 5.}, {14., 9., 8.}},
 Key63 → {{2.96656, 11., 5.}, {11., 16., 11.}}, Key64 → {{3.00204, 11., 6.}, {10., 8., 6.}},
 Key65 → {{3.10021, 13., 14.}, {9., 9., 4.}}, Key66 → {{3.13051, 4., 7.}, {9., 17., 6.}},
 Key67 → {{3.24167, 14., 11.}, {5., 12., 9.}}, Key68 → {{3.03607, 8., 10.}, {9., 13., 8.}},
 Key69 → {{3.06876, 11., 4.}, {6., 12., 13.}}, Key70 → {{3.06876, 13., 7.}, {16., 12., 14.}},
 Key71 → {{3.18796, 2., 9.}, {13., 12., 9.}}, Key72 → {{3.13051, 13., 9.}, {8., 10., 13.}},
 Key73 → {{3.21525, 6., 8.}, {12., 9., 10.}}, Key74 → {{3.10021, 11., 7.}, {10., 5., 13.}},
 Key75 → {{3.13051, 11., 8.}, {4., 5., 14.}}, Key76 → {{3.26726, 10., 11.}, {6., 6., 11.}},
 Key77 → {{3.03607, 12., 7.}, {8., 15., 7.}}, Key78 → {{3.29208, 11., 7.}, {15., 11., 7.}},
 Key79 → {{3.26726, 6., 12.}, {10., 11., 12.}}, Key80 → {{3.36232, 10., 12.}, {17., 6., 9.}},
 Key81 → {{3.29208, 7., 12.}, {10., 5., 16.}}, Key82 → {{3.06876, 13., 9.}, {6., 8., 5.}},
 Key83 → {{3.10021, 8., 16.}, {7., 11., 13.}}, Key84 → {{3.10021, 10., 8.}, {10., 4., 14.}},
 Key85 → {{3.15973, 9., 13.}, {14., 7., 11.}}, Key86 → {{3.13051, 11., 8.}, {7., 12., 9.}},
 Key87 → {{3.13051, 14., 12.}, {8., 10., 13.}}, Key88 → {{3.15973, 17., 6.}, {15., 10., 7.}},
 Key89 → {{3.29208, 13., 6.}, {7., 10., 7.}}, Key90 → {{3.06876, 19., 10.}, {12., 9., 12.}},
 Key91 → {{3.15973, 8., 8.}, {12., 9., 6.}}, Key92 → {{3.24167, 10., 11.}, {10., 10., 6.}},
 Key93 → {{3.03607, 7., 11.}, {16., 10., 9.}}, Key94 → {{3.13051, 13., 8.}, {8., 18., 7.}},
 Key95 → {{3.15973, 12., 12.}, {8., 3., 7.}}, Key96 → {{3.13051, 11., 10.}, {15., 4., 11.}},
 Key97 → {{3.15973, 12., 7.}, {13., 9., 10.}}, Key98 → {{3.21525, 8., 9.}, {11., 10., 12.}},
 Key99 → {{3.15973, 6., 11.}, {10., 6., 13.}}, Key100 → {{3.26726, 8., 0.}, {8., 20., 9.}}|>
```

SearchMaxFactor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

We can extend the maximum of the range over which the optimization takes place (which by default is the data maximum).

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In[2]:=
```
dataRandomAssociationsExample = AssociationThread@
  (("Key" <> ToString[#]) & /@ Range[100] → RandomVariate[PoissonDistribution[10], {100, 2, 3}])
```

Out[2]=
```
<|Key1 → {{11, 6, 7}, {9, 8, 8}}, Key2 → {{9, 12, 14}, {8, 15, 7}}, Key3 → {{8, 11, 10}, {6, 11, 16}},
 Key4 → {{7, 7, 14}, {17, 7, 6}}, Key5 → {{14, 10, 14}, {12, 6, 11}}, Key6 → {{16, 19, 13}, {12, 10, 6}},
 Key7 → {{10, 12, 16}, {7, 8, 12}}, Key8 → {{12, 7, 11}, {11, 9, 10}}, Key9 → {{13, 11, 11}, {9, 7, 22}},
 Key10 → {{6, 10, 7}, {8, 7, 9}}, Key11 → {{15, 6, 5}, {11, 8, 18}}, Key12 → {{16, 8, 12}, {12, 12, 9}},
 Key13 → {{12, 10, 7}, {8, 7, 11}}, Key14 → {{6, 10, 14}, {4, 7, 8}}, Key15 → {{7, 9, 13}, {14, 8, 13}},
 Key16 → {{9, 10, 12}, {12, 11, 12}}, Key17 → {{10, 11, 15}, {10, 6, 9}}, Key18 → {{3, 13, 7}, {17, 12, 10}},
 Key19 → {{9, 12, 14}, {13, 7, 8}}, Key20 → {{18, 8, 10}, {16, 14, 8}}, Key21 → {{4, 11, 13}, {10, 15, 6}},
 Key22 → {{11, 9, 7}, {9, 10, 13}}, Key23 → {{9, 4, 9}, {14, 7, 13}}, Key24 → {{10, 17, 10}, {8, 10, 10}},
 Key25 → {{7, 15, 9}, {10, 8, 10}}, Key26 → {{7, 12, 13}, {6, 11, 7}}, Key27 → {{12, 13, 10}, {10, 9, 6}},
 Key28 → {{11, 6, 11}, {7, 10, 11}}, Key29 → {{9, 7, 4}, {11, 10, 10}}, Key30 → {{11, 9, 8}, {12, 17, 8}},
 Key31 → {{10, 15, 10}, {14, 9, 7}}, Key32 → {{7, 12, 10}, {7, 9, 14}}, Key33 → {{17, 10, 13}, {3, 15, 8}},
 Key34 → {{11, 6, 5}, {11, 9, 5}}, Key35 → {{12, 14, 13}, {15, 15, 10}}, Key36 → {{11, 9, 12}, {13, 15, 10}},
 Key37 → {{13, 11, 5}, {12, 13, 8}}, Key38 → {{7, 11, 4}, {12, 19, 11}}, Key39 → {{5, 11, 9}, {9, 15, 15}},
 Key40 → {{14, 14, 9}, {13, 14, 10}}, Key41 → {{12, 11, 7}, {12, 9, 13}}, Key42 → {{14, 4, 9}, {10, 14, 11}},
 Key43 → {{12, 15, 10}, {5, 13, 8}}, Key44 → {{12, 10, 14}, {11, 11, 13}},
 Key45 → {{13, 11, 11}, {15, 9, 11}}, Key46 → {{12, 12, 12}, {12, 8, 10}},
 Key47 → {{10, 8, 8}, {6, 10, 12}}, Key48 → {{10, 10, 7}, {22, 13, 7}}, Key49 → {{11, 6, 12}, {6, 11, 8}},
 Key50 → {{9, 15, 13}, {6, 14, 14}}, Key51 → {{8, 4, 6}, {10, 8, 10}}, Key52 → {{16, 9, 7}, {10, 15, 9}},
 Key53 → {{6, 10, 13}, {13, 9, 4}}, Key54 → {{6, 14, 12}, {7, 14, 11}}, Key55 → {{6, 8, 15}, {13, 7, 7}},
 Key56 → {{13, 7, 8}, {12, 11, 10}}, Key57 → {{7, 7, 11}, {14, 8, 9}}, Key58 → {{13, 3, 11}, {11, 13, 9}},
 Key59 → {{6, 9, 10}, {13, 9, 7}}, Key60 → {{9, 6, 12}, {5, 13, 9}}, Key61 → {{14, 5, 8}, {8, 13, 6}},
 Key62 → {{13, 15, 5}, {11, 11, 8}}, Key63 → {{9, 10, 16}, {9, 7, 9}}, Key64 → {{5, 12, 10}, {13, 13, 12}},
 Key65 → {{11, 7, 12}, {6, 9, 13}}, Key66 → {{8, 14, 5}, {16, 16, 6}}, Key67 → {{16, 13, 11}, {8, 9, 7}},
 Key68 → {{11, 14, 11}, {11, 14, 7}}, Key69 → {{11, 9, 15}, {10, 8, 13}}, Key70 → {{12, 9, 17}, {3, 7, 10}},
 Key71 → {{9, 12, 13}, {20, 14, 7}}, Key72 → {{10, 11, 15}, {13, 8, 10}}, Key73 → {{14, 13, 12}, {10, 9, 4}},
 Key74 → {{8, 6, 10}, {10, 8, 8}}, Key75 → {{20, 14, 13}, {11, 18, 6}}, Key76 → {{6, 11, 8}, {6, 16, 9}},
 Key77 → {{8, 11, 9}, {13, 9, 12}}, Key78 → {{9, 15, 12}, {14, 9, 3}}, Key79 → {{15, 11, 10}, {5, 6, 9}},
 Key80 → {{8, 11, 9}, {9, 17, 12}}, Key81 → {{14, 6, 8}, {10, 8, 14}}, Key82 → {{9, 15, 10}, {10, 15, 8}},
 Key83 → {{10, 7, 15}, {11, 7, 12}}, Key84 → {{7, 14, 8}, {10, 14, 9}}, Key85 → {{6, 8, 6}, {8, 18, 8}},
 Key86 → {{12, 8, 4}, {10, 8, 10}}, Key87 → {{3, 8, 6}, {8, 9, 8}}, Key88 → {{10, 15, 14}, {9, 9, 12}},
 Key89 → {{5, 8, 6}, {15, 8, 11}}, Key90 → {{7, 9, 9}, {9, 6, 8}}, Key91 → {{10, 11, 11}, {11, 10, 12}},
 Key92 → {{17, 14, 7}, {11, 8, 14}}, Key93 → {{14, 16, 11}, {12, 11, 9}}, Key94 → {{12, 10, 17}, {10, 9, 17}},
 Key95 → {{10, 12, 8}, {6, 15, 9}}, Key96 → {{9, 13, 6}, {6, 8, 7}}, Key97 → {{9, 9, 11}, {18, 9, 9}},
 Key98 → {{17, 9, 11}, {16, 8, 4}}, Key99 → {{9, 9, 9}, {8, 11, 11}}, Key100 → {{12, 12, 14}, {10, 4, 8}}|>
```

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In[3]:=
```
ApplyBoxCoxTransformExtended[dataRandomAssociationsExample,
 ListIndex → 1, ComponentIndex → 1, HorizontalSelection → True, SearchMaxFactor → 3]
```

Calculated Box-Cox parameter $\hat{\lambda}$ = {0.437395, -3.}

Out[3]=
```
⟨|Key1 → {{3.39093, 6., 7.}, {9., 8., 8.}}, Key2 → {{2.71968, 12., 14.}, {8., 15., 7.}},
 Key3 → {{2.33597, 11., 10.}, {6., 11., 16.}}, Key4 → {{1.90615, 7., 14.}, {17., 7., 6.}},
 Key5 → {{4.23942, 10., 14.}, {12., 6., 11.}}, Key6 → {{4.7341, 19., 13.}, {12., 10., 6.}},
 Key7 → {{3.06884, 12., 16.}, {7., 8., 12.}}, Key8 → {{3.69107, 7., 11.}, {11., 9., 10.}},
 Key9 → {{3.97297, 11., 11.}, {9., 7., 22.}}, Key10 → {{1.41046, 10., 7.}, {8., 7., 9.}},
 Key11 → {{4.49257, 6., 5.}, {11., 8., 18.}}, Key12 → {{4.7341, 8., 12.}, {12., 12., 9.}},
 Key13 → {{3.69107, 10., 7.}, {8., 7., 11.}}, Key14 → {{1.41046, 10., 14.}, {4., 7., 8.}},
 Key15 → {{1.90615, 9., 13.}, {14., 8., 13.}}, Key16 → {{2.71968, 10., 12.}, {12., 11., 12.}},
 Key17 → {{3.06884, 11., 15.}, {10., 6., 9.}}, Key18 → {{-2.28626, 13., 7.}, {17., 12., 10.}},
 Key19 → {{2.71968, 12., 14.}, {13., 7., 8.}}, Key20 → {{5.18756, 8., 10.}, {16., 14., 8.}},
 Key21 → {{1.0153×10^-15, 11., 13.}, {10., 15., 6.}}, Key22 → {{3.39093, 9., 7.}, {9., 10., 13.}},
 Key23 → {{2.71968, 4., 9.}, {14., 7., 13.}}, Key24 → {{3.06884, 17., 10.}, {8., 10., 10.}},
 Key25 → {{1.90615, 15., 9.}, {10., 8., 10.}}, Key26 → {{1.90615, 12., 13.}, {6., 11., 7.}},
 Key27 → {{3.69107, 13., 10.}, {10., 9., 6.}}, Key28 → {{3.39093, 6., 11.}, {7., 10., 11.}},
 Key29 → {{2.71968, 7., 4.}, {11., 10., 10.}}, Key30 → {{3.39093, 9., 8.}, {12., 17., 8.}},
 Key31 → {{3.06884, 15., 10.}, {14., 9., 7.}}, Key32 → {{1.90615, 12., 10.}, {7., 9., 14.}},
 Key33 → {{4.96539, 10., 13.}, {3., 15., 8.}}, Key34 → {{3.39093, 6., 5.}, {11., 9., 5.}},
 Key35 → {{3.69107, 14., 13.}, {15., 15., 10.}}, Key36 → {{3.39093, 9., 12.}, {13., 15., 10.}},
 Key37 → {{3.97297, 11., 5.}, {12., 13., 8.}}, Key38 → {{1.90615, 11., 4.}, {12., 19., 11.}},
 Key39 → {{0.809696, 11., 9.}, {9., 15., 15.}}, Key40 → {{4.23942, 14., 9.}, {13., 14., 10.}},
 Key41 → {{3.69107, 11., 7.}, {12., 9., 13.}}, Key42 → {{4.23942, 4., 9.}, {10., 14., 11.}},
 Key43 → {{3.69107, 15., 10.}, {5., 13., 8.}}, Key44 → {{3.69107, 10., 14.}, {11., 11., 13.}},
 Key45 → {{3.97297, 11., 11.}, {15., 9., 11.}}, Key46 → {{3.69107, 12., 12.}, {12., 8., 10.}},
 Key47 → {{3.06884, 8., 8.}, {6., 10., 12.}}, Key48 → {{3.06884, 10., 7.}, {22., 13., 7.}},
 Key49 → {{3.39093, 6., 12.}, {6., 11., 8.}}, Key50 → {{2.71968, 15., 13.}, {6., 14., 14.}},
 Key51 → {{2.33597, 4., 6.}, {10., 8., 10.}}, Key52 → {{4.7341, 9., 7.}, {10., 15., 9.}},
 Key53 → {{1.41046, 10., 13.}, {13., 9., 4.}}, Key54 → {{1.41046, 14., 12.}, {7., 14., 11.}},
 Key55 → {{1.41046, 8., 15.}, {13., 7., 7.}}, Key56 → {{3.97297, 7., 8.}, {12., 11., 10.}},
 Key57 → {{1.90615, 7., 11.}, {14., 8., 9.}}, Key58 → {{3.97297, 3., 11.}, {11., 13., 9.}},
 Key59 → {{1.41046, 9., 10.}, {13., 9., 7.}}, Key60 → {{2.71968, 6., 12.}, {5., 13., 9.}},
 Key61 → {{4.23942, 5., 8.}, {8., 13., 6.}}, Key62 → {{3.97297, 15., 5.}, {11., 11., 8.}},
 Key63 → {{2.71968, 10., 16.}, {9., 7., 9.}}, Key64 → {{0.809696, 12., 10.}, {13., 13., 12.}},
 Key65 → {{3.39093, 7., 12.}, {6., 9., 13.}}, Key66 → {{2.33597, 14., 5.}, {16., 16., 6.}},
 Key67 → {{4.7341, 13., 11.}, {8., 9., 7.}}, Key68 → {{3.39093, 14., 11.}, {11., 14., 7.}},
 Key69 → {{3.39093, 9., 15.}, {10., 8., 13.}}, Key70 → {{3.69107, 9., 17.}, {3., 7., 10.}},
 Key71 → {{2.71968, 12., 13.}, {20., 14., 7.}}, Key72 → {{3.06884, 11., 15.}, {13., 8., 10.}},
 Key73 → {{4.23942, 13., 12.}, {10., 9., 4.}}, Key74 → {{2.33597, 6., 10.}, {10., 8., 8.}},
 Key75 → {{5.60813, 14., 13.}, {11., 18., 6.}}, Key76 → {{1.41046, 11., 8.}, {6., 16., 9.}},
 Key77 → {{2.33597, 11., 9.}, {13., 9., 12.}}, Key78 → {{2.71968, 15., 12.}, {14., 9., 3.}},
 Key79 → {{4.49257, 11., 10.}, {5., 6., 9.}}, Key80 → {{2.33597, 11., 9.}, {9., 17., 12.}},
 Key81 → {{4.23942, 6., 8.}, {10., 8., 14.}}, Key82 → {{2.71968, 15., 10.}, {10., 15., 8.}},
 Key83 → {{3.06884, 7., 15.}, {11., 7., 12.}}, Key84 → {{1.90615, 14., 8.}, {10., 14., 9.}},
 Key85 → {{1.41046, 8., 6.}, {8., 18., 8.}}, Key86 → {{3.69107, 8., 4.}, {10., 8., 10.}},
 Key87 → {{-2.28626, 8., 6.}, {8., 9., 8.}}, Key88 → {{3.06884, 15., 14.}, {9., 9., 12.}},
 Key89 → {{0.809696, 8., 6.}, {15., 8., 11.}}, Key90 → {{1.90615, 9., 9.}, {9., 6., 8.}},
 Key91 → {{3.06884, 11., 11.}, {11., 10., 12.}}, Key92 → {{4.96539, 14., 7.}, {11., 8., 14.}},
 Key93 → {{4.23942, 16., 11.}, {12., 11., 9.}}, Key94 → {{3.69107, 10., 17.}, {10., 9., 17.}},
 Key95 → {{3.06884, 12., 8.}, {6., 15., 9.}}, Key96 → {{2.71968, 13., 6.}, {6., 8., 7.}},
 Key97 → {{2.71968, 9., 11.}, {18., 9., 9.}}, Key98 → {{4.96539, 9., 11.}, {16., 8., 4.}},
 Key99 → {{2.71968, 9., 9.}, {8., 11., 11.}}, Key100 → {{3.69107, 12., 14.}, {10., 4., 8.}}|⟩
```

See Also

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Applier ▪ **ApplyBoxCoxTransform** ▪ **BoxCoxTransform** ▪ **BoxCoxTransformExtended** ▪ **OmicsObject** ▪ **QuantileNormalization** ▪ **StandardizeExtended**

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Autocorrelation

`Autocorrelation[data, setTimes]`
calculates the normalized autocorrelation for a time series over specified set times, using a Lomb–Scargle based inverse autocovariance.

Details

- `Autocorrelation[data, setTimes]` calculates the autocorrelation of a dataset over a set of specified times using the inverse Fourier transform of a Lomb-Scargle based inverse autocovariance. It takes as input:

data	Time series (data as a list; list may be the value of a single key in an association). The series may include Missing data points. Data may be entered as list of N signal intensities corresponding one–to–one to the N setTimes with Missing inserted appropriately if the data is absent, $\{X_1 = X(t_1), X_2 = X(t_2), \ldots, X_N = X(t_N)\}$. Alternatively, the data may be a list of pairs of values $\{\{t_1,X_1\},\{t_2,X_2\},\ldots,\{t_N,X_N\}\}$ for only existing measurements.
setTimes	A complete set of all possible N times during which data could have been collected in the window of the experiment, including times for which no data was collected, $\{t_1, t_2, \ldots, t_N\}$.

- The Autocorrelation function returns a list of autocorrelations from `lag = 0` to n, in the form $\{\rho_X(0)=1, \rho_x(1), \rho_x(2), \rho_x(n)\}$, where where n=Floor[N/2].

- The following options can be given:

SpectrumFunction	InverseAutocovariance	Selection of specific function to use to generate periodogram on which inverse Fourier transform will be performed to obtain the autocorrelation function.
UpperFrequencyFactor	1	Value ≥ 1, by which to scale the upper Nyquist cutoff frequency and increase spectral resolution.

Background

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- This function calculates, for a given discrete time series of a signal $x(t)$, the corresponding discretization of the autocorrelation at different time lags τ, $\rho_x(\tau) = \frac{\gamma_x(\tau)}{\gamma_x(0)} = \frac{\langle x(t)\, x(t+\tau)\rangle}{\langle x^2(t)\rangle}$, where the autocovariance $\gamma_x(\tau) = \langle x(t)\, x(t+\tau)\rangle$ is an average over all initial times t, and $\rho_x(\tau)$ is normalized so that $\rho_x(0) = 1$. Note that in the case that the data is perfectly evenly spaced in real-time, then we may use *Mathematica*'s built-in ListCorrelate function. However, if the data are unevenly spaced, as many biological time series are, instead an alternative route may involve performing an inverse Fourier transform of $S_x(f)$ in order to get the autocovariance $\gamma_x(\tau)$.

- By the Wiener-Khinchin Theorem, if a signal $x(t)$ has corresponding Inverse Fourier Transformed Autocovariance $S_x(f)$, then $\gamma_x(\tau) = \int_{-\infty}^{\infty} df\, S_x(f)\, \mathrm{Cos}(2\pi f t) = 2\int_0^{\infty} df\, S_x(f)\, \mathrm{Cos}(2\pi f t)$, taking advantage of the symmetry of the integrand under frequency reversal. The complete time window of the experiment is defined by the range of $\{t_{\mathrm{complete}}\}$, $t_{\mathrm{window}} = \mathrm{Max}[\{t_{\mathrm{complete}}\}] - \mathrm{Min}[\{t_{\mathrm{complete}}\}]$. From this time window, the Nyquist frequency is defined to be $f_{\mathrm{Nyq}} = \frac{N}{2}\, \frac{1}{t_{\mathrm{window}}}$, and a given UpperFrequencyFactor factor ≥ 1 sets the cutoff frequency f_{cutoff} for calculation by $\frac{f_{\mathrm{cutoff}}}{f_{\mathrm{Nyq}}}$ = UpperFrequencyFactor . It is recommended to set UpperFrequencyFactor close to 1 unless one has an explicit reason to do otherwise.

- In the context of experimental data, we often work with a discrete time series $\{x(t_1),\ x(t_2),\ \ldots,\ x(t_N)\}$ for times $t_1 < t_2 < \ldots < t_N$, rather than a continuous time series. This leads to a natural discretization of $S_x(f) \to \{S_x(f_1),\ S_x(f_2),\ \ldots,\ S_x(f_M)\}$, where M is the total number of positive frequencies. The estimation of this discretized spectral sequence, and the corresponding input frequencies $\{f_1,\ f_2,\ \ldots,\ f_M\}$, is handled through the InverseAutocovariance function. Thus given a sequence $\{S_x(f_i)\}$, we may apply *Mathematica*'s built-in Inverse Discrete Cosine Transform, and normalize to get the real time autocorrelation $\{\rho_x(\tau_j)\} = \left\{\frac{\gamma_x(\tau_j)}{\gamma_x(0)}\right\}$. This choice of normalization sets autocorrelation at lag 0 to be 1 but does not impose other restrictions due to normalization on autocorrelations at other lags.

References

- Lomb, N.R, *Least-squares frequency analysis of unequally spaced data*, Astrophysics and Space Science 39 (2) : 447–462 (1976). External link: http://dx.doi.org/10.1007/BF00648343.

- Scargle, J.D., *Studies in astronomical time series analysis II - Statistical aspects of spectral analysis of unevenly spaced data*, Astrophysical Journal 263 : 835 (1982). External link: http://dx.doi.org/10.1086/160554.

- Scargle, J.D., *Studies in astronomical time series analysis. III - Fourier transforms, autocorrelation functions, and cross-correlation functions of unevenly spaced data*, Astrophysical Journal 343 : 874 (1989). External link: http://dx.doi.org/10.1086/167757.

Examples (10)

Basic Examples (7)

Package Dependencies (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

```
In[2]:= Autocorrelation[{1, 2, 3, 4, 5}, {1, 2, 3, 4, 5}]
Out[2]= {1., 0.292437, 0.143869}
```

General Example: Linear Signal (1)

Below are some examples of the normalized Autocorrelation for linear signals.

We first generate a linear signal with pairs of data:

```
In[1]:= timeSetLinear = Transpose[{Range[1, 100], Range[1, 100]}];
```

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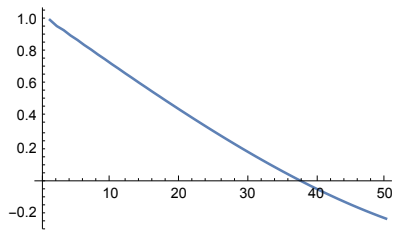
We can calculate the Autocorrelation list as:

In[2]:=
```
linearAutocorrelationA = Autocorrelation[timeSetLinear, Range[1, 100]]
```

Out[2]=
```
{1., 0.961875, 0.936586, 0.903624, 0.876079, 0.844471, 0.81624, 0.785374, 0.756886, 0.726568, 0.698027,
 0.668191, 0.639725, 0.610352, 0.582055, 0.553152, 0.525102, 0.496686, 0.468951, 0.441048, 0.413691,
 0.386331, 0.35941, 0.332625, 0.306198, 0.280023, 0.254145, 0.228615, 0.20334, 0.178492, 0.153874, 0.129745,
 0.105836, 0.0824643, 0.0593158, 0.0367417, 0.0144045, -0.00733269, -0.0288082, -0.049668, -0.0702323,
 -0.0901735, -0.109778, -0.128759, -0.147354, -0.165332, -0.182872, -0.199804, -0.216241, -0.232083}
```

In[3]:=
```
ListLinePlot[linearAutocorrelationA, PlotRange → All]
```

Out[3]=


We can instead introduce the data as a list and still obtain the same result:

In[4]:=
```
linearAutocorrelationB = Autocorrelation[Range[1, 100], Range[1, 100]]
```

Out[4]=
```
{1., 0.961875, 0.936586, 0.903624, 0.876079, 0.844471, 0.81624, 0.785374, 0.756886, 0.726568, 0.698027,
 0.668191, 0.639725, 0.610352, 0.582055, 0.553152, 0.525102, 0.496686, 0.468951, 0.441048, 0.413691,
 0.386331, 0.35941, 0.332625, 0.306198, 0.280023, 0.254145, 0.228615, 0.20334, 0.178492, 0.153874, 0.129745,
 0.105836, 0.0824643, 0.0593158, 0.0367417, 0.0144045, -0.00733269, -0.0288082, -0.049668, -0.0702323,
 -0.0901735, -0.109778, -0.128759, -0.147354, -0.165332, -0.182872, -0.199804, -0.216241, -0.232083}
```

The function also works on an association:

In[5]:=
```
linearAutocorrelationC = Autocorrelation[<|"Data Key" → Range[1, 100]|>, Range[1, 100]]
```

Out[5]=
```
<|Data Key → {1., 0.961875, 0.936586, 0.903624, 0.876079, 0.844471, 0.81624, 0.785374,
   0.756886, 0.726568, 0.698027, 0.668191, 0.639725, 0.610352, 0.582055, 0.553152, 0.525102,
   0.496686, 0.468951, 0.441048, 0.413691, 0.386331, 0.35941, 0.332625, 0.306198, 0.280023,
   0.254145, 0.228615, 0.20334, 0.178492, 0.153874, 0.129745, 0.105836, 0.0824643, 0.0593158,
   0.0367417, 0.0144045, -0.00733269, -0.0288082, -0.049668, -0.0702323, -0.0901735,
   -0.109778, -0.128759, -0.147354, -0.165332, -0.182872, -0.199804, -0.216241, -0.232083}|>
```

We now create an unevenly sampled dataset through a function that samples n random points,

In[6]:=
```
timeSeriesLine[n_] := SortBy[RandomSample[Transpose[{Range[1, 100, 1], Range[1, 100, 1]}], n], First];
```

We also create another function to calculate the corresponding Autocorrelation list:

In[7]:=
```
lineUnevenAutocorrelation[n_] := Autocorrelation[timeSeriesLine[n] , Range[1, 100, 1]];
```

Here are some examples of sampling this set with 50 to 100 points in steps of 10:

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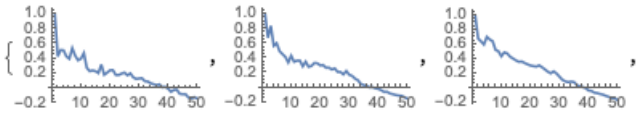
In[8]:=
```
ListLinePlot[lineUnevenAutocorrelation[#], PlotRange → All] & /@ Range[50, 100, 10]
```

Out[8]=


We can instead have a list provided with data missing at timepoints and tagged Missing. Let's introduce missing data at random integer positions, say 10 points missing :

In[9]:=
```
timeSetLinearMissing = Nest[ReplacePart[#, RandomInteger[{1, 100}] → Missing[]] &, Range[1, 100], 10]
```

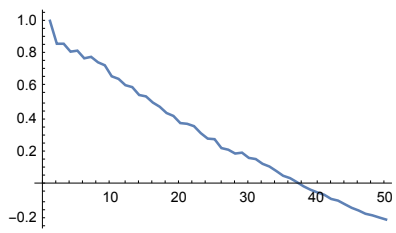
Out[9]=
```
{1, 2, 3, Missing[], 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23,
 24, 25, 26, 27, Missing[], 29, Missing[], 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43,
 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, Missing[], 60, 61, Missing[], 63,
 64, 65, 66, 67, 68, 69, 70, 71, 72, Missing[], Missing[], 75, 76, 77, 78, 79, Missing[], 81,
 82, 83, 84, 85, Missing[], 87, 88, 89, 90, 91, 92, 93, Missing[], 95, 96, 97, 98, 99, 100}
```

We can again calculate the Autocorrelation list as:

In[10]:=
```
timeSetLinearMissingAutocorrelation = Autocorrelation[timeSetLinearMissing, Range[1, 100]]
```

Out[10]=
```
{1., 0.860894, 0.860952, 0.812875, 0.818931, 0.772493, 0.781305, 0.748214, 0.730004,
 0.663181, 0.647439, 0.609122, 0.597426, 0.549605, 0.540998, 0.503578, 0.478172, 0.440039,
 0.422289, 0.378911, 0.374448, 0.360181, 0.317338, 0.284497, 0.281068, 0.226967, 0.217092,
 0.193781, 0.199159, 0.167222, 0.160299, 0.131322, 0.114913, 0.087646, 0.0587123,
 0.0444784, 0.0200936, -0.00588926, -0.0263054, -0.0426099, -0.0569644, -0.0821212,
 -0.0922038, -0.114435, -0.136146, -0.152265, -0.172072, -0.181579, -0.194706, -0.20732}
```

In[11]:=
```
ListLinePlot[timeSetLinearMissingAutocorrelation, PlotRange → All]
```

Out[11]=


Examples of Autocorrelation Based on Lomb-Scargle Vs. Exact Calculations (5)

Linear Trend Expansions (1)

We can use the inbuilt CorrelationFunction for an exact calculation not based on Fourier transforms, particularly with a regularly sampled time series with no missing data sets:

In[14]:=
```
linearAutocorrelationExact = N[CorrelationFunction[timeSetLinear, {Floor@(Length[timeSetLinear]/2)}]]
```

Out[14]=
```
{1., 0.97, 0.940012, 0.910048, 0.88012, 0.85024, 0.82042, 0.790672, 0.761008, 0.73144, 0.70198, 0.67264,
 0.643432, 0.614368, 0.585461, 0.556721, 0.528161, 0.499793, 0.471629, 0.443681, 0.415962, 0.388482,
 0.361254, 0.33429, 0.307603, 0.281203, 0.255104, 0.229316, 0.203852, 0.178725, 0.153945, 0.129526, 0.105479,
 0.0818152, 0.0585479, 0.0356886, 0.0132493, -0.00875788, -0.030321, -0.0514281, -0.0720672, -0.0922262,
 -0.111893, -0.131056, -0.149703, -0.167822, -0.185401, -0.202427, -0.21889, -0.234776, -0.250075}
```

We see that the functions agree to a great extend:

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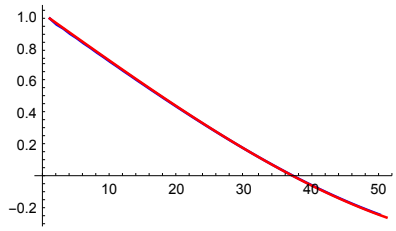
In[17]:=
```
ListLinePlot[{linearAutocorrelationA, linearAutocorrelationExact}, PlotRange → All, PlotStyle → {Blue, Red}]
```

Out[17]=



Sinusoidal Series Example (1)

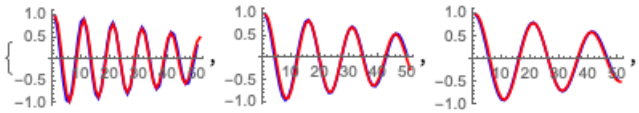
Let's consider a sinusoidal signal set:

In[280]:=
```
sineSignalAutocorrelation[n_] := Autocorrelation[Sin[2 π/n * Range[1, 100]], Range[1, 100, 1]];
```

We can plot the Autocorrelation and the CorrelationFunction results together:

In[283]:=
```
ListLinePlot[{sineSignalAutocorrelation[#], N@CorrelationFunction[N@Sin[2 π/# Range[1, 100, 1]], {50}]},
  PlotRange → All, PlotStyle → {Blue, Red}] & /@ Range[10, 50, 5]
```

Out[283]=



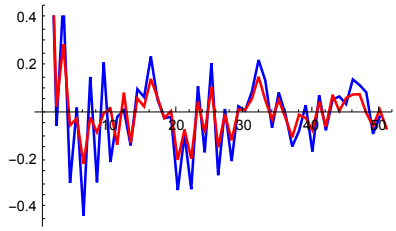
Random Series Comparison (1)

In[284]:=
```
randomList = RandomReal[{-1, 1}, 100]
```

Out[284]=
```
{-0.113701, 0.624505, -0.892958, -0.460071, -0.906059, -0.528756, 0.0708229, 0.0510381, -0.912449, 0.573578,
 -0.630059, -0.428088, -0.0472665, -0.775668, -0.462054, 0.135251, -0.380577, -0.283162, -0.753539,
 0.779901, -0.475683, 0.179572, -0.44581, 0.121062, -0.313655, 0.183515, -0.861918, 0.574134,
 0.455197, -0.136364, 0.701933, 0.666348, -0.835509, -0.130473, -0.351923, 0.271977, 0.113012,
 0.0976132, 0.692681, 0.427684, 0.0172706, 0.732223, 0.281962, 0.6758, -0.0831782, 0.00022431,
 -0.58553, -0.429202, -0.849788, -0.929066, 0.10129, 0.0068542, -0.497111, -0.93755, -0.996348,
 -0.180912, -0.16323, 0.0222051, 0.6439, 0.681129, -0.251591, 0.944286, 0.243733, -0.639921,
 -0.310725, 0.384989, -0.325639, -0.329954, -0.0957975, -0.587486, -0.0315639, -0.898231, 0.853212,
 0.839692, 0.876916, 0.416309, 0.0862606, -0.991755, -0.869665, -0.772733, -0.85974, -0.182331,
 -0.816338, 0.80589, -0.657445, 0.919816, -0.760071, 0.270243, -0.911859, 0.0197175, 0.646593,
 -0.410873, -0.0121278, -0.862593, -0.646296, -0.990035, 0.559137, -0.967805, 0.727959, 0.0100112}
```

In[286]:=
```
ListLinePlot[{Autocorrelation[randomList, Range[1, 100, 1]],
  N@CorrelationFunction[randomList, {50}]}, PlotStyle → {Blue, Red}]
```

Out[286]=



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Sinusoidal Signals with Uneven Sampling (1)

Below are some examples of the normalized Autocorrelation for sinusoidal signals:

In[292]:=
```
sineSignalAuto[n_] :=
  Autocorrelation[Transpose[{Range[1, 100], Sin[2 π/n * Range[1, 100, 1]]}], Range[1, 100]];
```

We can randomly sample n of such signals using the function:

In[299]:=
```
timeSeriesSine[m_, n_] :=
  SortBy[RandomSample[Transpose[{Range[1, 100, 1], Sin[2 π/m * Range[1, 100, 1]]}], n], First];
```

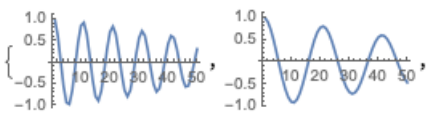
For these signals with n points sampled we can calculate the autocorrelation:

In[296]:=
```
sineUnevenAuto[m_, n_] := Autocorrelation[timeSeriesSine[m, n] , Range[1, 100]] ;
```

A plot of the regularly sampled autocorrelations:

In[301]:=
```
ListLinePlot[sineSignalAuto[#], PlotRange → All] & /@ Range[10, 50, 10]
```

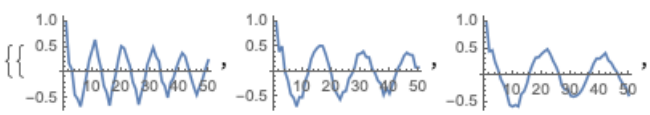
Out[301]=



In[302]:=
```
sineUnevenAutoDisplay[n_] := ListLinePlot[sineUnevenAuto[#, n], PlotRange → All] & /@ Range[10, 50, 5];
```

In[305]:=
```
sineUnevenAutoDisplay[#] & /@ Range[50, 100, 10]
```

Out[305]=

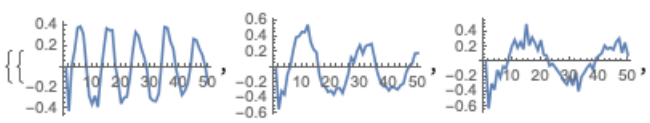


Let's display the numerical difference error in autocorrelation for uneven vs. even sampling.

In[306]:=
```
errorSineUnevenAuto[n_] :=
  ListLinePlot[sineUnevenAuto[#, n] - sineSignalAuto[#], PlotRange → All] & /@ Range[10, 50, 10];
```

In[307]:=
```
errorSineUnevenAuto[#] & /@ Range[50, 100, 10]
```

Out[307]=



Noisy Signals with Uneven Sampling (1)

Below are some examples of the normalized Autocorrelation for random noise:

In[308]:=
```
randomList = RandomReal[{-1, 1}, 100];
```

In[312]:=
```
randomAutocorrelation = Autocorrelation[randomList, Range[1, 100, 1]];
```

We can also randomly sample n of such signals using the function:

In[310]:=
```
timeSeriesRandom[n_] := SortBy[RandomSample[Transpose[{Range[1, 100, 1], randomList}], n], First];
```

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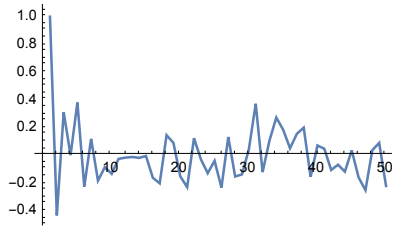
For these signals with n points sampled we can calculate the autocorrelations:

In[316]:=
```
randomUnevenAutocorrelation[n_] := Autocorrelation[timeSeriesRandom[n], Range[1, 100, 1]];
```

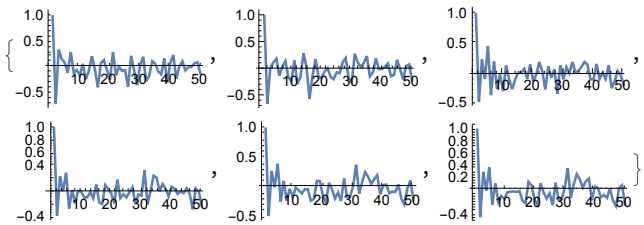
In[317]:=
```
ListLinePlot[randomAutocorrelation, PlotRange → All]
```

Out[317]=



In[318]:=
```
ListLinePlot[randomUnevenAutocorrelation[#], PlotRange → All] & /@ Range[50, 100, 10]
```

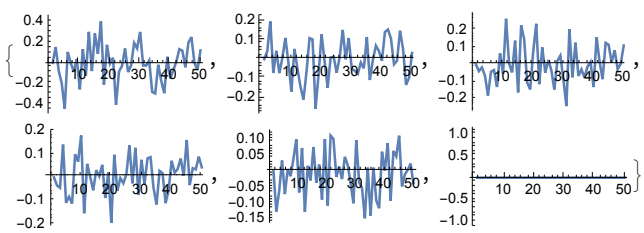
Out[318]=



We can also display the numerical difference error in autocorrelation for uneven vs. even sampling:

In[319]:=
```
ListLinePlot[randomUnevenAutocorrelation[#] - randomAutocorrelation, PlotRange → All] & /@ Range[50, 100, 10]
```

Out[319]=



Options (2)

UpperFrequencyFactor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

UpperFrequencyFactor takes values ≥ 1, by which to scale the upper Nyquist cutoff frequency and increase spectral resolution. It is recommended to set UpperFrequencyFactor close to 1. The default value is 1.

We consider the following example data

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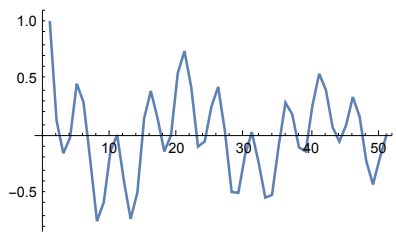
In[2]:=
```
dataExample = Table[{n, Cos[0.05 * 2 π n ] + Cos[0.2 * 2 π n] + RandomReal[{-1, 1}]}, {n, 0, 100}]
```

Out[2]=
```
{{0, 1.00735}, {1, 0.807902}, {2, -0.0376538}, {3, -0.93852}, {4, -0.250372}, {5, 0.825871},
 {6, -0.665125}, {7, -1.76222}, {8, -1.35841}, {9, 0.18426}, {10, 0.122237}, {11, -0.496553},
 {12, -1.43812}, {13, -1.09048}, {14, -0.562625}, {15, 0.557508}, {16, 1.49009}, {17, 0.660269},
 {18, -0.0933526}, {19, 2.00843}, {20, 1.05233}, {21, 1.98897}, {22, -0.777257}, {23, -0.23375},
 {24, 0.0468363}, {25, 0.498077}, {26, -0.697378}, {27, -1.76892}, {28, -2.43567},
 {29, -0.389525}, {30, 0.480958}, {31, -1.32861}, {32, -2.1679}, {33, -1.5162}, {34, 0.968314},
 {35, 1.85186}, {36, 1.43127}, {37, -0.866525}, {38, -0.140132}, {39, 0.310858}, {40, 2.09166},
 {41, 2.02717}, {42, -0.998684}, {43, -0.476606}, {44, 1.41584}, {45, 0.453212}, {46, 0.677018},
 {47, -0.560606}, {48, -2.29885}, {49, -1.34956}, {50, 0.605601}, {51, -0.300362}, {52, -2.57057},
 {53, -0.823656}, {54, -0.209321}, {55, 0.731399}, {56, 0.963195}, {57, 0.0895538}, {58, 0.79142},
 {59, 0.435578}, {60, 1.59708}, {61, 1.46375}, {62, 0.611611}, {63, -0.574368}, {64, 1.08383},
 {65, 1.21262}, {66, -0.439262}, {67, -2.08671}, {68, -1.9629}, {69, 0.0489416}, {70, 0.93799},
 {71, -1.47406}, {72, -0.768705}, {73, -1.46383}, {74, 0.0891103}, {75, 0.024698}, {76, 1.01306},
 {77, 0.176178}, {78, -0.136365}, {79, 2.05029}, {80, 1.68548}, {81, 1.30762}, {82, -0.726454},
 {83, 0.743665}, {84, -0.219236}, {85, 1.68396}, {86, 0.086708}, {87, -1.53947}, {88, -2.20758},
 {89, -0.398815}, {90, 0.602264}, {91, -1.08813}, {92, -1.80126}, {93, -0.875818}, {94, -0.584195},
 {95, 1.50239}, {96, 0.306663}, {97, 0.194243}, {98, 0.905891}, {99, 0.913972}, {100, 1.11155}}
```

In[3]:=
```
ListLinePlot[Autocorrelation[dataExample, Range[0, 100], UpperFrequencyFactor → 1], PlotRange → All]
```

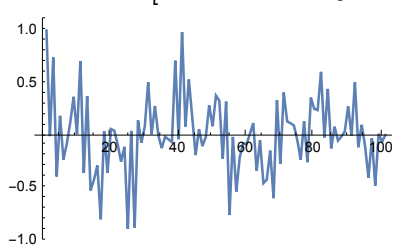
Out[3]=



Changing the upper Nyquist frequency has a direct effect on the autocorrelation with more noisy output:

In[4]:=
```
ListLinePlot[Autocorrelation[dataExample, Range[0, 100], UpperFrequencyFactor → 2], PlotRange → All]
```

Out[4]=



SpectrumFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

SpectrumFunction allows selection of specific function to use to internally for the power spectrum equivalent (c.f. periodogram) on which inverse Fourier transform will be performed to obtain the autocorrelation function. The default function used is the InverseAutocovariance. We can also use LombScargle as an alternative.

In[2]:=
```
timeSetLinear = Transpose[{Range[1, 100], Range[1, 100]}];
```

We can calculate the Autocorrelation list as:

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```
In[3]:= linearAutocorrelationA =
         Autocorrelation[timeSetLinear, Range[1, 100], SpectrumFunction → InverseAutocovariance]
Out[3]= {1., 0.961875, 0.936586, 0.903624, 0.876079, 0.844471, 0.81624, 0.785374, 0.756886, 0.726568, 0.698027,
         0.668191, 0.639725, 0.610352, 0.582055, 0.553152, 0.525102, 0.496686, 0.468951, 0.441048, 0.413691,
         0.386331, 0.35941, 0.332625, 0.306198, 0.280023, 0.254145, 0.228615, 0.20334, 0.178492, 0.153874, 0.129745,
         0.105836, 0.0824643, 0.0593158, 0.0367417, 0.0144045, -0.00733269, -0.0288082, -0.049668, -0.0702323,
         -0.0901735, -0.109778, -0.128759, -0.147354, -0.165332, -0.182872, -0.199804, -0.216241, -0.232083}
```

We can instead use directly the LombScarlge function:

```
In[4]:= linearAutocorrelationA = Autocorrelation[timeSetLinear, Range[1, 100], SpectrumFunction → LombScargle]
Out[4]= {1., 0.907961, 0.791084, 0.680177, 0.573758, 0.472297,
         0.375624, 0.283795, 0.196804, 0.114634, 0.0373119, -0.0351931, -0.102849}
```

We notice that the samplings and also number of lags are different in this case.

Properties & Relations (1)

In calculating the Autocorrelation as an inverse Fourier transform of a periodogram a modified version of the LombScargle function is used by InverseAutocovariance .

The function CorrelationFunction can calculate exact autocorrelations for a series of evenly spaced time points, and can also employ linear interpolation as an alternative to the Lomb-Scargle approach of the Autocorrelation function.

See Also

InverseAutocovariance ▪ **LombScargle** ▪ **TimeSeriesClassification**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

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BenjaminiHochbergFDR

BenjaminiHochbergFDR[*pValues*]
calculates for a list of *pValues* the Benjamini Hochberg approach false discovery rates (FDR).

Details

- BenjaminiHochbergFDR[*pValues*] calculates for a list of p-Values, $\{p_1, p_2, \ldots p_N\}$, the Benjamini Hochberg approach false discovery rates (FDR). The procedure is outlined below. The output for the function is a list of length N comprised of results for each of N input p-Values is an association of the results and the associated cutoff values:

```
output = <|"Results" → {{original p - value1, adjusted p - value1,
      True or False based on whether this value is considered statistically significant or not respectively},
     {original p - value2, adjusted p - value2, True or False based on whether p -
       value2 value is considered statistically significant or not respectively}, ...,
     {original p - valueN, adjusted p - valueN, True or False based on whether p -
       value2 value is considered statistically significant or not respectively}},
  "p-Value Cutoff" → actual p - Value surviving cutoff,
  "q-Value Cutoff" → adjusted p - Value surviving cutoff
 |>
```

- With a large number of hypotheses tested, the chance of getting false-discoveries just by chance alone increases. The Benjamini-Hochberg procedure corrects for this by, first, calculating a set of adjusted p-values (q-values) from input p-Values set. These adjusted p-Values are then used to test for significance (with a significance cutoff set by default to $\alpha = 0.05$).

- To get the adjusted p-value (q-values), the input p-values are first ranked in ascending order, $\{p_1^{ranked}, p_2^{ranked}, \ldots p_j^{ranked}, \ldots, p_N^{ranked}\}$ such that, $\text{Min}[\{\{p_1, p_2, \ldots p_N\}] = p_1^{ranked} < \ldots < p_j^{ranked} < p_{j+1}^{ranked} < \ldots < p_N^{ranked} = \text{Max}[\{\{p_1, p_2, \ldots p_N\}]$.

- Then, the ranked p-values are weighted by the formula $p_i^{weighted} = \frac{N}{i} \times p_i^{ranked}$. To get q values, any local maxima in the $p_i^{weighted}$ are smoothed out, so as to preserve the original ordering, via the following iterative procedure:

- First, set $q_N = p_N^{weighted}$; then, for $m = 1, 2, \ldots, N - 1$, set:

- $q_{N-m}^{weighted} = \text{Min}[\{p_{N-m}^{weighted}, q_{N-m+1}\}]$.

- Finally, these q-values are compared against the cutoff used to assess statistical significance, meaning if we are testing for significance level S (default option SignificanceLevel = 0.05), we reject any hypotheses with adjusted values less than S.

- The following options can be given:

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SignificanceLevel	0.05	SignificanceLevel is an option to that controls cutoffs for diagnostic tests as well as test conclusions. Adjuste p–values less than the cutoff will be marked as True for significance, and values higher will be marked as False for significance.

Examples (2)

Basic Examples (1)

We first load the MathIOmica package:

```
In[1]:= Needs["MathIOmica`"]
```

Let us consider the following example for a list of p-Values:

```
In[2]:= pValueExamples =
  {0.03, 0.02, 0.04, 0.01, 0.001, 0.0001, 0.05, 0.01, 0.03, 0.04, 0.03, 0.63, 0.70, 0.80, 0.30, 0.11, 0.01,
   0.30, 0.25, 0.45, 0.1, 0.01, 0.77, 0.9, 0.33, 0.41, 0.000001, 0.02, 0.33, 0.21, 0.41, 0.55, 0.66};
```

We can calculate the Benjamini-Hochberg adjusted valued:

```
In[3]:= BenjaminiHochbergFDR[pValueExamples]

Out[3]= ⟨|Results → {{0.03, 0.0825, False}, {0.02, 0.0733333, False}, {0.04, 0.0942857, False},
    {0.01, 0.0471429, True}, {0.001, 0.011, True}, {0.0001, 0.00165, True}, {0.05, 0.11, False},
    {0.01, 0.0471429, True}, {0.03, 0.0825, False}, {0.04, 0.0942857, False}, {0.03, 0.0825, False},
    {0.63, 0.7425, False}, {0.7, 0.77, False}, {0.8, 0.825, False}, {0.3, 0.471429, False},
    {0.11, 0.213529, False}, {0.01, 0.0471429, True}, {0.3, 0.471429, False},
    {0.25, 0.434211, False}, {0.45, 0.571154, False}, {0.1, 0.20625, False}, {0.01, 0.0471429, True},
    {0.77, 0.819677, False}, {0.9, 0.9, False}, {0.33, 0.473478, False}, {0.41, 0.5412, False},
    {1.×10^-6, 0.000033, True}, {0.02, 0.0733333, False}, {0.33, 0.473478, False},
    {0.21, 0.385, False}, {0.41, 0.5412, False}, {0.55, 0.672222, False}, {0.66, 0.751034, False}},
  p-Value Cutoff → 0.01, q-Value Cutoff → 0.0471429|⟩
```

Options (1)

SignificanceLevel (1)

```
In[1]:= Needs["MathIOmica`"]
```

SignificanceLevel is an option to that controls cutoffs for diagnostic tests as well as test conclusions. Adjuste p-values less than the cutoff will be marked as True for significance, and values higher will be marked as False for significance.

We consider the following data:

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```
In[2]:= pValueExamples =
  {0.03, 0.02, 0.04, 0.01, 0.001, 0.0001, 0.05, 0.01, 0.03, 0.04, 0.03, 0.63, 0.70, 0.80, 0.30, 0.11, 0.01,
   0.30, 0.25, 0.45, 0.1, 0.01, 0.77, 0.9, 0.33, 0.41, 0.000001, 0.02, 0.33, 0.21, 0.41, 0.55, 0.66};
```

We can calculate the Benjamini-Hochberg adjusted valued, setting the SignificanceLevel to 0.01:

```
In[3]:= BenjaminiHochbergFDR[pValueExamples, SignificanceLevel → 0.01]

Out[3]= ⟨|Results → {{0.03, 0.0825, False}, {0.02, 0.0733333, False}, {0.04, 0.0942857, False},
    {0.01, 0.0471429, False}, {0.001, 0.011, False}, {0.0001, 0.00165, True}, {0.05, 0.11, False},
    {0.01, 0.0471429, False}, {0.03, 0.0825, False}, {0.04, 0.0942857, False}, {0.03, 0.0825, False},
    {0.63, 0.7425, False}, {0.7, 0.77, False}, {0.8, 0.825, False}, {0.3, 0.471429, False},
    {0.11, 0.213529, False}, {0.01, 0.0471429, False}, {0.3, 0.471429, False},
    {0.25, 0.434211, False}, {0.45, 0.571154, False}, {0.1, 0.20625, False}, {0.01, 0.0471429, False},
    {0.77, 0.819677, False}, {0.9, 0.9, False}, {0.33, 0.473478, False}, {0.41, 0.5412, False},
    {1.×10^-6, 0.000033, True}, {0.02, 0.0733333, False}, {0.33, 0.473478, False},
    {0.21, 0.385, False}, {0.41, 0.5412, False}, {0.55, 0.672222, False}, {0.66, 0.751034, False}},
   p-Value Cutoff → 0.0001, q-Value Cutoff → 0.00165|⟩
```

See Also

GOAnalysis ▪ **KEGGAnalysis**

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- MathIOmica Dynamic Transcriptome

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- MathIOmicaGuide
- MathIOmicaOverview

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BootstrapGeneral

BootstrapGeneral[*omicsObject*, *numberResampled*]
performs a resampling of the *omicsObject* data with replacement, and generates a new association structure with numbering corresponding to the *numberResampled* of new identities.

Details

- BootstrapGeneral[*omicsObject*, *numberResampled*] is an assistive function for generating resampled datasets for statistical considerations or simulations, particularly involving data in series. It takes two inputs:

omicsObject	OmicsObject of raw data out of which to create the bootstrap dataset.
numberResampled	Number of elements to create in each association.

- The following options can be given:

LabelFunction	Range	Which function to use to generate the labels for the simulated data.
SamplingFunction	RandomChoice	What kind of sampling strategy to use.

Examples (3)

Basic Examples (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

Let's import the example protein data. These are located at:

```
In[2]:= proteinExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinExample"}
```

We can now get the data:

```
In[3]:= proteinExampleData = Get[proteinExampleFile];
```

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Let' s query the first 5 proteins across all datasets

In[4]:=
```
Query[All, 1 ;; 5]@proteinExampleData
```

Out[4]=
```
<|7 → <|{A0AVT1, Protein} → {{0.937}, {17}},
    {A0FGR8, Protein} → {{1.073}, {24}}, {A0MZ66, Protein} → {{1.059}, {9}},
    {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}}|>,
 9 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}}, {A0MZ66, Protein} →
    {{1.479}, {9}}, {A1A4S6, Protein} → {{0.779}, {11}}, {A1L0T0, Protein} → {{0.917}, {4}}|>,
 10 → <|{A0AVT1, Protein} → {{0.966}, {17}}, {A0FGR8, Protein} → {{1.007}, {24}}, {A0MZ66, Protein} →
    {{1.455}, {9}}, {A1A4S6, Protein} → {{0.951}, {11}}, {A1L0T0, Protein} → {{1.058}, {4}}|>,
 11 → <|{A0AVT1, Protein} → {{0.982}, {17}}, {A0FGR8, Protein} → {{0.913}, {24}}, {A0MZ66, Protein} →
    {{1.689}, {9}}, {A1A4S6, Protein} → {{0.78}, {11}}, {A1L0T0, Protein} → {{1.091}, {4}}|>,
 14 → <|{A0AVT1, Protein} → {{1.024}, {17}}, {A0FGR8, Protein} → {{0.937}, {24}}, {A0MZ66, Protein} →
    {{1.312}, {9}}, {A1A4S6, Protein} → {{0.818}, {11}}, {A1L0T0, Protein} → {{0.936}, {4}}|>,
 12 → <|{A0AVT1, Protein} → {{1.064}, {19}}, {A0FGR8, Protein} → {{0.87}, {23}}, {A0MZ66, Protein} →
    {{1.518}, {6}}, {A1A4S6, Protein} → {{0.545}, {5}}, {A1L0T0, Protein} → {{0.921}, {2}}|>,
 13 → <|{A0AVT1, Protein} → {{1.178}, {19}}, {A0FGR8, Protein} → {{0.77}, {23}}, {A0MZ66, Protein} →
    {{2.266}, {6}}, {A1A4S6, Protein} → {{0.428}, {5}}, {A1L0T0, Protein} → {{0.734}, {2}}|>,
 15 → <|{A0AVT1, Protein} → {{0.841}, {19}}, {A0FGR8, Protein} → {{1.12}, {23}}, {A0MZ66, Protein} →
    {{1.517}, {6}}, {A1A4S6, Protein} → {{0.447}, {5}}, {A1L0T0, Protein} → {{1.153}, {2}}|>,
 16 → <|{A0AVT1, Protein} → {{1.086}, {19}}, {A0FGR8, Protein} → {{0.941}, {23}}, {A0MZ66, Protein} →
    {{1.374}, {6}}, {A1A4S6, Protein} → {{0.749}, {5}}, {A1L0T0, Protein} → {{1.016}, {2}}|>,
 17 → <|{A0AVT1, Protein} → {{1.071}, {16}}, {A0FGR8, Protein} → {{0.846}, {22}}, {A0MZ66, Protein} →
    {{1.283}, {4}}, {A1A4S6, Protein} → {{0.654}, {5}}, {A1L0T0, Protein} → {{0.833}, {3}}|>,
 19 → <|{A0AVT1, Protein} → {{0.951}, {16}}, {A0FGR8, Protein} → {{0.882}, {22}},
    {A0MZ66, Protein} → {{1.473}, {4}}, {A1A4S6, Protein} → {{0.71}, {5}}, {A1L0T0, Protein} → {{0.952}, {3}}|>,
 20 → <|{A0AVT1, Protein} → {{0.873}, {16}}, {A0FGR8, Protein} → {{0.852}, {22}}, {A0MZ66, Protein} →
    {{1.213}, {4}}, {A1A4S6, Protein} → {{0.882}, {5}}, {A1L0T0, Protein} → {{1.065}, {3}}|>,
 21 → <|{A0AVT1, Protein} → {{0.988}, {16}}, {A0FGR8, Protein} → {{0.916}, {22}}, {A0MZ66, Protein} →
    {{1.066}, {4}}, {A1A4S6, Protein} → {{0.796}, {5}}, {A1L0T0, Protein} → {{0.992}, {3}}|>|>
```

We can now perform a resampling of this set. For the example let's only create 10000 data in each set:

In[5]:=
```
bootstrapSets = BootstrapGeneral[proteinExampleData, 10 000];
```

We can look at this example (please note that if you repeat the steps above you will most likely get a different dataset as this is a random selection process). We query again the first 5 elements in each dataset:

In[6]:=
```
Query[All, 1 ;; 5]@bootstrapSets
```

Out[6]=
```
<|7 → <|1 → Missing[], 2 → {{1.161}, {12}}, 3 → {{1.947}, {4}}, 4 → {{0.974}, {2}}, 5 → {{0.956}, {4}}|>,
 9 → <|1 → Missing[], 2 → {{1.135}, {2}}, 3 → Missing[], 4 → {{1.013}, {2}}, 5 → {{1.344}, {2}}|>,
 10 → <|1 → {{0.906}, {11}}, 2 → {{0.937}, {8}}, 3 → Missing[], 4 → Missing[], 5 → {{0.922}, {17}}|>,
 11 → <|1 → {{1.082}, {9}}, 2 → {{1.175}, {2}}, 3 → {{1.023}, {3}}, 4 → {{1.016}, {6}}, 5 → {{1.288}, {1}}|>,
 14 → <|1 → {{0.897}, {9}}, 2 → {{1.044}, {7}}, 3 → {{1.282}, {5}}, 4 → {{1.001}, {8}}, 5 → {{0.74}, {1}}|>,
 12 → <|1 → {{1.407}, {18}}, 2 → Missing[], 3 → {{1.231}, {3}}, 4 → {{1.092}, {9}}, 5 → {{1.622}, {1}}|>,
 13 → <|1 → Missing[], 2 → {{0.955}, {6}}, 3 → {{1.592}, {16}}, 4 → Missing[], 5 → {{1.295}, {5}}|>,
 15 → <|1 → {{0.554}, {4}}, 2 → {{1.408}, {2}}, 3 → Missing[], 4 → {{0.832}, {1}}, 5 → Missing[]|>,
 16 → <|1 → Missing[], 2 → {{1.244}, {5}}, 3 → Missing[], 4 → Missing[], 5 → {{1.168}, {2}}|>,
 17 → <|1 → {{0.768}, {3}}, 2 → Missing[], 3 → {{0.892}, {32}}, 4 → {{1.217}, {1}}, 5 → {{0.814}, {3}}|>,
 19 → <|1 → Missing[], 2 → {{1.077}, {3}}, 3 → Missing[], 4 → {{1.353}, {13}}, 5 → {{1.225}, {6}}|>,
 20 → <|1 → {{0.534}, {2}}, 2 → Missing[], 3 → {{0.906}, {3}}, 4 → {{0.829}, {2}}, 5 → {{1.24}, {10}}|>,
 21 → <|1 → {{0.835}, {11}}, 2 → Missing[], 3 → {{1.112}, {18}}, 4 → {{0.732}, {2}}, 5 → Missing[]|>|>
```

Options (2)

LabelFunction (1)

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In[1]:=
```
Needs["MathIOmica`"]
```

We can change the labeling of the samples using a function of the sampling (2nd input for the BoostrapGeneral function) to keep enumeration. For a fun example, let's enumerate the set by selecting 10000 random words from the dictionary:

We consider the example protein data. If these are not imported we can load them:

In[2]:=
```
proteinExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinExample"};
proteinExampleData = Get[proteinExampleFile];
```

```
testLabelFunction= RandomSample[DictionaryLookup[___],#]&;
```

In[4]:=
```
proteinExampleDataLabeled = BootstrapGeneral[proteinExampleData, 10 000, LabelFunction → testLabelFunction]
```

Out[4]=
```
<|7 → <|backward → {{0.957}, {27}}, cottages → {{0.999}, {7}}, tiebreak → {{1.05}, {8}},
   limiter → {{0.983}, {2}}, ⋯ 9992 ⋯, glowered → Missing[], mudpack → {{0.795}, {3}},
   typewrote → {{0.829}, {7}}, profiles → {{1.074}, {18}}|>, ⋯ 11 ⋯, 21 → <| ⋯ 1 ⋯ |> |>
```

large output | show less | show more | show all | set size limit...

SamplingFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

We can change the sampling strategy of the simulation. The default function used is RandomChoice using sampling with replacement. If we want a permutation of the data with no replacement we can use RandomSample as an example.

We consider again the example protein data. If these are not imported we can load them:

In[2]:=
```
proteinExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinExample"};
proteinExampleData = Get[proteinExampleFile];
```

In[3]:=
```
proteinExampleDataSamplingFunction2 =
 BootstrapGeneral[proteinExampleData, 5000, SamplingFunction → RandomSample]
```

Out[3]=
```
<|7 → <|1 → {{0.96}, {4}}, 2 → Missing[], 3 → {{1.086}, {9}}, 4 → Missing[], 5 → {{0.95}, {22}},
   6 → {{1.227}, {1}}, ⋯ 4989 ⋯, 4996 → Missing[], 4997 → {{1.099}, {1}}, 4998 → {{2.969}, {2}},
   4999 → {{1.566}, {1}}, 5000 → {{0.696}, {1}}|>, 9 → <| ⋯ 1 ⋯ |>, ⋯ 9 ⋯, ⋯ 1 ⋯, 21 → <| ⋯ 1 ⋯ |> |>
```

large output | show less | show more | show all | set size limit...

We note that if we try this for 10000 samplings, we run into an error, as we have less than 10000 entries in our original dataset:

In[4]:=
```
proteinExampleDataSamplingFunction2 =
 BootstrapGeneral[proteinExampleData, 10 000, SamplingFunction → RandomSample]
```

Out[4]= Failure[

Message: RandomSample cannot generate a sample of length 10000, which is greater than the length of the sample set {{{0.937}, {17}}, {{1.0

Tag: RandomSample

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See Also

QuantileEstimator ▪ **OmicsObject**

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BoxCoxTransform

`BoxCoxTransform[data, lambda]`
computes the Box–Cox transformation for a given parameter λ.

Details

- `BoxCoxTransform[data, lambda]` is a compiled function that performs a Box-Cox transformation for a given transformation parameter λ. It takes as inputs:

data	Numeric data for which the transformation will be performed.
lambda	Real valued Box–Cox transformation variable λ.

- The Box-Cox transformation for a single variable x is a piecewise power transformation defined by $x^{(\lambda)} = \{ \frac{x^{\lambda}-1}{\lambda} \text{ if } \lambda \neq 0, \ \ln x \text{ if } \lambda = 0 \}$. This transformation is used to standardize a group of disparate data sets to all be approximately normally distributed, through the ApplyBoxCoxTransform function.

Examples (1)

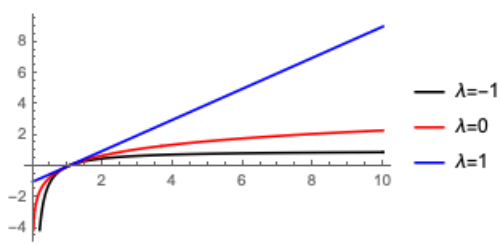
Basic Examples (1)

In[1]:=
```
Needs["MathIOmica`"]
```

Plots of the BoxCoxTransform for various values of λ

In[2]:=
```
Plot[{BoxCoxTransform[x, -1], BoxCoxTransform[x, 0], BoxCoxTransform[x, 1]},
 {x, 0, 10}, PlotStyle → {Black, Red, Blue}, PlotLegends → {"λ=-1", "λ=0", "λ=1"}]
```

Out[2]=



See Also

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ApplyBoxCoxTransform ▪ ApplyBoxCoxTransformExtended ▪ BoxCoxTransformExtended

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BoxCoxTransformExtended

BoxCoxTransformExtended[*data*, *lambda1*, *lambda2*]
computes the two parameter Box–Cox transformation for the *data*, for given parameter set *lambda1*, *lambda2*.

Details

- BoxCoxTransform[*data*, *lambda*, *lambda2*] is a compiled function that performs a two parameter Box-Cox transformation for a given transformation parameter set $\lambda = \{\lambda_1, \lambda_2\}$. It takes as inputs:

data	Numeric data for which the transformation will be performed.
lambda1	Real valued Box–Cox transformation scaling parameter λ_1.
lambda2	Real valued Box–Cox transformation shift parameter λ_2.

- Piecewise[{{((x + lambda2)^lamda1 - 1)/lamda1, Chop[Abs[lamda1]] > 0.}, {Log[x + lambda2], (x + lambda2) > 0}}]

- The two parameter Box-Cox transformation for a single variable $X^{(\lambda)}$ is a piecewise power transformation defined by $X^{(\lambda)} = \log(X + \lambda_2)$ for $\lambda_1 = 0$ and $X^{(\lambda)} = \frac{(X+\lambda_2)^{\lambda_1} - 1}{\lambda_1}$ for $\lambda_1 \neq 0$. This transformation is used to standardize a group of disparate data sets to all be approximately normally distributed, through the ApplyBoxCoxTransformExtended function.

Examples (1)

Basic Examples (1)

In[1]:=
```
Needs["MathIOmica`"]
```

Plots of the BoxCoxTransform for various values of λ_1, λ_2:

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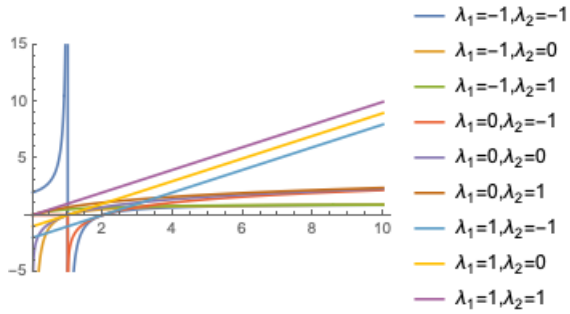
In[2]:=
```
Plot[{BoxCoxTransformExtended[x, -1, -1], BoxCoxTransformExtended[x, -1, 0],
  BoxCoxTransformExtended[x, -1, 1], BoxCoxTransformExtended[x, 0, -1],
  BoxCoxTransformExtended[x, 0, 0], BoxCoxTransformExtended[x, 0, 1], BoxCoxTransformExtended[x, 1, -1],
  BoxCoxTransformExtended[x, 1, 0], BoxCoxTransformExtended[x, 1, 1]}, {x, 0, 10}, PlotStyle → Automatic,
 PlotRange → {Full, {-5, 15}}, PlotLegends → {"λ1=-1,λ2=-1", "λ1=-1,λ2=0", "λ1=-1,λ2=1",
   "λ1=0,λ2=-1", "λ1=0,λ2=0", "λ1=0,λ2=1", "λ1=1,λ2=-1", "λ1=1,λ2=0", "λ1=1,λ2=1"}]
```

Out[2]=



See Also

ApplyBoxCoxTransform ▪ **ApplyBoxCoxTransformExtended** ▪ **BoxCoxTransformExtended**

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ComponentIndex

`ComponentIndex`
is an option for MathIOmica functions, such as Applier, that allows selection of which component of a list to use in an association or OmicsObject input or output values.

Details

- ComponentIndex allows the selection of a component of a list (e.g. in an OmicsObject internal value) to be used by various functions, (e.g. FilteringFunction).

See Also

Applier ▪ **ApplierList** ▪ **FilteringFunction** ▪ **ListIndex** ▪ **MeasurementApplier** ▪ **OmicsObject** ▪ **Returner**

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ConstantAssociator

ConstantAssociator[*inputAssociation*, *associationAddition*]
adds multi–key constant to an OmicsObject (or an association of associations) *inputAssociation*, with each addition specified in a single association *associationAddition*, of form <|addition1→ Value1,addition2→ Value2,...|>.

Details

- ConstantAssociator[*inputAssociation*, *associationAddition*] adds constants to OmicsObject (and also associations of associations). ConstantAssociator takes as inputs:

inputAssociation	OmicsObject (or association of associations) to be modified.
associationAddition	Association of modifications and values.

- ConstantAssociator returns the same kind of object as its input.

Examples (1)

Basic Examples (1)

We first load MathIOmica:

In[1]:=
```
Needs["MathIOmica`"]
```

Let' s consider the OmicsObject:

In[2]:=
```
omicsObjectExample = <|FirstSample → <|{A0AVT1} → {{0.937}, {17}}, {A0MZ66} → {{1.059}, {9}},
      {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[]|>,
    SecondSample → <|{A0AVT1} → {{1.003}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.779}, {11}},
      {A1L0T0} → {{0.917}, {4}}, {A0FGR8} → {{0.921}, {24}}|>, ThirdSample → <|{A0AVT1} → {{1.064}, {19}},
      {A0MZ66} → Missing[], {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {23}}|>|>;
```

We add a new sample, FourthSample, where all protein data is Missing:

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In[3]:=
```
ConstantAssociator[omicsObjectExample, <|FourthSample → Missing[]|>]
```

Out[3]=
```
<|FirstSample → <|{A0AVT1} → {{0.937}, {17}}, {A0MZ66} → {{1.059}, {9}},
    {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[]|>,
  SecondSample → <|{A0AVT1} → {{1.003}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.779}, {11}},
    {A1L0T0} → {{0.917}, {4}}, {A0FGR8} → {{0.921}, {24}}|>,
  ThirdSample → <|{A0AVT1} → {{1.064}, {19}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.545}, {5}},
    {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {23}}|>, FourthSample → <|{A0AVT1} → Missing[],
    {A0MZ66} → Missing[], {A1A4S6} → Missing[], {A1L0T0} → Missing[], {A0FGR8} → Missing[]|>|>
```

We can add multiple constant samples with different values:

In[4]:=
```
ConstantAssociator[
 omicsObjectExample, <|FourthSample → Missing[], FifthSample → {{1}, {2}}, "TestKey" → "TestConstant"|>]
```

Out[4]=
```
<|FirstSample → <|{A0AVT1} → {{0.937}, {17}}, {A0MZ66} → {{1.059}, {9}},
    {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[]|>,
  SecondSample → <|{A0AVT1} → {{1.003}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.779}, {11}},
    {A1L0T0} → {{0.917}, {4}}, {A0FGR8} → {{0.921}, {24}}|>,
  ThirdSample → <|{A0AVT1} → {{1.064}, {19}}, {A0MZ66} → Missing[],
    {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {23}}|>,
  FourthSample → <|{A0AVT1} → Missing[], {A0MZ66} → Missing[], {A1A4S6} → Missing[],
    {A1L0T0} → Missing[], {A0FGR8} → Missing[]|>, FifthSample → <|{A0AVT1} → {{1}, {2}},
    {A0MZ66} → {{1}, {2}}, {A1A4S6} → {{1}, {2}}, {A1L0T0} → {{1}, {2}}, {A0FGR8} → {{1}, {2}}|>,
  TestKey → <|{A0AVT1} → TestConstant, {A0MZ66} → TestConstant, {A1A4S6} → TestConstant,
    {A1L0T0} → TestConstant, {A0FGR8} → TestConstant|>|>
```

We can also perform constant addition to associations of associations:

In[5]:=
```
associations = <|1 → <|1 → a11, 2 → a12, 3 → a13, 4 → a14, 5 → Missing["KeyAbsent", 5]|>,
  2 → <|1 → a21, 2 → a22, 3 → Missing["KeyAbsent", 3], 4 → a24, 5 → a25|>,
  3 → <|1 → a31, 2 → a32, 3 → Missing["KeyAbsent", 3], 4 → a34, 5 → a35|>,
  5 → <|1 → a31m, 2 → Missing["KeyAbsent", 2 m], 3 → a33m, 4 → a34m, 5 → a35m|>|>
```

Out[5]=
```
<|1 → <|1 → a11, 2 → a12, 3 → a13, 4 → a14, 5 → Missing[KeyAbsent, 5]|>,
 2 → <|1 → a21, 2 → a22, 3 → Missing[KeyAbsent, 3], 4 → a24, 5 → a25|>,
 3 → <|1 → a31, 2 → a32, 3 → Missing[KeyAbsent, 3], 4 → a34, 5 → a35|>,
 5 → <|1 → a31m, 2 → Missing[KeyAbsent, 2 m], 3 → a33m, 4 → a34m, 5 → a35m|>|>
```

Let's add 0s to a new key 6:

In[6]:=
```
ConstantAssociator[associations, <|6 → 0|>]
```

Out[6]=
```
<|1 → <|1 → a11, 2 → a12, 3 → a13, 4 → a14, 5 → Missing[KeyAbsent, 5]|>,
 2 → <|1 → a21, 2 → a22, 3 → Missing[KeyAbsent, 3], 4 → a24, 5 → a25|>,
 3 → <|1 → a31, 2 → a32, 3 → Missing[KeyAbsent, 3], 4 → a34, 5 → a35|>,
 5 → <|1 → a31m, 2 → Missing[KeyAbsent, 2 m], 3 → a33m, 4 → a34m, 5 → a35m|>, 6 → <|1 → 0, 2 → 0, 3 → 0, 4 → 0, 5 → 0|>|>
```

We can also make general additions of associations, lists, etc.:

In[7]:=
```
ConstantAssociator[associations, <|6 → <|10 → "testValue1"|>, 7 → {1, 1}|>]
```

Out[7]=
```
<|1 → <|1 → a11, 2 → a12, 3 → a13, 4 → a14, 5 → Missing[KeyAbsent, 5]|>,
 2 → <|1 → a21, 2 → a22, 3 → Missing[KeyAbsent, 3], 4 → a24, 5 → a25|>,
 3 → <|1 → a31, 2 → a32, 3 → Missing[KeyAbsent, 3], 4 → a34, 5 → a35|>,
 5 → <|1 → a31m, 2 → Missing[KeyAbsent, 2 m], 3 → a33m, 4 → a34m, 5 → a35m|>,
 6 → <|1 → <|10 → testValue1|>, 2 → <|10 → testValue1|>, 3 → <|10 → testValue1|>, 4 → <|10 → testValue1|>,
   5 → <|10 → testValue1|>|>, 7 → <|1 → {1, 1}, 2 → {1, 1}, 3 → {1, 1}, 4 → {1, 1}, 5 → {1, 1}|>|>
```

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See Also

Applier ▪ **ApplierList** ▪ **EnlargeInnerAssociation** ▪ **EnlargeOuterAssociation** ▪ **FilteringFunction** ▪ **ListIndex** ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **Returner**

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ConstantGeneDictionary

`ConstantGeneDictionary`
is a global gene/protein dictionary variable typically created by `GetGeneDictionary`.

Details

- `ConstantGeneDictionary` is created through functions that implement GetGeneDictionary, such as GOAnalysis and KEGGAnalysis, as a reference translation between various gene or protein accessions. The associations that appear in `ConstantGeneDictionary` indicate a class (e.g. species) to database relationship.
- For `i` species, each having m_i possible annotations (kinds of IDs) for n_i entities each (e.g. corresponding to n_i genes) the format is schematically:

```
ConstantGeneDictionary = <|
  Species_1 → <|Kind of ID_11 → {accessions list_11 of length n_1},
    Kind of ID_12 → {accessions list_12 of length n_1}, ...,
    Kind of ID_1 m_1→ {accessions list_1 m_1 of length n_1}|>,
  Species_2 → <|Kind of ID_21 → {accessions list_21 of length n_2},
    Kind of ID_22 → {accessions list_22 of length n_2}, ...,
    Kind of ID_2 m_2→ {accessions list_2 m_2 of length n_2}|>,
  ...,
  Species_i → <|Kind of ID_i1 → {accessions list_i2 of length n_i},
    Kind of ID_i2 → {accessions list_12 of length n_i}, ...,
    Kind of ID_i m_i→ {accessions list_12 of length n_i}|>
 |>
```

Examples (1)

Basic Examples (1)

First we need to load the MathIOmica package:

```
In[1]:= Needs["MathIOmica`"]
```

When called, functions like GOAnalysis and KEGGAnalysis will create the `ConstantGeneDictionary` variable if it does not already exist (please note not to evaluate the example below if you already have an existing `ConstantGeneDictionary`

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variable, as it may modify your existing dictionary):

GetGeneDictionary by itself generates a gene translation reference dictionary:

In[2]:=
```
GetGeneDictionary[]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
      uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
      uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, HGU13 … ix ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

Let's carry out an example KEGGAnalysis for three genes of interest

In[3]:=
```
KEGGAnalysis[{"NFKB2", "RELB", "TNFAIP3"}]
```

Out[3]=
```
<|path:hsa04064 → {{2.18924×10^-6, 0.0000240816, True}, {3, 93, 7086, 3},
    {NF-kappa B signaling pathway - Homo sapiens (human), {{NFKB2}, {RELB}, {TNFAIP3}}}},
  path:hsa05169 → {{0.0000235211, 0.000129366, True}, {3, 204, 7086, 3},
    {Epstein-Barr virus infection - Homo sapiens (human), {{NFKB2}, {RELB}, {TNFAIP3}}}},
  path:hsa04380 → {{0.00102066, 0.00374241, True}, {3, 132, 7086, 2},
    {Osteoclast differentiation - Homo sapiens (human), {{NFKB2}, {RELB}}}},
  path:hsa04010 → {{0.00377823, 0.00857214, True}, {3, 255, 7086, 2},
    {MAPK signaling pathway - Homo sapiens (human), {{NFKB2}, {RELB}}}},
  path:hsa05166 → {{0.00389643, 0.00857214, True}, {3, 259, 7086, 2},
    {HTLV-I infection - Homo sapiens (human), {{NFKB2}, {RELB}}}}, path:hsa05134 →
   {{0.0231083, 0.0376229, True}, {3, 55, 7086, 1}, {Legionellosis - Homo sapiens (human), {{NFKB2}}}},
  path:hsa04621 → {{0.0239418, 0.0376229, True}, {3, 57, 7086, 1},
    {NOD-like receptor signaling pathway - Homo sapiens (human), {{TNFAIP3}}}}|>
```

In[4]:=
```
ConstantGeneDictionary
```

Out[4]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
      uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
      uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, HGU13 … ix ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

In[5]:=
```
Keys[ConstantGeneDictionary]
```

Out[5]=
```
{human}
```

We see that the `ConstantGeneDictionary` variable is now populated. We can get the database accessions included in the `ConstantGeneDictionary`

In[6]:=
```
Query[All, Keys]@ConstantGeneDictionary
```

Out[6]=
```
<|human → {UCSC ID, UniProt ID, Gene Symbol, RefSeq ID,
    NCBI Protein Accession, Ensembl ID, KEGG Gene ID, HGU133Plus2 Affymetrix ID}|>
```

For any entry we can get all corresponding IDs. For example for entry 12252

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```
In[7]:= Query[All, All, 12 252]@ConstantGeneDictionary

Out[7]= ⟨|human → ⟨|UCSC ID → uc001jpk.4, UniProt ID → P19367-2,
    Gene Symbol → HK1, RefSeq ID → NM_033496, NCBI Protein Accession → NP_277031,
    Ensembl ID → ENST00000298649, KEGG Gene ID → 3098, HGU133Plus2 Affymetrix ID → 200697_at|⟩|⟩
```

See Also

GeneTranslation ▪ **GetGeneDictionary** ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGDictionary** ▪ **KEGGPathwayVisual** ▪ **MassDictionary** ▪ **MassMatcher** ▪ **OBOGODictionary** ▪ **TimeSeriesClusters** ▪ **UCSCBrowserSQL**

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ConstantMathIOmicaDataDirectory

`ConstantMathIOmicaDataDirectory`
is a global variable pointing to the MathIOmica data directory.

Details

- `ConstantMathIOmicaDataDirectory` is a global variable pointing to the MathIOmica data directory.

Examples (1)

Basic Examples (1)

In[1]:=
```
Needs["MathIOmica`"]
```

We can evaluate the current MathIOmica data directory:

In[2]:=
```
ConstantMathIOmicaDataDirectory
```

See Also

ConstantMathIOmicaExamplesDirectory ▪ **ConstantMathIOmicaExampleVideosDirectory**

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ConstantMathIOmicaExampleVideosDirectory

`ConstantMathIOmicaExampleVideosDirectory`
is a global variable pointing to the MathIOmica example videos directory.

Details

- ConstantMathIOmicaExampleVideosDirectory is a global variable pointing to the MathIOmica example videos directory.

See Also

ConstantMathIOmicaDataDirectory ▪ **ConstantMathIOmicaExamplesDirectory**

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ConstantMathIOmicaExamplesDirectory

`ConstantMathIOmicaExamplesDirectory`
is a global variable pointing to the MathIOmica example data directory.

Details

- `ConstantMathIOmicaExamplesDirectory` is a global variable pointing to the MathIOmica example data directory.

See Also

ConstantMathIOmicaDataDirectory ▪ **ConstantMathIOmicaExampleVideosDirectory**

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ConstantSeriesClean

`ConstantSeriesClean[associationOfLists]`
removes constant list series from *associationOfLists* values.

Details

- `ConstantSeriesClean[associationOfLists]` takes as input an association of series (lists), *associationOfLists*, and returns a filtered association where constant series have been removed.
- The following options can be given:

InverseSelection	False	`InverseSelection` can be set to True to invert the selection/filtering process and return the constant series instead of the non–constant ones.
ReturnDropped	False	`ReturnDropped` can be set to True to return the keys of the constant series in addition to the filtered list. The data is returned in an association: `<|"Data" → non - constant data, "Dropped keys" → keys of dropped values|>`

Examples (3)

Basic Examples (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

We consider the following set of series measurements:

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```
In[2]:= dataSeriesConstants = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
          {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {1, 1, 1, 1, 1, 1},
          {"Measurement4"} → {0.2, 3, Missing[], 3, 0.3, 2}, {"Measurement5"} → {3, 3, 3, 3, 3}|>;

In[3]:= ConstantSeriesClean[dataSeriesConstants]

        Removed series and returning filtered
          list. If you would like a list of removed keys run the
          command ConstantSeriesClean[data,ReturnDropped → True]

Out[3]= <|{Measurement1} → {0.8, 2, 0.7, 1, 0.9, 2},
         {Measurement2} → {Missing[], 0.7, 1, 0.3, 5}, {Measurement4} → {0.2, 3, Missing[], 3, 0.3, 2}|>
```

If data are provided in list form, a list is returned instead:

```
In[4]:= ConstantSeriesClean[Values@dataSeriesConstants]

        Removed series and returning filtered
          list. If you would like a list of removed keys run the
          command ConstantSeriesClean[data,ReturnDropped → True]

Out[4]= {{0.8, 2, 0.7, 1, 0.9, 2}, {Missing[], 0.7, 1, 0.3, 5}, {0.2, 3, Missing[], 3, 0.3, 2}}
```

Options (2)

ReturnDropped (1)

```
In[1]:= Needs["MathIOmica`"]
```

ReturnDropped can return the constant series that were removed:

```
In[2]:= dataSeriesConstants = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
          {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {1, 1, 1, 1, 1, 1},
          {"Measurement4"} → {0.2, 3, Missing[], 3, 0.3, 2}, {"Measurement5"} → {3, 3, 3, 3, 3}|>;

In[3]:= ConstantSeriesClean[dataSeriesConstants, ReturnDropped → True]

Out[3]= <|Data → <|{Measurement1} → {0.8, 2, 0.7, 1, 0.9, 2}, {Measurement2} → {Missing[], 0.7, 1, 0.3, 5},
          {Measurement4} → {0.2, 3, Missing[], 3, 0.3, 2}|>, Dropped Keys → {{Measurement3}, {Measurement5}}|>
```

The data is returned in an association:

```
<|"Data" -> non - constant data,
 "Dropped Keys" -> keys of dropped values |>
```

InverseSelection (1)

```
In[1]:= Needs["MathIOmica`"]
```

InverseSelection can inverse the selection/filtering to return the constant series instead of the non-constant ones.

```
In[2]:= dataSeriesConstants = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
          {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {1, 1, 1, 1, 1, 1},
          {"Measurement4"} → {0.2, 3, Missing[], 3, 0.3, 2}, {"Measurement5"} → {3, 3, 3, 3, 3}|>;
```

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In[3]:=
```
ConstantSeriesClean[dataSeriesConstants, InverseSelection → True]
```

```
Removed series and returning filtered
  list. If you would like a list of removed keys run the
  command ConstantSeriesClean[data,ReturnDropped → True]
```

Out[3]=
```
<|{Measurement3} → {1, 1, 1, 1, 1, 1}, {Measurement5} → {3, 3, 3, 3, 3}|>
```

See Also

CreateTimeSeries ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **SeriesCompare** ▪ **SeriesApplier** ▪ **SeriesInternalCompare**

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CreateTimeSeries

`CreateTimeSeries[omicsObject]`
creates a time series list across an OmicsObject using outer keys as times.

Details

- `CreateTimeSeries[dataIn]` takes as input an OmicsObject that has been created so that its outer keys are strings of numbers corresponding to time points for a time series, and constructs the time series for each inner key across the timepoints returning a list of associations. The selection of intensities is from the first data list in the OmicsObject, i.e. the measurement.

- For a general OmicsObject with N inner associations (inner keys), M timepoints, we have:

- $<|t_1 \to <|\ InnerKey_1 \to \{\{Measurements1_{t1}\}, \{Metadata1_{t1}\}\},$
  $InnerKey_2 \to \{\{Measurements2_{t1}\}, \{Metadata2_{t1}\}\}, \ldots, InnerKey_N \to \{\{MeasurementsN_{t1}\}, \{MetadataN_{t1}\}\}|>,$
  $t_2 \to <|InnerKey_1 \to \{\{Measurements1_{t2}\}, \{Metadata1_{t2}\}\}, InnerKey_2 \to \{\{Measurements2_{t2}\}, \{Metadata2_{t2}\}\}, \ldots,$
  $InnerKey_N \to \{\{MeasurementsN_{t2}\}, \{MetadataN_{t2}\}\}|>, \ldots,$
  $t_M \to <|InnerKey_1 \to \{\{Measurements1_{tM}\}, \{Metadata1_{tM}\}\}, InnerKey_2 \to \{\{Measurements2_{tM}\}, \{Metadata2_{tM}\}\}, \ldots,$
  $InnerKey_N \to \{\{MeasurementsN_{tM}\}, \{MetadataN_{tM}\}\}|>|>$

- The output data looks after we apply CreateTimeSeries will look like:

- $<|InnerKey_1 \to \{Measurements1_{t1}, Measurements1_{t2}, \ldots, Measurements1_{tM}\},$
  $InnerKey_2 \to \{Measurements2_{t1}, Measurements2_{t2}, \ldots, Measurements2_{tM}\}, \ldots,$
  $InnerKeyN \to \{MeasurementsN_{t1}, MeasurementsN_{t2}, \ldots, MeasurementsN_{tM}\}|>$

- CreateTimeSeries will attempt to sort the outer labels to obtain the correct order for the measurements.

Examples (1)

Basic Examples (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

For an OmicsObject that was created from a series we have:

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```
In[2]:= omicsObject1 = <|"7" → <|{"A0AVT1"} → {{0.937`}, {17}}, {"A0FGR8"} → {{1.073`}, {24}},
          {"A0MZ66"} → {{1.059`}, {9}}, {"A1A4S6"} → {{1.03`}, {11}}, {"A1L0T0"} → {{1.268`}, {4}}|>,
        "9" → <|{"A0AVT1"} → {{1.003`}, {17}}, {"A0FGR8"} → {{0.921`}, {24}}, {"A0MZ66"} → {{1.479`}, {9}},
          {"A1A4S6"} → {{0.779`}, {11}}, {"A1L0T0"} → {{0.917`}, {4}}|>,
        "10" → <|{"A0AVT1"} → {{0.966`}, {17}}, {"A0FGR8"} → {{1.007`}, {24}}, {"A0MZ66"} → {{1.455`}, {9}},
          {"A1A4S6"} → {{0.951`}, {11}}, {"A1L0T0"} → {{1.058`}, {4}}|>,
        "11" → <|{"A0AVT1"} → {{0.982`}, {17}}, {"A0FGR8"} → {{0.913`}, {24}}, {"A0MZ66"} → {{1.689`}, {9}},
          {"A1A4S6"} → {{0.78`}, {11}}, {"A1L0T0"} → {{1.091`}, {4}}|>,
        "14" → <|{"A0AVT1"} → {{1.024`}, {17}}, {"A0FGR8"} → {{0.937`}, {24}}, {"A0MZ66"} → {{1.312`}, {9}},
          {"A1A4S6"} → {{0.818`}, {11}}, {"A1L0T0"} → {{0.936`}, {4}}|>|>;
```

We create the corresponding time series lists:

```
In[3]:= CreateTimeSeries[omicsObject1]

Out[3]= <|{A0AVT1} → {0.937, 1.003, 0.966, 0.982, 1.024},
  {A0FGR8} → {1.073, 0.921, 1.007, 0.913, 0.937}, {A0MZ66} → {1.059, 1.479, 1.455, 1.689, 1.312},
  {A1A4S6} → {1.03, 0.779, 0.951, 0.78, 0.818}, {A1L0T0} → {1.268, 0.917, 1.058, 1.091, 0.936}|>
```

As long as the labeling of the outer association can be sorted, the internal order of the outer keys does not affect the outcome. Let's shuffle the order of timepoints in the example above:

```
In[4]:= omicsObjectShuffled = <|"10" → <|{"A0AVT1"} → {{0.966`}, {17}}, {"A0FGR8"} → {{1.007`}, {24}},
          {"A0MZ66"} → {{1.455`}, {9}}, {"A1A4S6"} → {{0.951`}, {11}}, {"A1L0T0"} → {{1.058`}, {4}}|>,
        "11" → <|{"A0AVT1"} → {{0.982`}, {17}}, {"A0FGR8"} → {{0.913`}, {24}}, {"A0MZ66"} → {{1.689`}, {9}},
          {"A1A4S6"} → {{0.78`}, {11}}, {"A1L0T0"} → {{1.091`}, {4}}|>,
        "14" → <|{"A0AVT1"} → {{1.024`}, {17}}, {"A0FGR8"} → {{0.937`}, {24}}, {"A0MZ66"} → {{1.312`}, {9}},
          {"A1A4S6"} → {{0.818`}, {11}}, {"A1L0T0"} → {{0.936`}, {4}}|>,
        "9" → <|{"A0AVT1"} → {{1.003`}, {17}}, {"A0FGR8"} → {{0.921`}, {24}}, {"A0MZ66"} → {{1.479`}, {9}},
          {"A1A4S6"} → {{0.779`}, {11}}, {"A1L0T0"} → {{0.917`}, {4}}|>,
        "7" → <|{"A0AVT1"} → {{0.937`}, {17}}, {"A0FGR8"} → {{1.073`}, {24}}, {"A0MZ66"} → {{1.059`}, {9}},
          {"A1A4S6"} → {{1.03`}, {11}}, {"A1L0T0"} → {{1.268`}, {4}}|>|>;

In[5]:= CreateTimeSeries[omicsObjectShuffled]

Out[5]= <|{A0AVT1} → {0.937, 1.003, 0.966, 0.982, 1.024},
  {A0FGR8} → {1.073, 0.921, 1.007, 0.913, 0.937}, {A0MZ66} → {1.059, 1.479, 1.455, 1.689, 1.312},
  {A1A4S6} → {1.03, 0.779, 0.951, 0.78, 0.818}, {A1L0T0} → {1.268, 0.917, 1.058, 1.091, 0.936}|>
```

See Also

ConstantSeriesClean ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **SeriesApplier** ▪ **SeriesCompare** ▪ **SeriesInternalCompare** ▪ **TimeExtractor** ▪ **TimeSeriesClassification**

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DataImporter

DataImporter[*associationName*]
provides a graphical interface to extract data and create an OmicsObject variable *associationName* for associations of information.

Details

- DataImporter[*associationName*] provides a graphical interface to extract data and create an OmicsObject variable *associationName* for associations of information. At the end of the computation, the *associationName* variable will have the format:

- <|OuterLabel$_1$ → <|InnerLabel$_1$ → {{Measurements$_{11}$}, {Metadata$_{11}$}},
  InnerLabel$_2$ → {{Measurements$_{12}$}, {Metadata$_{12}$}},
  InnerLabel$_3$ → {{Measurements$_{13}$}, {Metadata$_{13}$}},
  ...,
  InnerLabel$_k$ → {{Measurements$_{1k}$}, {Metadata$_{1k}$}},
  ...,
  InnerLabel$_N$ → {{Measurements$_{1N}$}, {Metadata$_{1N}$}}|>,
  OuterLabel$_2$ → <|InnerLabel$_1$ → {{Measurements$_{21}$}, {Metadata$_{21}$}},
  InnerLabel$_2$ → {{Measurements$_{22}$}, {Metadata$_{22}$}},
  InnerLabel$_3$ → {{Measurements$_{23}$}, {Metadata$_{23}$}},
  ...,
  InnerLabel$_k$ → {{Measurements$_{2k}$}, {Metadata$_{2k}$}},
  ...,
  InnerLabel$_N$ → {{Measurements$_{2N}$}, {Metadata$_{2N}$}}|>,
  ...,
  OuterLabel$_j$ → <|InnerLabel$_1$ → {{Measurements$_{j1}$}, {Metadata$_{j1}$}},
  InnerLabel$_2$ → {{Measurements$_{j2}$}, {Metadata$_{j2}$}},
  InnerLabel$_3$ → {{Measurements$_{j3}$}, {Metadata$_{j3}$}},
  ...,
  InnerLabel$_k$ → {{Measurements$_{jk}$}, {Metadata$_{jk}$}},
  ...,
  InnerLabel$_N$ → {{Measurements$_{jN}$}, {Metadata$_{jN}$}}|>,
  ...,
  OuterLabel$_M$ → <|InnerLabel$_1$ → {{Measurements$_{M1}$}, {Metadata$_{M1}$}},
  InnerLabel$_2$ → {{Measurements$_{M2}$}, {Metadata$_{M2}$}},
  InnerLabel$_3$ → {{Measurements$_{M3}$}, {Metadata$_{M3}$}},
  ...,
  InnerLabel$_k$ → {{Measurements$_{Mk}$}, {Metadata$_{Mk}$}},
  ...,
  InnerLabel$_N$ → {{Measurements$_{MN}$}, {Metadata$_{MN}$}}|>
  |>

- In this example there are M outer labels, corresponding to M samples. Across the samples there are N inner labels (e.g. identifiers for genes/proteins), and the the inner labels are the same across samples. For a given j^{th} outer label, OuterLabel$_j$, the kth inner label, InnerLabel$_k$ has a value of the form: InnerLabel$_k$ → {{Measurements$_{jk}$}, {Metadata$_{jk}$}}.

- For any j^{th} outer label, OuterLabel$_j$, it is possible that the mth inner label, InnerLabel$_m$ is missing and takes a Missing[] value in the form InnerLabel$_m$ → Missing[]. This can happen if the measurement was not performed for the sample, or no value was recorded (e.g. mass spectrometry data).

- For example here is a list of 3 samples using protein identifiers (specifically, these are UniProt accessions). The measurements are relative intensities in this case and the metadata is the number of peptides per sample.

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```
<| FirstSample → <| {A0AVT1} → {{0.937}, {17}}, {A0MZ66} → {{1.059}, {9}},
    {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[] |>,
 SecondSample → <| {A0AVT1} → {{1.003}, {17}}, {A0MZ66} → Missing[],
    {A1A4S6} → {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A0FGR8} → {{0.921}, {24}} |>,
 ThirdSample → <| {A0AVT1} → {{1.064}, {19}}, {A0MZ66} → Missing[],
    {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {23}} |> |>
```

- The `DataImporter` function uses the header of each file selected to provide an easy way to make multiple selections across files using the headers as guides/labels. This facilitates the selection of which columns to import.
- Advanced users can select columns by number using a manual selection.
- The following options can be given for `DataImporter`:

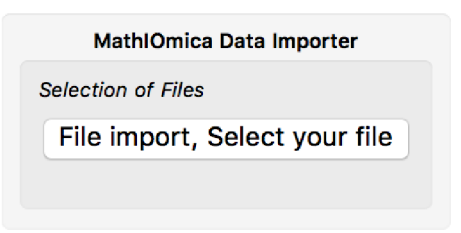
AssociationLabels	None	Set of labels for the associations to be created.
DelimiterList	{","}	DelimiterList provides a list of delimiters to use when importing text files.
JavaGBs	None	How much memory to use for Java.

- It is recommended to use simple text files in the importer with single line headers for each column. Spreadsheet files have limitations due to number of columns and rows allowed by their format.

Graphical Interface

Initialization

- When `DataImporter` is first evaluated a button appears that when pressed will open a file selector:



- The file selector allows us to navigate to any directory to select multiple files.(using standard way of selecting multiple files depending on the operating system). Upon selection the next panel will appear:

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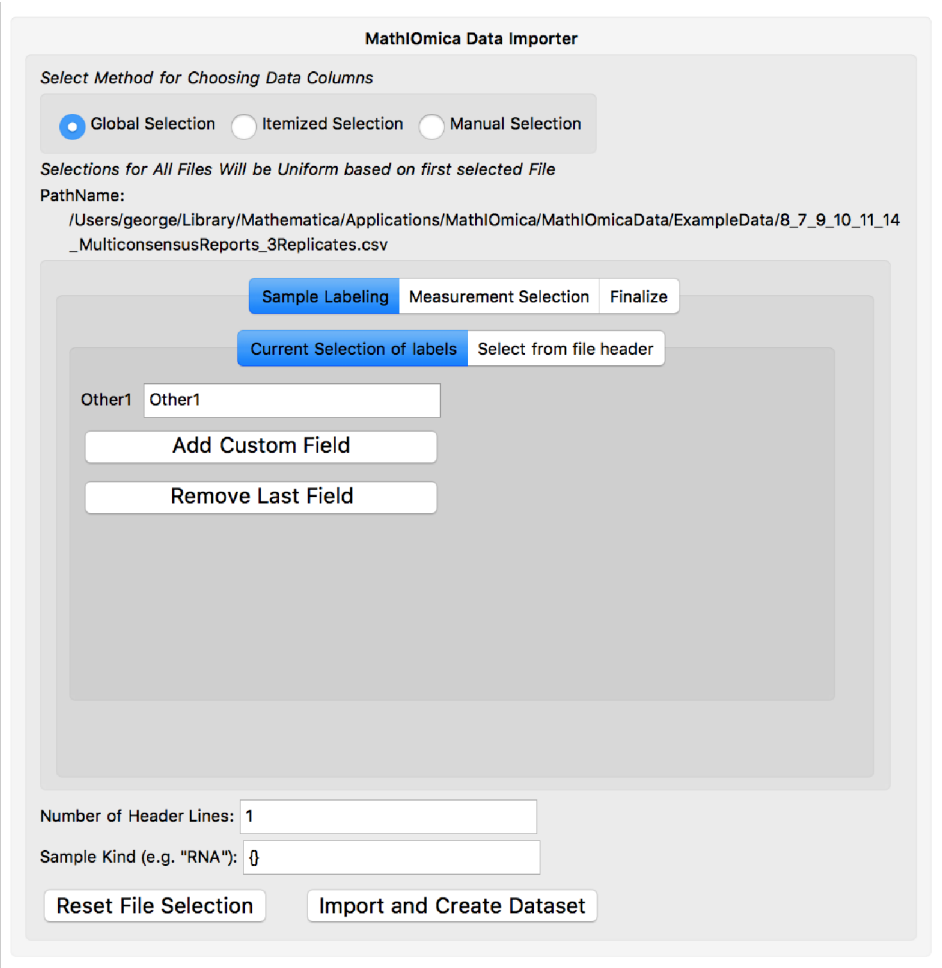
In[1]:=



- There are three choices for the selection method:

Select Method for Choosing Data Columns	Selection Description
Global Selection	Select columns with the same positions across multiple files.
Itemized Selection	Select columns with different positions across individual files.
Manual Selection	Select columns by providing a list of positions – for advanced user selection.

"Global Selection" Method

- Global Selection has a five step workflow:

"Global Selection" Steps	Step Description
1. Select labels ("Sample Labeling" tab).	The selection creates labels for selection of multiple samples from single files. The labels can be custom selected or selected from a list populated from the first provided file header (sub panel "Select from file header").

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2. Select measurements ("Measurement Selection" tab).	For each of the labels created corresponding to each sample a subpanel is created. Selections must be made for each subpanel for three items: (i) "Unique ID", a unique identifier column for the entries of the sample, (ii) "Measurements", which columns to use as measurements, (iii) "Extras", which column to select fo additional metadata for each entry. At least one field must be selected. Multiple selections for each of i–iii above are possible.
3. Finalize measurements ("Finalize" tab).	The information collected can be checked and if correct the "Finalize Selection" button can be pressed.
4. Modify other fields as necessary ("Number of Header Lines", "Sample Kind") at the bottom of the panel.	Values are adjusted for the text fields: "Number of Header Lines" to skip when the files are imported. The default is to skip one line. "Sample Kind" label that will be used to label identifiers. For protein or RNA a standard usage would be to enter a label as {"Protein"} or {"RNA"} respectively. An empty list {} will not provide labeling for the identifiers.
5. Press the "Import and Create Dataset" button at the bottom of the panel.	The "Import and Create Dataset" button will import the dataset and create an OmicsObject corresponding to the input choices.

- Here are some example screenshots for each step:

  Step 1. Select labels ("Sample Labeling" tab).

- Selection of 3 labels shown across files (labels can be added or removed using the "Add Custom Field" or "Remove Last Field" respectively):

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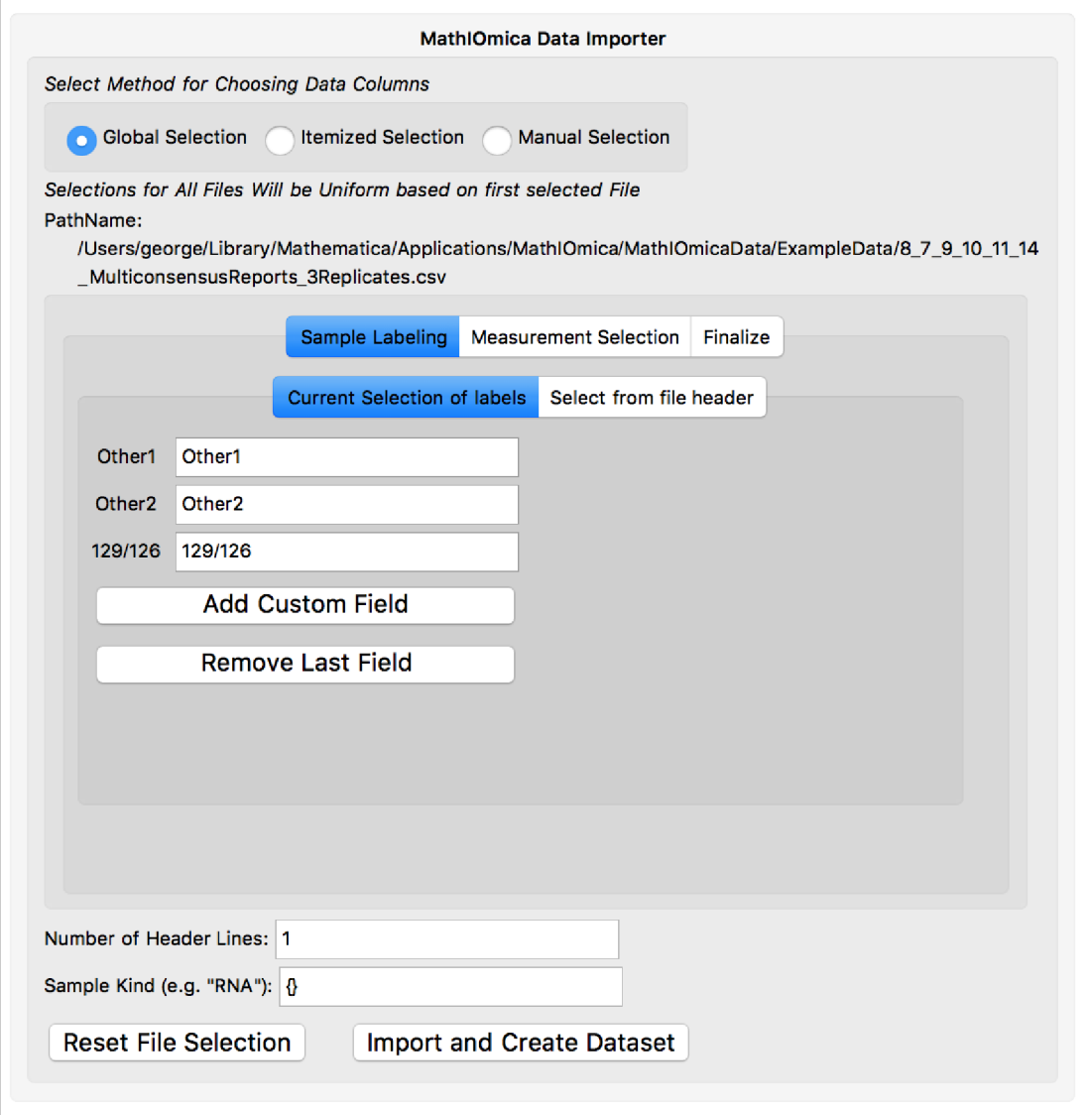

- More selections are facilitated by selecting from the file's header line for choices of labels:

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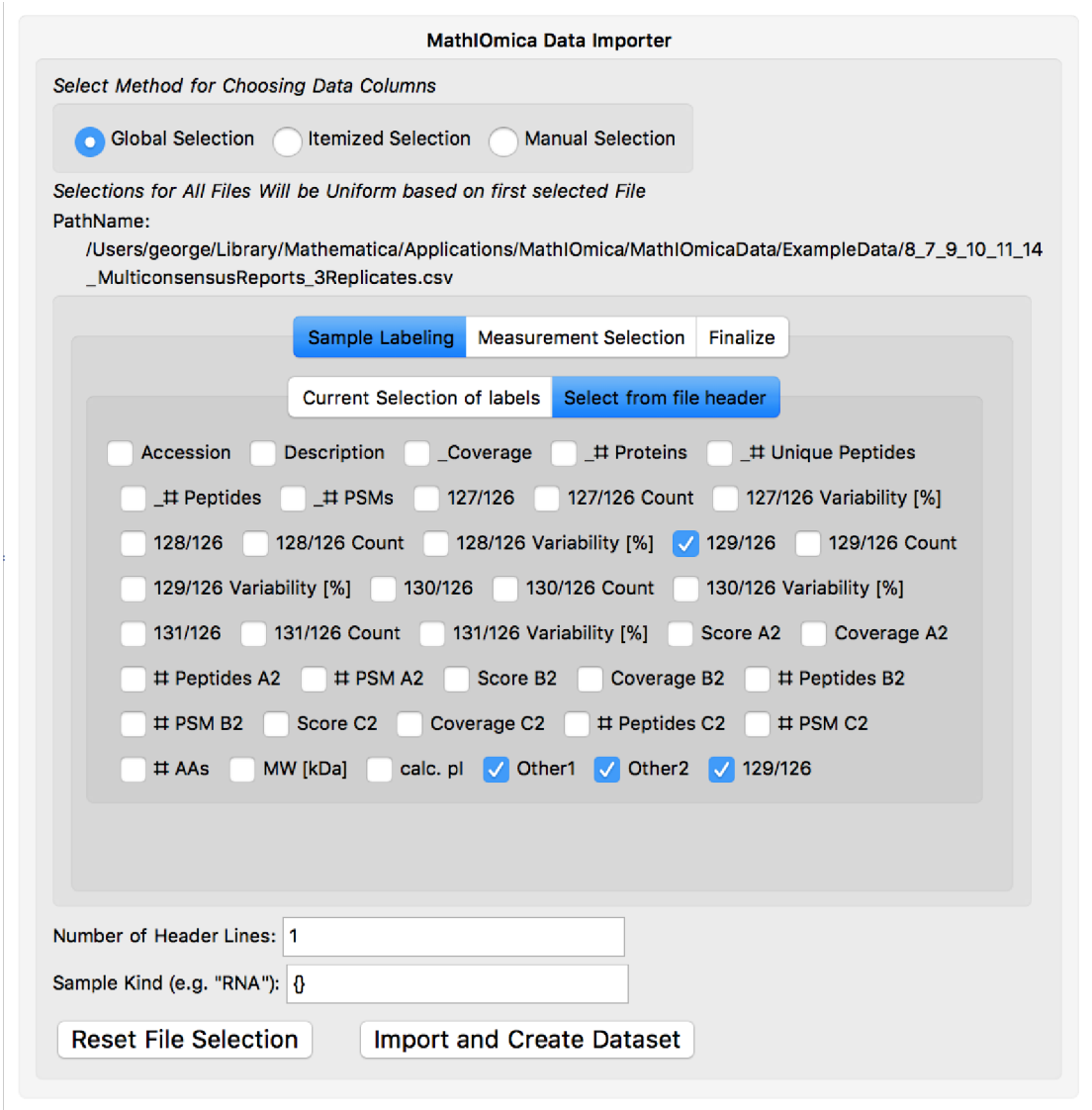

Step 2. Select measurements ("Measurement Selection" tab).

- For each tab representing a sample label we make 3 selections by selecting the tabs below:

- a. The "Unique Id"

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- b. The "Measurements":

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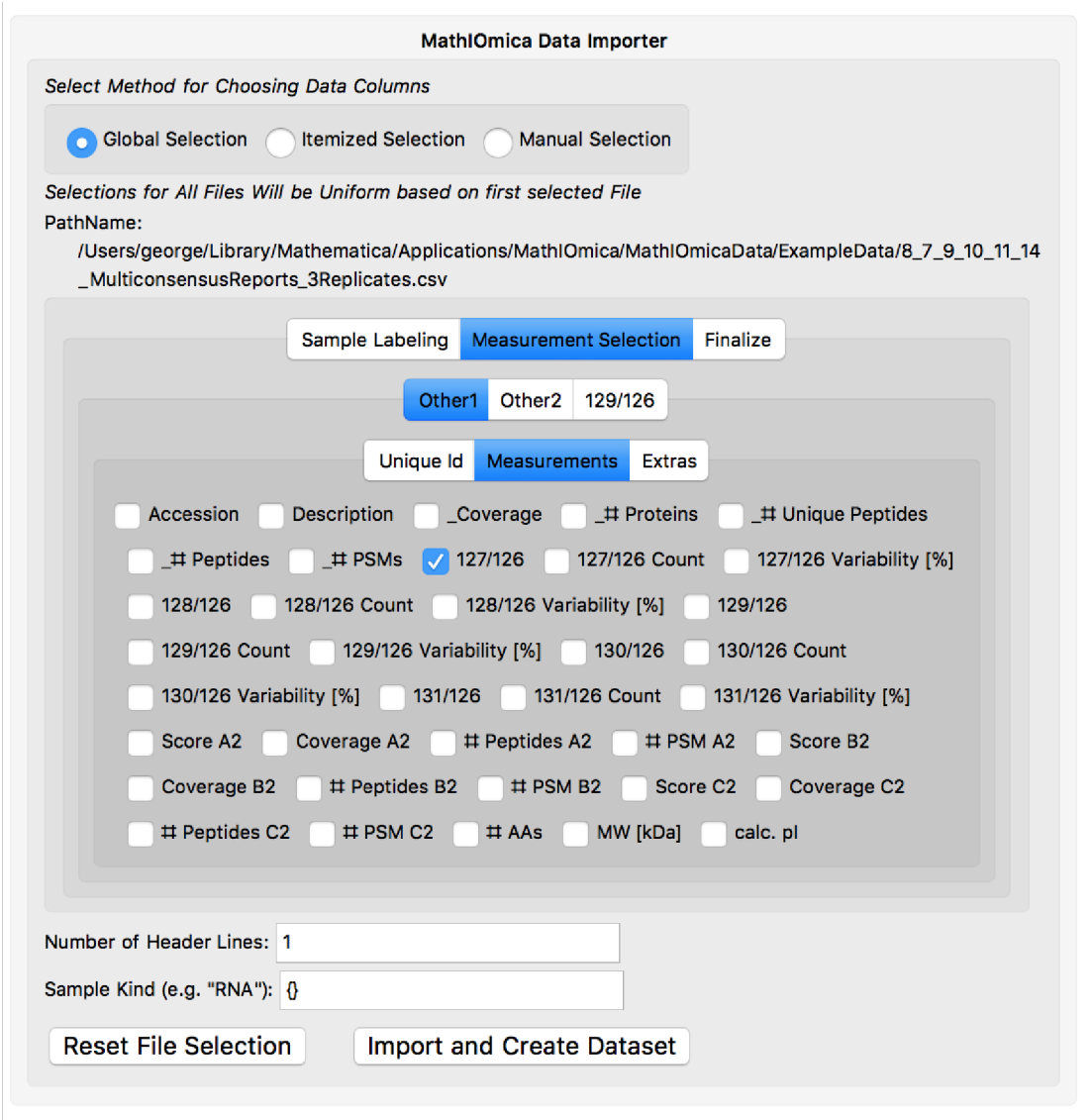

- c. The "Extras" (i.e. metadata):

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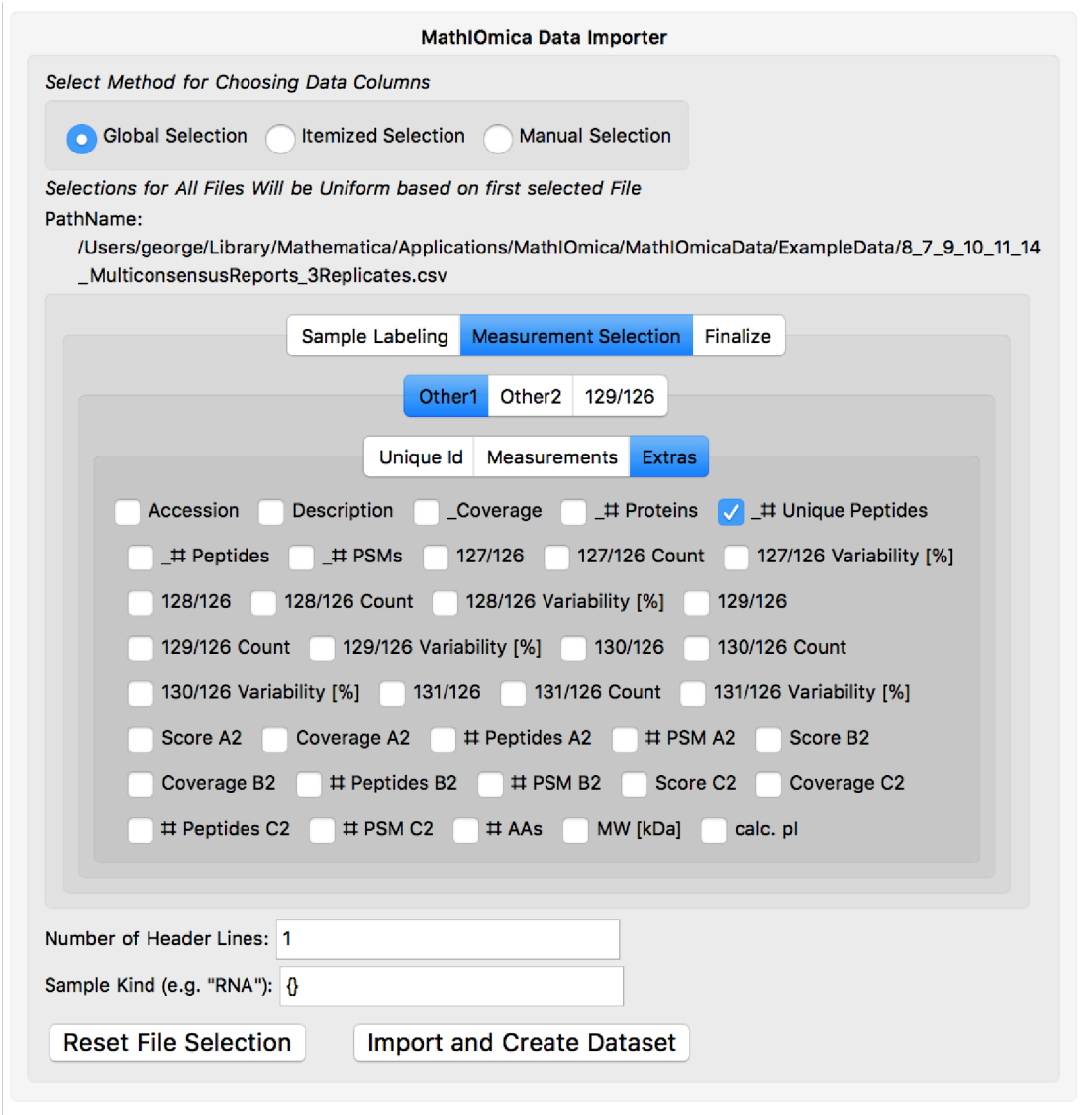

- We repeate for each sample label:

- Label "Other2", "Unique Id" Selection:

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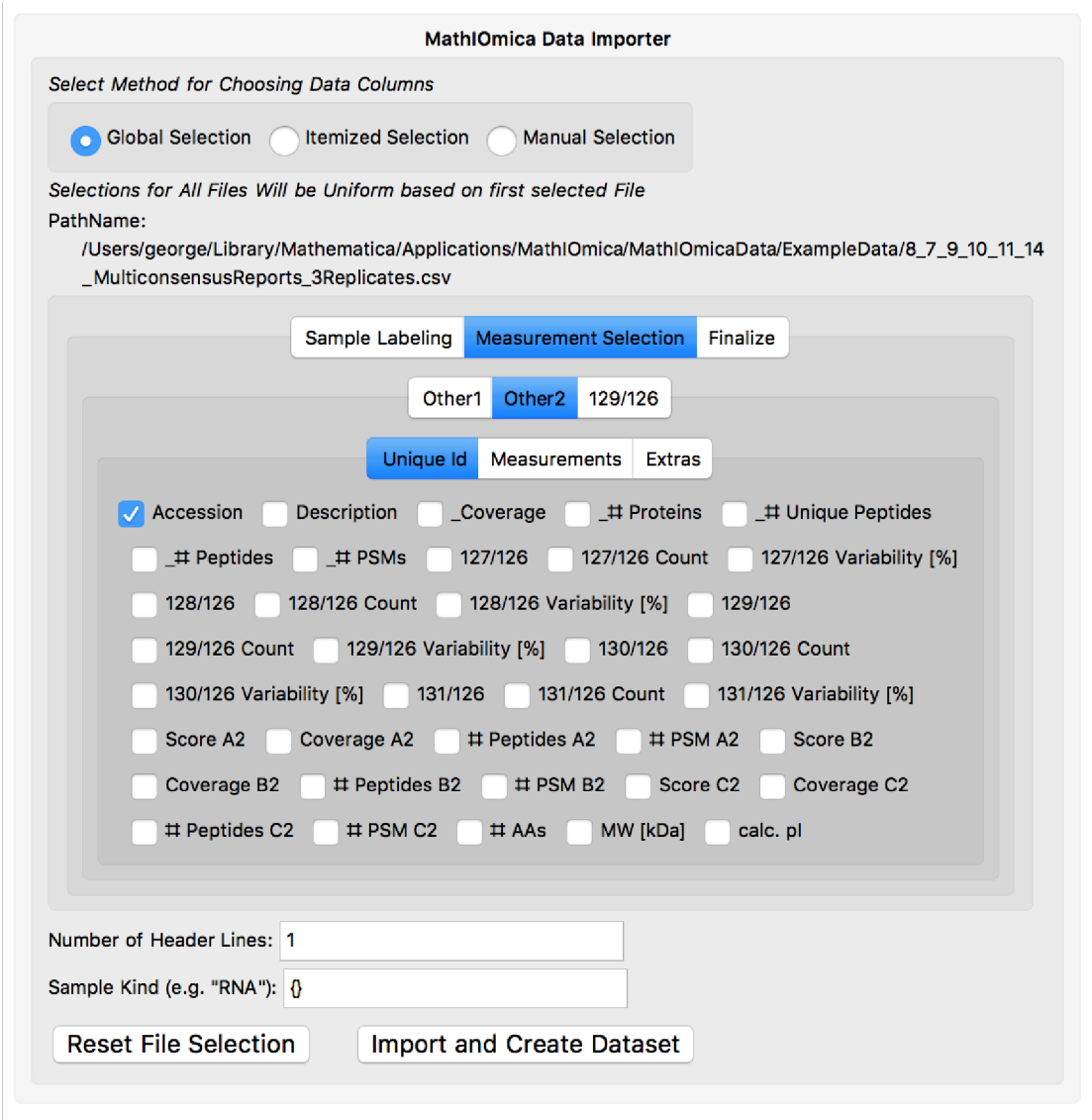

- Label "Other2", "Measurements" Selection:

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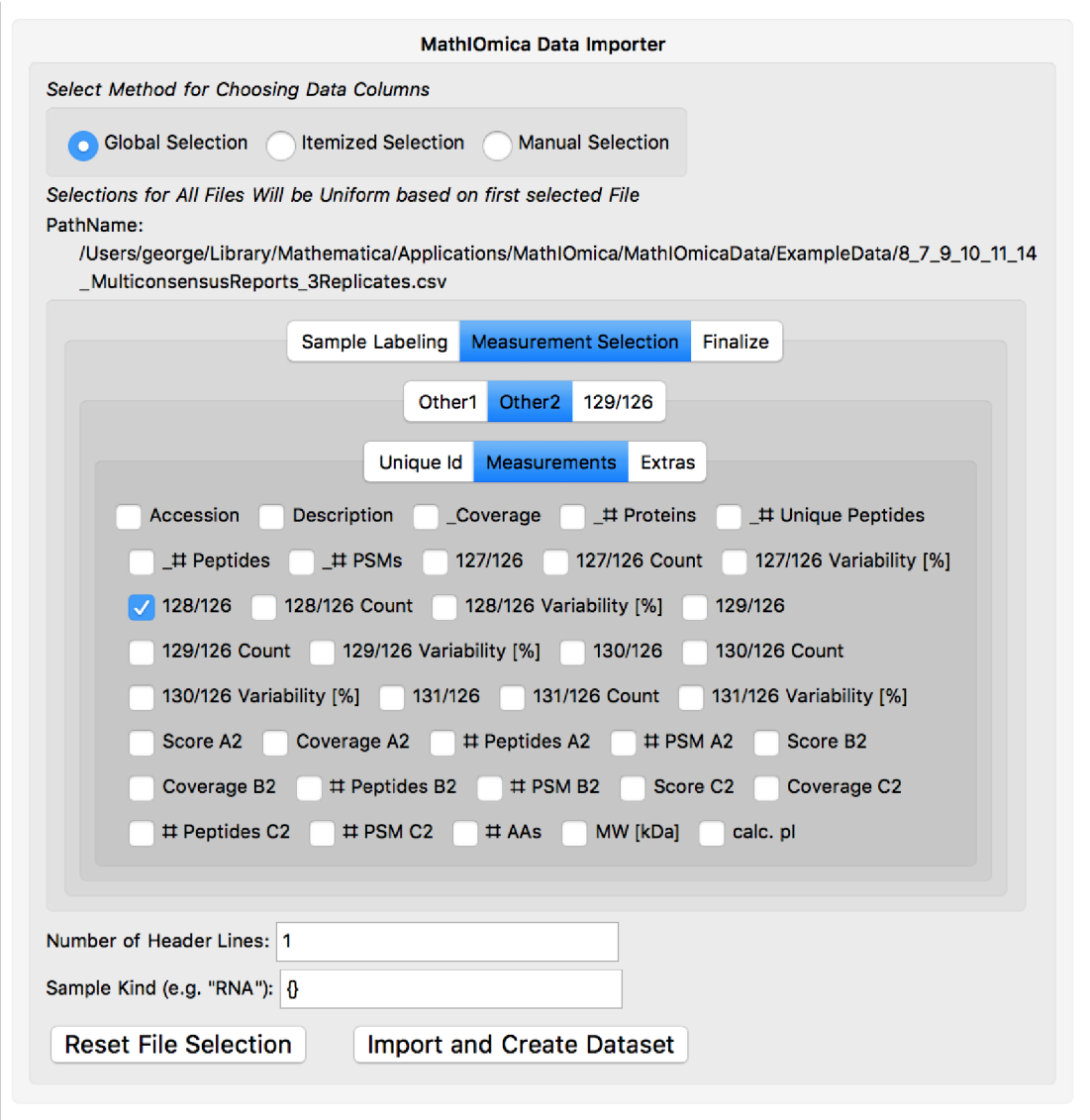

- Label "Other2", "Extras" Selection:

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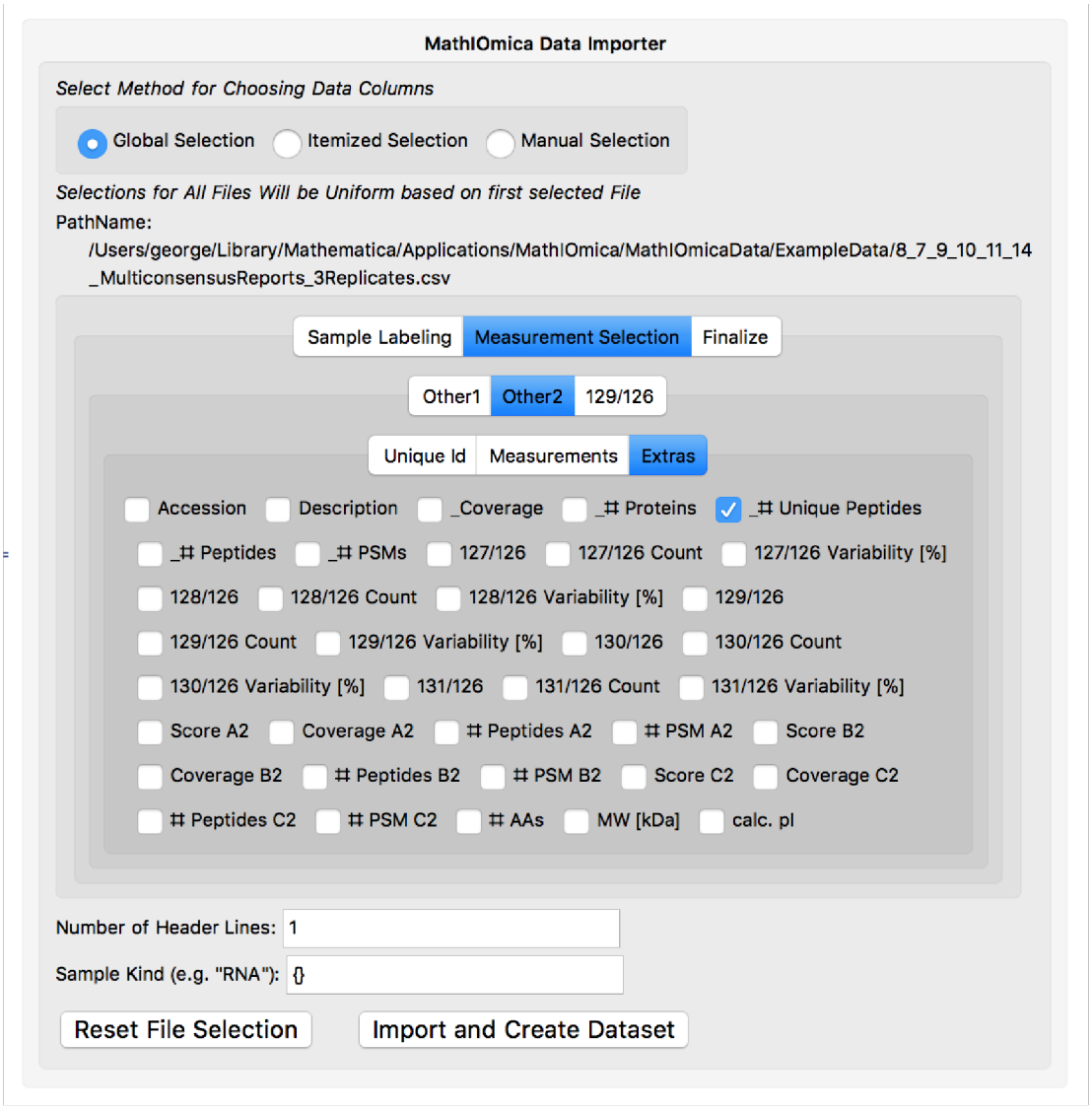

- Label "129/126", "Unique Id" Selection:

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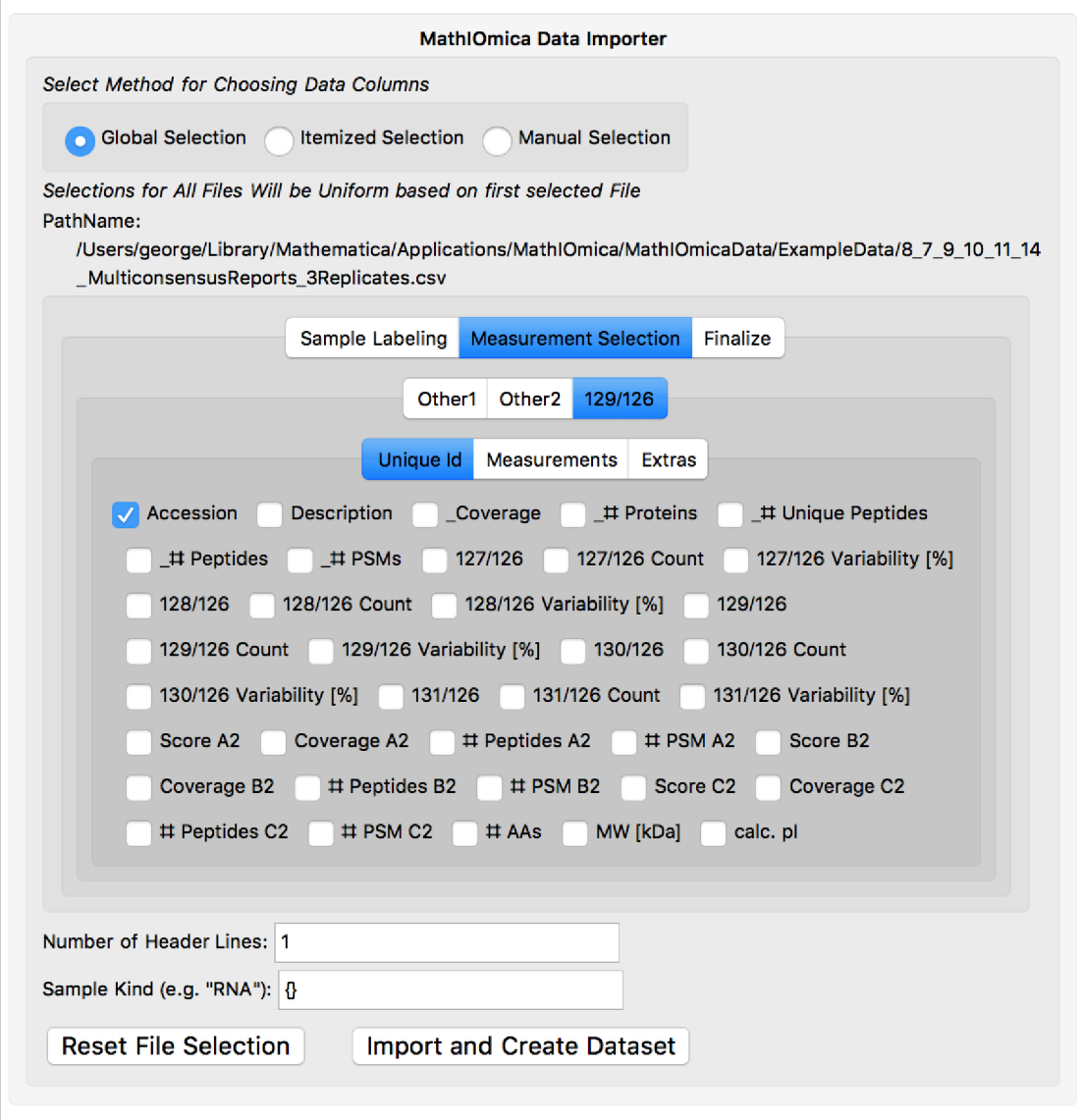

- Label "129/126", "Measurements" Selection:

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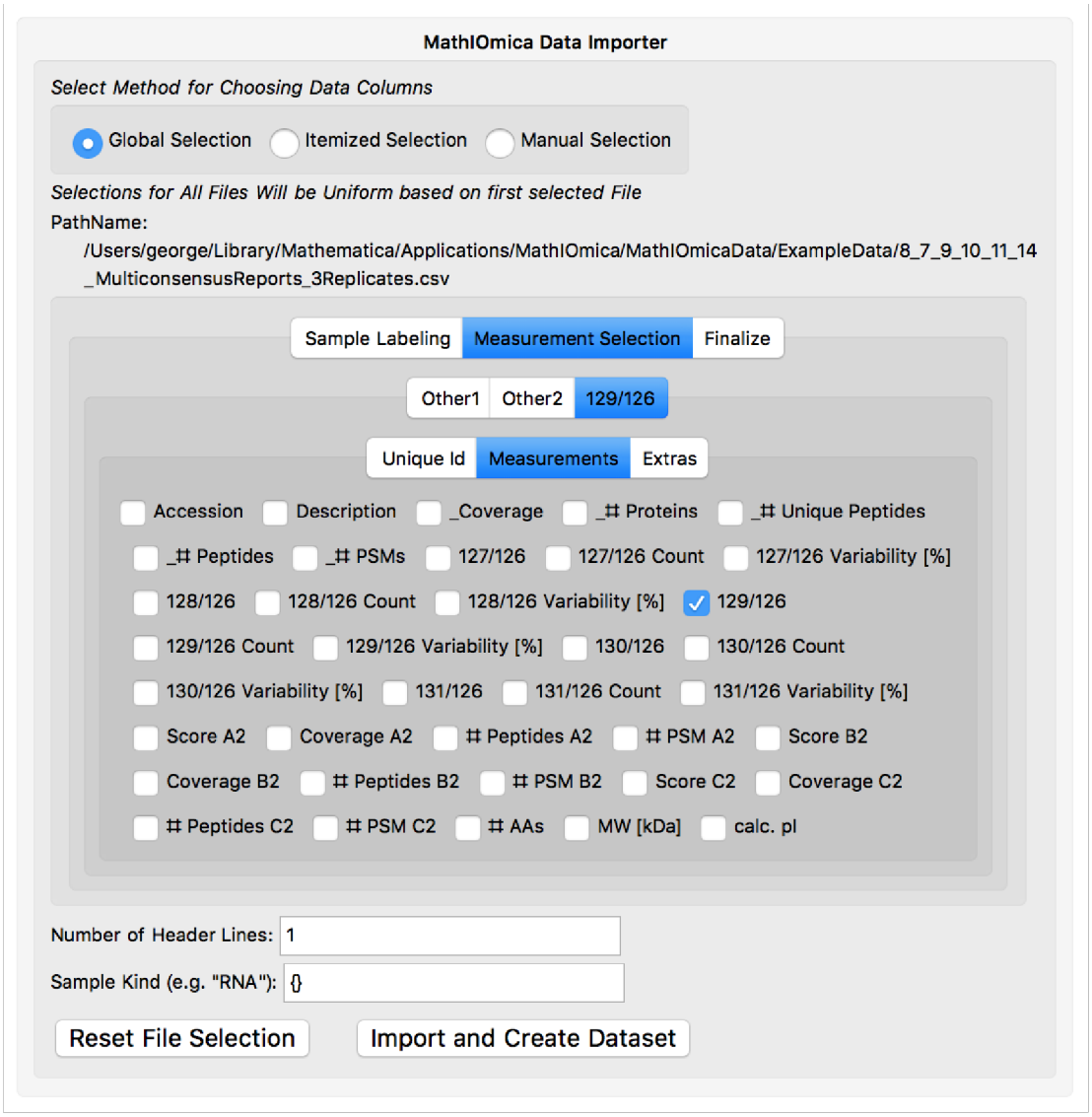

- Label "129/126", "Extras" Selection:

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Step 3. Finalize measurements ("Finalize" tab).

- If we are satisfied with our selection we press "Set Input Measurement". The message to the left below the button will change from "Selection Pending" to "Selection Made"

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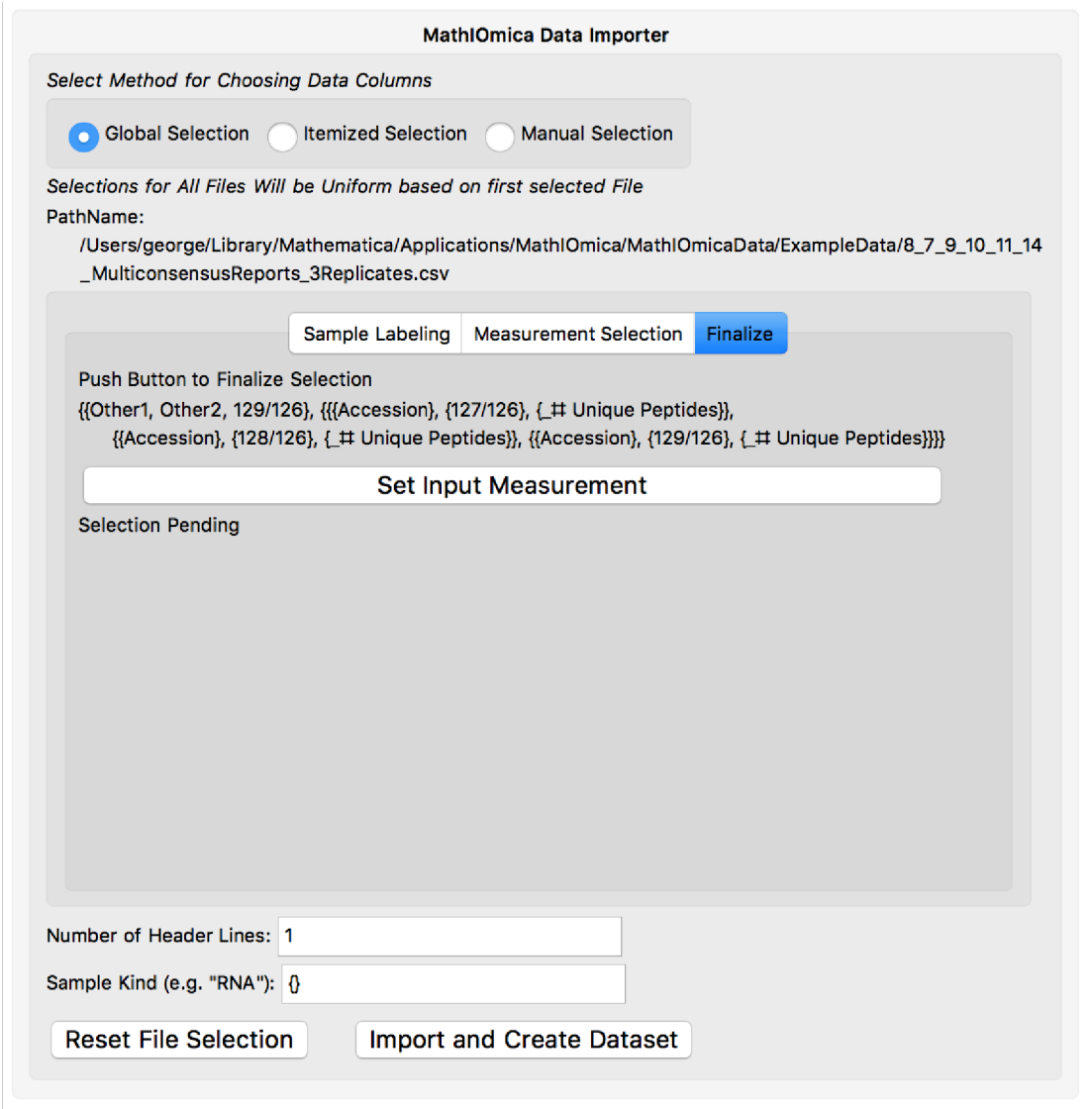

- After the button "Set Input Measurement" has been pressed:

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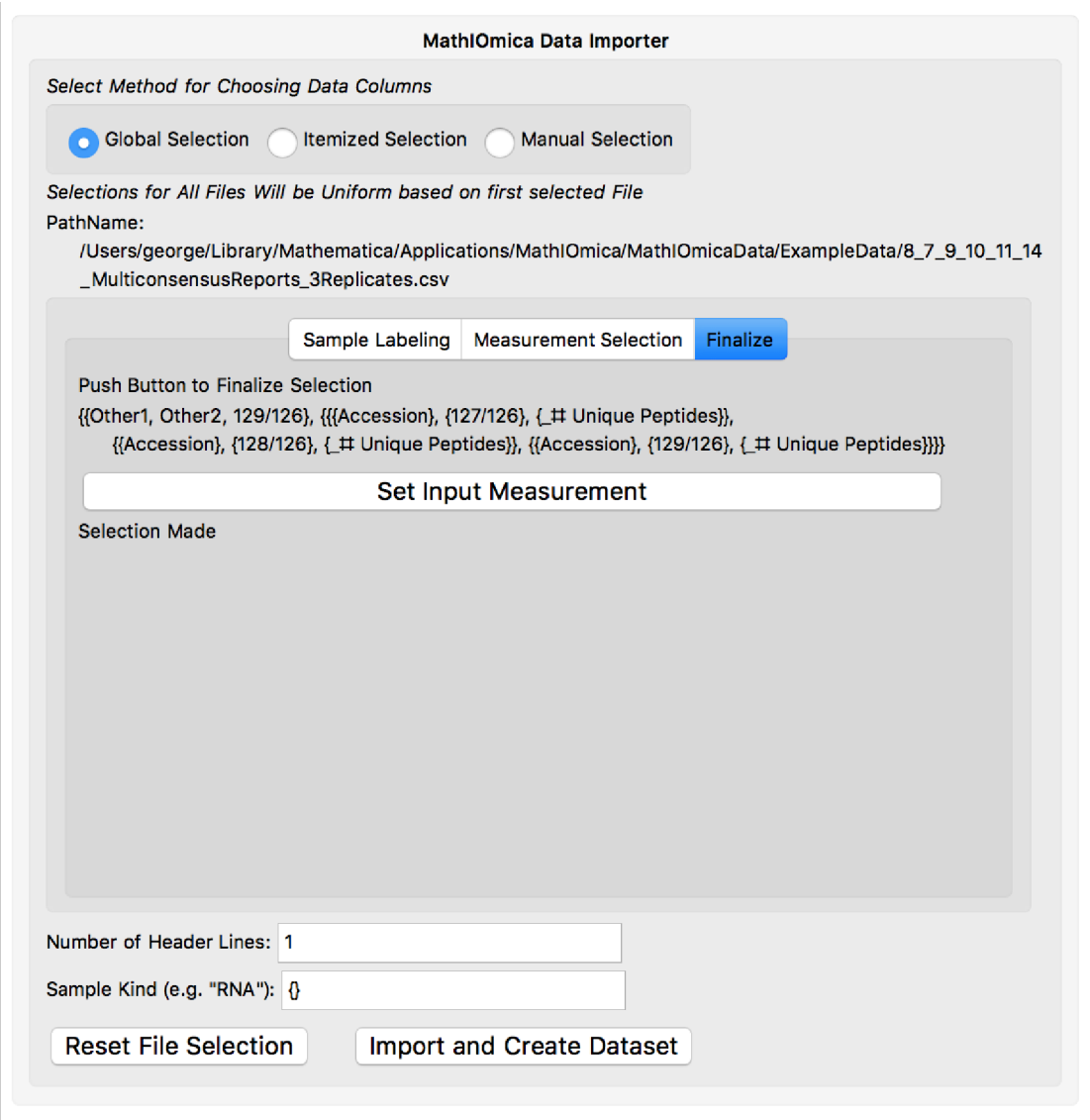

Step 4. Modify other fields as necessary ("Number of Header Lines", "Sample Kind").

- We can modify other fields, e.g. labeling {"Protein"} as the sample kind, by changing the "Sample Kind" text field:

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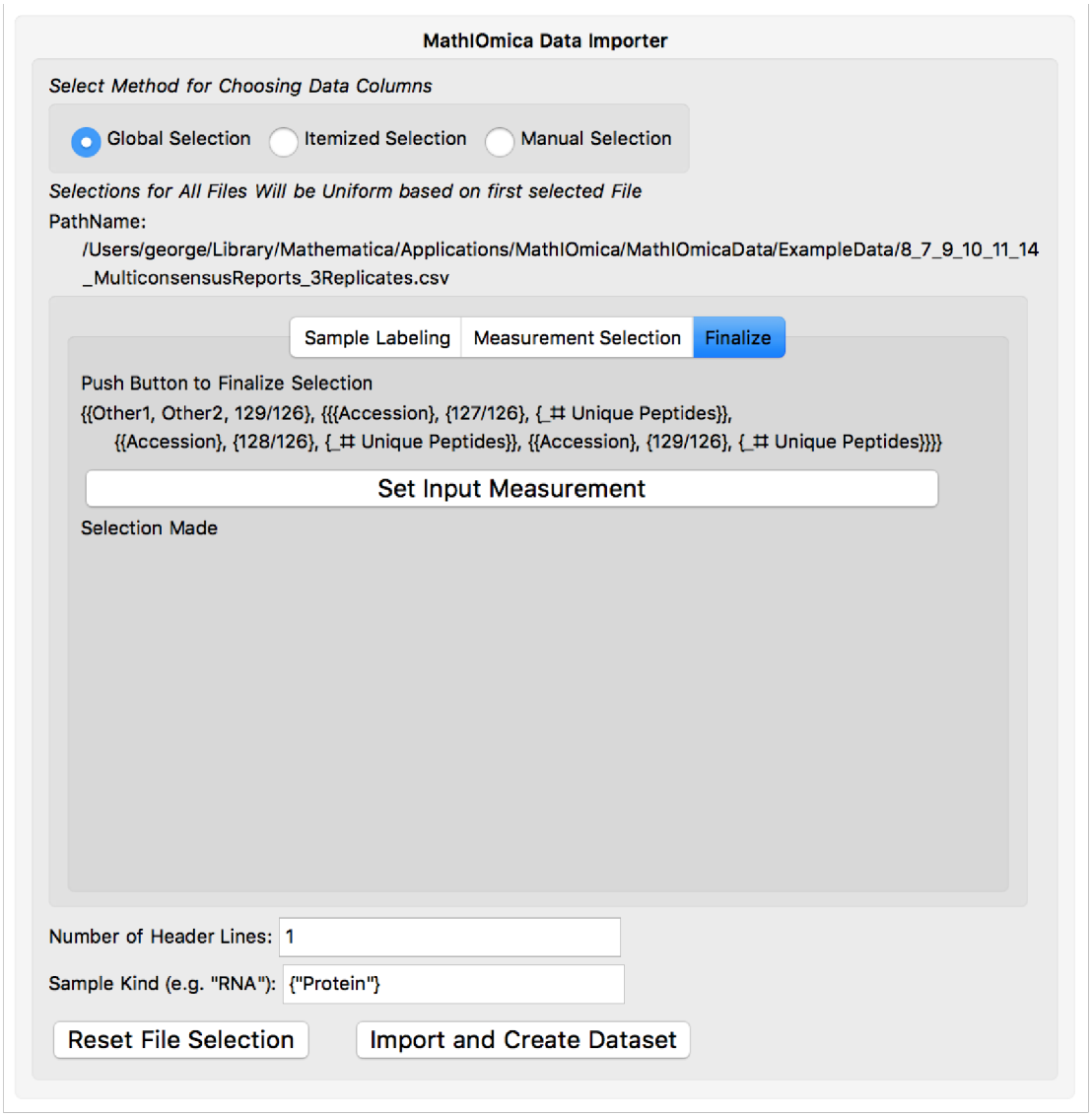
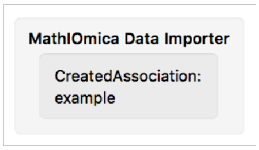


Step 5. Press the "Import and Create Dataset" button at the bottom of the panel.

- After the "Import and Create Dataset" button is pressed, and the computation concludes a verification that the variable with the OmicsObject has been created (in this case "example") is displayed.



"Itemized Selection" Method

- Itemized Selection has a six step workflow:

"Itemized Selection" Steps	Step Description
1. Select labels ("Sample Labeling" tab ").	The selection creates labels for selection of multiple samples from single files. The labels can be custom selected or selected from a list populated from the first provided file header (sub panel "Select from file header").

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2. Select measurements ("Measurement Selection" tab).	For each of the labels created corresponding to each sample a subpanel is created. Selections must be made for each subpanel for three items: (i) "Unique ID", a unique identifier column for the entries of the sample, (ii) "Measurements", which columns to use as measurements, (iii) "Extras", which column to select fo additional metadata for each entry. At least one field must be selected. Multiple selections for each of i–iii above are possible.
3. Finalize measurements ("Finalize" tab).	The information collected can be checked and if correct the "Finalize Selection" button can be pressed.
4. Repeat steps 2 and 3 for each file in the dropdown menu.	Steps 2 and 3 are iterated for each file selected from the dropdown menu. This allows for individualized selection of columns from each of the files.
5. Modify other fields as necessary ("Number of Header Lines", "Sample Kind") at the bottom of the panel.	Values are adjusted for the text fields: "Number of Header Lines" to skip when the files are imported. The default is to skip one line. "Sample Kind" label that will be used to label identifiers. For protein or RNA a standard usage would be to enter a label as {"Protein"} or {"RNA"} respectively. An empty list {} will not provide labeling for the identifiers.
6. Press the "Import and Create Dataset" button at the bottom of the panel.	The "Import and Create Dataset" button will import the dataset and create an OmicsObject corresponding to the input choices.

- Compared to "Global Selection", "Itemized Selection" iterates steps 2 and 3 for each file selected from a dropdown menu in sequence.
- Here are some example screenshots for each step:

Step 1. Select labels ("Sample Labeling" tab).

- Selection of 1 labels shown for the first file (of two) selected (labels can be added or removed using the "Add Custom Field" or "Remove Last Field" respectively):

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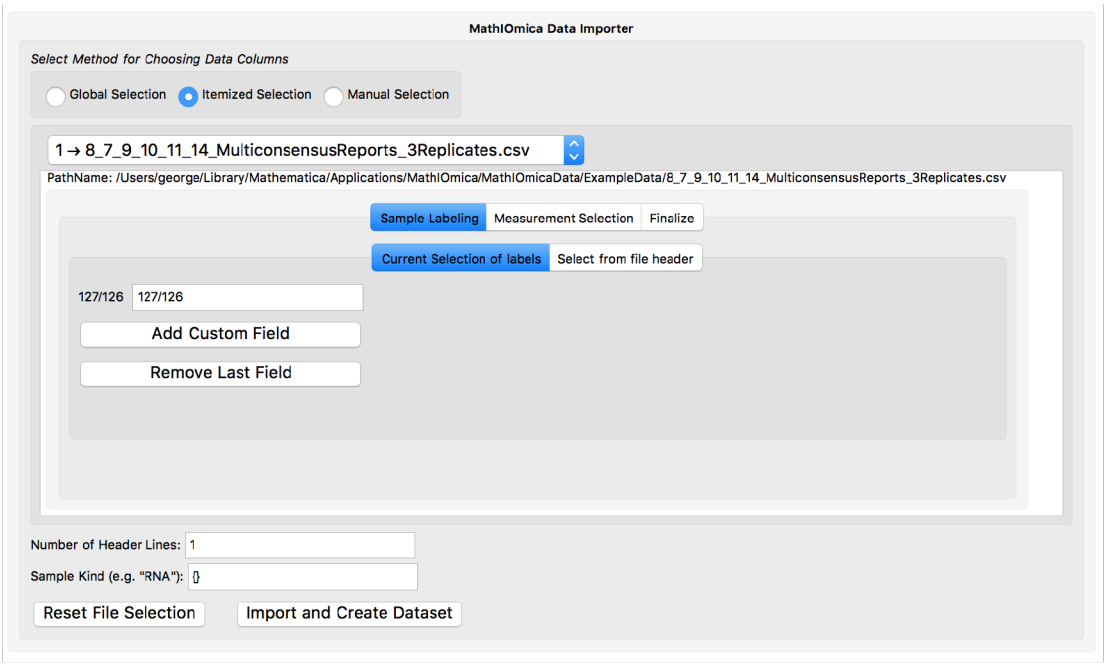
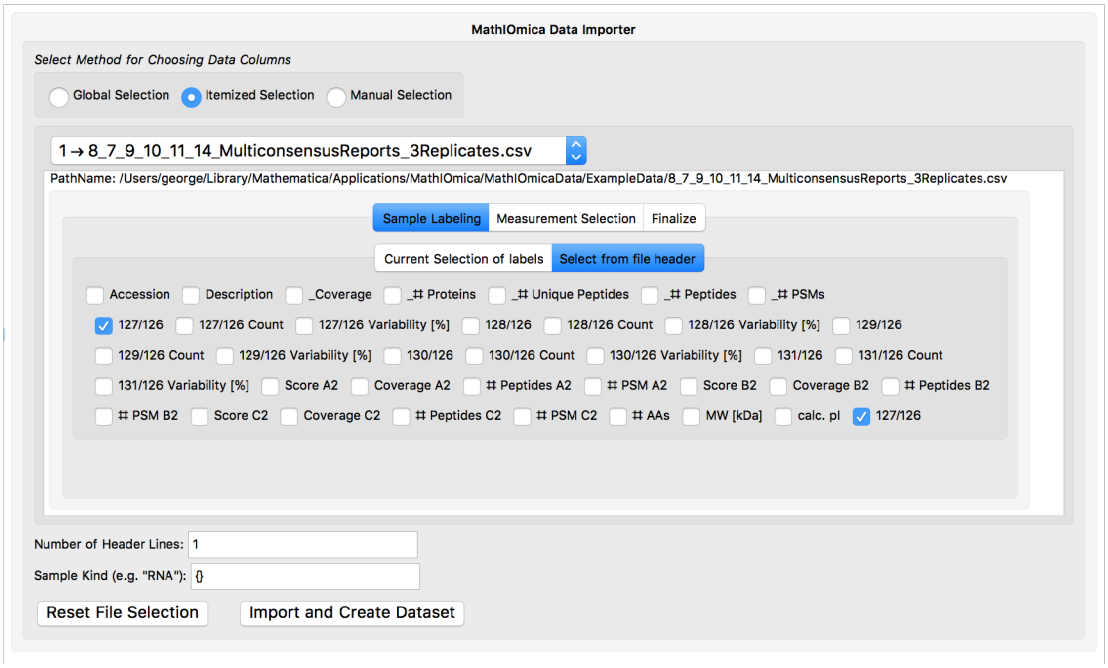


- More selections can be facilitated by selecting from the file's header line for choices of labels.



Step 2. Select measurements ("Measurement Selection" tab).

- For each tab representing a sample label we make 3 selections by selecting the tabs below:

- a. The "Unique Id"

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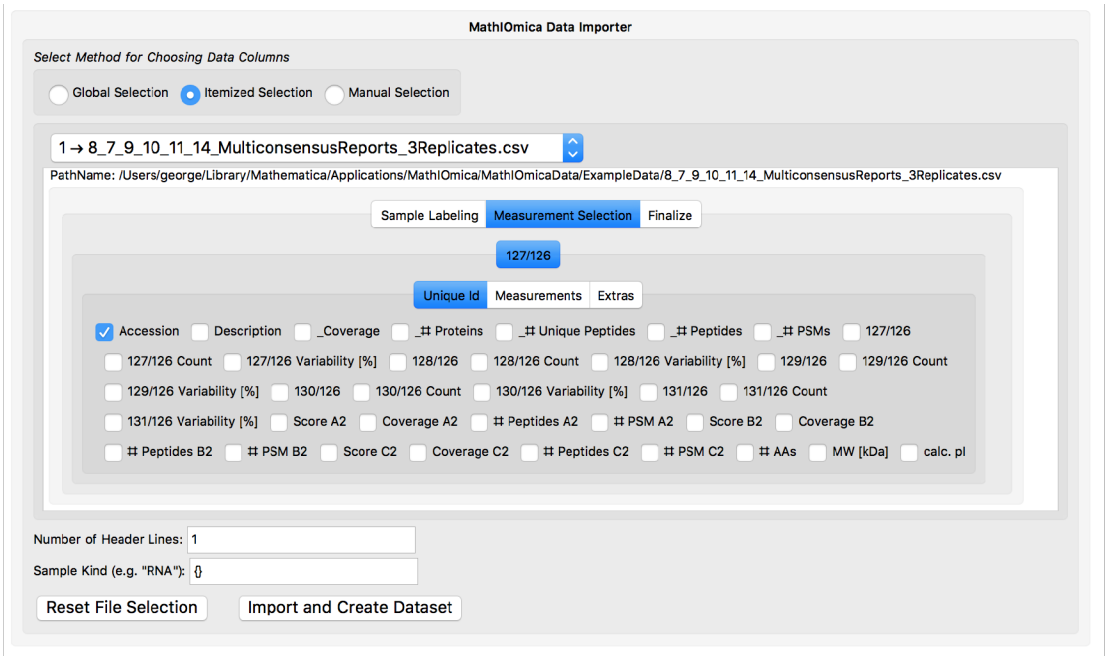
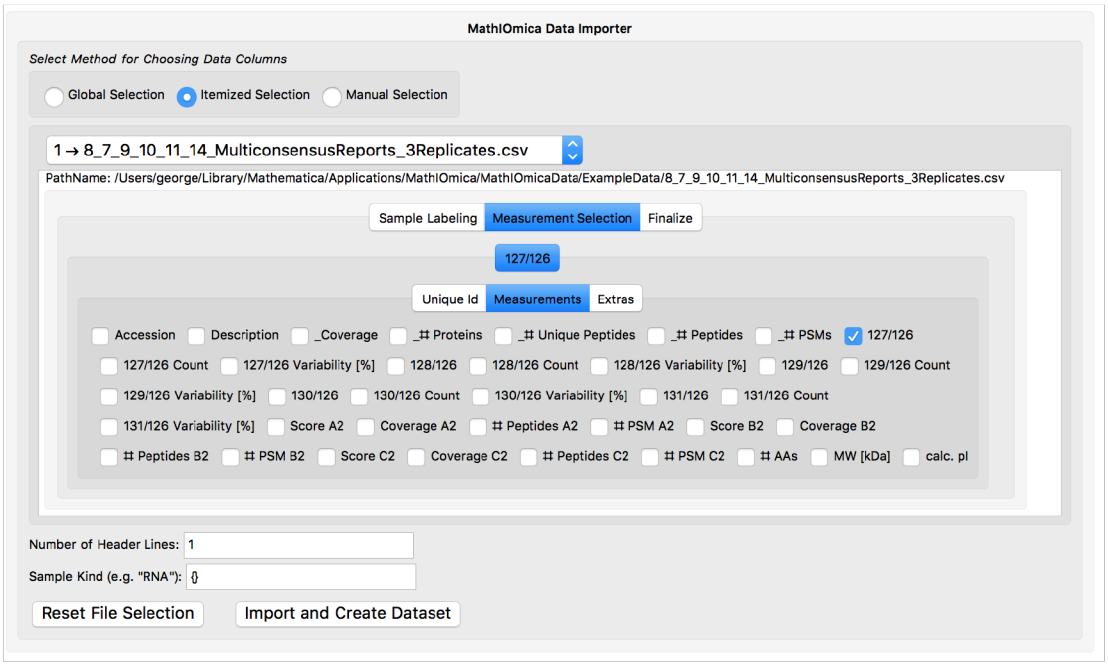


- b. The "Measurements":



- c. The "Extras" (i.e. metadata):

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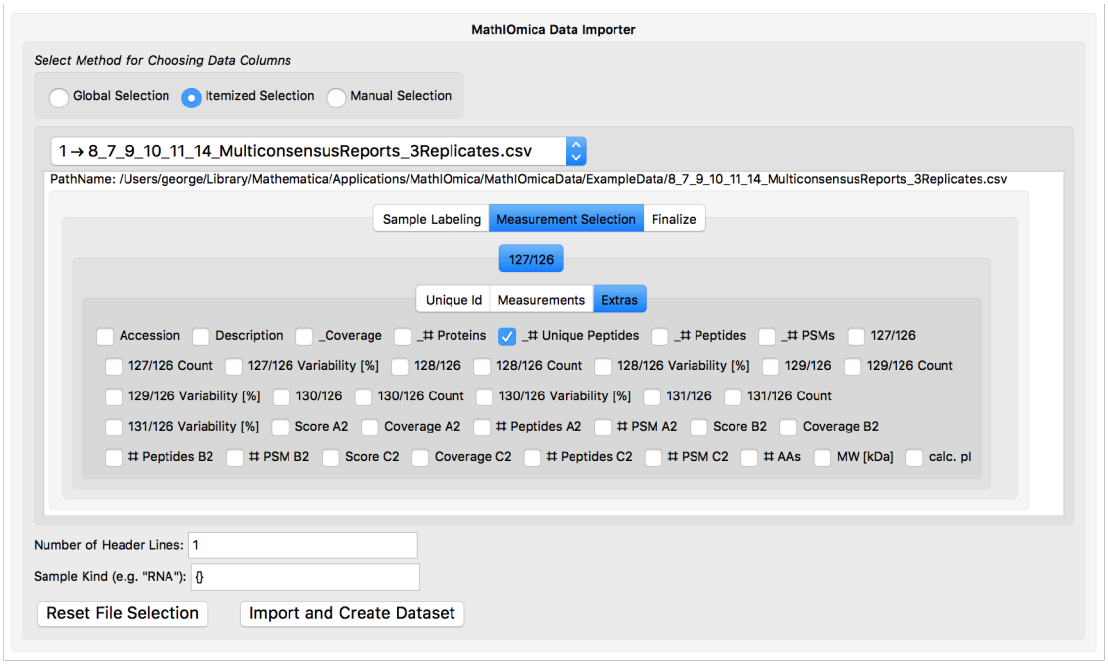
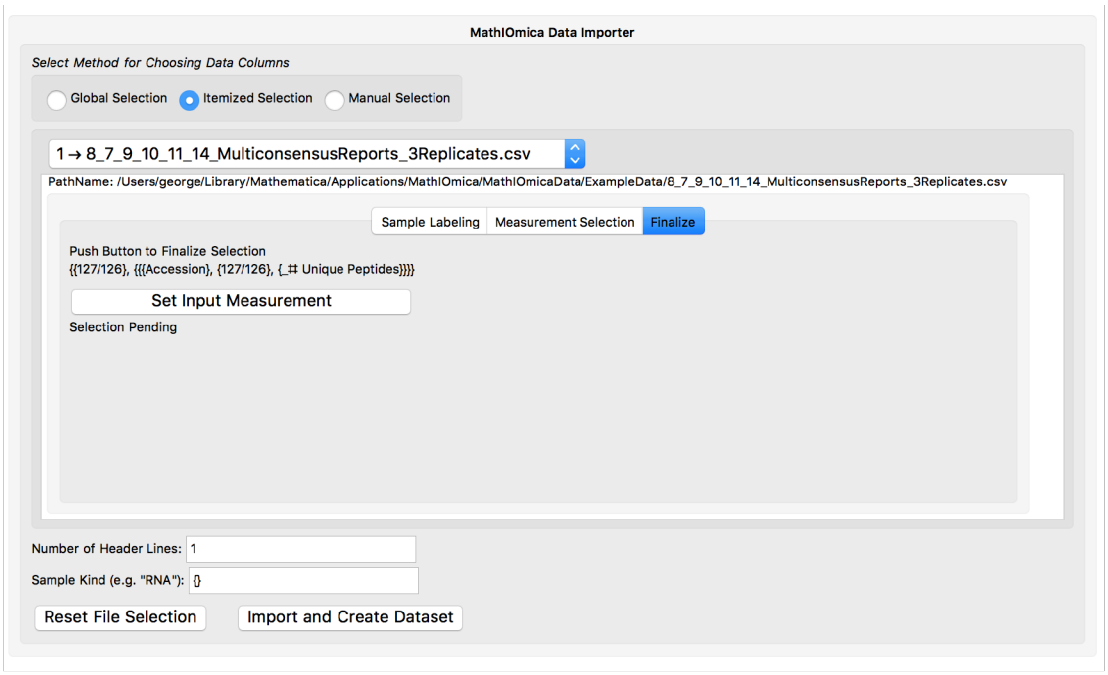


Step 3. Finalize measurements ("Finalize" tab).

- If we are satisfied with our selection we press "Set Input Measurement". The message to the left below the button will change from "Selection Pending" to "Selection Made":



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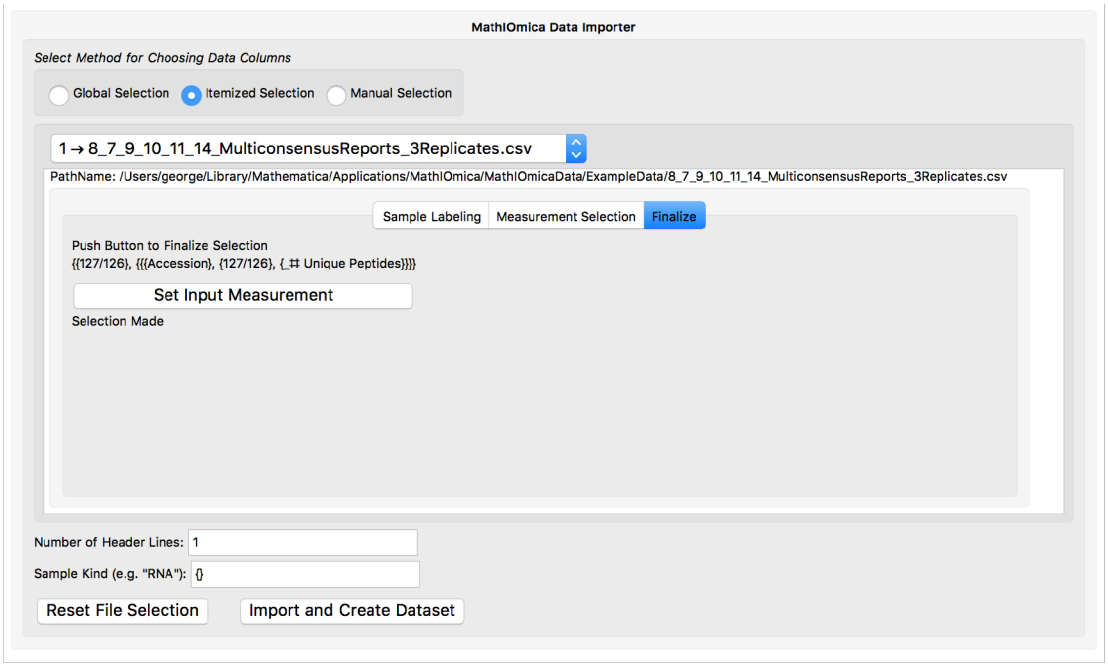
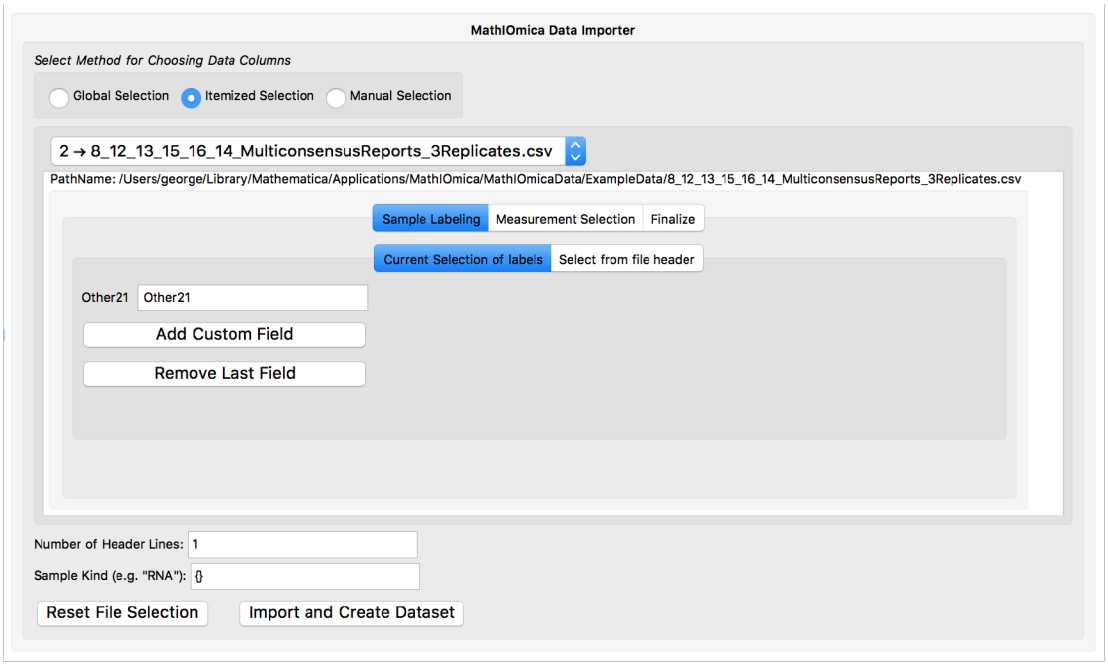


Step 4. Repeat steps 2 and 3 for each file in the dropdown menu.

- Select label(s) for the sample(s) in the second file:



- Select "Measurement Selection for the second file, Sample "Other 22", "Unique Id" column":

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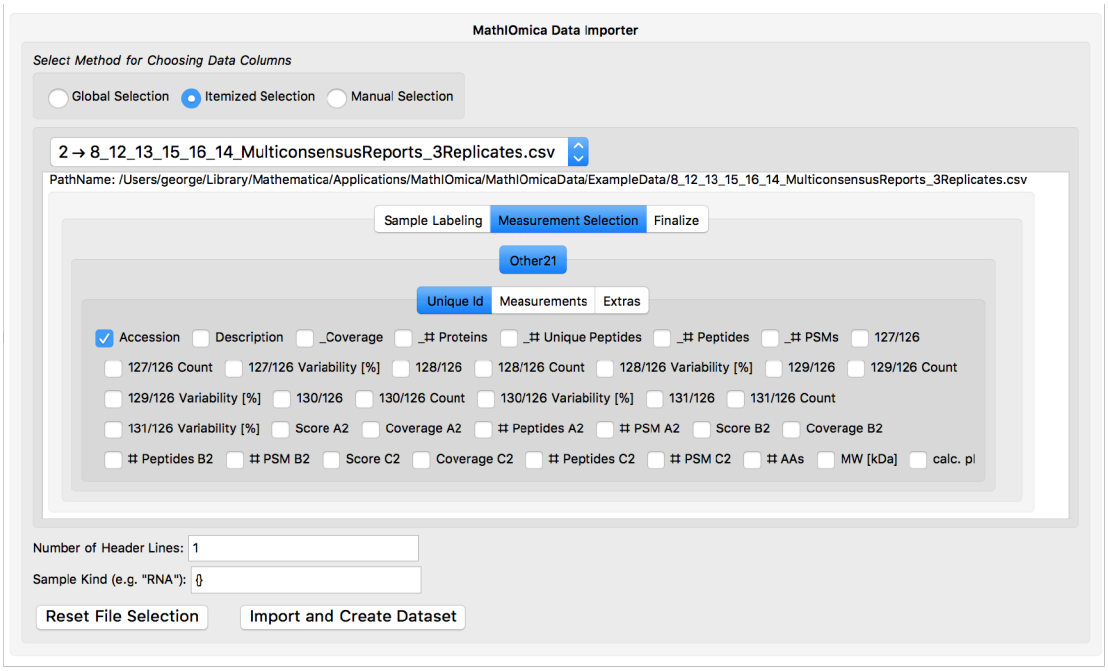
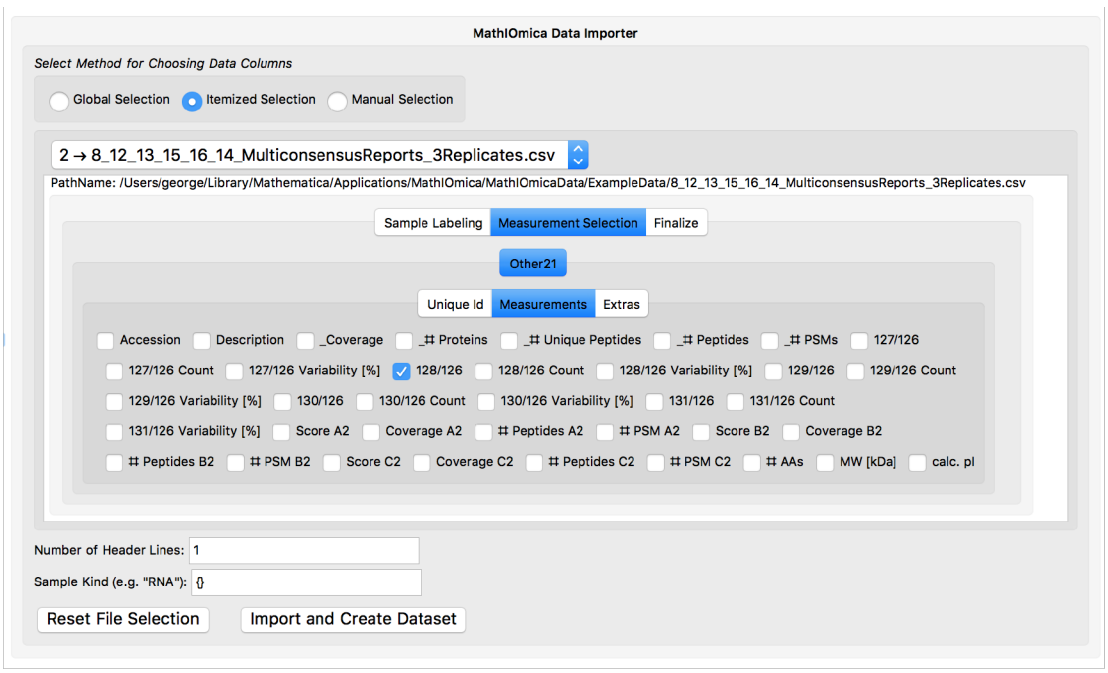


- Select "Measurement Selection for the second file, Sample "Other 22", "Measurements" column":



- Select "Measurement Selection for the second file, Sample "Other 22", "Extras" column":

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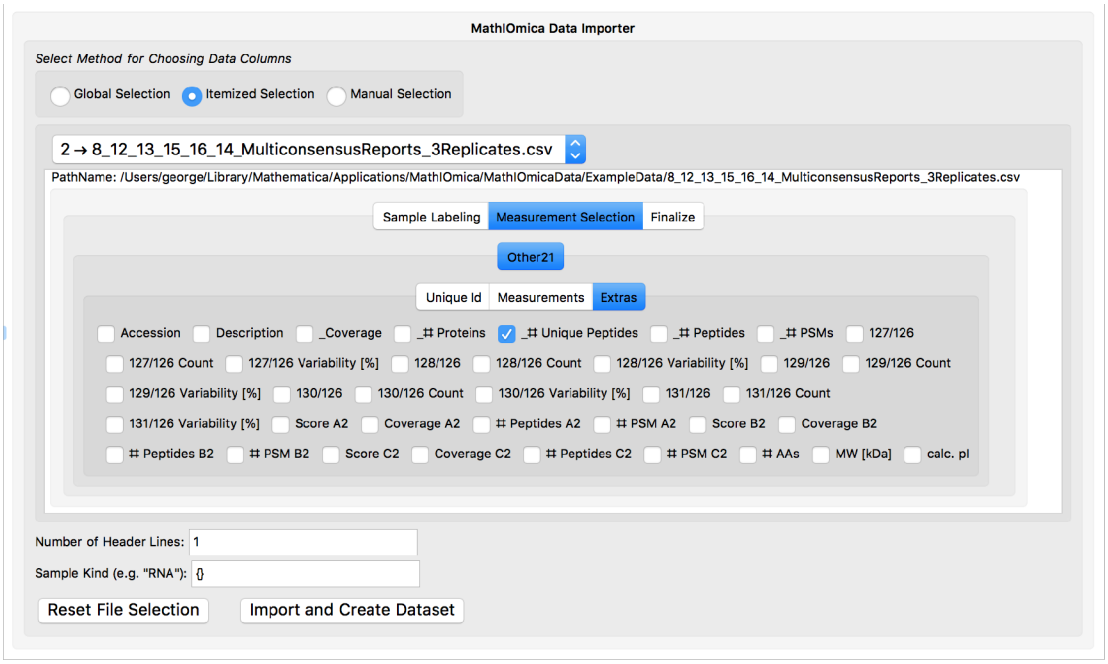
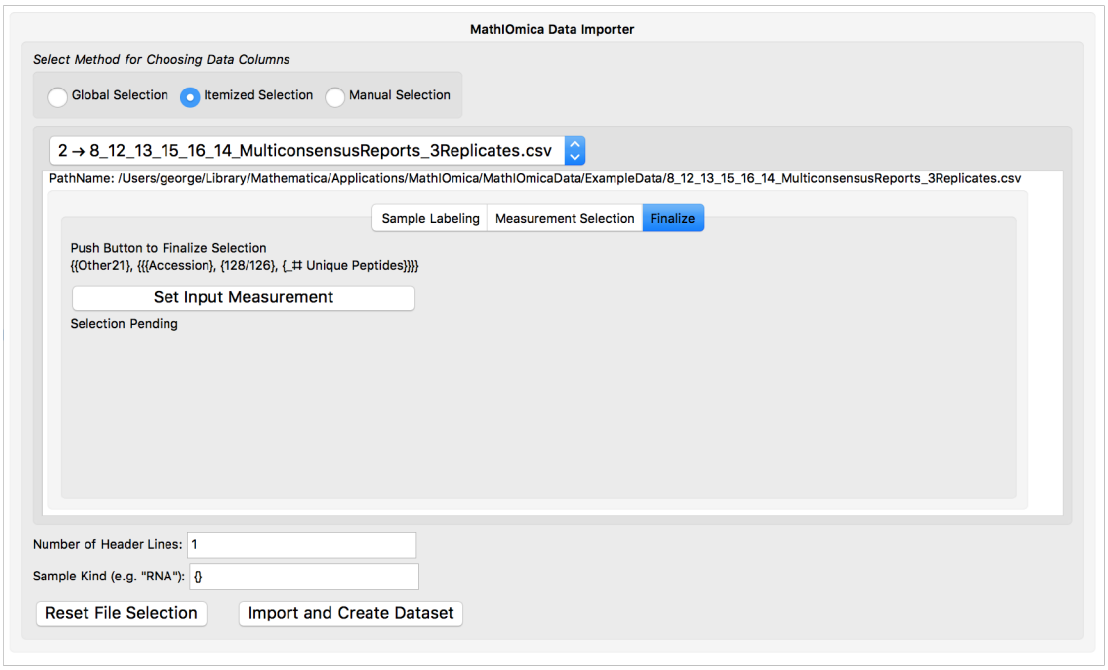


- Check the selection:



- Finalize the selection by pressing "Set Input Measurement":

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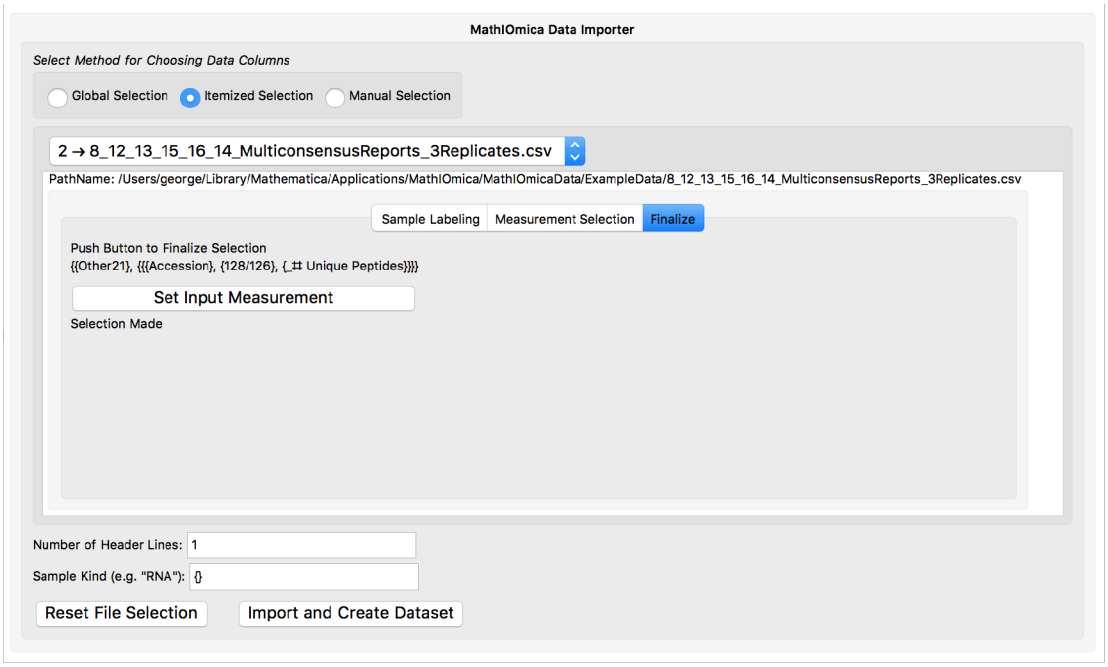
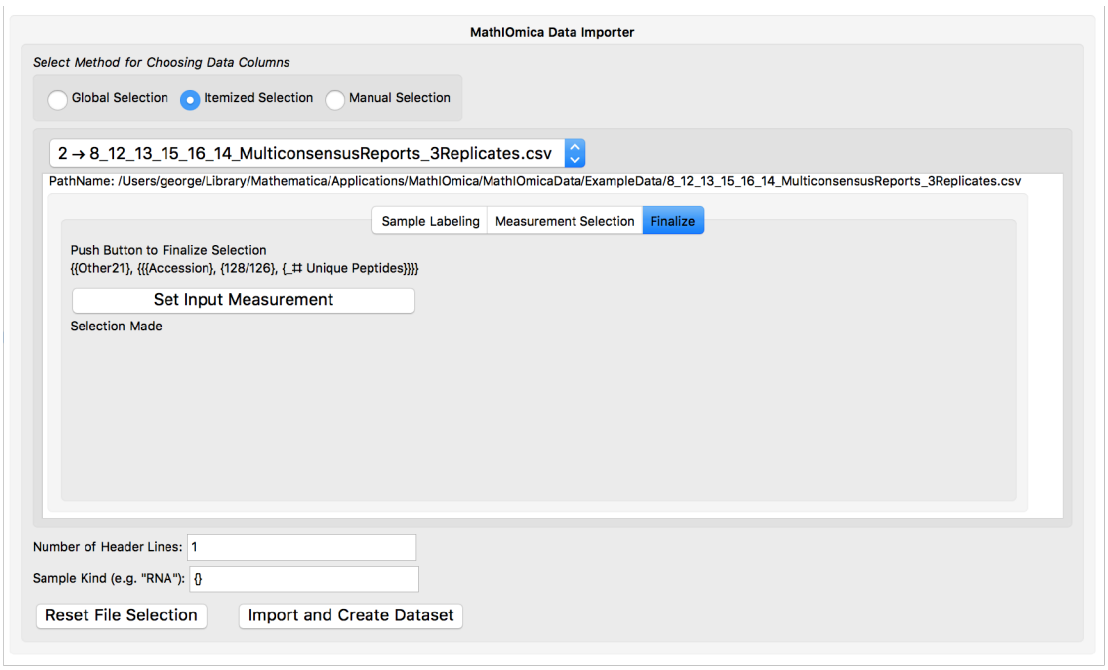


Step 5. Modify other fields as necessary ("Number of Header Lines", "Sample Kind").

- Once selections have been finalized for each of the files, we can modify other fields, e.g. labeling {"Protein"} as the sample kind:



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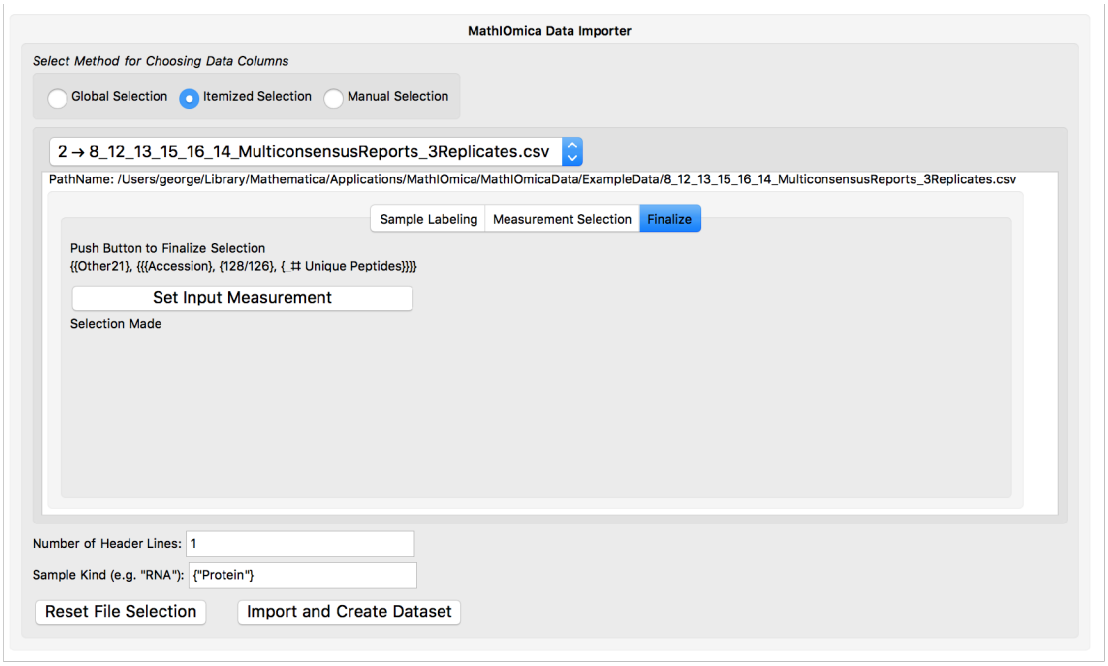
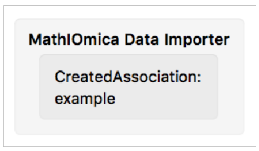


Step 6. Press the "Import and Create Dataset" button at the bottom of the panel.

- After the "Import and Create Dataset" button is pressed, and the computation concludes a verification that the variable with the OmicsObject has been created (in this case "example") is displayed.



"Manual Selection" Method

- Manual Selection has a four step workflow:

"Manual Selection" Steps	Step Description
1. Select from "Global Selection" or "Individual Selection" from the subpanel.	The selection allows to enter one list for structured positions of columns to be imported across files ("Global Selection"), or a list of lists structured positions of columns to be imported for each individual file ("Individual Selection").

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2. Fill out the text box with the list of positions structured as indicated.	For "Global Selection" enter columns to be imported across files in the format: {{{"identifier1"},{"measurement1"},{"metadata1"}},{{"identifier2"},{"measurement2"},{"metadata2"}}}. "identifierj" refers to the column(s) used for unique identifiers for sample j. "measurementj" refers to the column(s) used for measurements for sample j. "metadataj" refers to the column(s) used for metadata for sample j. For "Individual Selection" enter the columns to be imported in lists for each file: {{{{"identifier1f1"},{"measurement1f1"},{"metadata1f1"}},{{"identifier2f1"},{"measurement2f1"},{"metadata2f1"}},{{"identifier3f1"},{"measurement3f1"},{"metadata3f1"}}},{{{"identifier1f2"},{"measurement1f2"},{"metadata1f2"}},{{"identifier2f2"},{"measurement2f2"},{"metadata2f2"}}}}. Here the suffix "fk" refers to the information for file k.
3. Modify other fields as necessary ("Number of Header Lines", "Sample Kind") at the bottom of the panel.	Values are adjusted for the text fields: "Number of Header Lines" to skip when the files are imported. The default is to skip one line. "Sample Kind" label that will be used to label identifiers. For protein or RNA a standard usage would be to enter a label as {"Protein"} or {"RNA"} respectively. An empty list {} will not provide labeling for the identifiers.
4. Press the "Import and Create Dataset" button at the bottom of the panel.	The "Import and Create Dataset" button will import the dataset and create an OmicsObject corresponding to the input choices.

- Here are some example screenshots for each step for each of "Global Selection" or "Individual Selection" workflows:

  Step 1: "Global Selection". Select from "Global Selection" or "Individual Selection" from the subpanel.

- Selection of "Manual Selection" method and "Global Selection":

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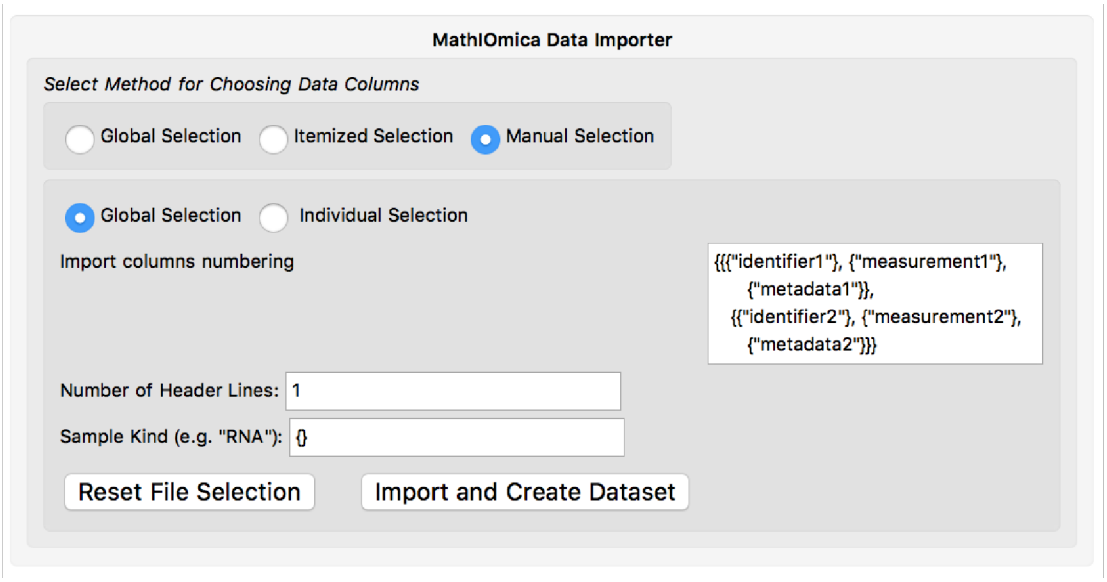
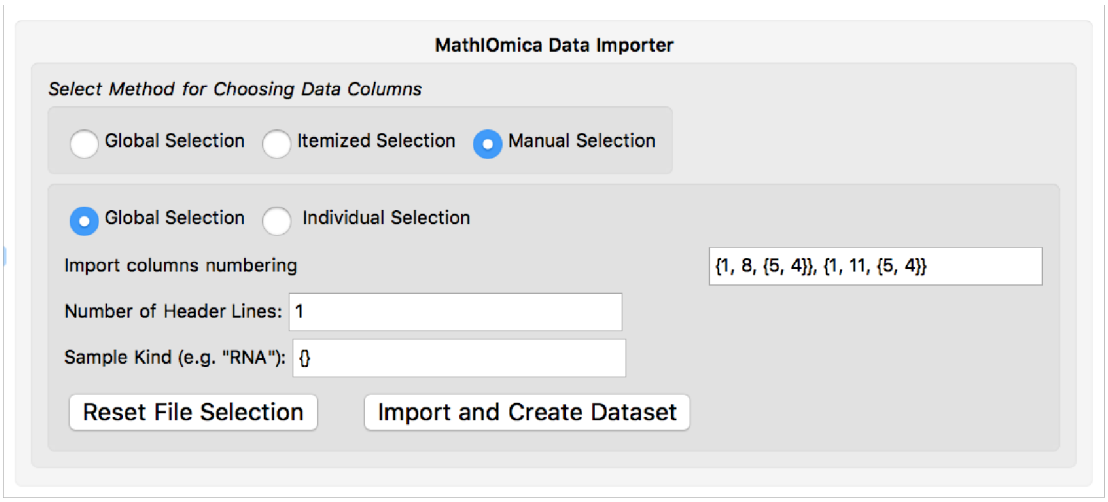


Step 2: "Global Selection". Fill out the text box with the list of positions structured as indicated.

- For this example, in each file two samples are extracted. All identifiers are taken from the first column, measurements for the first sample are from column 8, for the second sample from column 11. The metadata is taken as a two member list, populated from columns 5 and 4 for both samples:



Step 3: "Global Selection". Modify other fields as necessary ("Number of Header Lines", "Sample Kind").

- We can modify other fields, e.g. labeling {"Protein"} as the sample kind:

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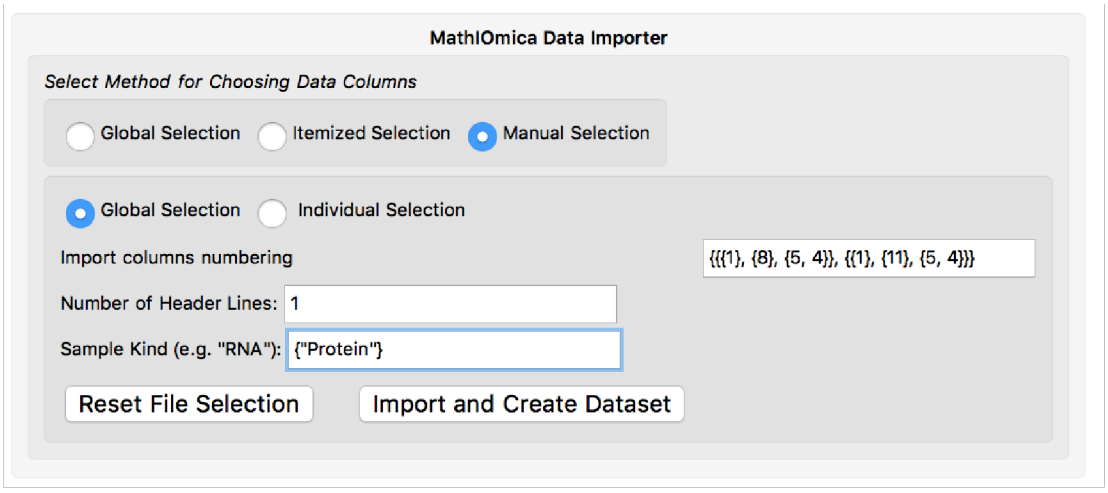
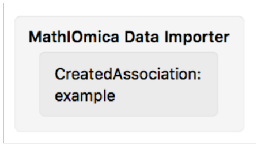


Step 4: "Global Selection". Press the "Import and Create Dataset" button at the bottom of the panel.

- After the "Import and Create Dataset" button is pressed, and the computation concludes a verification that the variable with the OmicsObject has been created (in this case "example") is displayed.



Step 1: "Individual Selection". Select from "Global Selection" or "Individual Selection" from the subpanel.

- Selection of "Manual Selection" method and "Individual Selection":

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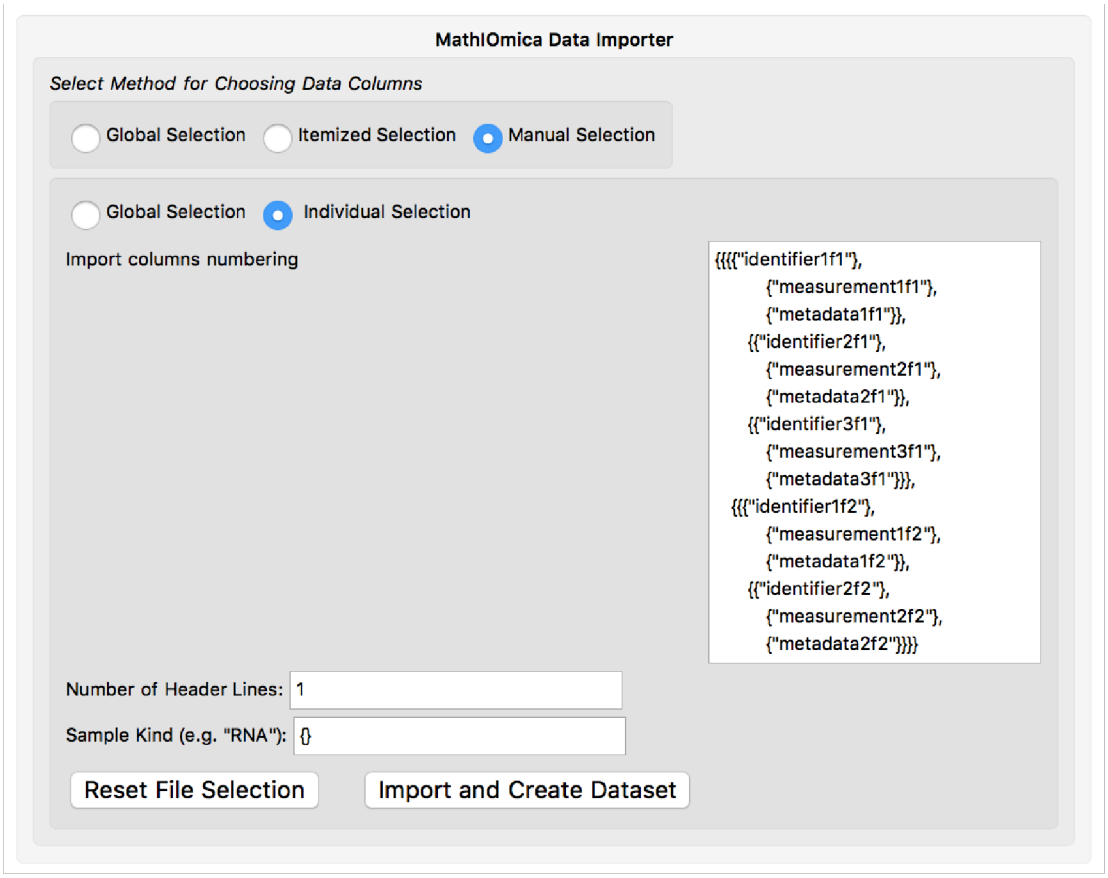

Step 2: "Individual Selection". Fill out the text box with the list of positions structured as indicated.

- For this example, there are two files and we take two samples from each:

File 1 column used for:	Sample 1 file 1	Sample 2 file 1
Identifiers	1	1
Measurements	8	11
Metadata	5,4	5,4

File 2 column used for:	Sample 1 file 2	Sample 2 file 2
Identifiers	1	1
Measurements	8	14
Metadata	5,4	5,4

- The information is entered as a list:

- `{{{{1}, {8}, {5, 4}}, {{1}, {11}, {5, 4}}}, {{{1}, {8}, {5, 4}}, {{1}, {14}, {5, 4}}}}`

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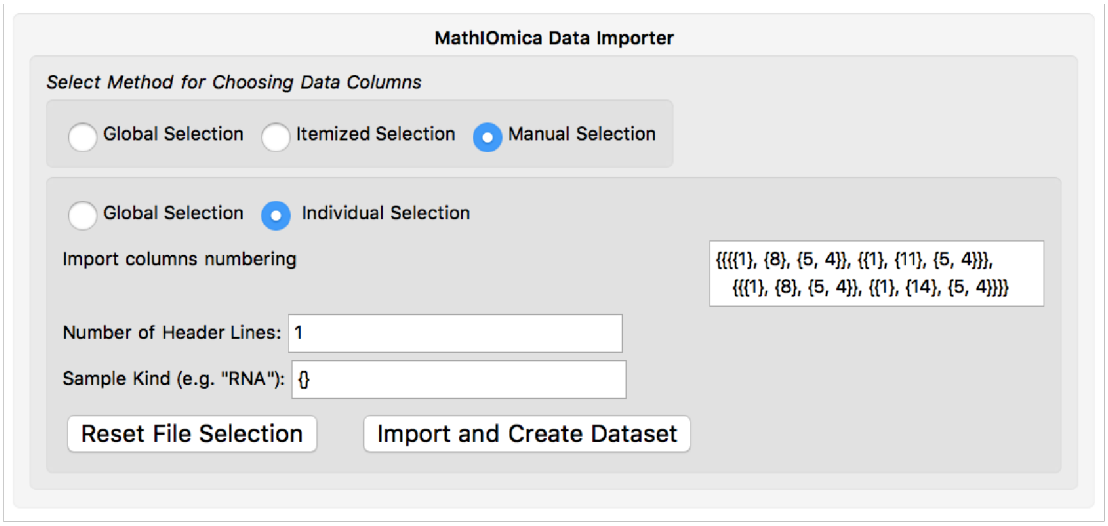
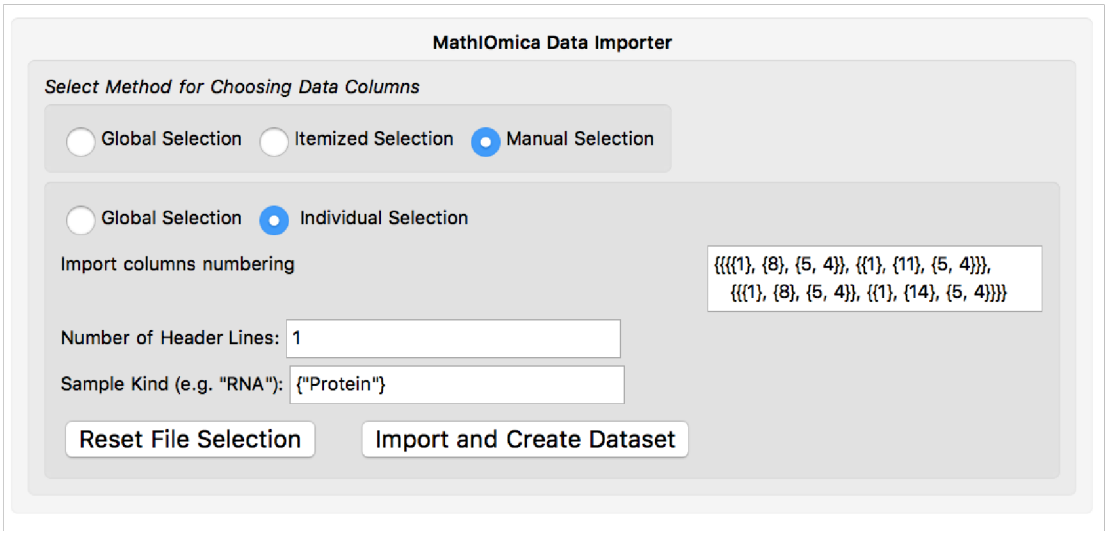


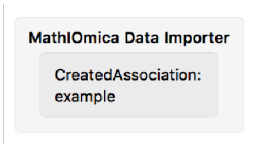
Step 3: "Individual Selection". Modify other fields as necessary ("Number of Header Lines", "Sample Kind").

- We can modify other fields, e.g. labeling {"Protein"} as the sample kind:



Step 4: "Individual Selection". Press the "Import and Create Dataset" button at the bottom of the panel.

- After the "Import and Create Dataset" button is pressed, and the computation concludes a verification that the variable with the OmicsObject has been created (in this case "example") is displayed.



Examples (4)

Basic Examples (1)

In[1]:=
```
Needs["MathIOmica`"]
```

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DataImporter uses a dynamical user interface to assist in importing datasets (screenshots are provided in the information above).

The example uses MathIOmica example data files. We can see the full paths where the files are stored by evaluating:

In[2]:=
```
fileNames = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, #} & /@
  {"8_7_9_10_11_14_MulticonsensusReports_3Replicates.csv",
   "8_12_13_15_16_14_MulticonsensusReports_3Replicates.csv"}
```

Data is imported for time points 7,9,10,11,14 from the first file, and 12,13,15,16 from the second file. The process can be viewed in a video at:

If the system can open .wmv files use (e.g. Windows):

In[3]:=
```
wmvExampleLocation =
 FileNameJoin[{ConstantMathIOmicaExampleVideosDirectory, "DataImporter.wmv"}] (*wmv format*)
```

In[4]:=
```
SystemOpen[wmvExampleLocation]
```

If the system can open .mp4 files use (e.g. Mac OS):

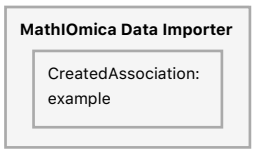
In[5]:=
```
mp4ExampleLocation =
 FileNameJoin[{ConstantMathIOmicaExampleVideosDirectory, "DataImporter.mp4"}] (*mp4 format*)
```

In[6]:=
```
SystemOpen[mp4ExampleLocation]
```

To begin the example we call DataImporter:

In[7]:=
```
DataImporter[example]
```

Out[7]=



At the end of the example the data will look like:

In[8]:=
```
example
```

Out[8]=
```
<|7 → <|{A0AVT1, Protein} → {{0.937}, {17}}, {A0FGR8, Protein} → {{1.073}, {24}},
   ⋯ 4942 ⋯, {Q9Y6R9, Protein} → Missing[KeyAbsent, {Q9Y6R9, Protein}]|>,
 ⋯ 7 ⋯, 16 → <|{A0AVT1, Protein} → {{1.086}, ⋯ 1 ⋯}, ⋯ 4943 ⋯, ⋯ 1 ⋯|>|>
```

large output | show less | show more | show all | set size limit...

Options (3)

AssociationLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

AssociationLabels provides a list of labels for the associations to be created. If a list is

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provided it will supersed any custom/default sample label displayed by the DataImporter interface. The number of labels provided must match exactly the number of samples imported. For example if we are creating a two sample object:

```
In[2]:= DataImporter[example, AssociationLabels → {"LabelForSample1", "LabelForSample2"}]
```

DelimiterList (1)

```
In[1]:= Needs["MathIOmica`"]
```

DelimiterList provides a list of delimiters to use when importing text files. The default is to use {","}, i.e. commas, for comma separated values.

```
In[2]:= DataImporter[example, DelimiterList → {","}]
```

JavaGBs (1)

```
In[1]:= Needs["MathIOmica`"]
```

The JavaGBs option assigns the value of GBs of memory to be used by Java by running an internal ReinstallJava command with option JVMArgurments-> "-Xmx" <> OptionValue[JavaGBs] <> "g". The default is to use 8 GBs of memory. This is used particularly when importing spreadsheets.

```
In[2]:= DataImporter[example, JavaGBs → 12]
```

See Also

DataImporterDirect ▪ **DataImporterDirectLabeled** ▪ **FileSelector** ▪ **OmicsObjectCreator** ▪ **OmicsObject**

Tutorials

- MathIOmicaTutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

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Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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DataImporterDirect

`DataImporterDirect[positionsList, fileList, headerLines]`
creates an OmicsObject association by importing data from the files at the paths specified in the fileList, using the positionsList to select columns, and importing data by skipping a number of headerLines.

Details

- *Expert Usage:* The `DataImporterDirect` function is a helper function originally created for DataImporter.
  `DataImporterDirect[positionsList, fileList, headerLines]` creates an OmicsObject importing the column number in *positionsList* from the *fileList* file path list, and importing data by skipping a number of *headerLines*.
- It allows the creation of an OmicsObject using a selection from columns in multiple files. It takes the following inputs:

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positionList	A list of positions for columns to be imported from each file specified by *fileList*, $\{f_1, f_2, \ldots, f_j, \ldots f_N\}$, which takes the following list structure: $\mathtt{positionList} =$ $\{\{\{id_{11}, x_{11}, e_{11}\}, \{id_{12}, x_{12}, e_{12}\}, \ldots,$ $\{id_{1k}, x_{1k}, e_{1k}\}, \ldots,$ $\{id_{1n_1}, x_{1n_1}, e_{1n_1}\}\},$ $\{\{id_{21}, x_{21}, e_{21}\}, \{id_{22}, x_{22}, e_{22}\}, \ldots,$ $\{id_{2k}, x_{2k}, e_{2k}\}, \ldots,$ $\{id_{2n_2}, x_{2n_2}, e_{2n_2}\}\},$ $\ldots,$ $\{\{id_{j1}, x_{j1}, e_{j1}\}, \{id_{j2}, x_{j2}, e_{j2}\}, \ldots,$ $\{id_{jk}, x_{jk}, e_{jk}\}, \ldots,$ $\{id_{jn_j}, x_{jn_j}, e_{jn_j}\}\},$ $\ldots,$ $\{\{id_{N1}, x_{N1}, e_{N1}\}, \{id_{N2}, x_{N2}, e_{N2}\}, \ldots,$ $\{id_{Nk}, x_{Nk}, e_{Nk}\}, \ldots,$ $\{id_{Nn_N}, x_{Nn_N}, e_{Nn_N}\}\}\}$ Where: If in in each file f_j there are n_j samples, $\{sample_{j1}, sample_{j2}, \ldots,$ $sample_{jk} \ldots, sample_{jn_j},\}$ then for each sample k in file f_j a list of column locations is provided as a sublist $\{id_{jk}, x_{jk}, e_{jk}\}$, where: id_{jk} is a list of positions for columns with identifiers, x_{jk} is a list of positions for columns with measurements, and e_{jk} is a list of positions for columns with extra information (e.g. metadata).
fileNames	List of file paths $\{f_1, f_2, \ldots, f_j, \ldots f_N\}$ from which the data will be extracted.
headerLines	Number of lines to skip as a header on importing.

- The following options can be given:

AssociationLabels	None	Set of labels for the associations to be created.
SampleKind	{}	A label for the sample kind, e.g. {"Protein"}.

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Examples (4)

Basic Examples (1)

We first need the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

The function can be used to extract information from files by direct selection without the use of the GUI. We can follow the following steps as an example. First, let's obtain a file list. Evaluate the following:

In[2]:=
```
fileNames = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, #} & /@
  {"8_7_9_10_11_14_MulticonsensusReports_3Replicates.csv",
   "8_12_13_15_16_14_MulticonsensusReports_3Replicates.csv"}
```

For each of the files, we can now use the FileSelector to obtain the header if needed as a guide for selection. Alternatively we could have imported the files directly using Import. Evaluate the following, and navigate to the locations indicated above, and select both files listed.

In[3]:=
```
FileSelector[fileHeaders]
```

Out[3]= File Import: Select your file(s)

Now we can evaluate the fileHeaders to see the headers and path for each of the two files. This can help in choosing the positions to select:

In[4]:=
```
fileHeaders
```

Out[4]=
```
{{{Accession, Description, _Coverage, _# Proteins, _# Unique Peptides, _# Peptides,
    _# PSMs, 127/126, 127/126 Count, 127/126 Variability [%], 128/126, 128/126 Count,
    128/126 Variability [%], 129/126, 129/126 Count, 129/126 Variability [%], 130/126,
    130/126 Count, 130/126 Variability [%], 131/126, 131/126 Count, 131/126 Variability [%],
    Score A2, Coverage A2, # Peptides A2, # PSM A2, Score B2, Coverage B2, # Peptides B2,
    # PSM B2, Score C2, Coverage C2, # Peptides C2, # PSM C2, # AAs, MW [kDa], calc. pI},
   /Users/george/Library/Mathematica/Applications/MathIOmica/MathIOmicaData/ExampleData/8_7_9_10_11_14
    _MulticonsensusReports_3Replicates.csv},
  {{Accession, Description, _Coverage, _# Proteins, _# Unique Peptides, _# Peptides,
    _# PSMs, 127/126, 127/126 Count, 127/126 Variability [%], 128/126, 128/126 Count,
    128/126 Variability [%], 129/126, 129/126 Count, 129/126 Variability [%], 130/126,
    130/126 Count, 130/126 Variability [%], 131/126, 131/126 Count, 131/126 Variability [%],
    Score A2, Coverage A2, # Peptides A2, # PSM A2, Score B2, Coverage B2, # Peptides B2,
    # PSM B2, Score C2, Coverage C2, # Peptides C2, # PSM C2, # AAs, MW [kDa], calc. pI},
   /Users/george/Library/Mathematica/Applications/MathIOmica/MathIOmicaData/ExampleData/8_12_13_15_16_14
    _MulticonsensusReports_3Replicates.csv}}
```

A list of positions for columns to be imported from each file is specified by *fileList*, $\{f_1, f_2, \ldots, f_j, \ldots f_N\}$. In each file f_j are n_j samples, $\{sample_{j1}, sample_{j2}, \ldots, sample_{jk} \ldots, sample_{jn_j}\}$. For each sample k in

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file f_j a list of column locations is provided as a sublist $\{id_{jk}, x_{jk}, e_{jk}\}$, where:

id_{jk} is a list of positions for columns with identifiers,

x_{jk} is a list of positions for columns with measurements,

and e_{jk} is a list of positions for columns with extra information (e.g. metadata).

The structure of the list then has the form:

$$\begin{aligned}
&\{\{\{id_{11}, x_{11}, e_{11}\}, \{id_{12}, x_{12}, e_{12}\}, \ldots, \\
&\quad \{id_{1k}, x_{1k}, e_{1k}\}, \ldots, \{id_{1n_1}, x_{1n_1}, e_{1n_1}\}\}, \\
&\{\{id_{21}, x_{21}, e_{21}\}, \{id_{22}, x_{22}, e_{22}\}, \ldots, \\
&\quad \{id_{2k}, x_{2k}, e_{2k}\}, \ldots, \{id_{2n_2}, x_{2n_2}, e_{2n_2}\}\}, \\
&\ldots, \\
&\{\{id_{j1}, x_{j1}, e_{j1}\}, \{id_{j2}, x_{j2}, e_{j2}\}, \ldots, \\
&\quad \{id_{jk}, x_{jk}, e_{jk}\}, \ldots, \{id_{jn_j}, x_{jn_j}, e_{jn_j}\}\}, \\
&\ldots, \\
&\{\{id_{N1}, x_{N1}, e_{N1}\}, \{id_{N2}, x_{N2}, e_{N2}\}, \ldots, \\
&\quad \{id_{Nk}, x_{Nk}, e_{Nk}\}, \ldots, \{id_{Nn_N}, x_{Nn_N}, e_{Nn_N}\}\}\}
\end{aligned}$$

Now we can define our selection for multiple data from each file by using the column number.

In our example here we select two samples from the first file, and one from the second, importing the following columns :

File 1 column used for:	Sample 1 file 1	Sample 2 file 1
Identifiers	1	1
Measurements	8	11
Metadata	5	5

File 2 column used for:	Sample 1 file 2
Identifiers	1
Measurements	8
Metadata	5

```
In[5]:= positionList = {{{{1}, {8}, {5}}, {{1}, {11}, {5}}}, {{{1}, {8}, {5}}}};
```

We can now evaluate the function to create an OmicsObject with our selection choices:

```
In[6]:= associationCreatedDirect = DataImporterDirect[positionList, fileNames, 1];
```

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For our association of protein data we now can loo at what was imported. For example, we can query the first fifteen entries in each sample.

```
In[7]:= Query[All, 1 ;; 15]@associationCreatedDirect

Out[7]= <|Other1f1 → <|{A0AVT1} → {{0.937}, {17}}, {A0FGR8} → {{1.073}, {24}},
    {A0MZ66} → {{1.059}, {9}}, {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}},
    {A1X283} → {{1.277}, {1}}, {A2RRP1} → {{0.977}, {12}}, {A2RTX5} → {{1.351}, {4}},
    {A2RUS2} → {{1.017}, {12}}, {A3KMH1} → Missing[], {A3KN83} → {{0.88}, {1}}, {A4D1P6} → {{1.665}, {6}},
    {A5D8V6} → {{0.792}, {2}}, {A5PLN9} → {{1.022}, {3}}, {A5YKK6} → {{0.983}, {14}}|>,
  Other2f1 → <|{A0AVT1} → {{1.003}, {17}}, {A0FGR8} → {{0.921}, {24}}, {A0MZ66} → {{1.479}, {9}},
    {A1A4S6} → {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A1X283} → {{0.926}, {1}},
    {A2RRP1} → {{0.922}, {12}}, {A2RTX5} → {{1.182}, {4}}, {A2RUS2} → {{0.867}, {12}},
    {A3KMH1} → Missing[], {A3KN83} → {{1.42}, {1}}, {A4D1P6} → {{1.142}, {6}},
    {A5D8V6} → {{0.778}, {2}}, {A5PLN9} → {{1.004}, {3}}, {A5YKK6} → {{0.973}, {14}}|>,
  Other1f2 → <|{A0AVT1} → {{1.064}, {19}}, {A0FGR8} → {{0.87}, {23}}, {A0MZ66} → {{1.518}, {6}},
    {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → {{0.921}, {2}}, {A1X283} → Missing[], {A2RRP1} → {{0.971}, {12}},
    {A2RTX5} → Missing[], {A2RUS2} → {{0.641}, {6}}, {A3KMH1} → {{0.99}, {2}}, {A3KN83} → {{0.925}, {3}},
    {A4D1P6} → Missing[], {A5D8V6} → {{0.577}, {1}}, {A5PLN9} → {{1.057}, {3}}, {A5YKK6} → {{0.912}, {14}}|>|>
```

Options (2)

AssociationLabels (1)

AssociationLabels allows us to use a list to specify the Keys for the outer association in our OmicsObject.

```
In[1]:= Needs["MathIOmica`"]
```

We use example proteomics data files, so for this example we import the data. We can define our selection for multiple data from each file by using the positions of the columns directly using the column number.

```
In[2]:= fileNames = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, #} & /@
    {"8_7_9_10_11_14_MulticonsensusReports_3Replicates.csv",
     "8_12_13_15_16_14_MulticonsensusReports_3Replicates.csv"};
  positionList = {{{{1}, {8}, {5}}, {{1}, {11}, {5}}}, {{{1}, {8}, {5}}}};
```

In our example here we select two samples from the first file, and one from the second, importing the following columns :

File 1 column used for:	Sample 1 file 1	Sample 2 file 1
Identifiers	1	1
Measurements	8	11
Metadata	5	5

File 2 column used for:	Sample 1 file 2
Identifiers	1
Measurements	8
Metadata	5

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Now we can create the OmicsObject with custom labeling:

```
In[3]:= associationCreatedDirectLabels = DataImporterDirect[positionList,
          fileNames, 1, AssociationLabels → {"FirstSample", "SecondSample", "ThirdSample"}];

In[4]:= Query[All, 1 ;; 15]@associationCreatedDirectLabels

Out[4]= <|FirstSample → <|{A0AVT1} → {{0.937}, {17}}, {A0FGR8} → {{1.073}, {24}},
          {A0MZ66} → {{1.059}, {9}}, {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}},
          {A1X283} → {{1.277}, {1}}, {A2RRP1} → {{0.977}, {12}}, {A2RTX5} → {{1.351}, {4}},
          {A2RUS2} → {{1.017}, {12}}, {A3KMH1} → Missing[], {A3KN83} → {{0.88}, {1}}, {A4D1P6} → {{1.665}, {6}},
          {A5D8V6} → {{0.792}, {2}}, {A5PLN9} → {{1.022}, {3}}, {A5YKK6} → {{0.983}, {14}}|>,
        SecondSample → <|{A0AVT1} → {{1.003}, {17}}, {A0FGR8} → {{0.921}, {24}}, {A0MZ66} → {{1.479}, {9}},
          {A1A4S6} → {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A1X283} → {{0.926}, {1}},
          {A2RRP1} → {{0.922}, {12}}, {A2RTX5} → {{1.182}, {4}}, {A2RUS2} → {{0.867}, {12}},
          {A3KMH1} → Missing[], {A3KN83} → {{1.42}, {1}}, {A4D1P6} → {{1.142}, {6}},
          {A5D8V6} → {{0.778}, {2}}, {A5PLN9} → {{1.004}, {3}}, {A5YKK6} → {{0.973}, {14}}|>,
        ThirdSample → <|{A0AVT1} → {{1.064}, {19}}, {A0FGR8} → {{0.87}, {23}}, {A0MZ66} → {{1.518}, {6}},
          {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → {{0.921}, {2}}, {A1X283} → Missing[], {A2RRP1} → {{0.971}, {12}},
          {A2RTX5} → Missing[], {A2RUS2} → {{0.641}, {6}}, {A3KMH1} → {{0.99}, {2}}, {A3KN83} → {{0.925}, {3}},
          {A4D1P6} → Missing[], {A5D8V6} → {{0.577}, {1}}, {A5PLN9} → {{1.057}, {3}}, {A5YKK6} → {{0.912}, {14}}|>|>
```

SampleKind (1)

```
In[1]:= Needs["MathIOmica`"]
```

SampleKind allows the insertion of a text for each identifier in the inner association.

We use example proteomics data files, so for this example we import the data, indicating these are protein data. We can define our selection for multiple data from each file by using the positions of the columns directly.

```
In[2]:= fileNames = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, #} & /@
          {"8_7_9_10_11_14_MulticonsensusReports_3Replicates.csv",
           "8_12_13_15_16_14_MulticonsensusReports_3Replicates.csv"};
        positionList = {{{{1}, {8}, {5}}, {{1}, {11}, {5}}}, {{{1}, {8}, {5}}}};
```

In our example here we select two samples from the first file, and one from the second, importing the following columns :

File 1 column used for:	Sample 1 file 1	Sample 2 file 1
Identifiers	1	1
Measurements	8	11
Metadata	5	5

File 2 column used for:	Sample 1 file 2
Identifiers	1
Measurements	8
Metadata	5

We now import the data, indicating that the samples are "Protein" data:

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```
In[3]:= associationCreatedDirectSampleKind =
          DataImporterDirect[positionList, fileNames, 1, SampleKind → {"Protein"}];

In[4]:= Query[All, 1 ;; 15]@associationCreatedDirectSampleKind

Out[4]= <|Other1f1 → <|{A0AVT1, Protein} → {{0.937}, {17}}, {A0FGR8, Protein} → {{1.073}, {24}},
           {A0MZ66, Protein} → {{1.059}, {9}}, {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}},
           {A1X283, Protein} → {{1.277}, {1}}, {A2RRP1, Protein} → {{0.977}, {12}},
           {A2RTX5, Protein} → {{1.351}, {4}}, {A2RUS2, Protein} → {{1.017}, {12}}, {A3KMH1, Protein} → Missing[],
           {A3KN83, Protein} → {{0.88}, {1}}, {A4D1P6, Protein} → {{1.665}, {6}}, {A5D8V6, Protein} → {{0.792}, {2}},
           {A5PLN9, Protein} → {{1.022}, {3}}, {A5YKK6, Protein} → {{0.983}, {14}}|>,
         Other2f1 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}},
           {A0MZ66, Protein} → {{1.479}, {9}}, {A1A4S6, Protein} → {{0.779}, {11}},
           {A1L0T0, Protein} → {{0.917}, {4}}, {A1X283, Protein} → {{0.926}, {1}}, {A2RRP1, Protein} → {{0.922}, {12}},
           {A2RTX5, Protein} → {{1.182}, {4}}, {A2RUS2, Protein} → {{0.867}, {12}}, {A3KMH1, Protein} → Missing[],
           {A3KN83, Protein} → {{1.42}, {1}}, {A4D1P6, Protein} → {{1.142}, {6}}, {A5D8V6, Protein} → {{0.778}, {2}},
           {A5PLN9, Protein} → {{1.004}, {3}}, {A5YKK6, Protein} → {{0.973}, {14}}|>,
         Other1f2 → <|{A0AVT1, Protein} → {{1.064}, {19}}, {A0FGR8, Protein} → {{0.87}, {23}},
           {A0MZ66, Protein} → {{1.518}, {6}}, {A1A4S6, Protein} → {{0.545}, {5}},
           {A1L0T0, Protein} → {{0.921}, {2}}, {A1X283, Protein} → Missing[], {A2RRP1, Protein} → {{0.971}, {12}},
           {A2RTX5, Protein} → Missing[], {A2RUS2, Protein} → {{0.641}, {6}}, {A3KMH1, Protein} → {{0.99}, {2}},
           {A3KN83, Protein} → {{0.925}, {3}}, {A4D1P6, Protein} → Missing[], {A5D8V6, Protein} → {{0.577}, {1}},
           {A5PLN9, Protein} → {{1.057}, {3}}, {A5YKK6, Protein} → {{0.912}, {14}}|>|>
```

Properties & Relations (1)

`DataImporterDirect` uses direct indexing of columns to be imported by number. This is to be compared to DataImporterDirectLabeled that uses text identifications and an association to assign the text to column number. Both functions are utilized internally by the graphical interface for importing data, DataImporter.

See Also

DataImporter ▪ **DataImporterDirectLabeled** ▪ **FileSelector** ▪ **OmicsObjectCreator** ▪ **OmicsObject**

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- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

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DataImporterDirectLabeled

`DataImporterDirectLabeled[sampleRules, fileList, headerLines, headerColumnAssociations]`
creates an OmicsObject association for *variableName*, by imporing data from the files at the paths specified in *fileList*, using *sampleRules* as rules from labels to column–headers being imported for each file, and the *headerColumnAssociations* list of associations to associate column headers to column positions for each file.

Details

- *Expert Usage:* `DataImporterDirectLabeled[sampleRules, fileList, headerLines, headerColumnAssociations]` function is a helper function originally created for DataImporter. It allows the creation of an omics association object (OmicsObject) using a selection from columns in multiple files. It takes the following inputs:

sampleRules	A list of rules from samples to column names per file to be imported specified by *fileList*, $\{f_1, f_2, \ldots, f_j, \ldots f_N\}$ where the structure takes the form:

$$
\begin{aligned}
&\text{sampleRules} = \\
&\{\{\text{sampleS}_{11}, \text{sampleS}_{12}, \ldots, \\
&\quad \text{sampleS}_{1k} \ldots, \text{sampleS}_{1n_1}\} \to \\
&\quad \{\{\text{idS}_{11}, \text{xS}_{11}, \text{eS}_{11}\}, \\
&\quad \{\text{idS}_{12}, \text{xS}_{12}, \text{eS}_{12}\}, \ldots, \\
&\quad \{\text{idS}_{1k}, \text{xS}_{1k}, \text{eS}_{1k}\}, \ldots, \\
&\quad \{\text{idS}_{1n_1}, \text{xS}_{1n_1}, \text{eS}_{1n_1}\}\}, \\
&\{\text{sampleS}_{21}, \text{sampleS}_{22}, \ldots, \\
&\quad \text{sampleS}_{2k} \ldots, \text{sampleS}_{2n_2}\} \to \\
&\quad \{\{\text{idS}_{21}, \text{xS}_{21}, \text{eS}_{21}\}, \\
&\quad \{\text{idS}_{22}, \text{xS}_{22}, \text{eS}_{22}\}, \ldots, \\
&\quad \{\text{idS}_{2k}, \text{xS}_{2k}, \text{eS}_{2k}\}, \ldots, \\
&\quad \{\text{idS}_{2n_2}, \text{xS}_{2n_2}, \text{eS}_{2n_2}\}\}, \\
&\ldots, \\
&\{\text{sampleS}_{j1}, \text{sampleS}_{j2}, \ldots, \\
&\quad \text{sampleS}_{jk} \ldots, \text{sampleS}_{jn_j}\} \to \\
&\quad \{\{\text{idS}_{j1}, \text{xS}_{j1}, \text{eS}_{j1}\}, \{\text{idS}_{j2}, \text{xS}_{j2}, \\
&\quad \text{eS}_{j2}\}, \ldots, \{\text{idS}_{jk}, \text{xS}_{jk}, \text{eS}_{jk}\}, \ldots, \\
&\quad \{\text{idS}_{jn_j}, \text{xS}_{jn_j}, \text{eS}_{jn_j}\}\}, \\
&\ldots.
\end{aligned}
$$

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$\{sampleS_{N1}, sampleS_{N2}, \ldots, sampleS_{Nk} \ldots, sampleS_{Nn_N}\} \to \{\{idS_{N1}, xS_{N1}, eS_{N1}\}, \{idS_{N2}, xS_{N2}, eS_{N2}\}, \ldots, \{idS_{Nk}, xS_{Nk}, eS_{Nk}\}, \ldots, \{idS_{Nn_N}, xS_{Nn_N}, eS_{Nn_N}\}\}\}$

Where:

There are n_j samples,

$\{sample_{j1}, sample_{j2}, \ldots, sample_{jk} \ldots, sample_{jn_j}\}$

in each file f_j with corresponding label strings,

$\{sampleS_{j1}, sampleS_{j2}, \ldots, sampleS_{jk} \ldots, sampleS_{jn_j}\}$

For each sample k in file f_j a list of column locations is provided by using the header names (string exactly matching the headers in the file being imported) of the columns as a sublist $\{idS_{jk}, xS_{jk}, eS_{jk}\}$, of string lists where:

idS_{jk} is a list of strings for the column header of columns with identifiers,

xS_{jk} is a list of strings for the column header for columns with measurements,

and eS_{jk} is a list of strings for the column header for columns with extra information (e.g. metadata).

fileNames	List of file paths $\{f_1, f_2, \ldots, f_{j,\ldots} f_N\}$ from which the data will be extracted.
headerLines	Number of lines to skip as a header on importing.
headerColumnAssociations	A list of associations connecting the column headers in each file from *fileList*, $\{f_1, f_2, \ldots, f_{j,\ldots} f_N\}$ to a column position. The structure takes the form:

$headerColumnAssociations = \{<|header_{11} \to 1, header_{12} \to 2, \ldots, header_{1m} \to m, \ldots, header_{1c_1} \to c_1|>, <|header_{21} \to 1, header_{22} \to 2, \ldots, header_{2m} \to m, \ldots, header_{2c_1} \to c_2|>, \ldots, <|header_{j1} \to 1, header_{j2} \to 2, \ldots, header_{jm} \to m, \ldots, header_{1c_j} \to c_j|>, \ldots, <|header_{N1} \to 1, header_{12} \to 2, \ldots$

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$\langle|\text{header}_{N1} \to 1, \text{header}_{12} \to 1, \ldots,$
$\text{header}_{Nm} \to m, \ldots, \text{header}_{Nc_N} \to c_N|\rangle\}$

Where:

Each file f_j has c_j number of columns, with the mth column having a column header string header_{jm}.

- The following options can be given:

AssociationLabels	None	Set of labels for the associations to be created.
SampleKind	{}	A label for the sample kind, e.g. {"Protein"}.

Examples (4)

Basic Examples (1)

We first need the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

The function can be used to extract information from files by direct selection without the use of the GUI. We can follow the following steps as an example. First, let's obtain a file list. Evaluate the following:

In[2]:=
```
fileNames = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, #} & /@
  {"8_7_9_10_11_14_MulticonsensusReports_3Replicates.csv",
   "8_12_13_15_16_14_MulticonsensusReports_3Replicates.csv"}
```

For each of the files, we can now use the FileSelector to obtain the header. Alternatively we could have imported the files directly. Evaluate the following, and navigate to the locations indicated above, and select both files listed.

In[3]:=
```
FileSelector[fileHeaders]
```

Out[3]= File Import: Select your file(s)

We can create an association for each file of the header:column relationships

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```
In[4]:= headerColumnAssociations = Query[All, 1 /* (AssociationThread[# → Range[Length[#]]] &)] @ fileHeaders

Out[4]= {<|Accession → 1, Description → 2, _Coverage → 3, _# Proteins → 4, _# Unique Peptides → 5,
    _# Peptides → 6, _# PSMs → 7, 127/126 → 8, 127/126 Count → 9, 127/126 Variability [%] → 10,
    128/126 → 11, 128/126 Count → 12, 128/126 Variability [%] → 13, 129/126 → 14, 129/126 Count → 15,
    129/126 Variability [%] → 16, 130/126 → 17, 130/126 Count → 18, 130/126 Variability [%] → 19, 131/126 → 20,
    131/126 Count → 21, 131/126 Variability [%] → 22, Score A2 → 23, Coverage A2 → 24, # Peptides A2 → 25,
    # PSM A2 → 26, Score B2 → 27, Coverage B2 → 28, # Peptides B2 → 29, # PSM B2 → 30, Score C2 → 31,
    Coverage C2 → 32, # Peptides C2 → 33, # PSM C2 → 34, # AAs → 35, MW [kDa] → 36, calc. pI → 37|>,
   <|Accession → 1, Description → 2, _Coverage → 3, _# Proteins → 4, _# Unique Peptides → 5,
    _# Peptides → 6, _# PSMs → 7, 127/126 → 8, 127/126 Count → 9, 127/126 Variability [%] → 10,
    128/126 → 11, 128/126 Count → 12, 128/126 Variability [%] → 13, 129/126 → 14, 129/126 Count → 15,
    129/126 Variability [%] → 16, 130/126 → 17, 130/126 Count → 18, 130/126 Variability [%] → 19, 131/126 → 20,
    131/126 Count → 21, 131/126 Variability [%] → 22, Score A2 → 23, Coverage A2 → 24, # Peptides A2 → 25,
    # PSM A2 → 26, Score B2 → 27, Coverage B2 → 28, # Peptides B2 → 29, # PSM B2 → 30, Score C2 → 31,
    Coverage C2 → 32, # Peptides C2 → 33, # PSM C2 → 34, # AAs → 35, MW [kDa] → 36, calc. pI → 37|>}
```

Now we can define our selection for multiple data from each file by using the header string instead of the column number. For each file f (e.g. f1 and f2) a rule of {Key list} to {identifierList, measurementList, metadataList} lists is to be provided in the following format:

```
{{"Key1:File f1", "Key2:File f1", "Key3:File f1"} →
  {{{"identifier1f1"}, {"measurement1f1"}, {"metadata1f1"}}, {{"identifier2f1"}, {"measurement2f1"},
    {"metadata2f1"}}, {{"identifier3f1"}, {"measurement3f1"}, {"metadata3f1"}}}},
 {"Key1:File f2" , "Key2: File f2"} → {{{"identifier1f2"}, {"measurement1f2"}, {"metadata1f2"}},
   {{"identifier2f2"}, {"measurement2f2"}, {"metadata2f2"}}}}
```

Typically a Key per measurement/sample is chosen. As an example, we create a rule per file, where in our example below we select two samples from file 1 ("Sample11" and "Sample12"), and one from file 2 ("Sample 21").

```
In[5]:= sampleRules = {{"Sample11", "Sample12"} → {{{"Accession"}, {"127/126"}, {"_# Unique Peptides"}},
      {{"Accession"}, {"128/126"}, {"_# Unique Peptides"}}},
    {"Sample21"} → {{{"Accession"}, {"127/126"}, {"_# Unique Peptides"}}}};
```

We can now evaluate the function to create an OmicsObject with our selection choices:

```
In[6]:= associationCreated = DataImporterDirectLabeled[sampleRules, fileNames, 1, headerColumnAssociations];
```

For our association of protein data we now can look at what was imported. For example, we can query the first 15 entries in each sample.

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In[7]:=
```
Query[All, 1 ;; 15] @ (associationCreated /. _Missing → Missing[])
```

Out[7]=
```
<|Sample11 → <|{A0AVT1} → {{0.937}, {17}}, {A0FGR8} → {{1.073}, {24}},
    {A0MZ66} → {{1.059}, {9}}, {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}},
    {A1X283} → {{1.277}, {1}}, {A2RRP1} → {{0.977}, {12}}, {A2RTX5} → {{1.351}, {4}},
    {A2RUS2} → {{1.017}, {12}}, {A3KMH1} → Missing[], {A3KN83} → {{0.88}, {1}}, {A4D1P6} → {{1.665}, {6}},
    {A5D8V6} → {{0.792}, {2}}, {A5PLN9} → {{1.022}, {3}}, {A5YKK6} → {{0.983}, {14}}|>,
  Sample12 → <|{A0AVT1} → {{1.003}, {17}}, {A0FGR8} → {{0.921}, {24}}, {A0MZ66} → {{1.479}, {9}},
    {A1A4S6} → {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A1X283} → {{0.926}, {1}},
    {A2RRP1} → {{0.922}, {12}}, {A2RTX5} → {{1.182}, {4}}, {A2RUS2} → {{0.867}, {12}},
    {A3KMH1} → Missing[], {A3KN83} → {{1.42}, {1}}, {A4D1P6} → {{1.142}, {6}},
    {A5D8V6} → {{0.778}, {2}}, {A5PLN9} → {{1.004}, {3}}, {A5YKK6} → {{0.973}, {14}}|>,
  Sample21 → <|{A0AVT1} → {{1.064}, {19}}, {A0FGR8} → {{0.87}, {23}}, {A0MZ66} → {{1.518}, {6}},
    {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → {{0.921}, {2}}, {A1X283} → Missing[], {A2RRP1} → {{0.971}, {12}},
    {A2RTX5} → Missing[], {A2RUS2} → {{0.641}, {6}}, {A3KMH1} → {{0.99}, {2}}, {A3KN83} → {{0.925}, {3}},
    {A4D1P6} → Missing[], {A5D8V6} → {{0.577}, {1}}, {A5PLN9} → {{1.057}, {3}}, {A5YKK6} → {{0.912}, {14}}|>|>
```

Options (2)

AssociationLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

AssociationLabels allows us to use a list to specify the Keys for the outer association in our OmicsObject.

We need to import some data for this example. First, let's obtain a file list. Evaluate the following:

In[2]:=
```
fileNames = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, #} & /@
  {"8_7_9_10_11_14_MulticonsensusReports_3Replicates.csv",
   "8_12_13_15_16_14_MulticonsensusReports_3Replicates.csv"}
```

For each of the files, we can now use the FileSelector to obtain the header. Evaluate the following, and navigate to the locations indicated above, and select both files listed.

In[3]:=
```
FileSelector[fileHeaders]
```

Out[3]= File Import: Select your file(s)

We can create an association for each file of the header:column relationships

In[4]:=
```
headerColumnAssociations = Query[All, 1 /* (AssociationThread[# → Range[Length[#]]] &)] @ fileHeaders
```

Out[4]=
```
{<|Accession → 1, Description → 2, _Coverage → 3, _# Proteins → 4, _# Unique Peptides → 5,
  _# Peptides → 6, _# PSMs → 7, 127/126 → 8, 127/126 Count → 9, 127/126 Variability [%] → 10,
  128/126 → 11, 128/126 Count → 12, 128/126 Variability [%] → 13, 129/126 → 14, 129/126 Count → 15,
  129/126 Variability [%] → 16, 130/126 → 17, 130/126 Count → 18, 130/126 Variability [%] → 19, 131/126 → 20,
  131/126 Count → 21, 131/126 Variability [%] → 22, Score A2 → 23, Coverage A2 → 24, # Peptides A2 → 25,
  # PSM A2 → 26, Score B2 → 27, Coverage B2 → 28, # Peptides B2 → 29, # PSM B2 → 30, Score C2 → 31,
  Coverage C2 → 32, # Peptides C2 → 33, # PSM C2 → 34, # AAs → 35, MW [kDa] → 36, calc. pI → 37|>,
 <|Accession → 1, Description → 2, _Coverage → 3, _# Proteins → 4, _# Unique Peptides → 5,
  _# Peptides → 6, _# PSMs → 7, 127/126 → 8, 127/126 Count → 9, 127/126 Variability [%] → 10,
  128/126 → 11, 128/126 Count → 12, 128/126 Variability [%] → 13, 129/126 → 14, 129/126 Count → 15,
  129/126 Variability [%] → 16, 130/126 → 17, 130/126 Count → 18, 130/126 Variability [%] → 19, 131/126 → 20,
  131/126 Count → 21, 131/126 Variability [%] → 22, Score A2 → 23, Coverage A2 → 24, # Peptides A2 → 25,
  # PSM A2 → 26, Score B2 → 27, Coverage B2 → 28, # Peptides B2 → 29, # PSM B2 → 30, Score C2 → 31,
  Coverage C2 → 32, # Peptides C2 → 33, # PSM C2 → 34, # AAs → 35, MW [kDa] → 36, calc. pI → 37|>}
```

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```
In[5]:= sampleRules = {{"Sample11", "Sample12"} → {{{"Accession"}, {"127/126"}, {"_# Unique Peptides"}},
          {{"Accession"}, {"128/126"}, {"_# Unique Peptides"}}},
        {"Sample21"} → {{{"Accession"}, {"127/126"}, {"_# Unique Peptides"}}}};

In[6]:= associationCreatedLabels = DataImporterDirectLabeled[sampleRules, fileNames, 1,
        headerColumnAssociations, AssociationLabels → {"FirstLabel", "SecondLabel", "ThirdLabel"}];

In[7]:= Query[All, 1 ;; 15]@associationCreatedLabels

Out[7]= <|FirstLabel → <|{A0AVT1} → {{0.937}, {17}}, {A0FGR8} → {{1.073}, {24}},
          {A0MZ66} → {{1.059}, {9}}, {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}},
          {A1X283} → {{1.277}, {1}}, {A2RRP1} → {{0.977}, {12}}, {A2RTX5} → {{1.351}, {4}},
          {A2RUS2} → {{1.017}, {12}}, {A3KMH1} → Missing[], {A3KN83} → {{0.88}, {1}}, {A4D1P6} → {{1.665}, {6}},
          {A5D8V6} → {{0.792}, {2}}, {A5PLN9} → {{1.022}, {3}}, {A5YKK6} → {{0.983}, {14}}|>,
        SecondLabel → <|{A0AVT1} → {{1.003}, {17}}, {A0FGR8} → {{0.921}, {24}}, {A0MZ66} → {{1.479}, {9}},
          {A1A4S6} → {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A1X283} → {{0.926}, {1}},
          {A2RRP1} → {{0.922}, {12}}, {A2RTX5} → {{1.182}, {4}}, {A2RUS2} → {{0.867}, {12}},
          {A3KMH1} → Missing[], {A3KN83} → {{1.42}, {1}}, {A4D1P6} → {{1.142}, {6}},
          {A5D8V6} → {{0.778}, {2}}, {A5PLN9} → {{1.004}, {3}}, {A5YKK6} → {{0.973}, {14}}|>,
        ThirdLabel → <|{A0AVT1} → {{1.064}, {19}}, {A0FGR8} → {{0.87}, {23}}, {A0MZ66} → {{1.518}, {6}},
          {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → {{0.921}, {2}}, {A1X283} → Missing[], {A2RRP1} → {{0.971}, {12}},
          {A2RTX5} → Missing[], {A2RUS2} → {{0.641}, {6}}, {A3KMH1} → {{0.99}, {2}}, {A3KN83} → {{0.925}, {3}},
          {A4D1P6} → Missing[], {A5D8V6} → {{0.577}, {1}}, {A5PLN9} → {{1.057}, {3}}, {A5YKK6} → {{0.912}, {14}}|>|>
```

SampleKind (1)

```
In[1]:= Needs["MathIOmica`"]
```

SampleKind allows the insertion of a text for each identifier in the inner association.

We need to import some data for this example. First, let's obtain a file list. Evaluate the following:

```
In[2]:= fileNames = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, #} & /@
        {"8_7_9_10_11_14_MulticonsensusReports_3Replicates.csv",
         "8_12_13_15_16_14_MulticonsensusReports_3Replicates.csv"}
```

For each of the files, we can now use the FileSelector to obtain the header. Evaluate the following, and navigate to the locations indicated above, and select both files listed.

```
In[3]:= FileSelector[fileHeaders]

Out[3]= File Import: Select your file(s)
```

We can create an association for each file of the header:column relationships

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```
In[4]:= headerColumnAssociations = Query[All, 1 /* (AssociationThread[# → Range[Length[#]]] &)] @ fileHeaders

Out[4]= {<|Accession → 1, Description → 2, _Coverage → 3, _# Proteins → 4, _# Unique Peptides → 5,
    _# Peptides → 6, _# PSMs → 7, 127/126 → 8, 127/126 Count → 9, 127/126 Variability [%] → 10,
    128/126 → 11, 128/126 Count → 12, 128/126 Variability [%] → 13, 129/126 → 14, 129/126 Count → 15,
    129/126 Variability [%] → 16, 130/126 → 17, 130/126 Count → 18, 130/126 Variability [%] → 19, 131/126 → 20,
    131/126 Count → 21, 131/126 Variability [%] → 22, Score A2 → 23, Coverage A2 → 24, # Peptides A2 → 25,
    # PSM A2 → 26, Score B2 → 27, Coverage B2 → 28, # Peptides B2 → 29, # PSM B2 → 30, Score C2 → 31,
    Coverage C2 → 32, # Peptides C2 → 33, # PSM C2 → 34, # AAs → 35, MW [kDa] → 36, calc. pI → 37|>,
   <|Accession → 1, Description → 2, _Coverage → 3, _# Proteins → 4, _# Unique Peptides → 5,
    _# Peptides → 6, _# PSMs → 7, 127/126 → 8, 127/126 Count → 9, 127/126 Variability [%] → 10,
    128/126 → 11, 128/126 Count → 12, 128/126 Variability [%] → 13, 129/126 → 14, 129/126 Count → 15,
    129/126 Variability [%] → 16, 130/126 → 17, 130/126 Count → 18, 130/126 Variability [%] → 19, 131/126 → 20,
    131/126 Count → 21, 131/126 Variability [%] → 22, Score A2 → 23, Coverage A2 → 24, # Peptides A2 → 25,
    # PSM A2 → 26, Score B2 → 27, Coverage B2 → 28, # Peptides B2 → 29, # PSM B2 → 30, Score C2 → 31,
    Coverage C2 → 32, # Peptides C2 → 33, # PSM C2 → 34, # AAs → 35, MW [kDa] → 36, calc. pI → 37|>}

In[5]:= sampleRules = {{"Sample11", "Sample12"} → {{{"Accession"}, {"127/126"}, {"_# Unique Peptides"}},
      {{"Accession"}, {"128/126"}, {"_# Unique Peptides"}}},
    {"Sample21"} → {{{"Accession"}, {"127/126"}, {"_# Unique Peptides"}}}};

In[6]:= associationCreatedSampleKind =
    DataImporterDirectLabeled[sampleRules, fileNames, 1, headerColumnAssociations, SampleKind → {"Protein"}];
```

For example we import the data above, indicating these are protein data.

```
In[7]:= Query[All, 1 ;; 15] @ associationCreatedSampleKind

Out[7]= <|Sample11 → <|{A0AVT1, Protein} → {{0.937}, {17}}, {A0FGR8, Protein} → {{1.073}, {24}},
      {A0MZ66, Protein} → {{1.059}, {9}}, {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}},
      {A1X283, Protein} → {{1.277}, {1}}, {A2RRP1, Protein} → {{0.977}, {12}},
      {A2RTX5, Protein} → {{1.351}, {4}}, {A2RUS2, Protein} → {{1.017}, {12}}, {A3KMH1, Protein} → Missing[],
      {A3KN83, Protein} → {{0.88}, {1}}, {A4D1P6, Protein} → {{1.665}, {6}}, {A5D8V6, Protein} → {{0.792}, {2}},
      {A5PLN9, Protein} → {{1.022}, {3}}, {A5YKK6, Protein} → {{0.983}, {14}}|>,
    Sample12 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}},
      {A0MZ66, Protein} → {{1.479}, {9}}, {A1A4S6, Protein} → {{0.779}, {11}},
      {A1L0T0, Protein} → {{0.917}, {4}}, {A1X283, Protein} → {{0.926}, {1}}, {A2RRP1, Protein} → {{0.922}, {12}},
      {A2RTX5, Protein} → {{1.182}, {4}}, {A2RUS2, Protein} → {{0.867}, {12}}, {A3KMH1, Protein} → Missing[],
      {A3KN83, Protein} → {{1.42}, {1}}, {A4D1P6, Protein} → {{1.142}, {6}}, {A5D8V6, Protein} → {{0.778}, {2}},
      {A5PLN9, Protein} → {{1.004}, {3}}, {A5YKK6, Protein} → {{0.973}, {14}}|>,
    Sample21 → <|{A0AVT1, Protein} → {{1.064}, {19}}, {A0FGR8, Protein} → {{0.87}, {23}},
      {A0MZ66, Protein} → {{1.518}, {6}}, {A1A4S6, Protein} → {{0.545}, {5}},
      {A1L0T0, Protein} → {{0.921}, {2}}, {A1X283, Protein} → Missing[], {A2RRP1, Protein} → {{0.971}, {12}},
      {A2RTX5, Protein} → Missing[], {A2RUS2, Protein} → {{0.641}, {6}}, {A3KMH1, Protein} → {{0.99}, {2}},
      {A3KN83, Protein} → {{0.925}, {3}}, {A4D1P6, Protein} → Missing[], {A5D8V6, Protein} → {{0.577}, {1}},
      {A5PLN9, Protein} → {{1.057}, {3}}, {A5YKK6, Protein} → {{0.912}, {14}}|>|>
```

Applications (1)

`DataImporterDirectLabeled` uses text identifications and an association to assign the text to column number. In contrast DataImporterDirect uses direct indexing of columns to be imported by number. Both functions are utilized by DataImporter.

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- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

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DelimiterList

`DelimiterList`
is an option for DataImporter that allows the user to select the delimiters in importing text files.

See Also

DataImporter

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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EnlargeInnerAssociation

`EnlargeInnerAssociation[omicsObjectList]`
combines a list of OmicsObject (associations of associations) *omicsObjectList* elements by enlarging the inner associations – inner association Keys must be different.

Details

- `EnlargeInnerAssociation[omicsObjectList]` is designed to work on a list omicsObjectList of OmicsObject components (associations of associations), and allow the user to enlarge inner associations with additional keys and associated values.
- The input for `EnlargeInnerAssociation[omicsObjectList]` is a list of multiple OmicsObject variables that will generate the new OmicsObject. The inner association key must be different for each list element, otherwise the last key in the list will take precedent with its value reported in the output.
- The following options can be given:

KeyModifiers	None	Whether keys will be modified.
MergeFunction	Join[Sequence @@ #1] &	Function to use in the merging of the input omicObjectList OmicsObject variables' inner associations.
MissingReplacement	Missing[]	Value that is used to handle Missing keys.

- When enlarging an OmicsObject the output is still an OmicsObject, and thus the inner keys are the same across all outer key values. Appropriate Missing[] tags are added where necessary.

Examples (4)

Basic Examples (1)

We first load MathIOmica:

```
In[1]:= Needs["MathIOmica`"]
```

Let' s consider the following OmicsObject:

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```
In[2]:= omicsObject1 = <|"7" → <|{"A0AVT1"} → {{0.937`}, {17}}, {"A0FGR8"} → {{1.073`}, {24}},
          {"A0MZ66"} → {{1.059`}, {9}}, {"A1A4S6"} → {{1.03`}, {11}}, {"A1L0T0"} → {{1.268`}, {4}}|>,
        "9" → <|{"A0AVT1"} → {{1.003`}, {17}}, {"A0FGR8"} → {{0.921`}, {24}}, {"A0MZ66"} → {{1.479`}, {9}},
          {"A1A4S6"} → {{0.779`}, {11}}, {"A1L0T0"} → {{0.917`}, {4}}|>,
        "10" → <|{"A0AVT1"} → {{0.966`}, {17}}, {"A0FGR8"} → {{1.007`}, {24}}, {"A0MZ66"} → {{1.455`}, {9}},
          {"A1A4S6"} → {{0.951`}, {11}}, {"A1L0T0"} → {{1.058`}, {4}}|>,
        "11" → <|{"A0AVT1"} → {{0.982`}, {17}}, {"A0FGR8"} → {{0.913`}, {24}}, {"A0MZ66"} → {{1.689`}, {9}},
          {"A1A4S6"} → {{0.78`}, {11}}, {"A1L0T0"} → {{1.091`}, {4}}|>,
        "14" → <|{"A0AVT1"} → {{1.024`}, {17}}, {"A0FGR8"} → {{0.937`}, {24}}, {"A0MZ66"} → {{1.312`}, {9}},
          {"A1A4S6"} → {{0.818`}, {11}}, {"A1L0T0"} → {{0.936`}, {4}}|>|>;
```

We may want to include additional measurements, e.g. additional proteins in the set from another set:

```
In[3]:= omicsObject2 = <|"7" → <|{"A1X283"} → {{1.277`}, {1}}, {"A2RRP1"} → {{0.977`}, {12}}|>,
        "9" → <|{"A1X283"} → {{0.926`}, {1}}, {"A2RRP1"} → {{0.922`}, {12}}|>,
        "10" → <|{"A1X283"} → {{0.831`}, {1}}, {"A2RRP1"} → {{0.925`}, {12}}|>,
        "11" → <|{"A1X283"} → {{0.862`}, {1}}, {"A2RRP1"} → {{0.835`}, {12}}|>,
        "14" → <|{"A1X283"} → {{0.925`}, {1}}, {"A2RRP1"} → {{0.944`}, {12}}|>|>;
```

We combine the two OmicsObject variables:

```
In[4]:= EnlargeInnerAssociation[{omicsObject1, omicsObject2}]

Out[4]= <|7 → <|{A0AVT1} → {{0.937}, {17}},
          {A0FGR8} → {{1.073}, {24}}, {A0MZ66} → {{1.059}, {9}}, {A1A4S6} → {{1.03}, {11}},
          {A1L0T0} → {{1.268}, {4}}, {A1X283} → {{1.277}, {1}}, {A2RRP1} → {{0.977}, {12}}|>,
        9 → <|{A0AVT1} → {{1.003}, {17}}, {A0FGR8} → {{0.921}, {24}}, {A0MZ66} → {{1.479}, {9}}, {A1A4S6} →
           {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A1X283} → {{0.926}, {1}}, {A2RRP1} → {{0.922}, {12}}|>,
        10 → <|{A0AVT1} → {{0.966}, {17}}, {A0FGR8} → {{1.007}, {24}}, {A0MZ66} → {{1.455}, {9}}, {A1A4S6} →
           {{0.951}, {11}}, {A1L0T0} → {{1.058}, {4}}, {A1X283} → {{0.831}, {1}}, {A2RRP1} → {{0.925}, {12}}|>,
        11 → <|{A0AVT1} → {{0.982}, {17}}, {A0FGR8} → {{0.913}, {24}}, {A0MZ66} → {{1.689}, {9}}, {A1A4S6} →
           {{0.78}, {11}}, {A1L0T0} → {{1.091}, {4}}, {A1X283} → {{0.862}, {1}}, {A2RRP1} → {{0.835}, {12}}|>,
        14 → <|{A0AVT1} → {{1.024}, {17}}, {A0FGR8} → {{0.937}, {24}}, {A0MZ66} → {{1.312}, {9}}, {A1A4S6} →
           {{0.818}, {11}}, {A1L0T0} → {{0.936}, {4}}, {A1X283} → {{0.925}, {1}}, {A2RRP1} → {{0.944}, {12}}|>|>
```

We may have another set to add, (the example here is from RNA data):

```
In[5]:= omicsObject3 =
          <|"7" → <|{"FAM138A"} → {{0}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} → {{2.73998`}, {"OK"}},
            {"DDX11L1"} → {{6.75461`}, {"OK"}}, {"WASH7P"} → {{11.8883`}, {"OK"}}|>,
          "9" → <|{"FAM138A"} → {{0.00257233`}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} →
             {{5.15563`}, {"OK"}}, {"DDX11L1"} → {{3.57627`}, {"OK"}}, {"WASH7P"} → {{11.93`}, {"OK"}}|>,
          "11" → <|{"FAM138A"} → {{0}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} → {{5.71829`}, {"OK"}},
            {"DDX11L1"} → {{3.24942`}, {"OK"}}, {"WASH7P"} → {{10.4902`}, {"OK"}}|>,
          "14" → <|{"FAM138A"} → {{0.00429509`}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} →
             {{2.38838`}, {"OK"}}, {"DDX11L1"} → {{3.58037`}, {"OK"}}, {"WASH7P"} → {{9.0819`}, {"OK"}}|>|>;
```

We can combine all three objects to add the new inner associations:

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```
In[6]:= EnlargeInnerAssociation[{omicsObject1, omicsObject2, omicsObject3}]

Out[6]= <|7 → <|{A0AVT1} → {{0.937}, {17}}, {A0FGR8} → {{1.073}, {24}}, {A0MZ66} → {{1.059}, {9}},
          {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A1X283} → {{1.277}, {1}},
          {A2RRP1} → {{0.977}, {12}}, {FAM138A} → {{0}, {OK}}, {OR4F5} → {{0}, {OK}},
          {LOC729737} → {{2.73998}, {OK}}, {DDX11L1} → {{6.75461}, {OK}}, {WASH7P} → {{11.8883}, {OK}}|>,
        9 → <|{A0AVT1} → {{1.003}, {17}}, {A0FGR8} → {{0.921}, {24}}, {A0MZ66} → {{1.479}, {9}},
          {A1A4S6} → {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A1X283} → {{0.926}, {1}},
          {A2RRP1} → {{0.922}, {12}}, {FAM138A} → {{0.00257233}, {OK}}, {OR4F5} → {{0}, {OK}},
          {LOC729737} → {{5.15563}, {OK}}, {DDX11L1} → {{3.57627}, {OK}}, {WASH7P} → {{11.93}, {OK}}|>,
        10 → <|{A0AVT1} → {{0.966}, {17}}, {A0FGR8} → {{1.007}, {24}}, {A0MZ66} → {{1.455}, {9}},
          {A1A4S6} → {{0.951}, {11}}, {A1L0T0} → {{1.058}, {4}}, {A1X283} → {{0.831}, {1}},
          {A2RRP1} → {{0.925}, {12}}, {FAM138A} → Missing[], {OR4F5} → Missing[],
          {LOC729737} → Missing[], {DDX11L1} → Missing[], {WASH7P} → Missing[]|>,
        11 → <|{A0AVT1} → {{0.982}, {17}}, {A0FGR8} → {{0.913}, {24}}, {A0MZ66} → {{1.689}, {9}},
          {A1A4S6} → {{0.78}, {11}}, {A1L0T0} → {{1.091}, {4}}, {A1X283} → {{0.862}, {1}},
          {A2RRP1} → {{0.835}, {12}}, {FAM138A} → {{0}, {OK}}, {OR4F5} → {{0}, {OK}},
          {LOC729737} → {{5.71829}, {OK}}, {DDX11L1} → {{3.24942}, {OK}}, {WASH7P} → {{10.4902}, {OK}}|>,
        14 → <|{A0AVT1} → {{1.024}, {17}}, {A0FGR8} → {{0.937}, {24}}, {A0MZ66} → {{1.312}, {9}},
          {A1A4S6} → {{0.818}, {11}}, {A1L0T0} → {{0.936}, {4}}, {A1X283} → {{0.925}, {1}},
          {A2RRP1} → {{0.944}, {12}}, {FAM138A} → {{0.00429509}, {OK}}, {OR4F5} → {{0}, {OK}},
          {LOC729737} → {{2.38838}, {OK}}, {DDX11L1} → {{3.58037}, {OK}}, {WASH7P} → {{9.0819}, {OK}}|>|>
```

We notice that for the outer key "10" that did not exist in omicsObject1 and omicsObject2 the appropriate Missing[] values have been inserted.

Here is another example:

```
In[7]:= associationExample1 = <|"sample1" → <|1 → 11, 2 → "a", 3 → 1.3|>, "sample2" → <|1 → 21, 2 → "b", 3 → Missing[]|>,
          "sample3" → <|1 → 31, 2 → Missing[], 3 → 3.3|>, "sample5" → <|1 → 51, 2 → "e", 3 → 5.3|>|>;

In[8]:= associationExample2 = <|"sample2" → <|4 → 3, 5 → Missing[]|>, "sample6" → <|4 → 31, 5 → "ff"|>|>;

In[9]:= EnlargeInnerAssociation[{associationExample1, associationExample2}]

Out[9]= <|sample1 → <|1 → 11, 2 → a, 3 → 1.3, 4 → Missing[], 5 → Missing[]|>,
         sample2 → <|1 → 21, 2 → b, 3 → Missing[], 4 → 3, 5 → Missing[]|>,
         sample3 → <|1 → 31, 2 → Missing[], 3 → 3.3, 4 → Missing[], 5 → Missing[]|>,
         sample5 → <|1 → 51, 2 → e, 3 → 5.3, 4 → Missing[], 5 → Missing[]|>,
         sample6 → <|1 → Missing[], 2 → Missing[], 3 → Missing[], 4 → 31, 5 → ff|>|>
```

Options (3)

MissingReplacement (1)

```
In[1]:= Needs["MathIOmica`"]
```

MissingReplacement is an option on what value to insert in the case of missing data when enlarging OmicsObjects (e.g. one of the two OmicsObjects does not have the values). As a simple example:

```
In[2]:= associationExample3a = <|"sample1" → <|1 → 11, 2 → "a"|>, "sample2" → <|1 → 21, 2 → "b"|>|>;
        associationExample3b = <|"sample1" → <|3 → 3.1, 4 → "b"|>, "sample3" → <|3 → 5.2, 4 → "a"|>|>;

In[3]:= EnlargeInnerAssociation[{associationExample3a, associationExample3b}]

Out[3]= <|sample1 → <|1 → 11, 2 → a, 3 → 3.1, 4 → b|>, sample2 → <|1 → 21, 2 → b, 3 → Missing[], 4 → Missing[]|>,
         sample3 → <|1 → Missing[], 2 → Missing[], 3 → 5.2, 4 → a|>|>
```

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In[4]:=
```
EnlargeInnerAssociation[{associationExample3a, associationExample3b},
 MissingReplacement → "This value is missing."]
```

Out[4]=
```
<|sample1 → <|1 → 11, 2 → a, 3 → 3.1, 4 → b|>,
 sample2 → <|1 → 21, 2 → b, 3 → This value is missing., 4 → This value is missing.|>,
 sample3 → <|1 → This value is missing., 2 → This value is missing., 3 → 5.2, 4 → a|>|>
```

KeyModifiers (1)

In[1]:=
```
Needs["MathIOmica`"]
```

KeyModifiers allows us to select if any modifications are to be included in the inner keys of the associations being enlarged. The modification is provided as a list in the the form:

```
EnlargeInnerAssociation[{OmicsObject1, OmicsObject2, ...},
 KeyModifiers → {"Modifier for OmicsObject1",
   "Modifier for OmicsObject2", ...}]
```

For example we may have protein and RNA data that we want to label differently:

In[2]:=
```
omicsObject1 = <|"7" → <|{"A0AVT1"} → {{0.937`}, {17}}, {"A0FGR8"} → {{1.073`}, {24}},
      {"A0MZ66"} → {{1.059`}, {9}}, {"A1A4S6"} → {{1.03`}, {11}}, {"A1L0T0"} → {{1.268`}, {4}}|>,
    "9" → <|{"A0AVT1"} → {{1.003`}, {17}}, {"A0FGR8"} → {{0.921`}, {24}}, {"A0MZ66"} → {{1.479`}, {9}},
      {"A1A4S6"} → {{0.779`}, {11}}, {"A1L0T0"} → {{0.917`}, {4}}|>,
    "10" → <|{"A0AVT1"} → {{0.966`}, {17}}, {"A0FGR8"} → {{1.007`}, {24}}, {"A0MZ66"} → {{1.455`}, {9}},
      {"A1A4S6"} → {{0.951`}, {11}}, {"A1L0T0"} → {{1.058`}, {4}}|>,
    "11" → <|{"A0AVT1"} → {{0.982`}, {17}}, {"A0FGR8"} → {{0.913`}, {24}}, {"A0MZ66"} → {{1.689`}, {9}},
      {"A1A4S6"} → {{0.78`}, {11}}, {"A1L0T0"} → {{1.091`}, {4}}|>,
    "14" → <|{"A0AVT1"} → {{1.024`}, {17}}, {"A0FGR8"} → {{0.937`}, {24}}, {"A0MZ66"} → {{1.312`}, {9}},
      {"A1A4S6"} → {{0.818`}, {11}}, {"A1L0T0"} → {{0.936`}, {4}}|>|>;
omicsObject3 = <|"7" → <|{"FAM138A"} → {{0}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} →
       {{2.73998`}, {"OK"}}, {"DDX11L1"} → {{6.75461`}, {"OK"}}, {"WASH7P"} → {{11.8883`}, {"OK"}}|>,
    "9" → <|{"FAM138A"} → {{0.00257233`}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} →
       {{5.15563`}, {"OK"}}, {"DDX11L1"} → {{3.57627`}, {"OK"}}, {"WASH7P"} → {{11.93`}, {"OK"}}|>,
    "11" → <|{"FAM138A"} → {{0}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} → {{5.71829`}, {"OK"}},
      {"DDX11L1"} → {{3.24942`}, {"OK"}}, {"WASH7P"} → {{10.4902`}, {"OK"}}|>,
    "14" → <|{"FAM138A"} → {{0.00429509`}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} →
       {{2.38838`}, {"OK"}}, {"DDX11L1"} → {{3.58037`}, {"OK"}}, {"WASH7P"} → {{9.0819`}, {"OK"}}|>|>;
```

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In[3]:=
```
EnlargeInnerAssociation[{omicsObject1, omicsObject3}, KeyModifiers → {"Protein", "RNA"}]
```

Out[3]=
```
<|7 → <|{A0AVT1, Protein} → {{0.937}, {17}}, {A0FGR8, Protein} → {{1.073}, {24}},
    {A0MZ66, Protein} → {{1.059}, {9}}, {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}},
    {FAM138A, RNA} → {{0}, {OK}}, {OR4F5, RNA} → {{0}, {OK}}, {LOC729737, RNA} → {{2.73998}, {OK}},
    {DDX11L1, RNA} → {{6.75461}, {OK}}, {WASH7P, RNA} → {{11.8883}, {OK}}|>,
 9 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}},
    {A0MZ66, Protein} → {{1.479}, {9}}, {A1A4S6, Protein} → {{0.779}, {11}},
    {A1L0T0, Protein} → {{0.917}, {4}}, {FAM138A, RNA} → {{0.00257233}, {OK}}, {OR4F5, RNA} → {{0}, {OK}},
    {LOC729737, RNA} → {{5.15563}, {OK}}, {DDX11L1, RNA} → {{3.57627}, {OK}}, {WASH7P, RNA} → {{11.93}, {OK}}|>,
 10 → <|{A0AVT1, Protein} → {{0.966}, {17}}, {A0FGR8, Protein} → {{1.007}, {24}},
    {A0MZ66, Protein} → {{1.455}, {9}}, {A1A4S6, Protein} → {{0.951}, {11}},
    {A1L0T0, Protein} → {{1.058}, {4}}, {FAM138A, RNA} → Missing[], {OR4F5, RNA} → Missing[],
    {LOC729737, RNA} → Missing[], {DDX11L1, RNA} → Missing[], {WASH7P, RNA} → Missing[]|>,
 11 → <|{A0AVT1, Protein} → {{0.982}, {17}}, {A0FGR8, Protein} → {{0.913}, {24}},
    {A0MZ66, Protein} → {{1.689}, {9}}, {A1A4S6, Protein} → {{0.78}, {11}}, {A1L0T0, Protein} → {{1.091}, {4}},
    {FAM138A, RNA} → {{0}, {OK}}, {OR4F5, RNA} → {{0}, {OK}}, {LOC729737, RNA} → {{5.71829}, {OK}},
    {DDX11L1, RNA} → {{3.24942}, {OK}}, {WASH7P, RNA} → {{10.4902}, {OK}}|>,
 14 → <|{A0AVT1, Protein} → {{1.024}, {17}}, {A0FGR8, Protein} → {{0.937}, {24}},
    {A0MZ66, Protein} → {{1.312}, {9}}, {A1A4S6, Protein} → {{0.818}, {11}}, {A1L0T0, Protein} → {{0.936}, {4}},
    {FAM138A, RNA} → {{0.00429509}, {OK}}, {OR4F5, RNA} → {{0}, {OK}}, {LOC729737, RNA} → {{2.38838}, {OK}},
    {DDX11L1, RNA} → {{3.58037}, {OK}}, {WASH7P, RNA} → {{9.0819}, {OK}}|>|>
```

MergeFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MergeFunction is the function used internally to merge the list of OmicsObjects in a Merge Operation. The default value Joins the associations. We consider the simple examples:

In[2]:=
```
associationExample1 = <|"sample1" → <|1 → 11, 2 → "a", 3 → 1.3|>, "sample2" → <|1 → 21, 2 → "b", 3 → Missing[]|>,
   "sample3" → <|1 → 31, 2 → Missing[], 3 → 3.3|>, "sample5" → <|1 → 51, 2 → "e", 3 → 5.3|>|>;
associationExample2 = <|"sample2" → <|4 → 3, 5 → Missing[]|>, "sample6" → <|4 → 31, 5 → "ff"|>|>;
```

In[3]:=
```
EnlargeInnerAssociation[{associationExample1, associationExample2}]
```

Out[3]=
```
<|sample1 → <|1 → 11, 2 → a, 3 → 1.3, 4 → Missing[], 5 → Missing[]|>,
 sample2 → <|1 → 21, 2 → b, 3 → Missing[], 4 → 3, 5 → Missing[]|>,
 sample3 → <|1 → 31, 2 → Missing[], 3 → 3.3, 4 → Missing[], 5 → Missing[]|>,
 sample5 → <|1 → 51, 2 → e, 3 → 5.3, 4 → Missing[], 5 → Missing[]|>,
 sample6 → <|1 → Missing[], 2 → Missing[], 3 → Missing[], 4 → 31, 5 → ff|>|>
```

If instead we employ a MergeFunction that returns lists as an example we get:

In[4]:=
```
EnlargeInnerAssociation[{associationExample1, associationExample2}, MergeFunction → Identity]
```

Out[4]=
```
<|sample1 → {<|1 → 11, 2 → a, 3 → 1.3|>, <|4 → Missing[], 5 → Missing[]|>},
 sample2 → {<|1 → 21, 2 → b, 3 → Missing[]|>, <|4 → 3, 5 → Missing[]|>},
 sample3 → {<|1 → 31, 2 → Missing[], 3 → 3.3|>, <|4 → Missing[], 5 → Missing[]|>},
 sample5 → {<|1 → 51, 2 → e, 3 → 5.3|>, <|4 → Missing[], 5 → Missing[]|>},
 sample6 → {<|1 → Missing[], 2 → Missing[], 3 → Missing[]|>, <|4 → 31, 5 → ff|>}|>
```

For a generic function f we have:

In[5]:=
```
EnlargeInnerAssociation[{associationExample1, associationExample2}, MergeFunction → f]
```

Out[5]=
```
<|sample1 → f[{<|1 → 11, 2 → a, 3 → 1.3|>, <|4 → Missing[], 5 → Missing[]|>}],
 sample2 → f[{<|1 → 21, 2 → b, 3 → Missing[]|>, <|4 → 3, 5 → Missing[]|>}],
 sample3 → f[{<|1 → 31, 2 → Missing[], 3 → 3.3|>, <|4 → Missing[], 5 → Missing[]|>}],
 sample5 → f[{<|1 → 51, 2 → e, 3 → 5.3|>, <|4 → Missing[], 5 → Missing[]|>}],
 sample6 → f[{<|1 → Missing[], 2 → Missing[], 3 → Missing[]|>, <|4 → 31, 5 → ff|>}]|>
```

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See Also

ConstantAssociator ▪ **DataImporter** ▪ **DataImporterDirect** ▪ **DataImporterDirectLabeled** ▪ **EnlargeOuterAssociation** ▪ **FileSelector** ▪ **JoinNestedAssociations** ▪ **OmicsObject** ▪ **OmicsObjectCreator**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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EnlargeOuterAssociation

`EnlargeOuterAssociation[omicsObjectList]`
combines a list, *omicsObjectList*, of OmicsObject (or associations of associations) elements to a combined output by enlarging the outer associations – outer association keys must be different.

Details

- `EnlargeOuterAssociation[data]` is designed to work on data provided as an OmicsObject list (associations of associations), to allow the user to enlarge outer associations with additional keys and associated values.
- The input for EnlargeOuterAssociation is a list of multiple OmicsObject components that will generate the new OmicsObject. The outer association key must be different for each list element, otherwise the last key in the list will take precedent with its value reported in the output.
- When enlarging an OmicsObject the output is still an OmicsObject, and thus the inner keys are the same across all outer key values. Appropriate Missing[] tags are added where necessary.
- The following options can be given:

Examples (2)

Basic Examples (1)

We first load MathIOmica:

```
In[1]:= Needs["MathIOmica`"]
```

```
In[2]:= omicsObjectA = <|"7" → <|{"A0AVT1"} → {{0.937`}, {17}}, {"A0FGR8"} → {{1.073`}, {24}},
          {"A0MZ66"} → {{1.059`}, {9}}, {"A1A4S6"} → {{1.03`}, {11}}, {"A1L0T0"} → {{1.268`}, {4}}|>,
        "9" → <|{"A0AVT1"} → {{1.003`}, {17}}, {"A0FGR8"} → {{0.921`}, {24}}, {"A0MZ66"} → {{1.479`}, {9}},
          {"A1A4S6"} → {{0.779`}, {11}}, {"A1L0T0"} → {{0.917`}, {4}}|>,
        "10" → <|{"A0AVT1"} → {{0.966`}, {17}}, {"A0FGR8"} → {{1.007`}, {24}}, {"A0MZ66"} → {{1.455`}, {9}},
          {"A1A4S6"} → {{0.951`}, {11}}, {"A1L0T0"} → {{1.058`}, {4}}|>,
        "11" → <|{"A0AVT1"} → {{0.982`}, {17}}, {"A0FGR8"} → {{0.913`}, {24}}, {"A0MZ66"} → {{1.689`}, {9}},
          {"A1A4S6"} → {{0.78`}, {11}}, {"A1L0T0"} → {{1.091`}, {4}}|>,
        "14" → <|{"A0AVT1"} → {{1.024`}, {17}}, {"A0FGR8"} → {{0.937`}, {24}}, {"A0MZ66"} → {{1.312`}, {9}},
          {"A1A4S6"} → {{0.818`}, {11}}, {"A1L0T0"} → {{0.936`}, {4}}|>|>;
```

We may want to include additional measurements, e.g. additional proteins in the set from another set:

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```
In[3]:= omicsObjectB = <|"12" → <|{"A0MZ66"} → {{1.518`}, {6}}, {"A1A4S6"} → {{0.545`}, {5}},
          {"A1L0T0"} → {{0.921`}, {2}}, {"A1X283"} → Missing[], {"A2RRP1"} → {{0.971`}, {12}}|>,
        "14" → <|{"A0MZ66"} → {{1.312`}, {9}}, {"A1A4S6"} → {{0.818`}, {11}}, {"A1L0T0"} → {{0.936`}, {4}},
          {"A1X283"} → {{0.925`}, {1}}, {"A2RRP1"} → {{0.944`}, {12}}|>|>;

In[4]:= EnlargeOuterAssociation[{omicsObjectA, omicsObjectB}]

Out[4]= <|7 → <|{A0AVT1} → {{0.937}, {17}}, {A0FGR8} → {{1.073}, {24}}, {A0MZ66} → {{1.059}, {9}},
          {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A1X283} → Missing[], {A2RRP1} → Missing[]|>,
        9 → <|{A0AVT1} → {{1.003}, {17}}, {A0FGR8} → {{0.921}, {24}}, {A0MZ66} → {{1.479}, {9}},
          {A1A4S6} → {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A1X283} → Missing[], {A2RRP1} → Missing[]|>,
        10 → <|{A0AVT1} → {{0.966}, {17}}, {A0FGR8} → {{1.007}, {24}}, {A0MZ66} → {{1.455}, {9}},
          {A1A4S6} → {{0.951}, {11}}, {A1L0T0} → {{1.058}, {4}}, {A1X283} → Missing[], {A2RRP1} → Missing[]|>,
        11 → <|{A0AVT1} → {{0.982}, {17}}, {A0FGR8} → {{0.913}, {24}}, {A0MZ66} → {{1.689}, {9}},
          {A1A4S6} → {{0.78}, {11}}, {A1L0T0} → {{1.091}, {4}}, {A1X283} → Missing[], {A2RRP1} → Missing[]|>,
        14 → <|{A0AVT1} → Missing[], {A0FGR8} → Missing[], {A0MZ66} → {{1.312}, {9}}, {A1A4S6} → {{0.818}, {11}},
          {A1L0T0} → {{0.936}, {4}}, {A1X283} → {{0.925}, {1}}, {A2RRP1} → {{0.944}, {12}}|>,
        12 → <|{A0AVT1} → Missing[], {A0FGR8} → Missing[], {A0MZ66} → {{1.518}, {6}}, {A1A4S6} → {{0.545}, {5}},
          {A1L0T0} → {{0.921}, {2}}, {A1X283} → Missing[], {A2RRP1} → {{0.971}, {12}}|>|>
```

We notice how outer keys were combined, and inner keys were augmented with Missing values when not available.

Options (1)

MissingReplacement (1)

```
In[1]:= Needs["MathIOmica`"]
```

MissingReplacement is an option on what value to insert in the case of missing data when enlarging OmicsObjects (e.g. one of the two OmicsObjects does not have the values). As a simple example:

```
In[2]:= associationExampleA = <|"sample1" → <|1 → 11, 2 → "a"|>, "sample2" → <|1 → 21, 2 → "b"|>|>;
        associationExampleB = <|"sample3" → <|3 → 3.1, 4 → "b"|>, "sample4" → <|3 → 5.2, 4 → "a"|>|>;

In[3]:= EnlargeOuterAssociation[{associationExampleA, associationExampleB}]

Out[3]= <|sample1 → <|1 → 11, 2 → a, 3 → Missing[], 4 → Missing[]|>,
         sample2 → <|1 → 21, 2 → b, 3 → Missing[], 4 → Missing[]|>,
         sample3 → <|1 → Missing[], 2 → Missing[], 3 → 3.1, 4 → b|>,
         sample4 → <|1 → Missing[], 2 → Missing[], 3 → 5.2, 4 → a|>|>

In[4]:= EnlargeInnerAssociation[{associationExampleA, associationExampleB},
         MissingReplacement → "This value is missing."]

Out[4]= <|sample1 → <|1 → 11, 2 → a, 3 → This value is missing., 4 → This value is missing.|>,
         sample2 → <|1 → 21, 2 → b, 3 → This value is missing., 4 → This value is missing.|>,
         sample3 → <|1 → This value is missing., 2 → This value is missing., 3 → 3.1, 4 → b|>,
         sample4 → <|1 → This value is missing., 2 → This value is missing., 3 → 5.2, 4 → a|>|>
```

See Also

ConstantAssociator ▪ **DataImporter** ▪ **DataImporterDirect** ▪ **DataImporterDirectLabeled** ▪ **EnlargeInnerAssociation** ▪

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FileSelector ▪ JoinNestedAssociations ▪ OmicsObject ▪ OmicsObjectCreator

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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EnrichmentReportExport

EnrichmentReportExport[*results*]
exports results from enrichment analyses to Excel spreadsheets

Details

Examples (4)

Basic Examples (2)

In[1]:=
```
Needs["MathIOmica`"]
```

In[1]:=
```
Needs["MathIOmica`"]
```

Let's consider an example from real protein data. We will use already clustered data, from the MathIOmica proteomics examples. Let's import the data, which should be located at:

In[2]:=
```
proteinExampleClusterFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinClusteringExample"}
```

We can now get the data :

In[3]:=
```
proteinExampleClusters = Get[proteinExampleClusterFile]
```

Out[3]=
```
<|SpikeMax → <|Cluster → Cluster[
    Cluster[Cluster[ ··· 1 ··· , ··· 1 ··· , 0.680914, 7, 18], Cluster[ ··· 1 ··· ], 0.698225, 25, 28], ··· 3 ··· , 2],
  ··· 4 ··· , GroupAssociations → <|G1S1 → { ··· 1 ··· }, ··· 4 ··· |> |> , ··· 4 ··· , f7 → <| ··· 1 ··· |> |>
```

large output | show less | show more | show all | set size limit...

We can calculate the KEGGAnalysis for each group in each class:

In[4]:=
```
enrichmentKEGGprotein = KEGGAnalysis[proteinExampleClusters]
```

Out[4]=
```
<|SpikeMax → <|G1S1 → <|path:hsa03050 →
      {{0.0000356064, 0.000961373, True}, {11, 44, 7086, 3}, {Proteasome - Homo sapiens (human),
        {{{P60900, Protein}}, {{P25788, Protein}}, {{P35998, Protein}}}}}}|>,
  G1S2 → <| |>, G2S1 → <| |>, G2S2 → <|path:hsa00020 → {{9.68339×10^-7, 0.0000397019, True},
      {19, 30, 7086, 4}, {Citrate cycle (TCA cycle) - Homo sapiens (human),
        {{{Q96I99, Protein}}, {{P10515, Protein}}, {{Q02218, Protein}}, {{Q99798, Protein}}}}},
    path:hsa01200 → {{9.18132×10^-6, 0.000188217, True}, {19, 113, 7086, 5},
      {Carbon metabolism - Homo sapiens (human), {{{Q96I99, Protein}}, {{P10515, Protein}},
        {{Q02218, Protein}}, {{P40939, Protein}}, {{Q99798, Protein}}}}}, path:hsa01100 →
      {{0.0000883103, 0.00120691, True}, {19, 1243, 7086, 11}, {Metabolic pathways - Homo sapiens (human),
        {{{P22695, Protein}}, {{Q96I99, Protein}}, {{P20674, Protein}}, {{P10515, Protein}},
```

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```
        {{Q02218, Protein}}, {{P40939, Protein}}, {{P22307, Protein}}, {{Q9HAN9, Protein}},
        {{P17568, Protein}}, {{P06576, Protein}}, {{Q99798, Protein}}}}}},
    path:hsa00190 → {{0.000369405, 0.0037864, True}, {19, 133, 7086, 4},
      {Oxidative phosphorylation - Homo sapiens (human),
       {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}},
    path:hsa05012 → {{0.000474073, 0.0038874, True}, {19, 142, 7086, 4},
      {Parkinson's disease - Homo sapiens (human),
       {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}},
    path:hsa05010 → {{0.000894412, 0.00611181, True}, {19, 168, 7086, 4},
      {Alzheimer's disease - Homo sapiens (human),
       {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}},
    path:hsa05016 → {{0.00149973, 0.00878412, True}, {19, 193, 7086, 4},
      {Huntington's disease - Homo sapiens (human),
       {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}},
    path:hsa00640 → {{0.00322059, 0.0165055, True}, {19, 32, 7086, 2},
      {Propanoate metabolism - Homo sapiens (human), {{{Q96I99, Protein}}, {{P40939, Protein}}}}}},
    path:hsa00380 → {{0.00500038, 0.0227795, True}, {19, 40, 7086, 2},
      {Tryptophan metabolism - Homo sapiens (human), {{{Q02218, Protein}}, {{P40939, Protein}}}}}},
    path:hsa00071 → {{0.006026, 0.0247066, True}, {19, 44, 7086, 2},
      {Fatty acid degradation - Homo sapiens (human), {{{P42126, Protein}}, {{P40939, Protein}}}}}},
    path:hsa04932 → {{0.00715492, 0.0266683, True}, {19, 151, 7086, 3},
      {Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
       {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}}}},
    path:hsa00310 → {{0.00833956, 0.0284935, True}, {19, 52, 7086, 2},
      {Lysine degradation - Homo sapiens (human), {{{Q02218, Protein}}, {{P40939, Protein}}}}}},
    path:hsa05134 → {{0.00929502, 0.0293151, True}, {19, 55, 7086, 2},
      {Legionellosis - Homo sapiens (human), {{{P10809, Protein}}, {{O75396, Protein}}}}}},
    path:hsa03018 → {{0.0176847, 0.0495313, True}, {19, 77, 7086, 2},
      {RNA degradation - Homo sapiens (human), {{{P38646, Protein}}, {{P10809, Protein}}}}}},
    path:hsa04260 → {{0.0181212, 0.0495313, True}, {19, 78, 7086, 2},
      {Cardiac muscle contraction - Homo sapiens (human), {{{P22695, Protein}}, {{P20674, Protein}}}}}}|⟩,
  G3S1 → ‹|path:hsa03018 → {{0.0108665, 0.0108665, True}, {1, 77, 7086, 1},
      {RNA degradation - Homo sapiens (human), {{{O75175, Protein}}}}}}|›|⟩,
SpikeMin → ‹|G1S1 → ‹| |›, G1S2 → ‹| |›, G1S3 → ‹| |›|›,
f1 →
 ‹|G1S1 → ‹| |›,
  G1S2 → ‹|path:hsa05416 → {{0.0168643, 0.0329136, True}, {2, 60, 7086, 1},
      {Viral myocarditis - Homo sapiens (human), {{{P08174, Protein}}}}}},
    path:hsa04610 → {{0.0221747, 0.0329136, True}, {2, 79, 7086, 1},
      {Complement and coagulation cascades - Homo sapiens (human), {{{P08174, Protein}}}}}},
    path:hsa04640 → {{0.0246852, 0.0329136, True}, {2, 88, 7086, 1},
      {Hematopoietic cell lineage - Homo sapiens (human), {{{P08174, Protein}}}}}},
    path:hsa04360 → {{0.0490619, 0.0490619, True}, {2, 176, 7086, 1},
      {Axon guidance - Homo sapiens (human), {{{O15031, Protein}}}}}}|›, G2S1 → ‹| |›,
  G2S2 → ‹| |›, G3S1 → ‹|path:hsa03050 → {{0.000775901, 0.0178457, True}, {7, 44, 7086, 2},
      {Proteasome - Homo sapiens (human), {{{P40306, Protein}}, {{P55036, Protein}}}}}}|›,
  G3S2 → ‹|path:hsa01200 → {{0.00244281, 0.0293138, True}, {5, 113, 7086, 2},
      {Carbon metabolism - Homo sapiens (human), {{{P23368, Protein}}, {{Q96AT9, Protein}}}}}}|›|›,
f5 → ⟨|G1S1 → ⟨|path:hsa04960 → {{0.00550381, 0.0274431, True}, {1, 39, 7086, 1},
      {Aldosterone-regulated sodium reabsorption - Homo sapiens (human), {{{O00329, Protein}}}}}},
    path:hsa04973 → {{0.00649167, 0.0274431, True}, {1, 46, 7086, 1},
      {Carbohydrate digestion and absorption - Homo sapiens (human), {{{O00329, Protein}}}}}},
    path:hsa04930 → {{0.00677392, 0.0274431, True}, {1, 48, 7086, 1},
      {Type II diabetes mellitus - Homo sapiens (human), {{{O00329, Protein}}}}}},
    path:hsa05213 → {{0.00733841, 0.0274431, True}, {1, 52, 7086, 1},
      {Endometrial cancer - Homo sapiens (human), {{{O00329, Protein}}}}}},
    path:hsa04923 → {{0.00790291, 0.0274431, True}, {1, 56, 7086, 1},
      {Regulation of lipolysis in adipocytes - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa05223 → {{0.00790291, 0.0274431, True}, {1, 56, 7086, 1},
      {Non-small cell lung cancer - Homo sapiens (human), {{{O00329, Protein}}}}}},
    path:hsa05221 → {{0.00804403, 0.0274431, True}, {1, 57, 7086, 1},
      {Acute myeloid leukemia - Homo sapiens (human), {{{O00329, Protein}}}}}},
    path:hsa04370 → {{0.00860852, 0.0274431, True}, {1, 61, 7086, 1},
      {VEGF signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}}},
```

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```
path:hsa05210 → {{0.00874965, 0.0274431, True}, {1, 62, 7086, 1},
  {Colorectal cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04213 → {{0.00903189, 0.0274431, True}, {1, 64, 7086, 1},
  {Longevity regulating pathway - multiple species - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05214 → {{0.00917302, 0.0274431, True}, {1, 65, 7086, 1},
  {Glioma - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05212 → {{0.00931414, 0.0274431, True}, {1, 66, 7086, 1},
  {Pancreatic cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05211 → {{0.00945526, 0.0274431, True}, {1, 67, 7086, 1},
  {Renal cell carcinoma - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05230 → {{0.00945526, 0.0274431, True}, {1, 67, 7086, 1},
  {Central carbon metabolism in cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04664 → {{0.00959639, 0.0274431, True}, {1, 68, 7086, 1},
  {Fc epsilon RI signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa00562 → {{0.0100198, 0.0274431, True}, {1, 71, 7086, 1},
  {Inositol phosphate metabolism - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05218 → {{0.0100198, 0.0274431, True}, {1, 71, 7086, 1},
  {Melanoma - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04917 → {{0.0101609, 0.0274431, True}, {1, 72, 7086, 1},
  {Prolactin signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04662 → {{0.010302, 0.0274431, True}, {1, 73, 7086, 1},
  {B cell receptor signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05220 → {{0.010302, 0.0274431, True}, {1, 73, 7086, 1},
  {Chronic myeloid leukemia - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa01524 → {{0.0105843, 0.0274431, True}, {1, 75, 7086, 1},
  {Platinum drug resistance - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05100 → {{0.0110076, 0.0274431, True}, {1, 78, 7086, 1},
  {Bacterial invasion of epithelial cells - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa01521 → {{0.011431, 0.0274431, True}, {1, 81, 7086, 1},
  {EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05222 → {{0.0121366, 0.0274431, True}, {1, 86, 7086, 1},
  {Small cell lung cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04012 → {{0.0124189, 0.0274431, True}, {1, 88, 7086, 1},
  {ErbB signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05215 → {{0.01256, 0.0274431, True}, {1, 89, 7086, 1},
  {Prostate cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04666 → {{0.0131245, 0.0274431, True}, {1, 93, 7086, 1},
  {Fc gamma R-mediated phagocytosis - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04211 → {{0.0132656, 0.0274431, True}, {1, 94, 7086, 1},
  {Longevity regulating pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa01522 → {{0.013689, 0.0274431, True}, {1, 97, 7086, 1},
  {Endocrine resistance - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04070 → {{0.0138301, 0.0274431, True}, {1, 98, 7086, 1},
  {Phosphatidylinositol signaling system - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04750 → {{0.0138301, 0.0274431, True}, {1, 98, 7086, 1},
  {Inflammatory mediator regulation of TRP channels - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04914 → {{0.0138301, 0.0274431, True}, {1, 98, 7086, 1},
  {Progesterone-mediated oocyte maturation - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04915 → {{0.0139712, 0.0274431, True}, {1, 99, 7086, 1},
  {Estrogen signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05146 → {{0.0141123, 0.0274431, True}, {1, 100, 7086, 1},
  {Amoebiasis - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04933 → {{0.0142535, 0.0274431, True}, {1, 101, 7086, 1},
  {AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human),
   {{{O00329, Protein}}}}}, path:hsa05231 → {{0.0142535, 0.0274431, True}, {1, 101, 7086, 1},
  {Choline metabolism in cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04066 → {{0.0145357, 0.0274431, True}, {1, 103, 7086, 1},
  {HIF-1 signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05142 → {{0.0146768, 0.0274431, True}, {1, 104, 7086, 1},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04660 → {{0.014818, 0.0274431, True}, {1, 105, 7086, 1},
  {T cell receptor signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04620 → {{0.0149591, 0.0274431, True}, {1, 106, 7086, 1},
  {Toll-like receptor signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04931 → {{0.0153824, 0.0274431, True}, {1, 109, 7086, 1},
```

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```
  {Insulin resistance - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04668 → {{0.0155236, 0.0274431, True}, {1, 110, 7086, 1},
  {TNF signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04725 → {{0.0156647, 0.0274431, True}, {1, 111, 7086, 1},
  {Cholinergic synapse - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04670 → {{0.0166526, 0.0274431, True}, {1, 118, 7086, 1},
  {Leukocyte transendothelial migration - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04919 → {{0.0166526, 0.0274431, True}, {1, 118, 7086, 1},
  {Thyroid hormone signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05145 → {{0.0167937, 0.0274431, True}, {1, 119, 7086, 1},
  {Toxoplasmosis - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04722 → {{0.0169348, 0.0274431, True}, {1, 120, 7086, 1},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04071 → {{0.0170759, 0.0274431, True}, {1, 121, 7086, 1},
  {Sphingolipid signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04611 → {{0.017217, 0.0274431, True}, {1, 122, 7086, 1},
  {Platelet activation - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04152 → {{0.0176404, 0.0274431, True}, {1, 125, 7086, 1},
  {AMPK signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04380 → {{0.0186283, 0.0274431, True}, {1, 132, 7086, 1},
  {Osteoclast differentiation - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05160 → {{0.0187694, 0.0274431, True}, {1, 133, 7086, 1},
  {Hepatitis C - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04068 → {{0.0189105, 0.0274431, True}, {1, 134, 7086, 1},
  {FoxO signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04650 → {{0.0190517, 0.0274431, True}, {1, 135, 7086, 1},
  {Natural killer cell mediated cytotoxicity - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05162 → {{0.0191928, 0.0274431, True}, {1, 136, 7086, 1},
  {Measles - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04910 → {{0.0196161, 0.0274431, True}, {1, 139, 7086, 1},
  {Insulin signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04210 → {{0.0197573, 0.0274431, True}, {1, 140, 7086, 1},
  {Apoptosis - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04550 → {{0.0200395, 0.0274431, True}, {1, 142, 7086, 1},
  {Signaling pathways regulating pluripotency of stem cells - Homo sapiens (human),
   {{{O00329, Protein}}}}}, path:hsa04072 → {{0.0203218, 0.0274431, True}, {1, 144, 7086, 1},
  {Phospholipase D signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05161 → {{0.020604, 0.0274431, True}, {1, 146, 7086, 1},
  {Hepatitis B - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04261 → {{0.0210274, 0.0274431, True}, {1, 149, 7086, 1},
  {Adrenergic signaling in cardiomyocytes - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04932 → {{0.0213096, 0.0274431, True}, {1, 151, 7086, 1},
  {Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04150 → {{0.021733, 0.0274431, True}, {1, 154, 7086, 1},
  {mTOR signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04630 → {{0.0222975, 0.0274431, True}, {1, 158, 7086, 1},
  {Jak-STAT signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04921 → {{0.0222975, 0.0274431, True}, {1, 158, 7086, 1},
  {Oxytocin signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04022 → {{0.0235676, 0.0285668, True}, {1, 167, 7086, 1},
  {cGMP-PKG signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04360 → {{0.0248377, 0.0292208, True}, {1, 176, 7086, 1},
  {Axon guidance - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05164 → {{0.0248377, 0.0292208, True}, {1, 176, 7086, 1},
  {Influenza A - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04062 → {{0.0263901, 0.0305972, True}, {1, 187, 7086, 1},
  {Chemokine signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04024 → {{0.0280835, 0.031276, True}, {1, 199, 7086, 1},
  {cAMP signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04510 → {{0.028648, 0.031276, True}, {1, 203, 7086, 1},
  {Focal adhesion - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05169 → {{0.0287892, 0.031276, True}, {1, 204, 7086, 1},
  {Epstein-Barr virus infection - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa05203 → {{0.0289303, 0.031276, True}, {1, 205, 7086, 1},
```

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```
    {Viral carcinogenesis - Homo sapiens (human), {{{O00329, Protein}}}}},
  path:hsa05205 → {{0.0289303, 0.031276, True}, {1, 205, 7086, 1},
    {Proteoglycans in cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
  path:hsa04015 → {{0.029777, 0.0317622, True}, {1, 211, 7086, 1},
    {Rap1 signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
  path:hsa04810 → {{0.0303415, 0.0319384, True}, {1, 215, 7086, 1},
    {Regulation of actin cytoskeleton - Homo sapiens (human), {{{O00329, Protein}}}}},
  path:hsa04014 → {{0.0321761, 0.0334297, True}, {1, 228, 7086, 1},
    {Ras signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
  path:hsa05166 → {{0.0365509, 0.0374881, True}, {1, 259, 7086, 1},
    {HTLV-I infection - Homo sapiens (human), {{{O00329, Protein}}}}},
  path:hsa04151 → {{0.0482642, 0.0488751, True}, {1, 342, 7086, 1},
    {PI3K-Akt signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}}|>,
G1S2 → <|path:hsa04110 → {{0.0174993, 0.0174993, True}, {1, 124, 7086, 1},
    {Cell cycle - Homo sapiens (human), {{{Q8N3U4, Protein}}}}}|>,
G2S1 → <|path:hsa04961 → {{0.0066328, 0.0177815, True}, {1, 47, 7086, 1},
    {Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
     {{{O94973, Protein}}}}}, path:hsa04721 → {{0.00889077, 0.0177815, True},
    {1, 63, 7086, 1}, {Synaptic vesicle cycle - Homo sapiens (human), {{{O94973, Protein}}}}},
  path:hsa05016 → {{0.0272368, 0.0363157, True}, {1, 193, 7086, 1},
    {Huntington's disease - Homo sapiens (human), {{{O94973, Protein}}}}},
  path:hsa04144 → {{0.0366921, 0.0366921, True}, {1, 260, 7086, 1},
    {Endocytosis - Homo sapiens (human), {{{O94973, Protein}}}}}|>, G2S2 → <| |>|>,
f6 → <|G1S1 → <|path:hsa04144 → {{0.00134132, 0.00804791, True}, {2, 260, 7086, 2},
    {Endocytosis - Homo sapiens (human), {{{Q9Y371, Protein}}, {{P50570, Protein}}}}},
  path:hsa04961 → {{0.0132225, 0.0312942, True}, {2, 47, 7086, 1},
    {Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
     {{{P50570, Protein}}}}}, path:hsa04721 → {{0.0177037, 0.0312942, True},
    {2, 63, 7086, 1}, {Synaptic vesicle cycle - Homo sapiens (human), {{{P50570, Protein}}}}},
  path:hsa05100 → {{0.0218956, 0.0312942, True}, {2, 78, 7086, 1},
    {Bacterial invasion of epithelial cells - Homo sapiens (human), {{{P50570, Protein}}}}},
  path:hsa04666 → {{0.0260785, 0.0312942, True}, {2, 93, 7086, 1},
    {Fc gamma R-mediated phagocytosis - Homo sapiens (human), {{{P50570, Protein}}}}},
  path:hsa04072 → {{0.0402334, 0.0402334, True}, {2, 144, 7086, 1},
    {Phospholipase D signaling pathway - Homo sapiens (human), {{{P50570, Protein}}}}}|>,
G1S2 → <|path:hsa03010 → {{7.50786×10^-8, 3.37854×10^-6, True}, {13, 138, 7086, 6},
    {Ribosome - Homo sapiens (human), {{{Q02543, Protein}}, {{P62888, Protein}},
      {{P27635, Protein}}, {{P61353, Protein}}, {{P26373, Protein}}, {{P35268, Protein}}}}}|>,
G2S1 → <|path:hsa04966 → {{0.00381033, 0.0215919, True}, {1, 27, 7086, 1},
    {Collecting duct acid secretion - Homo sapiens (human), {{{Q9Y5K8, Protein}}}}},
  path:hsa05110 → {{0.00719729, 0.0215919, True}, {1, 51, 7086, 1},
    {Vibrio cholerae infection - Homo sapiens (human), {{{Q9Y5K8, Protein}}}}},
  path:hsa04721 → {{0.00889077, 0.0215919, True}, {1, 63, 7086, 1},
    {Synaptic vesicle cycle - Homo sapiens (human), {{{Q9Y5K8, Protein}}}}},
  path:hsa05120 → {{0.00959639, 0.0215919, True}, {1, 68, 7086, 1},
    {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
     {{{Q9Y5K8, Protein}}}}}, path:hsa05323 → {{0.0128422, 0.023116, True},
    {1, 91, 7086, 1}, {Rheumatoid arthritis - Homo sapiens (human), {{{Q9Y5K8, Protein}}}}},
  path:hsa00190 → {{0.0187694, 0.0246084, True}, {1, 133, 7086, 1},
    {Oxidative phosphorylation - Homo sapiens (human), {{{Q9Y5K8, Protein}}}}},
  path:hsa04150 → {{0.021733, 0.0246084, True}, {1, 154, 7086, 1},
    {mTOR signaling pathway - Homo sapiens (human), {{{Q9Y5K8, Protein}}}}},
  path:hsa04145 → {{0.0218741, 0.0246084, True}, {1, 155, 7086, 1},
    {Phagosome - Homo sapiens (human), {{{Q9Y5K8, Protein}}}}}|>|>,
f7 → <|G1S1 → <|path:hsa00052 → {{0.00873112, 0.0296223, True}, {2, 31, 7086, 1},
    {Galactose metabolism - Homo sapiens (human), {{{P07902, Protein}}}}},
  path:hsa00520 → {{0.0135029, 0.0296223, True}, {2, 48, 7086, 1},
    {Amino sugar and nucleotide sugar metabolism - Homo sapiens (human), {{{P07902, Protein}}}}},
  path:hsa04917 → {{0.0202199, 0.0296223, True}, {2, 72, 7086, 1},
    {Prolactin signaling pathway - Homo sapiens (human), {{{P07902, Protein}}}}},
  path:hsa04610 → {{0.0221747, 0.0296223, True}, {2, 79, 7086, 1},
    {Complement and coagulation cascades - Homo sapiens (human), {{{P13987, Protein}}}}},
  path:hsa04640 → {{0.0246852, 0.0296223, True}, {2, 88, 7086, 1},
```

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```
    {Hematopoietic cell lineage - Homo sapiens (human), {{{P13987, Protein}}}}}}|>,
G1S2 → <|path:hsa00512 → {{0.00873112, 0.0261934, True}, {2, 31, 7086, 1},
    {Mucin type O-Glycan biosynthesis - Homo sapiens (human), {{{Q10471, Protein}}}}},
  path:hsa03018 → {{0.0216164, 0.0324246, True}, {2, 77, 7086, 1},
    {RNA degradation - Homo sapiens (human), {{{Q9GZS3, Protein}}}}}}|>,
G2S1 → <|path:hsa04727 → {{0.0124189, 0.0298123, True}, {1, 88, 7086, 1},
    {GABAergic synapse - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa05032 → {{0.0128422, 0.0298123, True}, {1, 91, 7086, 1},
    {Morphine addiction - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa04713 → {{0.0134067, 0.0298123, True}, {1, 95, 7086, 1},
    {Circadian entrainment - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa04723 → {{0.0142535, 0.0298123, True}, {1, 101, 7086, 1},
    {Retrograde endocannabinoid signaling - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa04725 → {{0.0156647, 0.0298123, True}, {1, 111, 7086, 1},
    {Cholinergic synapse - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa04726 → {{0.0158058, 0.0298123, True}, {1, 112, 7086, 1},
    {Serotonergic synapse - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa04724 → {{0.0160881, 0.0298123, True}, {1, 114, 7086, 1},
    {Glutamatergic synapse - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa04728 → {{0.018346, 0.0298123, True}, {1, 130, 7086, 1},
    {Dopaminergic synapse - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa05034 → {{0.0252611, 0.0343071, True}, {1, 179, 7086, 1},
    {Alcoholism - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa04062 → {{0.0263901, 0.0343071, True}, {1, 187, 7086, 1},
    {Chemokine signaling pathway - Homo sapiens (human), {{{P62879, Protein}}}}},
  path:hsa04014 → {{0.0321761, 0.0380263, True}, {1, 228, 7086, 1},
    {Ras signaling pathway - Homo sapiens (human), {{{P62879, Protein}}}}}}|>|>|>
```

The data has multiple clusters:

```
Query[All,Keys]@enrichmentKEGGprotein
```

```
Out[5]= <|SpikeMax → {G1S1, G1S2, G2S1, G2S2, G3S1},
 SpikeMin → {G1S1, G1S2, G1S3}, f1 → {G1S1, G1S2, G2S1, G2S2, G3S1, G3S2},
 f5 → {G1S1, G1S2, G2S1, G2S2}, f6 → {G1S1, G1S2, G2S1}, f7 → {G1S1, G1S2, G2S1}|>
```

We can export all the results in Excel spreadsheets in the current notebook directory (if the notebook is saved):

```
In[6]:= EnrichmentReportExport[enrichmentKEGGprotein]
```

Options (2)

See Also

Export ▪ **GOAnalysis** ▪ **KEGGAnalysis** ▪ **KEGGPathwayVisual**

Tutorials

- MathIOmica Tutorial

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- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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URL ▾

FileSelector

```
FileSelector[variable]
```

allows assignment of multiple file names and first lines to a variable.

Details

- File Selector allows the user to select a file. It is a helper function that is used with DataImporter

Examples (1)

Basic Examples (1)

First we load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

We call the function to assign our selection to a variable. We the cell below and then click to import the first line and file name path.

In[2]:=
```
FileSelector[testVariable]
```

Out[2]= File Import: Select your file(s)

If we now evaluate the cell below we will get a list of the headers, and file paths for our selection.

In[3]:=
```
testVariable
```

See Also

DataImporter ▪ **DataImporterDirect** ▪ **DataImporterDirectLabeled** ▪ **OmicsObjectCreator** ▪ **OmicsObject**

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Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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FilterMissing

`FilterMissing[omicsObject, percentage]`
filters out data from *omicsObject*, retaining data across the datasets with a *percentage* of data points not missing.

Details

- `FilterMissing[omicsObject, percentage]` filters out data from *omicsObject* if across the datasets a *percentage* of data points is missing. It takes the following inputs:

omicsObject	OmicsObject data.
percentage	Fraction of points necessary to keep data with same label across datasets.

- The following options can be given:

MininumPoints	3	Minimum number of datapoints to keep.
Reference	{}	Select a reference outer key for which should remove dataset if the reference point has a Missing value.
ShowPlots	True	Whether to show summary plots.

Examples (6)

Basic Examples (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

Example Protein Data (1)

Let's import the example protein data. These are located at:

```
In[31]:= proteinExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinExample"}
```

We can now get the data:

```
In[48]:= proteinExampleData = Get[proteinExampleFile];
```

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Let' s query the first 5 proteins across all datasets

```
In[49]:= proteinSubset = Query[All, 1 ;; 5]@proteinExampleData

Out[49]= <|7 → <|{A0AVT1, Protein} → {{0.937}, {17}},
    {A0FGR8, Protein} → {{1.073}, {24}}, {A0MZ66, Protein} → {{1.059}, {9}},
    {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}}|>,
  9 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}}, {A0MZ66, Protein} →
    {{1.479}, {9}}, {A1A4S6, Protein} → {{0.779}, {11}}, {A1L0T0, Protein} → {{0.917}, {4}}|>,
  10 → <|{A0AVT1, Protein} → {{0.966}, {17}}, {A0FGR8, Protein} → {{1.007}, {24}}, {A0MZ66, Protein} →
    {{1.455}, {9}}, {A1A4S6, Protein} → {{0.951}, {11}}, {A1L0T0, Protein} → {{1.058}, {4}}|>,
  11 → <|{A0AVT1, Protein} → {{0.982}, {17}}, {A0FGR8, Protein} → {{0.913}, {24}}, {A0MZ66, Protein} →
    {{1.689}, {9}}, {A1A4S6, Protein} → {{0.78}, {11}}, {A1L0T0, Protein} → {{1.091}, {4}}|>,
  14 → <|{A0AVT1, Protein} → {{1.024}, {17}}, {A0FGR8, Protein} → {{0.937}, {24}}, {A0MZ66, Protein} →
    {{1.312}, {9}}, {A1A4S6, Protein} → {{0.818}, {11}}, {A1L0T0, Protein} → {{0.936}, {4}}|>,
  12 → <|{A0AVT1, Protein} → {{1.064}, {19}}, {A0FGR8, Protein} → {{0.87}, {23}}, {A0MZ66, Protein} →
    {{1.518}, {6}}, {A1A4S6, Protein} → {{0.545}, {5}}, {A1L0T0, Protein} → {{0.921}, {2}}|>,
  13 → <|{A0AVT1, Protein} → {{1.178}, {19}}, {A0FGR8, Protein} → {{0.77}, {23}}, {A0MZ66, Protein} →
    {{2.266}, {6}}, {A1A4S6, Protein} → {{0.428}, {5}}, {A1L0T0, Protein} → {{0.734}, {2}}|>,
  15 → <|{A0AVT1, Protein} → {{0.841}, {19}}, {A0FGR8, Protein} → {{1.12}, {23}}, {A0MZ66, Protein} →
    {{1.517}, {6}}, {A1A4S6, Protein} → {{0.447}, {5}}, {A1L0T0, Protein} → {{1.153}, {2}}|>,
  16 → <|{A0AVT1, Protein} → {{1.086}, {19}}, {A0FGR8, Protein} → {{0.941}, {23}}, {A0MZ66, Protein} →
    {{1.374}, {6}}, {A1A4S6, Protein} → {{0.749}, {5}}, {A1L0T0, Protein} → {{1.016}, {2}}|>,
  17 → <|{A0AVT1, Protein} → {{1.071}, {16}}, {A0FGR8, Protein} → {{0.846}, {22}}, {A0MZ66, Protein} →
    {{1.283}, {4}}, {A1A4S6, Protein} → {{0.654}, {5}}, {A1L0T0, Protein} → {{0.833}, {3}}|>,
  19 → <|{A0AVT1, Protein} → {{0.951}, {16}}, {A0FGR8, Protein} → {{0.882}, {22}},
    {A0MZ66, Protein} → {{1.473}, {4}}, {A1A4S6, Protein} → {{0.71}, {5}}, {A1L0T0, Protein} → {{0.952}, {3}}|>,
  20 → <|{A0AVT1, Protein} → {{0.873}, {16}}, {A0FGR8, Protein} → {{0.852}, {22}}, {A0MZ66, Protein} →
    {{1.213}, {4}}, {A1A4S6, Protein} → {{0.882}, {5}}, {A1L0T0, Protein} → {{1.065}, {3}}|>,
  21 → <|{A0AVT1, Protein} → {{0.988}, {16}}, {A0FGR8, Protein} → {{0.916}, {22}}, {A0MZ66, Protein} →
    {{1.066}, {4}}, {A1A4S6, Protein} → {{0.796}, {5}}, {A1L0T0, Protein} → {{0.992}, {3}}|>|>
```

Let' s also query the length of the inner association data:

```
In[50]:= Query[All, Length]@proteinExampleData

Out[50]= <|7 → 5225, 9 → 5225, 10 → 5225, 11 → 5225, 14 → 5225, 12 → 5225,
  13 → 5225, 15 → 5225, 16 → 5225, 17 → 5225, 19 → 5225, 20 → 5225, 21 → 5225|>
```

We notice that all datasets are exactly the same length, 5225 protein identifiers included. We now filter out Missing data.

```
In[52]:= proteinExampleDataFilteredMissing = FilterMissing[proteinExampleData, 3 / 4]
```

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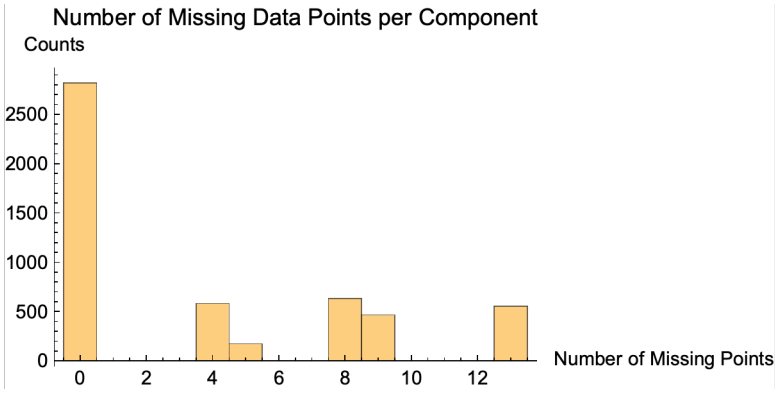
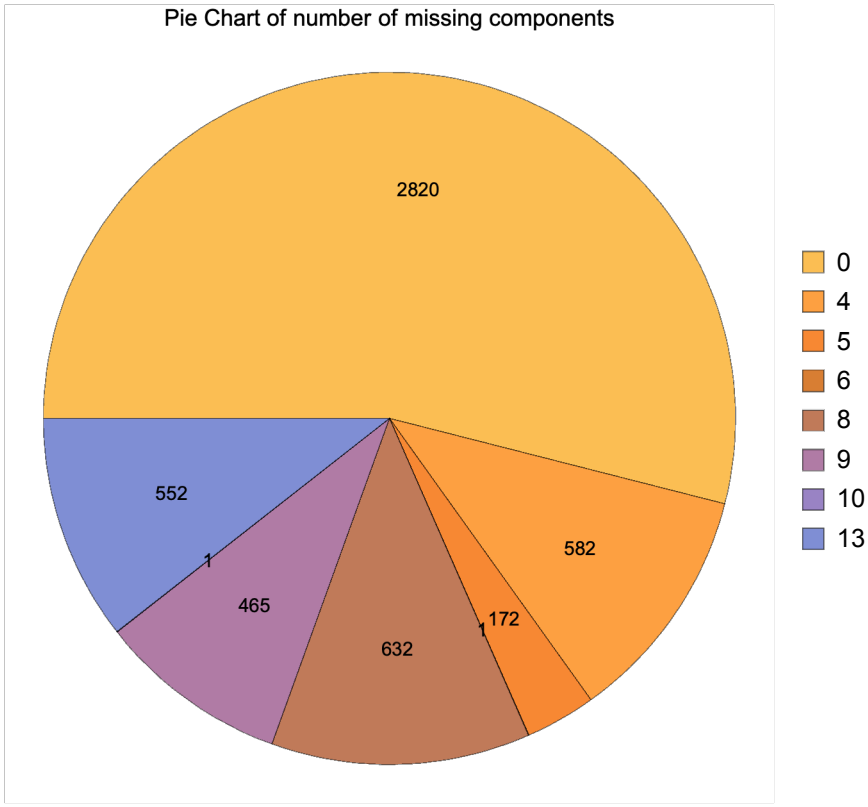



```
{Missing -> Counts: ,
 <|0 → 2820, 4 → 582, 5 → 172, 6 → 1, 8 → 632, 9 → 465, 10 → 1, 13 → 552|>}
```



Out[52]=

```
<|7 → <|{A0AVT1, Protein} → {{0.937}, {17}}, {A0FGR8, Protein} → {{1.073}, {24}},
   {A0MZ66, Protein} → {{1.059}, {9}}, ··· 2815 ···, {Q9Y6W5, Protein} → {{0.95}, {14}},
   {Q9Y6Y8, Protein} → {{0.974}, {10}}|>, ··· 11 ···, 21 → <|··· 1 ···|>|>
```

large output | **show less** | **show more** | **show all** | **set size limit...**

- We can see the number of points having Missing tags across the datasets (outer OmicObject keys).

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In[53]:=
```
Query[All, Length]@proteinExampleDataFilteredMissing
```

Out[53]=
```
<|7 → 2820, 9 → 2820, 10 → 2820, 11 → 2820, 14 → 2820, 12 → 2820,
 13 → 2820, 15 → 2820, 16 → 2820, 17 → 2820, 19 → 2820, 20 → 2820, 21 → 2820|>
```

We see that the filtering has removed 2405 proteins that had 1/4 datapoints Missing across datasets..

Example Simple Dataset (1)

Let's consider a simple dataset:

In[54]:=
```
omicsObjectMultiComponent =
  <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
     {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
     {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
     {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
     {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
   "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
     {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
     {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>,
   "FourthSample" → <|{"Measurement1"} → {{1.1, 3}, {11, "True"}}, {"Measurement2"} → Missing[],
     {"Measurement3"} → Missing[],
     {"Measurement4"} → {{0.8, 4}, {8, "True"}}, {"Measurement5"} → Missing[]|>|>;
```

In[55]:=
```
omicsObjectMultiFilterMissing = FilterMissing[omicsObjectMultiComponent, 1/3]
```

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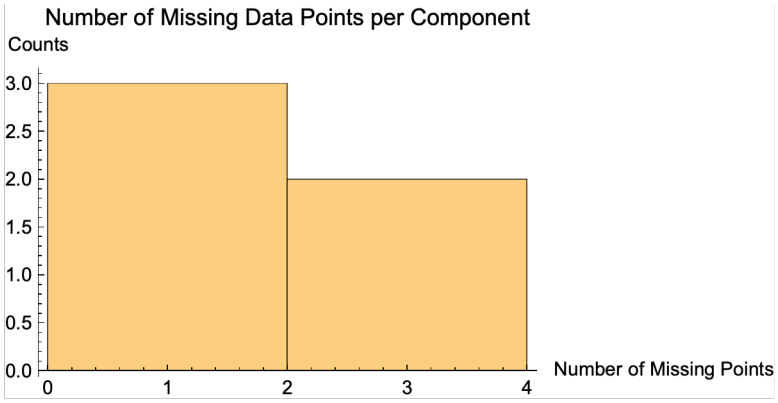
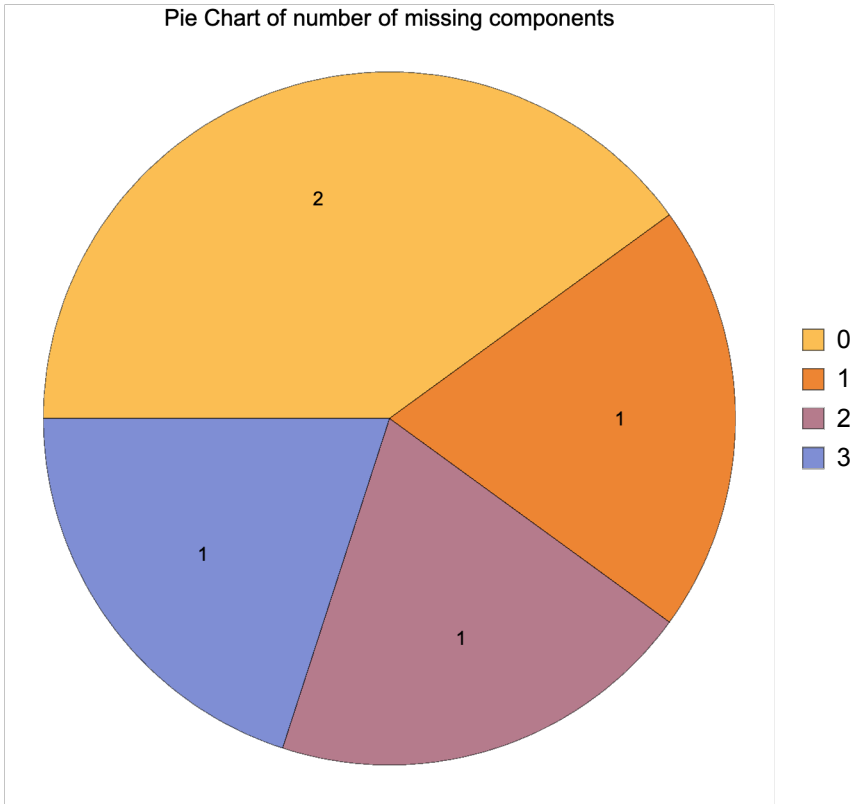



```
{Missing -> Counts: , <|0 → 2, 1 → 1, 2 → 1, 3 → 1|>}
```




```
Out[55]= <|FirstSample → <|{Measurement1} → {{0.8, 2}, {17, True}},
    {Measurement3} → {{0.5, 4}, {2, False}}, {Measurement4} → {{0.2, 3}, {5, True}}|>,
  SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement3} → {{0.3, 2}, {11, False}},
    {Measurement4} → {{0.3, 3}, {6, True}}|>, ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}},
    {Measurement3} → {{0.4, 6}, {8, False}}, {Measurement4} → {{0.3, 2}, {7, True}}|>,
  FourthSample → <|{Measurement1} → {{1.1, 3}, {11, True}}, {Measurement3} → Missing[],
    {Measurement4} → {{0.8, 4}, {8, True}}|>|>
```

```
In[56]:= Query[All, Keys]@omicsObjectMultiFilterMissing
```

```
Out[56]= <|FirstSample → {{Measurement1}, {Measurement3}, {Measurement4}},
  SecondSample → {{Measurement1}, {Measurement3}, {Measurement4}},
  ThirdSample → {{Measurement1}, {Measurement3}, {Measurement4}},
  FourthSample → {{Measurement1}, {Measurement3}, {Measurement4}}|>
```

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As we can see Measurement2 and Measurement5 have been removed.

Options (3)

MinimumPoints (1)

```
In[1]:= Needs["MathIOmica`"]
```

Minimum number of datapoints to keep in addition to filtering. For example using the simple dataset (see also above):

```
In[2]:= omicsObjectMultiComponent =
  <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
     {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
     {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
     {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
     {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
   "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
     {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
     {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>,
   "FourthSample" → <|{"Measurement1"} → {{1.1, 3}, {11, "True"}}, {"Measurement2"} → Missing[],
     {"Measurement3"} → Missing[],
     {"Measurement4"} → {{0.8, 4}, {8, "True"}}, {"Measurement5"} → Missing[]|>|>;
```

We filter out where 1/3 points exist, and minimum number of points is 2 (one less than default which is 3):

```
In[3]:= FilterMissing[omicsObjectMultiComponent, 1/3, MinimumPoints → 2]
```

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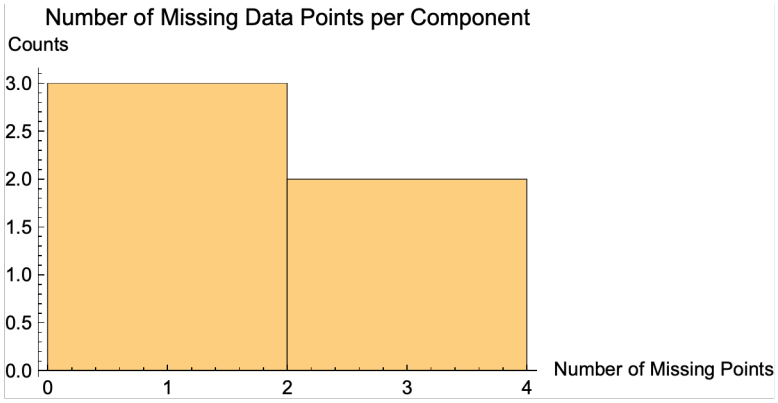
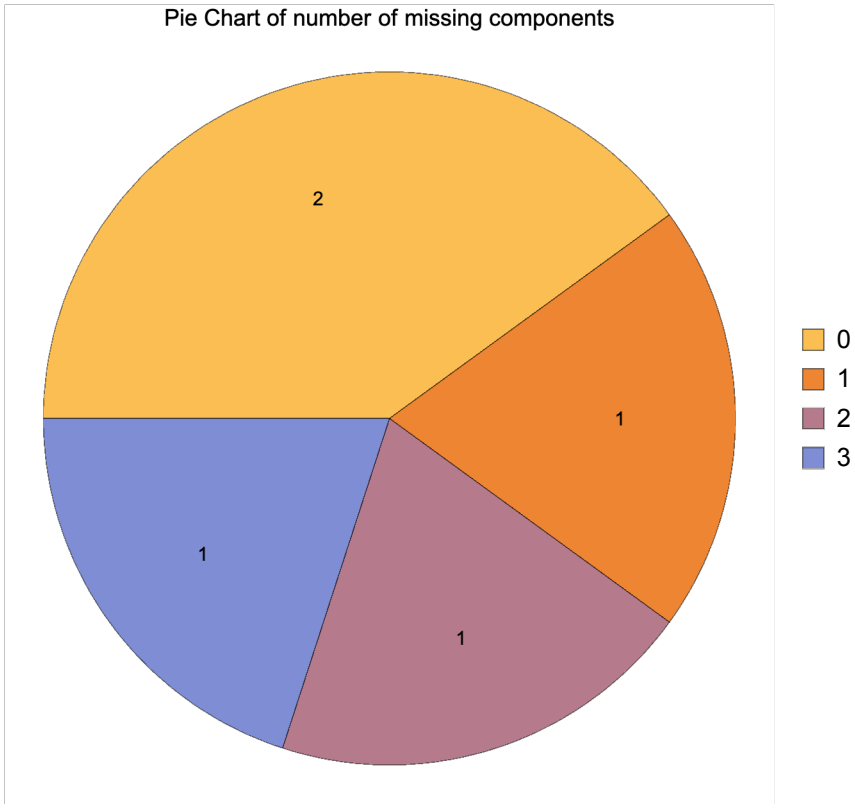



```
{Missing -> Counts: , <|0 → 2, 1 → 1, 2 → 1, 3 → 1|>}
```




```
Out[3]= <|FirstSample → <|{Measurement1} → {{0.8, 2}, {17, True}}, {Measurement2} → Missing[],
    {Measurement3} → {{0.5, 4}, {2, False}}, {Measurement4} → {{0.2, 3}, {5, True}}|>,
  SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement2} → {{0.7, 1}, {12, True}},
    {Measurement3} → {{0.3, 2}, {11, False}}, {Measurement4} → {{0.3, 3}, {6, True}}|>,
  ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}}, {Measurement2} → {{0.3, 5}, {11, True}},
    {Measurement3} → {{0.4, 6}, {8, False}}, {Measurement4} → {{0.3, 2}, {7, True}}|>,
  FourthSample → <|{Measurement1} → {{1.1, 3}, {11, True}}, {Measurement2} → Missing[],
    {Measurement3} → Missing[], {Measurement4} → {{0.8, 4}, {8, True}}|>|>
```

```
In[4]:= Query[All, Keys]@%
```

```
Out[4]= <|FirstSample → {{Measurement1}, {Measurement2}, {Measurement3}, {Measurement4}},
  SecondSample → {{Measurement1}, {Measurement2}, {Measurement3}, {Measurement4}},
  ThirdSample → {{Measurement1}, {Measurement2}, {Measurement3}, {Measurement4}},
  FourthSample → {{Measurement1}, {Measurement2}, {Measurement3}, {Measurement4}}|>
```

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As we can see now only Measurement 5 has been removed.

Reference (1)

```
In[1]:= Needs["MathIOmica`"]
```

The Reference option allows the selection of a reference of a reference point (outer association Key in OmicsObject) for which should remove data across datasets if the reference point is Missing. Let's consider again our example:

```
In[2]:= omicsObjectMultiComponent =
    <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
       {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
       {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
       {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
       {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
     "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
       {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
       {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>,
     "FourthSample" → <|{"Measurement1"} → {{1.1, 3}, {11, "True"}}, {"Measurement2"} → Missing[],
       {"Measurement3"} → Missing[],
       {"Measurement4"} → {{0.8, 4}, {8, "True"}}, {"Measurement5"} → Missing[]|>|>;;

In[3]:= omicsObjectMultiFilterMissing = FilterMissing[omicsObjectMultiComponent, 1/3]
```

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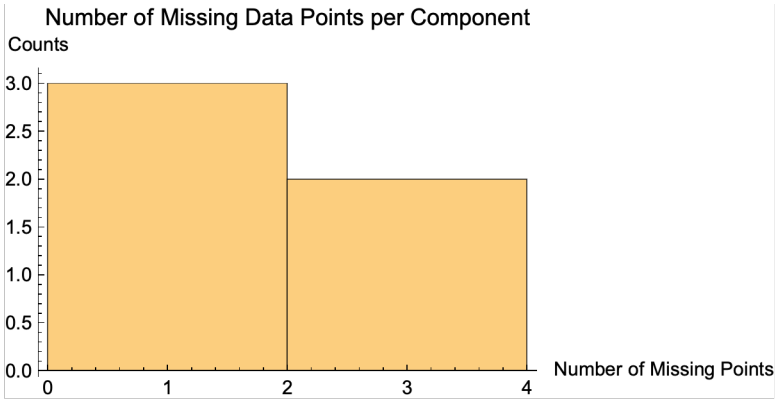
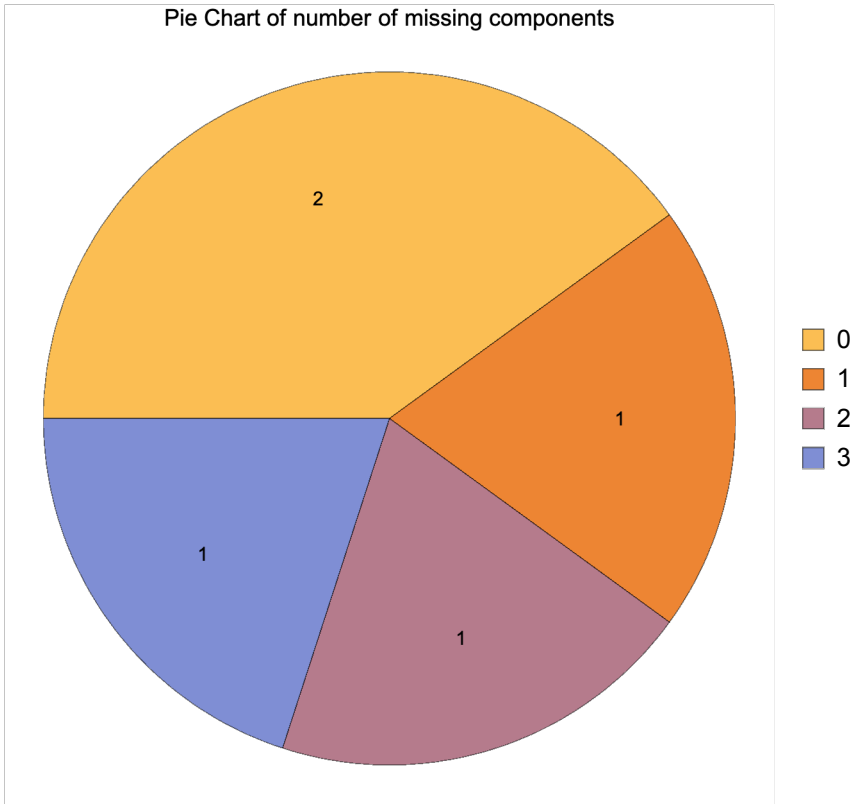



```
{Missing -> Counts: , <|0 → 2, 1 → 1, 2 → 1, 3 → 1|>}
```




```
Out[3]= <|FirstSample → <|{Measurement1} → {{0.8, 2}, {17, True}},
    {Measurement3} → {{0.5, 4}, {2, False}}, {Measurement4} → {{0.2, 3}, {5, True}}|>,
  SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement3} → {{0.3, 2}, {11, False}},
    {Measurement4} → {{0.3, 3}, {6, True}}|>, ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}},
    {Measurement3} → {{0.4, 6}, {8, False}}, {Measurement4} → {{0.3, 2}, {7, True}}|>,
  FourthSample → <|{Measurement1} → {{1.1, 3}, {11, True}}, {Measurement3} → Missing[],
    {Measurement4} → {{0.8, 4}, {8, True}}|>|>
```

With the Reference set to "FourthSample" the Measurement3 is also removed:

```
In[4]:= omicsObjectMultiFilterMissing = FilterMissing[omicsObjectMultiComponent, 1/3, Reference → "FourthSample"]
```

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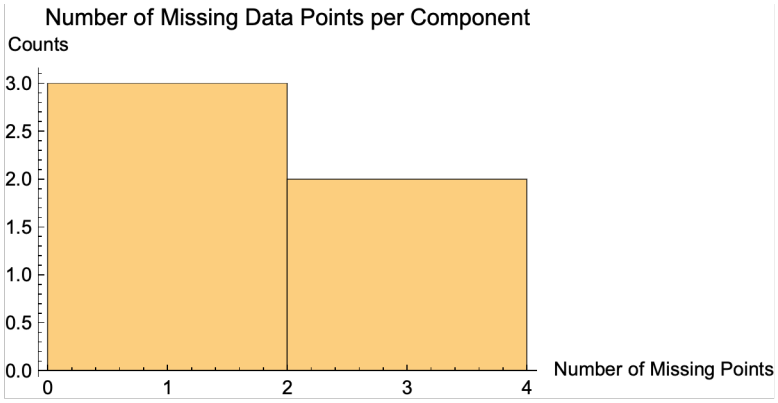
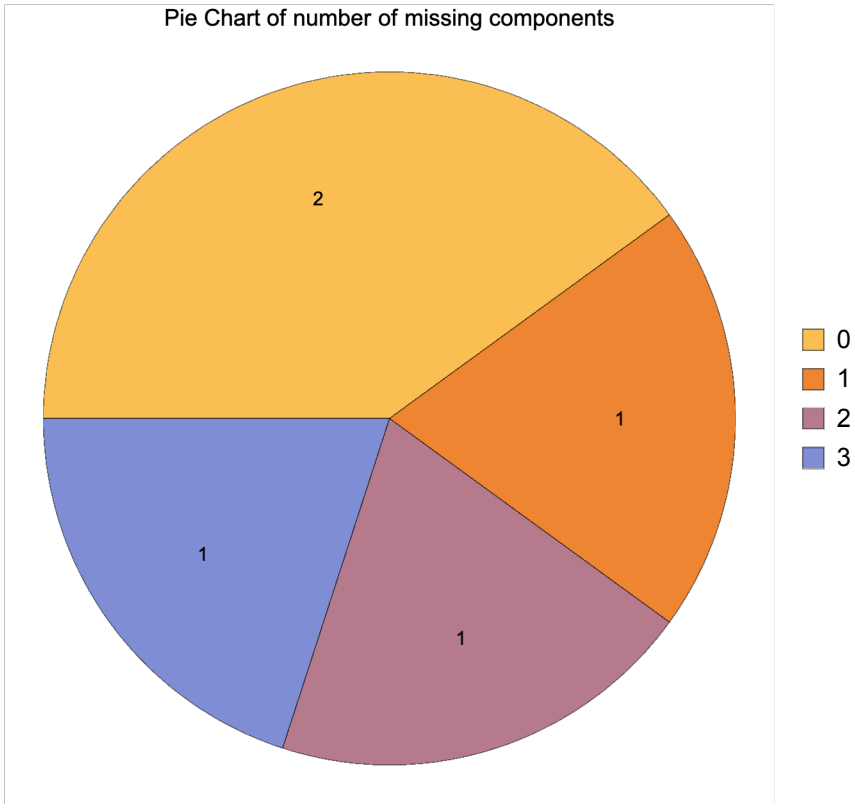



```
{Missing -> Counts: , <|0 → 2, 1 → 1, 2 → 1, 3 → 1|>}
```




```
Out[4]= <|FirstSample → <|{Measurement1} → {{0.8, 2}, {17, True}}, {Measurement4} → {{0.2, 3}, {5, True}}|>,
  SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement4} → {{0.3, 3}, {6, True}}|>,
  ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}}, {Measurement4} → {{0.3, 2}, {7, True}}|>,
  FourthSample → <|{Measurement1} → {{1.1, 3}, {11, True}}, {Measurement4} → {{0.8, 4}, {8, True}}|>|>
```

ShowPlots (1)

```
In[1]:= Needs["MathIOmica`"]
```

ShowPlots default is set as True to display the reference Pie plots and number of datapoints Missing across datasets:

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```
In[2]:= omicsObjectMultiComponent =
  <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
     {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
     {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
     {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
     {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
   "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
     {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
     {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>|>;
```

We can set ShowPlots to False :

```
In[3]:= omicsObjectMultiFilterMissing = FilterMissing[omicsObjectMultiComponent, 1/3, ShowPlots → False]

Out[3]= <|FirstSample → <|{Measurement1} → {{0.8, 2}, {17, True}},
     {Measurement3} → {{0.5, 4}, {2, False}}, {Measurement4} → {{0.2, 3}, {5, True}}|>,
   SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement3} → {{0.3, 2}, {11, False}},
     {Measurement4} → {{0.3, 3}, {6, True}}|>, ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}},
     {Measurement3} → {{0.4, 6}, {8, False}}, {Measurement4} → {{0.3, 2}, {7, True}}|>|>
```

See Also

FilteringFunction ▪ **LowValueTag** ▪ **OmicsObject** ▪ **OmicsObjectCreator**

Tutorials

- MathIOmicaTutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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FilteringFunction

`FilteringFunction[omicsObject, cutoff]`
filters OmicsObject data by a chosen comparison (by default greater or equal) to a *cutoff*.

Details

- `FilteringFunction[omicsObject, cutoff]`, filters an OmicsObject based on a chosen criterion. It takes the following inputs:

omicsObject	OmicsObject for which data will be filtered.
cutoff	Cutoff for which data will be filtererd.

- The following options can be given:

ListIndex	Missing[]	Selection of which list to use in the OmicsObject input.
ComponentIndex	Missing[]	Selection of which component of a list to use in the OmicsObject input.
SelectionFunction	GreaterEqual	Selection of comparison to use for filtering.

Examples (4)

Basic Examples (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

Let's import the example protein data. These are located at:

```
In[2]:= proteinExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinExample"}
```

We can now get the data:

```
In[3]:= proteinExampleData = Get[proteinExampleFile];
```

Let' s query the first 5 proteins across all datasets

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In[4]:=
```
proteinSubset = Query[All, 1 ;; 5]@proteinExampleData
```

Out[4]=
```
<|7 → <|{A0AVT1, Protein} → {{0.937}, {17}},
    {A0FGR8, Protein} → {{1.073}, {24}}, {A0MZ66, Protein} → {{1.059}, {9}},
    {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}}|>,
 9 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}}, {A0MZ66, Protein} →
    {{1.479}, {9}}, {A1A4S6, Protein} → {{0.779}, {11}}, {A1L0T0, Protein} → {{0.917}, {4}}|>,
 10 → <|{A0AVT1, Protein} → {{0.966}, {17}}, {A0FGR8, Protein} → {{1.007}, {24}}, {A0MZ66, Protein} →
    {{1.455}, {9}}, {A1A4S6, Protein} → {{0.951}, {11}}, {A1L0T0, Protein} → {{1.058}, {4}}|>,
 11 → <|{A0AVT1, Protein} → {{0.982}, {17}}, {A0FGR8, Protein} → {{0.913}, {24}}, {A0MZ66, Protein} →
    {{1.689}, {9}}, {A1A4S6, Protein} → {{0.78}, {11}}, {A1L0T0, Protein} → {{1.091}, {4}}|>,
 14 → <|{A0AVT1, Protein} → {{1.024}, {17}}, {A0FGR8, Protein} → {{0.937}, {24}}, {A0MZ66, Protein} →
    {{1.312}, {9}}, {A1A4S6, Protein} → {{0.818}, {11}}, {A1L0T0, Protein} → {{0.936}, {4}}|>,
 12 → <|{A0AVT1, Protein} → {{1.064}, {19}}, {A0FGR8, Protein} → {{0.87}, {23}}, {A0MZ66, Protein} →
    {{1.518}, {6}}, {A1A4S6, Protein} → {{0.545}, {5}}, {A1L0T0, Protein} → {{0.921}, {2}}|>,
 13 → <|{A0AVT1, Protein} → {{1.178}, {19}}, {A0FGR8, Protein} → {{0.77}, {23}}, {A0MZ66, Protein} →
    {{2.266}, {6}}, {A1A4S6, Protein} → {{0.428}, {5}}, {A1L0T0, Protein} → {{0.734}, {2}}|>,
 15 → <|{A0AVT1, Protein} → {{0.841}, {19}}, {A0FGR8, Protein} → {{1.12}, {23}}, {A0MZ66, Protein} →
    {{1.517}, {6}}, {A1A4S6, Protein} → {{0.447}, {5}}, {A1L0T0, Protein} → {{1.153}, {2}}|>,
 16 → <|{A0AVT1, Protein} → {{1.086}, {19}}, {A0FGR8, Protein} → {{0.941}, {23}}, {A0MZ66, Protein} →
    {{1.374}, {6}}, {A1A4S6, Protein} → {{0.749}, {5}}, {A1L0T0, Protein} → {{1.016}, {2}}|>,
 17 → <|{A0AVT1, Protein} → {{1.071}, {16}}, {A0FGR8, Protein} → {{0.846}, {22}}, {A0MZ66, Protein} →
    {{1.283}, {4}}, {A1A4S6, Protein} → {{0.654}, {5}}, {A1L0T0, Protein} → {{0.833}, {3}}|>,
 19 → <|{A0AVT1, Protein} → {{0.951}, {16}}, {A0FGR8, Protein} → {{0.882}, {22}},
    {A0MZ66, Protein} → {{1.473}, {4}}, {A1A4S6, Protein} → {{0.71}, {5}}, {A1L0T0, Protein} → {{0.952}, {3}}|>,
 20 → <|{A0AVT1, Protein} → {{0.873}, {16}}, {A0FGR8, Protein} → {{0.852}, {22}}, {A0MZ66, Protein} →
    {{1.213}, {4}}, {A1A4S6, Protein} → {{0.882}, {5}}, {A1L0T0, Protein} → {{1.065}, {3}}|>,
 21 → <|{A0AVT1, Protein} → {{0.988}, {16}}, {A0FGR8, Protein} → {{0.916}, {22}}, {A0MZ66, Protein} →
    {{1.066}, {4}}, {A1A4S6, Protein} → {{0.796}, {5}}, {A1L0T0, Protein} → {{0.992}, {3}}|>|>
```

Let' s also query the length of the inner association data:

In[5]:=
```
Query[All, Length]@proteinExampleData
```

Out[5]=
```
<|7 → 5225, 9 → 5225, 10 → 5225, 11 → 5225, 14 → 5225, 12 → 5225,
 13 → 5225, 15 → 5225, 16 → 5225, 17 → 5225, 19 → 5225, 20 → 5225, 21 → 5225|>
```

We notice that all datasets are exactly the same length, 5225 protein identifiers included. We now filter on the metadata list (ListIndex 2) which was set to contain the number of unique peptides (ComponentIndex 1), to filter out proteins that have less than two unique peptides identified.

In[6]:=
```
proteinExampleDataFiltered = FilteringFunction[proteinExampleData, 2, ListIndex → 2, ComponentIndex → 1];
```

Let' s again query the length of the inner association data:

In[7]:=
```
Query[All, Length]@proteinExampleDataFiltered
```

Out[7]=
```
<|7 → 3905, 9 → 3905, 10 → 3905, 11 → 3905, 14 → 3905, 12 → 3905,
 13 → 3905, 15 → 3905, 16 → 3905, 17 → 3905, 19 → 3905, 20 → 3905, 21 → 3905|>
```

We see that the filtering has removed 1320 proteins that only had one unique peptide.

Options (3)

ListIndex (1)

In[1]:=
```
Needs["MathIOmica`"]
```

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ListIndex allows selection of which list to filter on (list 1 or 2 in a typical OmicsObject contain data or metadata).

Let's look at the subset data from the standard examples (we repeat the data loading here for convenience):

```
In[2]:= proteinExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinExample"};
        proteinExampleData = Get[proteinExampleFile];

In[3]:= proteinSubset = Query[All, 1 ;; 5]@proteinExampleData

Out[3]= <|7 → <|{A0AVT1, Protein} → {{0.937}, {17}},
           {A0FGR8, Protein} → {{1.073}, {24}}, {A0MZ66, Protein} → {{1.059}, {9}},
           {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}}|>,
         9 → <|{A0AVT1, Protein} → {{1.003}, {17}}, {A0FGR8, Protein} → {{0.921}, {24}}, {A0MZ66, Protein} →
            {{1.479}, {9}}, {A1A4S6, Protein} → {{0.779}, {11}}, {A1L0T0, Protein} → {{0.917}, {4}}|>,
         10 → <|{A0AVT1, Protein} → {{0.966}, {17}}, {A0FGR8, Protein} → {{1.007}, {24}}, {A0MZ66, Protein} →
            {{1.455}, {9}}, {A1A4S6, Protein} → {{0.951}, {11}}, {A1L0T0, Protein} → {{1.058}, {4}}|>,
         11 → <|{A0AVT1, Protein} → {{0.982}, {17}}, {A0FGR8, Protein} → {{0.913}, {24}}, {A0MZ66, Protein} →
            {{1.689}, {9}}, {A1A4S6, Protein} → {{0.78}, {11}}, {A1L0T0, Protein} → {{1.091}, {4}}|>,
         14 → <|{A0AVT1, Protein} → {{1.024}, {17}}, {A0FGR8, Protein} → {{0.937}, {24}}, {A0MZ66, Protein} →
            {{1.312}, {9}}, {A1A4S6, Protein} → {{0.818}, {11}}, {A1L0T0, Protein} → {{0.936}, {4}}|>,
         12 → <|{A0AVT1, Protein} → {{1.064}, {19}}, {A0FGR8, Protein} → {{0.87}, {23}}, {A0MZ66, Protein} →
            {{1.518}, {6}}, {A1A4S6, Protein} → {{0.545}, {5}}, {A1L0T0, Protein} → {{0.921}, {2}}|>,
         13 → <|{A0AVT1, Protein} → {{1.178}, {19}}, {A0FGR8, Protein} → {{0.77}, {23}}, {A0MZ66, Protein} →
            {{2.266}, {6}}, {A1A4S6, Protein} → {{0.428}, {5}}, {A1L0T0, Protein} → {{0.734}, {2}}|>,
         15 → <|{A0AVT1, Protein} → {{0.841}, {19}}, {A0FGR8, Protein} → {{1.12}, {23}}, {A0MZ66, Protein} →
            {{1.517}, {6}}, {A1A4S6, Protein} → {{0.447}, {5}}, {A1L0T0, Protein} → {{1.153}, {2}}|>,
         16 → <|{A0AVT1, Protein} → {{1.086}, {19}}, {A0FGR8, Protein} → {{0.941}, {23}}, {A0MZ66, Protein} →
            {{1.374}, {6}}, {A1A4S6, Protein} → {{0.749}, {5}}, {A1L0T0, Protein} → {{1.016}, {2}}|>,
         17 → <|{A0AVT1, Protein} → {{1.071}, {16}}, {A0FGR8, Protein} → {{0.846}, {22}}, {A0MZ66, Protein} →
            {{1.283}, {4}}, {A1A4S6, Protein} → {{0.654}, {5}}, {A1L0T0, Protein} → {{0.833}, {3}}|>,
         19 → <|{A0AVT1, Protein} → {{0.951}, {16}}, {A0FGR8, Protein} → {{0.882}, {22}},
           {A0MZ66, Protein} → {{1.473}, {4}}, {A1A4S6, Protein} → {{0.71}, {5}}, {A1L0T0, Protein} → {{0.952}, {3}}|>,
         20 → <|{A0AVT1, Protein} → {{0.873}, {16}}, {A0FGR8, Protein} → {{0.852}, {22}}, {A0MZ66, Protein} →
            {{1.213}, {4}}, {A1A4S6, Protein} → {{0.882}, {5}}, {A1L0T0, Protein} → {{1.065}, {3}}|>,
         21 → <|{A0AVT1, Protein} → {{0.988}, {16}}, {A0FGR8, Protein} → {{0.916}, {22}}, {A0MZ66, Protein} →
            {{1.066}, {4}}, {A1A4S6, Protein} → {{0.796}, {5}}, {A1L0T0, Protein} → {{0.992}, {3}}|>|>
```

In this example, we can filter on the measurement (first list, ListIndex→1, first component), selecting values greater than 0.9 (these are relative intensity.

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```
In[4]:= FilteringFunction[proteinSubset, 1, ListIndex → 1, ComponentIndex → 1]

Out[4]= <|7 → <|{A0FGR8, Protein} → {{1.073}, {24}}, {A0MZ66, Protein} → {{1.059}, {9}},
          {A1A4S6, Protein} → {{1.03}, {11}}, {A1L0T0, Protein} → {{1.268}, {4}}, {A0AVT1, Protein} → Missing[]|>,
        9 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.479}, {9}}, {A1A4S6, Protein} → Missing[],
          {A1L0T0, Protein} → Missing[], {A0AVT1, Protein} → {{1.003}, {17}}|>,
        10 → <|{A0FGR8, Protein} → {{1.007}, {24}}, {A0MZ66, Protein} → {{1.455}, {9}},
          {A1A4S6, Protein} → Missing[], {A1L0T0, Protein} → {{1.058}, {4}}, {A0AVT1, Protein} → Missing[]|>,
        11 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.689}, {9}}, {A1A4S6, Protein} → Missing[],
          {A1L0T0, Protein} → {{1.091}, {4}}, {A0AVT1, Protein} → Missing[]|>,
        14 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.312}, {9}}, {A1A4S6, Protein} → Missing[],
          {A1L0T0, Protein} → Missing[], {A0AVT1, Protein} → {{1.024}, {17}}|>,
        12 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.518}, {6}}, {A1A4S6, Protein} → Missing[],
          {A1L0T0, Protein} → Missing[], {A0AVT1, Protein} → {{1.064}, {19}}|>,
        13 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{2.266}, {6}}, {A1A4S6, Protein} → Missing[],
          {A1L0T0, Protein} → Missing[], {A0AVT1, Protein} → {{1.178}, {19}}|>,
        15 → <|{A0FGR8, Protein} → {{1.12}, {23}}, {A0MZ66, Protein} → {{1.517}, {6}},
          {A1A4S6, Protein} → Missing[], {A1L0T0, Protein} → {{1.153}, {2}}, {A0AVT1, Protein} → Missing[]|>,
        16 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.374}, {6}}, {A1A4S6, Protein} → Missing[],
          {A1L0T0, Protein} → {{1.016}, {2}}, {A0AVT1, Protein} → {{1.086}, {19}}|>,
        17 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.283}, {4}}, {A1A4S6, Protein} → Missing[],
          {A1L0T0, Protein} → Missing[], {A0AVT1, Protein} → {{1.071}, {16}}|>,
        19 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.473}, {4}},
          {A1A4S6, Protein} → Missing[], {A1L0T0, Protein} → Missing[], {A0AVT1, Protein} → Missing[]|>,
        20 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.213}, {4}}, {A1A4S6, Protein} → Missing[],
          {A1L0T0, Protein} → {{1.065}, {3}}, {A0AVT1, Protein} → Missing[]|>,
        21 → <|{A0FGR8, Protein} → Missing[], {A0MZ66, Protein} → {{1.066}, {4}},
          {A1A4S6, Protein} → Missing[], {A1L0T0, Protein} → Missing[], {A0AVT1, Protein} → Missing[]|>|>
```

ComponentIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

ComponentIndex allows selection of which component of the selected list to filter on from the OmicsObject. Let's consider the following OmicsObject:

```
In[2]:= omicsObjectMultiComponent =
          <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
             {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
             {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
             {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
             {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
           "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
             {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
             {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>|>;
```

Let's first filter from the first list, on the first component being ≥ 0.6:

```
In[3]:= FilteringFunction[omicsObjectMultiComponent, 0.6, ListIndex → 1, ComponentIndex → 1]

Out[3]= <|FirstSample →
          <|{Measurement1} → {{0.8, 2}, {17, True}}, {Measurement2} → Missing[], {Measurement5} → Missing[]|>,
        SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement2} → {{0.7, 1}, {12, True}},
          {Measurement5} → {{0.6, 3}, {10, True}}|>, ThirdSample →
          <|{Measurement1} → {{0.9, 2}, {16, True}}, {Measurement2} → Missing[], {Measurement5} → Missing[]|>|>
```

We could also filter from component 2 on the same list, say values ≥ 6:

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```
In[4]:= FilteringFunction[omicsObjectMultiComponent, 6, ListIndex → 1, ComponentIndex → 2]

Out[4]= <|FirstSample → <|{Measurement3} → Missing[]|>, SecondSample → <|{Measurement3} → Missing[]|>,
  ThirdSample → <|{Measurement3} → {{0.4, 6}, {8, False}}|>|>
```

SelectionFunction (1)

```
In[1]:= Needs["MathIOmica`"]
```

Selection function allows us to select the function used for filtering. The default is GreaterEqual. We consider the following multi-component object.

```
In[2]:= omicsObjectMultiComponent =
  <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
     {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
     {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
     {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
     {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
   "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
     {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
     {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>|>;
```

We can filter the values ≥ 0.6 from the first list, first component:

```
In[3]:= FilteringFunction[omicsObjectMultiComponent, 0.6,
  ListIndex → 1, ComponentIndex → 1, SelectionFunction → GreaterEqual]

Out[3]= <|FirstSample →
    <|{Measurement1} → {{0.8, 2}, {17, True}}, {Measurement2} → Missing[], {Measurement5} → Missing[]|>,
  SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement2} → {{0.7, 1}, {12, True}},
     {Measurement5} → {{0.6, 3}, {10, True}}|>, ThirdSample →
    <|{Measurement1} → {{0.9, 2}, {16, True}}, {Measurement2} → Missing[], {Measurement5} → Missing[]|>|>
```

We can instead filter for values < 0.6 from the first list, first component:

```
In[4]:= FilteringFunction[omicsObjectMultiComponent, 0.6,
  ListIndex → 1, ComponentIndex → 1, SelectionFunction → Less]

Out[4]= <|FirstSample → <|{Measurement3} → {{0.5, 4}, {2, False}},
     {Measurement4} → {{0.2, 3}, {5, True}}, {Measurement2} → Missing[]|>,
  SecondSample → <|{Measurement3} → {{0.3, 2}, {11, False}}, {Measurement4} → {{0.3, 3}, {6, True}},
     {Measurement2} → Missing[]|>, ThirdSample → <|{Measurement3} → {{0.4, 6}, {8, False}},
     {Measurement4} → {{0.3, 2}, {7, True}}, {Measurement2} → {{0.3, 5}, {11, True}}|>|>
```

We can also filter for "True" values from the second list, second component.

```
In[5]:= FilteringFunction[omicsObjectMultiComponent, "True",
  ListIndex → 2, ComponentIndex → 2, SelectionFunction → MatchQ]

Out[5]= <|FirstSample → <|{Measurement1} → {{0.8, 2}, {17, True}},
     {Measurement4} → {{0.2, 3}, {5, True}}, {Measurement2} → Missing[], {Measurement5} → Missing[]|>,
  SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement4} → {{0.3, 3}, {6, True}},
     {Measurement2} → {{0.7, 1}, {12, True}}, {Measurement5} → {{0.6, 3}, {10, True}}|>,
  ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}}, {Measurement4} → {{0.3, 2}, {7, True}},
     {Measurement2} → {{0.3, 5}, {11, True}}, {Measurement5} → Missing[]|>|>
```

Equivalently we could have filtered for "False" values from the second list, second component.

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In[6]:=
```
FilteringFunction[omicsObjectMultiComponent, "False",
 ListIndex → 2, ComponentIndex → 2, SelectionFunction → MatchQ]
```

Out[6]=
```
<|FirstSample → <|{Measurement3} → {{0.5, 4}, {2, False}}|>,
 SecondSample → <|{Measurement3} → {{0.3, 2}, {11, False}}|>,
 ThirdSample → <|{Measurement3} → {{0.4, 6}, {8, False}}|>|>
```

See Also

OmicsObject ▪ **FilterMissing**

Tutorials

- MathIOmicaTutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾ URL ▾

GOAnalysis

GOAnalysis [*data*]

calculates input data over–representation analysis for Gene Ontology (GO) categories.

Details

- GOAnalysis[*data*] calculates input data over-representation analysis (ORA) for Gene Ontology (GO) categories. We note that the function utilizes ontologies obtained from the GO Consortium, and by default uses human data annotated with UniProt IDs.
- The input data can be a single list of n genes in the form:
- data = {ID_1, ID_2, ..., ID_n}
- The IDs may be provided as ID strings, or as labeled strings in the case of multiple omics being considered. Labeled IDs are provided as {{ID_1, $label_1$}, {ID_2, $label_2$}, ... {ID_3, $label_2$}}. The labels are typically a string, e.g. typically "RNA" or "Protein".
- The default output contains each GO:term that was considered and found to be statistically significant. For each GO term we schematically have an association with keys GO : Term → {{testing outcomes}, {statistics}, {{GO term}, {Membership}}. The output has the following structures: for a single list input:
- listOutput = <|
  GO : $Term_1$ → {{p – $value_1$, multiple hypothesis adjusted p – $value_1$, True / False for statistical significance},
    {{number of members in group being tested, number of successes for $term_1$ in population, total number of members in population, number of members (or more) in current group being tested associated to $term_1$},
     {{GO $term_1$ description, ontology category for $term_1$}, {input IDs associated to $Term_1$}}}},
  GO : $Term_2$ → {{p – $value_2$, multiple hypothesis adjusted p – $value_2$, True / False for statistical significance},
    {{number of members in group being tested, number of successes for $term_2$ in population, total number of members in population, number of members (or more) in current group being tested associated to $term_2$},
     {{GO $term_2$ description, ontology category for $term_2$}, {input IDs associated to $Term_2$}}}}, ...,
  GO : $Term_n$ → {{p – $value_n$, multiple hypothesis adjusted p – $value_n$, True / False for statistical significance},
    {{number of members in group being tested, number of successes for $term_n$ in population, total number of members in population, number of members (or more) in current group being tested associated to $term_n$},
     {{GO $term_n$ description, ontology category for $term_n$}, {input IDs associated to $term_n$}}}}
  |>
- The input data can also be an association of multiple L groups to be tested:
- data = <|$Group_1$ → {ID_{11}, ID_{12}, ..., $ID_{1\,n_1}$},
  $Group_2$ → {ID_{21}, ID_{22}, ..., $ID_{2\,n2}$}, ...,
  $Group_L$ → {ID_{11}, ID_{12}, ..., $ID_{1\,n_L}$}|>.
- In this case the output for each group has the listOutput format described above:
- associationOutput = <|$Group_1$ → $listOutput_1$,
  $Group_2$ → $listOutput_2$, ...,
  $Group_L$ → $listOutput_L$|>

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- `GOAnalysis` can also take as input the output of clustering of time series classification data, e.g. TimeSeriesClusters or TimeSeriesSingleClusters association of associations. The groups for each class will then have keys labeled `"GroupAssociations"`, that include the labels used in the clustering. The labels must correspond to protein or gene accessions/IDs. For each class and group the corresponding GOAnalysis enrichment is computed and returned.

- The enrichment analysis is an over-representation calculation, using a hypergeometric test. For a given a given group (e.g. members of a cluster after classification), we try to identify which gene ontology terms are over-represented by membership of genes to that cluster. The GOAnalysis function allows us to select the background, and hence address selection bias. Additionally a Benjamini-Hochberg procedure false discovery rate (FDR) may be calculated for each representation.

- We assume here we are considering a population (possible measurements) of N total genes, and a given pathway or GO term T has M_T genes associated to it. For any group/cluster we are interested in (e.g. as differentially expressed), that contains a subset of $n_{group} < N$ genes, we can identify which x_T genes are associated to term T. Then we would like to calculate the probability, p_T, that at least x_T genes could have an association to term T randomly (i.e. more than x_T number of successes):

- $p_T\,(\text{at least } x \text{ successes}) = \sum_{i=x}^{n_{group}} \frac{\binom{M_T}{i}\binom{N-M_T}{n_{group}-i}}{\binom{N}{n_{group}}}$.

- Using this hypergeometric distribution calculation, we can choose a p-value cutoff, typically at 0.95, to consider any cluster/group's number of successes (for a specified term) to show enrichment in be enriched in a term T of interest.

- In practice, typically a database (such as KEGG, or GO) has annotated only a subset $N_a \subset N$ of these total genes. The calculation then is modified to reduce this bias, by performing the analysis on a subset of the genes of interest to the ones that belong to N_a, and effectively we also have $n_{group} \to n_{group,a} = \{j \in n_{group} : j \in N_a\}$.

- Additionally, there are cases when the overall measurements can be restricted to certain sets only, i.e. a different background or species, $N \to N_b \subset N$. Then the pathway/group terms are also restricted to the ones that belong to N_b, $M_{T,b} = \{k \in M_{T,b} : k \in N_b\}$.

- In the case that labeled multi-omics data is provided there are multiple choices. If no `MultipleList` options are invoked (see below), the identifiers are treated as equivalent and are simply grouped together. If the same identifier shows with the same label these identifiers are treated as equivalent (i.e. no over-counting). If the MultipleList and MultipleListCorrection are set, the population N is enlarged by a factor f_P and so is the membership of each term to accommodate the changes. In the case of two omics, the assumption is that they can each contribute equally to a term and the Automatic GOAnalysis function correction is a simple factor of $f_P = 2$.

- Finally, there is the need to address false discovery rates and account for multiple hypothesis testing. The default method is the computation of a Benjamini-Hochberg false discovery rate (FDR) using BenjaminiHochbergFDR .

- The following options can be given:

AdditionalFilter	None	AdditionalFilter provides additional filtering that may be applied to the standard output structure to be returned.
AugmentDictionary	True	AugmentDictionary provides a choice whether or not to augment the current ConstantGeneDictionary variable or create a new one.
BackgroundSet	All	BackgroundSet provides a list of IDs (e.g. gene accessions) that should be considered as the background for the calculation.

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FilterSignificant	True	FilterSignificant can be set to True to filter data based on whether the enrichment analysis is statistically significant, or if set to False to return all membership computations.
GeneDictionary	None	GeneDictionary points to an existing variable to use as a gene dictionary in annotations. If set to None the default ConstantGeneDictionary will be used.
GetGeneDictionaryOptions	{}	The GetGeneDictionaryOptions option specifies a list of options that will be passed to the internal GetGeneDictionary function.
GOAnalysisAssignerOptions	{}	The GOAnalysisAssignerOptions option specifies a list of options that will be passed to the internal GOAnalysisAssigner function.
HypothesisFunction	(Query["Results"][BenjaminiHochbergFDR[#1, SignificanceLevel –> #2]] &)	The HypothesisFunction option allows us to chose a function to implement multiple hypothesis testing. The default is using the BenjaminiHochbergFDR function. The user can use any function f with three inputs, of the form f[#1,#2,#3] where the inputs refer to: #1 is the p–value list, #2 is a significance cutoff, #3 is the number of GO associations overall being tested. The function f must output a list of 3 values: {original p–value, adjusted p–value, True or False based on whether this value is considered statistically significant or not respectively}.
InputID	{"UniProt ID", "Gene Symbol"}	The InputID option specifies the kind of identifiers/accessions used as input.

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MultipleList	False	MultipleList option specifies whether the input accessions list constituted a multi–omics list input that is annotated so. If this is the case, MultipleList is set to True and each input list ID should have the form {ID,"Omics Type Label"}, e.g. {"NFKB1","Protein"}, and the different omics type are treated as different for each ID. If MultipleList is set to False, and labeled IDs are provided, labels corresponding to the same ID are treated as equivalent to avoid overcounting.
MultipleListCorrection	None	MultipleListCorrection is an option whether or not to correct for multi–omics analysis. The choices are None, Automatic, or a custom number. This essentially enlarges the population by this factor to account for additional IDs being considered as the result of a multi–omics cluster analysis. If the value is set to Automatic the number of unique ID labels is used to make the correction.
OBOGODictionaryOptions	{}	OBOGODictionaryOptions specifies a list of options to be passed to the internal OBOGODictionary function that provides the GO annotations.
OBODictionaryVariable	None	OBODictionaryVariable can provide a GO annotation variable. If set to None, OBOGODictionary will be used internally to automatically generate the default GO annotation.
OntologyLengthFilter	2	OntologyLengthFilter can be used to set the value for which terms to consider in the computation, by excluding GO terms that have fewer items compared to the OntologyLengthFilter value. It is used by the internal GOAnalysisAssigner function.

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OutputID	"UniProt ID"	The OutputID option takes a string value that specifies what kind of IDs/accessions to convert the input IDs to compute the GO enrichment.
pValueCutoff	0.05	pValueCutoff provides a cutoff p–value for adjusted p–values to assess statistical significance.
ReportFilter	1	ReportFilter provides a cutoff for membership in ontologies in selecting which terms/categories to return. It is used in conjunction with ReportFilterFunction.
ReportFilterFunction	GreaterEqualThan	ReportFilterFunction specifies what operator form will be used to compare against ReportFilter option value in selecting which terms/categories to return. The default is to use GreaterEqualThan.
Species	"human"	The Species option specifies the species considered in the calculation.
TestFunction	(1 – N[CDF[HypergeometricDistribution[#1, #2, #3], #4 – 1]]) &	The TestFunction option provides a function used to calculate the p–values for the enrichment of each term. It can be a function of four inputs, f[#1,#2,#3,#4] (e.g. the default is using a hypergeometric distribution CDF, 1–N[CDF[HypergeometricDistribution[#1,#2,#3],#4–1]]]. The four inputs refer to: #1 is number of draws (members in group being tested), #2 is number of successes for category in population, #3 is total number of members in population, #4 is number of successes (or more) in current group being tested for specific category. The output is a p–value (real positive number ≤ 1).

- GOAnalysis generates a global ConstantGeneDictionary variable if one does not exist already.

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Examples (29)

Basic Examples (5)

We first load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

Let's do a GO analysis for a group of genes, annotated with their "Gene Symbol":

In[2]:=
```
goExample1 =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
   "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}]
```

Out[2]=
```
⟨|GO:0051092 → {{9.39023×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
  GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
  GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
    {{protein serine/threonine kinase activity, molecular_function},
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
  GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
    {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
  GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
    {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
   {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
     {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
  GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
```

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```
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
   {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
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GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
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GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
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  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
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GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
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GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
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   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
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GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
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GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
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GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
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   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
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GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
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GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
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GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
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GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
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GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
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GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
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  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19 774, 10}, {{nucleoplasm, cellular_component},
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GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19 774, 2},
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GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19 774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19 774, 2},
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GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19 774, 2},
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  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
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GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19 774, 2},
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GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
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GO:2000630 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0071359 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0042159 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0043208 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0043504 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0048273 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0061041 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:1904354 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
 {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
```

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```
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
```

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```
    {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
  GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{response to testosterone, biological_process}, {{CSNK2B}}}},
  GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
  GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
  GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
    {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
  GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{DNA damage checkpoint, biological_process}, {{ATM}}}},
  GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
  GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
  GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
  GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|⟩
```

We can obtain the results for any of the data:

```
In[3]:= Query[{1}]@goExample1
```

Out[3]= ⟨|GO:0051092 → {{9.39023×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
{{positive regulation of NF-kappaB transcription factor activity, biological_process},
{{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}}|⟩

We see that the result is statistically significant. GO term GO:0051092 is a Biological Process term, namely, positive regulation of NF-kappaB transcription factor activity. 7 of the 20 input genes with annotation are associated to this term. The term has 151 genes associated to it.

```
In[1]:= Needs["MathIOmica`"]
```

The information can be computed for multiple groups, if these are provided as an association:

```
In[2]:= analysisGOAssociation = GOAnalysis[<|
    "Group1" → {"C6orf57", "CD46", "DHX58", "HMGB3", "MAP3K5", "NFKB2", "NOS2", "PYCARD", "PYDC1", "SSC5D"},
    "Group2" → {"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C",
      "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88",
      "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}|>]
```

Out[2]=
```
⟨|Group1 → ⟨|GO:0045087 → {{3.51337×10^-18, 8.29156×10^-16, True},
      {10, 425, 47250, 9}, {{innate immune response, biological_process},
       {{C6orf57}, {CD46}, {DHX58}, {HMGB3}, {MAP3K5}, {NFKB2}, {PYCARD}, {PYDC1}, {SSC5D}}}},
    ⋯ 180 ⋯, GO:0007568 → {{0.0372477, 0.0482993, True}, {10, 179, 47250, 1},
      {{aging, biological_process}, {{NFKB2}}}}|⟩,
 Group2 → ⟨|GO:0051092 → {⋯ 1 ⋯}, ⋯ 400 ⋯, GO:0002020 → {⋯ 1 ⋯}|⟩|⟩
```

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We can obtain the results for any of the data. Let's look at the top (lowest p-value) two

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results in both groups:

```
In[3]:= Query[All, {1, 2}]@analysisGOAssociation
```

```
Out[3]= ⟨|Group1 → ⟨|GO:0045087 → {{3.51337×10^-18, 8.29156×10^-16, True},
      {10, 425, 47250, 9}, {{innate immune response, biological_process},
       {{C6orf57}, {CD46}, {DHX58}, {HMGB3}, {MAP3K5}, {NFKB2}, {PYCARD}, {PYDC1}, {SSC5D}}}},
    GO:0050829 → {{8.99901×10^-8, 9.51286×10^-6, True}, {10, 44, 47250, 3},
      {{defense response to Gram-negative bacterium, biological_process}, {{NOS2}, {PYCARD}, {SSC5D}}}}|⟩,
  Group2 → ⟨|GO:0051092 → {{3.98878×10^-13, 1.97046×10^-10, True}, {21, 155, 47250, 7},
      {{positive regulation of NF-kappaB transcription factor activity, biological_process},
       {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}, GO:0005515 →
     {{1.90129×10^-12, 4.69619×10^-10, True}, {21, 8801, 47250, 19}, {{protein binding, molecular_function},
       {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
        {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}}|⟩|⟩
```

```
In[1]:= Needs["MathIOmica`"]
```

The data can be computed with or without a label. If labeled, the gene ID must be the first element for each ID provided. The data is in the form {ID,label}:

```
In[2]:= analysisGOLabel = GOAnalysis[{{"C6orf57", "Protein"}, {"CD46", "Protein"},
    {"DHX58", "Protein"}, {"HMGB3", "Protein"}, {"MAP3K5", "Protein"}, {"NFKB2", "Protein"},
    {"NOS2", "Protein"}, {"PYCARD", "Protein"}, {"PYDC1", "Protein"}, {"SSC5D", "Protein"}}];
```

We can query the first 5 results :

```
In[3]:= analysisGOLabel[[1 ;; 5]]
```

```
Out[3]= ⟨|GO:0045087 →
    {{3.51337×10^-18, 8.29156×10^-16, True}, {10, 425, 47250, 9}, {{innate immune response, biological_process},
      {{{C6orf57, Protein}}, {{CD46, Protein}}, {{DHX58, Protein}}, {{HMGB3, Protein}}, {{MAP3K5, Protein}},
       {{NFKB2, Protein}}, {{PYCARD, Protein}}, {{PYDC1, Protein}}, {{SSC5D, Protein}}}}},
  GO:0050829 → {{8.99901×10^-8, 9.51286×10^-6, True}, {10, 44, 47250, 3},
    {{defense response to Gram-negative bacterium, biological_process},
     {{{NOS2, Protein}}, {{PYCARD, Protein}}, {{SSC5D, Protein}}}}},
  GO:0002588 → {{1.20926×10^-7, 9.51286×10^-6, True}, {10, 3, 47250, 2},
    {{positive regulation of antigen processing and presentation of peptide antigen via MHC class II,
      biological_process}, {{{PYCARD, Protein}}, {{PYDC1, Protein}}}}},
  GO:0002277 → {{2.41825×10^-7, 0.0000142677, True}, {10, 4, 47250, 2},
    {{myeloid dendritic cell activation involved in immune response, biological_process},
     {{{PYCARD, Protein}}, {{PYDC1, Protein}}}}},
  GO:0044351 → {{1.45013×10^-6, 0.0000587192, True}, {10, 9, 47250, 2},
    {{macropinocytosis, biological_process}, {{{PYCARD, Protein}}, {{PYDC1, Protein}}}}}|⟩
```

```
In[1]:= Needs["MathIOmica`"]
```

The data can be mixed, e.g. proteins and RNA with different labels:

```
In[2]:= analysisGOMixed = GOAnalysis[{{"C6orf57", "Protein"}, {"CD46", "Protein"}, {"DHX58", "Protein"},
    {"HMGB3", "RNA"}, {"HMGB3", "Protein"}, {"MAP3K5", "Protein"}, {"NFKB2", "RNA"}, {"NFKB2", "Protein"},
    {"NOS2", "RNA"}, {"PYCARD", "RNA"}, {"PYDC1", "Protein"}, {"SSC5D", "Protein"}}];
```

The data in this case treated as originating from a single population. Protein and RNA labeled data for the same identifier are treated as equivalent.We can query the first 5 results

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:

In[3]:=
```
analysisGOMixed[[1 ;; 5]]
```

Out[3]=
```
⟨|GO:0045087 →
  {{6.48663×10^-12, 1.69301×10^-9, True}, {10, 497, 19774, 8}, {{innate immune response, biological_process},
    {{{C6orf57, Protein}}, {{CD46, Protein}}, {{DHX58, Protein}}, {{HMGB3, Protein}, {HMGB3, RNA}},
     {{MAP3K5, Protein}}, {{PYCARD, RNA}}, {{PYDC1, Protein}}, {{SSC5D, Protein}}}}},
 GO:0050829 → {{7.49698×10^-6, 0.000719577, True}, {10, 80, 19774, 3},
   {{defense response to Gram-negative bacterium, biological_process},
    {{{NOS2, RNA}}, {{PYCARD, RNA}}, {{SSC5D, Protein}}}}},
 GO:0008385 → {{8.271×10^-6, 0.000719577, True}, {10, 9, 19774, 2},
   {{IkappaB kinase complex, cellular_component}, {{{PYCARD, RNA}}, {{PYDC1, Protein}}}}},
 GO:0050718 → {{0.000120525, 0.00786425, True}, {10, 33, 19774, 2},
   {{positive regulation of interleukin-1 beta secretion, biological_process},
    {{{PYCARD, RNA}}, {{PYDC1, Protein}}}}},
 GO:0032481 → {{0.00028963, 0.0130993, True}, {10, 51, 19774, 2},
   {{positive regulation of type I interferon production, biological_process},
    {{{DHX58, Protein}}, {{NFKB2, Protein}, {NFKB2, RNA}}}}}|⟩
```

We can instead treat the data as different by setting the `MultipleList` and MultipleListCorrection options:

In[4]:=
```
analysisGOMixedMulti = GOAnalysis[{{"C6orf57", "Protein"}, {"CD46", "Protein"}, {"DHX58", "Protein"},
    {"HMGB3", "RNA"}, {"HMGB3", "Protein"}, {"MAP3K5", "Protein"}, {"NFKB2", "RNA"}, {"NFKB2", "Protein"},
    {"NOS2", "RNA"}, {"PYCARD", "RNA"}, {"PYDC1", "Protein"}, {"SSC5D", "Protein"}},
   MultipleList → True, MultipleListCorrection → Automatic];
```

In[5]:=
```
analysisGOMixedMulti[[1 ;; 5]]
```

Out[5]=
```
⟨|GO:0045087 →
  {{7.94077×10^-13, 2.07254×10^-10, True}, {12, 994, 39548, 9}, {{innate immune response, biological_process},
    {{{C6orf57, Protein}}, {{CD46, Protein}}, {{DHX58, Protein}}, {{HMGB3, RNA}}, {{HMGB3, Protein}},
     {{MAP3K5, Protein}}, {{PYCARD, RNA}}, {{PYDC1, Protein}}, {{SSC5D, Protein}}}}},
 GO:0002268 → {{5.06222×10^-7, 0.0000440413, True}, {12, 4, 39548, 2},
   {{follicular dendritic cell differentiation, biological_process},
    {{{NFKB2, RNA}}, {{NFKB2, Protein}}}}},
 GO:0033257 → {{5.06222×10^-7, 0.0000440413, True}, {12, 4, 39548, 2},
   {{Bcl3/NF-kappaB2 complex, cellular_component}, {{{NFKB2, RNA}}, {{NFKB2, Protein}}}}},
 GO:0032392 → {{2.36077×10^-6, 0.000154041, True}, {12, 8, 39548, 2},
   {{DNA geometric change, biological_process}, {{{HMGB3, RNA}}, {{HMGB3, Protein}}}}},
 GO:0032481 → {{3.60297×10^-6, 0.000164988, True}, {12, 102, 39548, 3},
   {{positive regulation of type I interferon production, biological_process},
    {{{DHX58, Protein}}, {{NFKB2, RNA}}, {{NFKB2, Protein}}}}}|⟩
```

In[1]:=
```
Needs["MathIOmica`"]
```

Let's consider an example from real protein data. We will use already clustered data, from the MathIOmica proteomics examples. Let's import the data, which should be located at:

In[2]:=
```
proteinExampleClusterFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinClusteringExample"}
```

We can now get the data :

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In[3]:=
```
proteinExampleClusters = Get[proteinExampleClusterFile]
```

Out[3]=
```
<|SpikeMax →
  <|Cluster → <··· 1 ···>, <··· 4 ···>, GroupAssociations → <|G1S1 → {{O14933, Protein}, {O94979, Protein},
      {P13612, Protein}, {P60900, Protein}, <··· 16 ···>, {Q86UP2, Protein}, {Q8N1G4, Protein},
      {P55263, Protein}, {Q01082, Protein}}, <··· 3 ···>, G3S1 → <··· 1 ···>|>|>, <··· 4 ···>, f7 → <··· 1 ···>|>
```

large output | show less | show more | show all | set size limit...

We can calculate the GOAnalysis for each group in each class:

In[4]:=
```
enrichmentGOprotein = GOAnalysis[proteinExampleClusters]
```

Out[4]=
```
<|SpikeMax → <|G1S1 → <|GO:0003723 →
      {{2.20201×10^-6, 0.000537863, True}, {24, 1387, 19774, 10}, {{RNA binding, molecular_function},
        {{{P60900, Protein}}, {{Q9Y333, Protein}}, <··· 7 ···>, {{Q01082, Protein}}}}},
    <··· 147 ···>, GO:0050901 → {<··· 1 ···>}|>, <··· 4 ···>|>, <··· 4 ···>, f7 → <|<··· 1 ···>|>|>
```

large output | show less | show more | show all | set size limit...

The data has multiple clusters:

In[5]:=
```
Query[All,Keys]@enrichmentGOprotein
```

Out[5]=
```
<|SpikeMax → {G1S1, G1S2, G2S1, G2S2, G3S1},
 SpikeMin → {G1S1, G1S2, G1S3}, f1 → {G1S1, G1S2, G2S1, G2S2, G3S1, G3S2},
 f5 → {G1S1, G1S2, G2S1, G2S2}, f6 → {G1S1, G1S2, G2S1}, f7 → {G1S1, G1S2, G2S1}|>
```

Let's look at the top category in each group in each class:

In[6]:=
```
Query[All, All, {1}]@enrichmentGOprotein
```

Out[6]=
```
<|SpikeMax → <|G1S1 → <|GO:0003723 → {{2.20201×10^-6, 0.000537863, True}, {24, 1387, 19774, 10},
      {{RNA binding, molecular_function}, {{{P60900, Protein}}, {{Q9Y333, Protein}},
        {{P19474, Protein}}, {{O60841, Protein}}, {{O75534, Protein}}, {{P63220, Protein}},
        {{Q86UP2, Protein}}, {{Q8N1G4, Protein}}, {{P55263, Protein}}, {{Q01082, Protein}}}}}|>,
  G1S2 → Missing[PartAbsent, {1}], G2S1 → <|GO:1903203 → {{0.000101143, 0.00131486, True},
      {1, 2, 19774, 1}, {{regulation of oxidative stress-induced neuron death, biological_process},
       {{{O43813, Protein}}}}}|>,
  G2S2 → <|GO:0005739 → {{1.92957×10^-16, 5.75012×10^-14, True}, {26, 1240, 19774, 18},
      {{mitochondrion, cellular_component}, {{{P22695, Protein}}, {{Q9NUJ1, Protein}},
        {{O95571, Protein}}, {{Q96I99, Protein}}, {{Q9NSE4, Protein}}, {{O96008, Protein}},
        {{P10515, Protein}}, {{P42126, Protein}}, {{Q02218, Protein}}, {{P40939, Protein}},
        {{P22307, Protein}}, {{P13804, Protein}}, {{P17568, Protein}}, {{O75323, Protein}},
        {{P06576, Protein}}, {{Q99798, Protein}}, {{P38646, Protein}}, {{P10809, Protein}}}}}|>,
  G3S1 → <|GO:0006032 → {{0.000505663, 0.0037556, True}, {2, 5, 19774, 1},
      {{chitin catabolic process, biological_process}, {{{Q01459, Protein}}}}}|>|>,
 SpikeMin → <|G1S1 → <|GO:0005829 → {{1.03428×10^-7, 0.0000587469, True}, {35, 5035, 19774, 24},
      {{cytosol, cellular_component}, {{{O00116, Protein}}, {{O94925, Protein}}, {{Q99816, Protein}},
        {{Q96CW5, Protein}}, {{Q9UQ13, Protein}}, {{Q08209, Protein}}, {{P49591, Protein}}, {{Q9UNH7,
          Protein}}, {{Q16512, Protein}}, {{Q9UL15, Protein}}, {{P60953, Protein}}, {{Q93100, Protein}},
        {{P02794, Protein}}, {{Q9Y5K5, Protein}}, {{O15144, Protein}}, {{P49720, Protein}},
        {{Q6N069, Protein}}, {{Q8ND71, Protein}}, {{O00231, Protein}}, {{P67775, Protein}},
        {{P10398, Protein}}, {{Q9UKV8, Protein}}, {{P45985, Protein}}, {{Q9UPN7, Protein}}}}}|>,
```

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```
    G1S2 → ⟨|GO:0005829 → {{2.56612×10^-13, 1.17015×10^-10, True}, {32, 5035, 19774, 28},
        {{cytosol, cellular_component}, {{{P60174, Protein}}, {{Q92598, Protein}}, {{Q9NQR4, Protein}},
          {{P50395, Protein}}, {{Q96KP4, Protein}}, {{Q9UEW8, Protein}}, {{P29350, Protein}}, {{Q16851,
            Protein}}, {{Q99614, Protein}}, {{Q9UHJ6, Protein}}, {{P29218, Protein}}, {{P50991, Protein}},
          {{O75347, Protein}}, {{O95336, Protein}}, {{P48147, Protein}}, {{Q8IUI8, Protein}},
          {{P31948, Protein}}, {{Q99497, Protein}}, {{Q15172, Protein}}, {{O00154, Protein}},
          {{P41240, Protein}}, {{Q9HAB8, Protein}}, {{Q9UNZ2, Protein}}, {{Q9Y2Z0, Protein}},
          {{P31939, Protein}}, {{P17987, Protein}}, {{P30566, Protein}}, {{P63151, Protein}}}}}}|⟩,
    G1S3 → ⟨|GO:0035456 → {{0.00151645, 0.0241862, True}, {3, 10, 19774, 1},
        {{response to interferon-beta, biological_process}, {{{P13164, Protein}}}}}}|⟩|⟩,
  f1 → ⟨|G1S1 → ‹|GO:0051707 → {{0.00121329, 0.0262915, True}, {8, 3, 19774, 1},
        {{response to other organism, biological_process}, {{{O43516, Protein}}}}}}|›,
    G1S2 → ⟨|GO:0019829 → {{0.000404541, 0.0125613, True}, {4, 2, 19774, 1},
        {{ATPase-coupled cation transmembrane transporter activity, molecular_function},
         {{{Q9Y2Q0, Protein}}}}}}|⟩,
    G2S1 → ⟨|GO:0005654 → {{1.70148×10^-7, 0.0000624443, True}, {26, 3142, 19774, 16},
        {{nucleoplasm, cellular_component}, {{{O00267, Protein}}, {{Q92499, Protein}}, {{P51531, Protein}},
          {{Q13151, Protein}}, {{Q9BTE3, Protein}}, {{O75792, Protein}}, {{Q86YP4, Protein}}, {{Q9UQ35,
            Protein}}, {{Q15291, Protein}}, {{Q9H0D6, Protein}}, {{O75643, Protein}}, {{P12956, Protein}},
          {{Q9NYB0, Protein}}, {{Q9H4Z3, Protein}}, {{O00273, Protein}}, {{Q14653, Protein}}}}}}|⟩,
    G2S2 → ⟨|GO:0016020 → {{6.94216×10^-6, 0.00370017, True}, {24, 1974, 19774, 11},
        {{membrane, cellular_component}, {{{P04844, Protein}}, {{Q13217, Protein}}, {{P11021, Protein}},
          {{Q14165, Protein}}, {{P42892, Protein}}, {{Q99439, Protein}}, {{P54920, Protein}},
          {{P09496, Protein}}, {{P60660, Protein}}, {{P33176, Protein}}, {{Q07021, Protein}}}}}}|⟩,
    G3S1 → ⟨|GO:0090263 → {{0.0000295074, 0.0063441, True}, {9, 142, 19774, 3},
        {{positive regulation of canonical Wnt signaling pathway, biological_process},
         {{{O00571, Protein}}, {{P40306, Protein}}, {{P55036, Protein}}}}}}|⟩,
    G3S2 → ‹|GO:0070062 → {{0.0000332807, 0.00382728, True}, {11, 2095, 19774, 7}, {{extracellular exosome,
          cellular_component}, {{{Q709C8, Protein}}, {{Q68D91, Protein}}, {{P32189, Protein}},
          {{Q01518, Protein}}, {{Q9NVJ2, Protein}}, {{Q9BWS9, Protein}}, {{Q96AT9, Protein}}}}}}|›|⟩,
  f5 → ⟨|G1S1 → ‹|GO:0035747 → {{0.000101143, 0.00154749, True}, {1, 2, 19774, 1},
        {{natural killer cell chemotaxis, biological_process}, {{{O00329, Protein}}}}}}|›,
    G1S2 → ‹|GO:0099041 → {{0.000606765, 0.0115889, True}, {3, 4, 19774, 1},
        {{vesicle tethering to Golgi, biological_process}, {{{Q9NUY8, Protein}}}}}}|›,
    G2S1 → ‹|GO:0002183 → {{0.000303413, 0.0093163, True}, {2, 3, 19774, 1},
        {{cytoplasmic translational initiation, biological_process}, {{{P60842, Protein}}}}}}|›,
    G2S2 → ⟨|GO:0008253 → {{0.000708, 0.002124, True}, {1, 14, 19774, 1},
        {{5'-nucleotidase activity, molecular_function}, {{{Q5TFE4, Protein}}}}}}|⟩|⟩,
  f6 → ⟨|G1S1 → ‹|GO:0006909 → {{0.000113129, 0.0154987, True}, {6, 55, 19774, 2},
        {{phagocytosis, biological_process}, {{{Q14696, Protein}}, {{P50570, Protein}}}}}}|›,
    G1S2 → ⟨|GO:0022625 → {{4.89955×10^-10, 1.56785×10^-7, True}, {29, 66, 19774, 6},
        {{cytosolic large ribosomal subunit, cellular_component}, {{{Q02543, Protein}}, {{P62888, Protein}},
          {{P27635, Protein}}, {{P61353, Protein}}, {{P26373, Protein}}, {{P35268, Protein}}}}}}|⟩,
    G2S1 → ⟨|GO:0046961 → {{0.00222396, 0.0209181, True}, {2, 22, 19774, 1},
        {{proton-transporting ATPase activity, rotational mechanism, molecular_function},
         {{{Q9Y5K8, Protein}}}}}}|⟩|⟩,
  f7 → ⟨|G1S1 → ‹|GO:0030133 → {{0.000738401, 0.0227526, True}, {9, 91, 19774, 2},
        {{transport vesicle, cellular_component}, {{{O14579, Protein}}, {{P13987, Protein}}}}}}|›,
    G1S2 → ‹|GO:0042645 → {{0.000128264, 0.0118316, True}, {8, 43, 19774, 2},
        {{mitochondrial nucleoid, cellular_component}, {{{Q9BQ52, Protein}}, {{Q8IYB8, Protein}}}}}}|›,
    G2S1 → ⟨|GO:0051020 → {{0.00171943, 0.0168403, True}, {1, 34, 19774, 1},
        {{GTPase binding, molecular_function}, {{{P62879, Protein}}}}}}|⟩|⟩|⟩
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Options (24)

AdditionalFilter (4)

In[1]:=
```
Needs["MathIOmica`"]
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AdditionalFilter provides additional filtering that may be applied to the standard output structure to be returned. This is typically implemented by a Select statement.

Let's do a GO analysis for a group of genes, annotated with their "Gene Symbol":

```
In[2]:= goExample1 =
  GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
    "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}]

Out[2]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
  GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
  GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
    {{protein serine/threonine kinase activity, molecular_function},
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
  GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
    {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
  GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
    {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
   {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
     {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
  GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
    {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
     {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
    {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
    {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
  GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
    {{regulation of signal transduction by p53 class mediator, biological_process},
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    {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
   {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
    {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
  {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
   {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
   {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
  {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
    {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
   {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
   {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
   {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
   {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
   {{negative regulation of NF-kappaB transcription factor activity, biological_process},
    {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
   {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
   {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
   {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
   {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
   {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
   {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
   {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
    {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
   {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
     {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
   {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
   {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
   {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
   {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
   {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
   {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
     {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
   {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
   {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
    {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
   {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
   {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
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GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19 774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19 774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19 774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19 774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19 774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19 774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19 774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19 774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19 774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19 774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19 774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19 774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19 774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19 774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19 774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19 774, 2},
  {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{B-1 B cell differentiation, biological_process}, {{MALT1}}}},
GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{positive regulation of Fc receptor mediated stimulatory signaling pathway, biological_process},
   {{LYN}}}}, GO:0061847 → {{0.00202189, 0.0130219, True},
  {20, 2, 19 774, 1}, {{response to cholecystokinin, biological_process}, {{CHUK}}}},
GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{negative regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0070668 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{positive regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{cellular response to bacterial lipopeptide, biological_process}, {{TIRAP}}}},
GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{establishment of RNA localization to telomere, biological_process}, {{ATM}}}},
GO:0097695 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{establishment of protein-containing complex localization to telomere, biological_process}, {{ATM}}}},
GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
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  {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of single strand break repair, biological_process}, {{PARP1}}}},
GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
  {{ATP binding, molecular_function}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {LYN}, {ATM}, {IRAK4}}}},
GO:0016301 → {{0.00292933, 0.0149088, True}, {20, 80, 19774, 2},
  {{kinase activity, molecular_function}, {{CSNK2A1}, {LYN}}}},
GO:0002331 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{tolerance induction to self antigen, biological_process}, {{LYN}}}},
GO:0002553 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{histamine secretion by mast cell, biological_process}, {{LYN}}}},
GO:0002762 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of myeloid leukocyte differentiation, biological_process}, {{LYN}}}},
GO:0002774 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{Fc receptor mediated inhibitory signaling pathway, biological_process}, {{LYN}}}},
GO:0002902 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{regulation of B cell apoptotic process, biological_process}, {{LYN}}}},
GO:0004677 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{DNA-dependent protein kinase activity, molecular_function}, {{ATM}}}},
GO:0008384 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{IkappaB kinase activity, molecular_function}, {{CHUK}}}},
GO:0010956 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of calcidiol 1-monooxygenase activity, biological_process}, {{NFKB1}}}},
GO:0030592 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{DNA ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:2001170 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0000724 → {{0.00314887, 0.0153472, True}, {20, 83, 19774, 2},
  {{double-strand break repair via homologous recombination, biological_process}, {{PARP1}, {ATM}}}},
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GO:0010957 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:1900127 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0016363 → {{0.00536146, 0.0202836, True}, {20, 109, 19774, 2},
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GO:0010884 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
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GO:0036092 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
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GO:0032731 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of interleukin-1 beta production, biological_process}, {{MALT1}}}},
GO:0045410 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of interleukin-6 biosynthetic process, biological_process}, {{TIRAP}}}},
GO:0060252 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of glial cell proliferation, biological_process}, {{LYN}}}},
GO:0071044 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{histone mRNA catabolic process, biological_process}, {{ATM}}}},
GO:0010744 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKB1}}}}, GO:0010875 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cholesterol efflux, biological_process}, {{NFKBIA}}}},
GO:0016540 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein autoprocessing, biological_process}, {{PARP1}}}},
GO:0019789 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{SUMO transferase activity, molecular_function}, {{PIAS4}}}},
GO:0032270 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cellular protein metabolic process, biological_process}, {{NFKBIA}}}},
GO:0034142 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{toll-like receptor 4 signaling pathway, biological_process}, {{NFKBIA}}}},
GO:0071354 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{cellular response to interleukin-6, biological_process}, {{NFKB1}}}},
GO:1901222 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{regulation of NIK/NF-kappaB signaling, biological_process}, {{NFKBIA}}}},
GO:1990404 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein ADP-ribosylase activity, molecular_function}, {{PARP1}}}},
GO:2000679 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of transcription regulatory region DNA binding, biological_process}, {{PARP1}}}},
GO:0042493 → {{0.0163579, 0.0341685, True}, {20, 195, 19774, 2},
  {{response to drug, biological_process}, {{CHUK}, {LYN}}}},
GO:0004724 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{magnesium-dependent protein serine/threonine phosphatase activity, molecular_function}, {{TAB1}}}},
GO:0008340 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{determination of adult lifespan, biological_process}, {{ATM}}}},
GO:0034162 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{toll-like receptor 9 signaling pathway, biological_process}, {{IRAK4}}}},
GO:1903146 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{regulation of autophagy of mitochondrion, biological_process}, {{CSNK2A2}}}},
GO:0010469 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of signaling receptor activity, biological_process}, {{PLAU}}}},
GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid cell differentiation, biological_process}, {{TIRAP}}}},
GO:0031668 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{cellular response to extracellular stimulus, biological_process}, {{LYN}}}},
GO:0043011 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid dendritic cell differentiation, biological_process}, {{LTBR}}}},
GO:0043537 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of blood vessel endothelial cell migration, biological_process}, {{CSNK2B}}}},
```

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```
GO:0045638 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of myeloid cell differentiation, biological_process}, {{NFKBIA}}}}, GO:0090734 →
 {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1}, {{site of DNA damage, cellular_component}, {{PARP1}}}},
GO:1903827 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of cellular protein localization, biological_process}, {{PARP1}}}},
GO:0010008 → {{0.0188076, 0.0374078, True}, {20, 210, 19774, 2},
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196568, 0.0385302, True}, {20, 215, 19774, 2},
  {{regulation of apoptotic process, biological_process}, {{MALT1}, {ATM}}}},
GO:0002756 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{macrophage differentiation, biological_process}, {{PARP1}}}},
GO:0032991 → {{0.0204617, 0.0395348, True}, {20, 588, 19774, 3},
  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
 {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1}, {{aorta development, biological_process}, {{TAB1}}}},
GO:0042098 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{T cell proliferation, biological_process}, {{MALT1}}}},
GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
 {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
```

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```
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
```

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```
    {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
  GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
    {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
  GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{DNA damage checkpoint, biological_process}, {{ATM}}}},
  GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
  GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
  GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
  GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|⟩
```

We can obtain the first 10 results for the data:

```
In[3]:= Query[1 ;; 10]@goExample1
```

```
Out[3]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
  GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}|⟩
```

Now let's apply a filter, to only select biological process ontologies. In the output this label is in the 3rd list, 1st sublist, 2nd component:

```
In[4]:= goExample1FilteredBP = GOAnalysis[
    {"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B",
     "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
    AdditionalFilter → Select[MatchQ[#[[3, 1, 2]], "biological_process"] &]];
```

We can see that the results are now filtered:

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In[5]:=
```
Query[1 ;; 10]@goExample1FilteredBP
```

Out[5]=
```
<|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
  GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
  GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}}|>
```

In[1]:=
```
Needs["MathIOmica`"]
```

Now let's apply a different filter, to only select cellular component ontologies. In the output this label is also in the 3rd list, 1st sublist, 2nd component:

In[2]:=
```
goExample1FilteredCC = GOAnalysis[
   {"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B",
    "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
   AdditionalFilter → Select[MatchQ[#[[3, 1, 2]], "cellular_component"] &]];
```

We can see that the results are now filtered:

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```
In[3]:= Query[1 ;; 10]@goExample1FilteredCC

Out[3]= ⟨|GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
    {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
  GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
    {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
      {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
  GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
    {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
      {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
  GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
     {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
  GO:0005829 → {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12},
    {{cytosol, cellular_component}, {{TAB1}, {MALT1}, {TIRAP}, {CHUK},
      {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
  GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
    {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
      {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
  GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
    {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
  GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{integrin alpha2-beta1 complex, cellular_component}, {{LYN}}}}|⟩
```

```
In[1]:= Needs["MathIOmica`"]
```

Now let's apply a different filter, to only select ontology results for which "NFKB2" is included in the membership ontologies. In the output this membership list is the 3rd list, 2nd sublist,:

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In[2]:=
```
goExample1FilteredMember =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
   "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
  AdditionalFilter → Select[MemberQ[#[[3, 2]], {"NFKB2"}] &]]
```

Out[2]=
```
⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}}, GO:0005515 →
   {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
    {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
      {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
  GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
    {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
      {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
  GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
    {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
  GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
     {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
  GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
    {{positive regulation of transcription by RNA polymerase II, biological_process},
     {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}}, GO:0005829 →
   {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
      {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
  GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
    {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
  GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
    {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
  GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
    {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
  GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
    {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
  GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
    {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
  GO:0002467 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
    {{germinal center formation, biological_process}, {{NFKB2}}}},
  GO:0001228 → {{0.00958954, 0.0268386, True}, {20, 443, 19774, 3},
    {{DNA-binding transcription activator activity, RNA polymerase II-specific, molecular_function},
     {{PARP1}, {NFKB1}, {NFKB2}}}}|⟩
```

In[1]:=
```
Needs["MathIOmica`"]
```

Now let's apply a filter, to only select results for which the pathway text inlcudes the term "NF-kappaB"". In the output this would mean checking for this pattern in the in the 3rd list, 1st sublist, 1st component

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```
In[2]:= goExample1FilteredText =
         GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
           "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
          AdditionalFilter → Select[StringMatchQ[#[[3, 1, 1]], ___ ~~ "NF-kappaB" ~~ ___] &]]

Out[2]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
           {{positive regulation of NF-kappaB transcription factor activity, biological_process},
            {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
         GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
           {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
            {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
         GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
           {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
         GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
           {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
         GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
           {{negative regulation of NF-kappaB transcription factor activity, biological_process},
            {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
           {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
         GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
           {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
         GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
           {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
         GO:0007253 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
           {{cytoplasmic sequestering of NF-kappaB, biological_process}, {{NFKBIA}}}},
         GO:1901222 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
           {{regulation of NIK/NF-kappaB signaling, biological_process}, {{NFKBIA}}}},
         GO:0051059 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
           {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}}|⟩
```

AugmentDictionary (1)

```
In[1]:= Needs["MathIOmica`"]
```

AugmentDictionary provides a choice whether or not to augment the current ConstantGeneDictionary variable or create a new one. In the example below gene dictionary already exists, and set a simple dictionary as an example (please note that this will reset your variable if you have one already created, so use with caution):

```
In[2]:= ConstantGeneDictionary =
          ⟨|"humanExample" → ⟨|"UCSC ID" → {"uc001aaa.3", "uc010nxr.1", "uc010nxq.1", "uc001aal.1", "uc001aaq.2",
               "uc001aar.2", "uc001aau.3", "uc021oeh.1", "uc009vjk.2", "uc021oei.1", "uc010nxu.2", "uc001aax.1",
               "uc001abb.3", "uc001abp.2", "uc021oem.2", "uc009vjn.2", "uc009vjo.2", "uc031pjk.1", "uc031pjj.1",
               "uc001abu.1", "uc001abw.1", "uc031pjv.1", "uc031pkd.1", "uc031pkk.1", "uc031pkl.1"},
             "Gene Symbol" → {"DDX11L1", "DDX11L1", "DDX11L1", "OR4F5", "DQ597235", "DQ599768",
               "LOC100132062", "LOC100133331", "LOC100133331", "LOC388312", "OR4F29", "BC036251",
               "M37726", "LOC643837", "LOC643837", "LOC643837", "LOC643837", "LOC643837",
               "LOC643837", "AK056486", "SAMD11", "SAMD11", "SAMD11", "SAMD11", "SAMD11"}|⟩|⟩;
```

If we now run a standard analysis with the `AugmentDictionary` option set to True we have:

```
In[3]:= goExampleAugmentTrue = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
          "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
          "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, AugmentDictionary → True]

Out[3]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
           {{positive regulation of NF-kappaB transcription factor activity, biological_process},
            {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
```

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```
GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
  {{interleukin-1-mediated signaling pathway, biological_process},
   {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
  {{stimulatory C-type lectin receptor signaling pathway, biological_process},
   {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
  {{tumor necrosis factor-mediated signaling pathway, biological_process},
   {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
  {{Fc-epsilon receptor signaling pathway, biological_process},
   {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
 {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
   {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
  {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
   {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
  {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
  {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
  {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
  {{protein serine/threonine kinase activity, molecular_function},
   {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
  {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
  {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
 {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
   {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
   {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
  {{regulation of signal transduction by p53 class mediator, biological_process},
   {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
```

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```
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
```

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```
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
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GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
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  {{positive regulation of lipid storage, biological_process}, {{NFKB1}}}},
GO:0031639 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{plasminogen activation, biological_process}, {{PLAU}}}},
GO:0035631 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{CD40 receptor complex, cellular_component}, {{CHUK}}}},
GO:0042994 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{cytoplasmic sequestering of transcription factor, biological_process}, {{NFKBIA}}}},
GO:0050855 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{regulation of B cell receptor signaling pathway, biological_process}, {{LYN}}}},
GO:0070213 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{protein auto-ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0090073 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{positive regulation of protein homodimerization activity, biological_process}, {{TIRAP}}}},
GO:1904385 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
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  {{cellular response to angiotensin, biological_process}, {{NFKB1}}}},
GO:0043312 → {{0.0119849, 0.0290293, True}, {20, 481, 19774, 3},
  {{neutrophil degranulation, biological_process}, {{CSNK2B}, {NFKB1}, {PLAU}}}},
GO:0001666 → {{0.0120525, 0.0290293, True}, {20, 166, 19774, 2},
  {{response to hypoxia, biological_process}, {{ATM}, {PLAU}}}},
GO:0007252 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{I-kappaB phosphorylation, biological_process}, {{CHUK}}}},
GO:0016572 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{histone phosphorylation, biological_process}, {{ATM}}}},
GO:0032495 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{response to muramyl dipeptide, biological_process}, {{NFKBIA}}}},
GO:0033148 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of intracellular estrogen receptor signaling pathway, biological_process},
   {{PARP1}}}}, GO:0042359 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{vitamin D metabolic process, biological_process}, {{PIAS4}}}}, GO:0042805 →
 {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1}, {{actinin binding, molecular_function}, {{NFKB1}}}},
GO:0043517 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of DNA damage response, signal transduction by p53 class mediator,
    biological_process}, {{ATM}}}}, GO:0051168 →
 {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1}, {{nuclear export, biological_process}, {{MALT1}}}},
GO:0060391 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of SMAD protein signal transduction, biological_process}, {{PARP1}}}},
GO:0090399 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{replicative senescence, biological_process}, {{ATM}}}},
GO:0097028 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{dendritic cell differentiation, biological_process}, {{LYN}}}},
GO:0043066 → {{0.0122555, 0.0293372, True}, {20, 485, 19774, 3},
  {{negative regulation of apoptotic process, biological_process}, {{MALT1}, {NFKB1}, {NFKBIA}}}},
GO:0046982 → {{0.0123921, 0.0295335, True}, {20, 487, 19774, 3},
  {{protein heterodimerization activity, molecular_function}, {{TIRAP}, {CHUK}, {NFKB1}}}},
GO:0007596 → {{0.0126116, 0.029925, True}, {20, 170, 19774, 2},
  {{blood coagulation, biological_process}, {{LYN}, {PLAU}}}},
GO:0046777 → {{0.0128955, 0.0302244, True}, {20, 172, 19774, 2},
  {{protein autophosphorylation, biological_process}, {{LYN}, {ATM}}}},
GO:0010745 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{negative regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKBIA}}}}, GO:0044030 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{regulation of DNA methylation, biological_process}, {{PARP1}}}}, GO:0048599 →
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GO:0050777 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{negative regulation of immune response, biological_process}, {{LYN}}}},
GO:0051279 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{regulation of release of sequestered calcium ion into cytosol, biological_process}, {{LYN}}}},
GO:0005149 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{interleukin-1 receptor binding, molecular_function}, {{IRAK4}}}}, GO:0016580 →
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GO:0032743 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{positive regulation of interleukin-2 production, biological_process}, {{MALT1}}}},
GO:0036092 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{phosphatidylinositol-3-phosphate biosynthetic process, biological_process}, {{ATM}}}},
GO:0045078 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{positive regulation of interferon-gamma biosynthetic process, biological_process}, {{TNFRSF13C}}}},
GO:0051146 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{striated muscle cell differentiation, biological_process}, {{CHUK}}}},
GO:0060397 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{growth hormone receptor signaling pathway via JAK-STAT, biological_process}, {{LYN}}}},
GO:0000729 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{DNA double-strand break processing, biological_process}, {{ATM}}}},
GO:0005161 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{platelet-derived growth factor receptor binding, molecular_function}, {{LYN}}}}, GO:0016581 →
 {{0.0150698, 0.032874, True}, {20, 15, 19774, 1}, {{NuRD complex, cellular_component}, {{CSNK2A1}}}},
GO:0032731 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
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  {{positive regulation of interleukin-1 beta production, biological_process}, {{MALT1}}}},
GO:0045410 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of interleukin-6 biosynthetic process, biological_process}, {{TIRAP}}}},
GO:0060252 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of glial cell proliferation, biological_process}, {{LYN}}}},
GO:0071044 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{histone mRNA catabolic process, biological_process}, {{ATM}}}},
GO:0010744 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKB1}}}}, GO:0010875 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cholesterol efflux, biological_process}, {{NFKBIA}}}},
GO:0016540 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein autoprocessing, biological_process}, {{PARP1}}}},
GO:0019789 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{SUMO transferase activity, molecular_function}, {{PIAS4}}}},
GO:0032270 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cellular protein metabolic process, biological_process}, {{NFKBIA}}}},
GO:0034142 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{toll-like receptor 4 signaling pathway, biological_process}, {{NFKBIA}}}},
GO:0071354 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{cellular response to interleukin-6, biological_process}, {{NFKB1}}}},
GO:1901222 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{regulation of NIK/NF-kappaB signaling, biological_process}, {{NFKBIA}}}},
GO:1990404 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein ADP-ribosylase activity, molecular_function}, {{PARP1}}}},
GO:2000679 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of transcription regulatory region DNA binding, biological_process}, {{PARP1}}}},
GO:0042493 → {{0.0163579, 0.0341685, True}, {20, 195, 19774, 2},
  {{response to drug, biological_process}, {{CHUK}, {LYN}}}},
GO:0004724 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{magnesium-dependent protein serine/threonine phosphatase activity, molecular_function}, {{TAB1}}}},
GO:0008340 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{determination of adult lifespan, biological_process}, {{ATM}}}},
GO:0034162 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{toll-like receptor 9 signaling pathway, biological_process}, {{IRAK4}}}},
GO:1903146 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{regulation of autophagy of mitochondrion, biological_process}, {{CSNK2A2}}}},
GO:0010469 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of signaling receptor activity, biological_process}, {{PLAU}}}},
GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid cell differentiation, biological_process}, {{TIRAP}}}},
GO:0031668 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{cellular response to extracellular stimulus, biological_process}, {{LYN}}}},
GO:0043011 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid dendritic cell differentiation, biological_process}, {{LTBR}}}},
GO:0043537 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of blood vessel endothelial cell migration, biological_process}, {{CSNK2B}}}},
GO:0045638 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of myeloid cell differentiation, biological_process}, {{NFKBIA}}}}, GO:0090734 →
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GO:1903827 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of cellular protein localization, biological_process}, {{PARP1}}}},
GO:0010008 → {{0.0188076, 0.0374078, True}, {20, 210, 19774, 2},
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196568, 0.0385302, True}, {20, 215, 19774, 2},
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  {{regulation of apoptotic process, biological_process}, {{MALT1}, {ATM}}}},
GO:0002756 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{macrophage differentiation, biological_process}, {{PARP1}}}},
GO:0032991 → {{0.0204617, 0.0395348, True}, {20, 588, 19774, 3},
  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
 {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1}, {{aorta development, biological_process}, {{TAB1}}}},
GO:0042098 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{T cell proliferation, biological_process}, {{MALT1}}}},
GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
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GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
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GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
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GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
  {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{DNA damage checkpoint, biological_process}, {{ATM}}}},
GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

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We now check again the ConstantGeneDictionary :

In[4]:=
```
ConstantGeneDictionary
```

Out[4]=
```
<|humanExample →
  <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1, uc001aaq.2, uc001aar.2, uc001aau.3,
     uc021oeh.1, uc009vjk.2, uc021oei.1, uc010nxu.2, uc001aax.1, uc001abb.3,
     uc001abp.2, uc021oem.2, uc009vjn.2, uc009vjo.2, uc031pjk.1, uc031pjj.1,
     uc001abu.1, uc001abw.1, uc031pjv.1, uc031pkd.1, uc031pkk.1, uc031pkl.1},
   Gene Symbol → {DDX11L1, DDX11L1, DDX11L1, OR4F5, DQ597235, DQ599768, LOC100132062,
     LOC100133331, LOC100133331, ··· 7 ···, LOC643837, LOC643837, LOC643837,
     AK056486, SAMD11, SAMD11, SAMD11, SAMD11, SAMD11}|>, human → <| ··· 1 ··· |>|>
```

large output | show less | show more | show all | set size limit...

We see that this has augmented the previous dictionary with the "human" annotation used in the example. We now repeat with `AugmentDictionary` set to False:

In[5]:=
```
goExampleAugmentFalse = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, AugmentDictionary → False]
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Out[5]=
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<|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
   {{positive regulation of NF-kappaB transcription factor activity, biological_process},
    {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
 GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
   {{interleukin-1-mediated signaling pathway, biological_process},
    {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
   {{stimulatory C-type lectin receptor signaling pathway, biological_process},
    {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
 GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
   {{tumor necrosis factor-mediated signaling pathway, biological_process},
    {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
 GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
   {{Fc-epsilon receptor signaling pathway, biological_process},
    {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
  {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
    {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
 GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
   {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
    {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
 GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
   {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
 GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
   {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
 GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
   {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
 GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
   {{protein serine/threonine kinase activity, molecular_function},
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
 GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
   {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
 GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
   {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
 GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
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  {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
  {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
 {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
   {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
   {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
  {{regulation of signal transduction by p53 class mediator, biological_process},
   {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
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  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
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GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{B-1 B cell differentiation, biological_process}, {{MALT1}}}},
GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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  {{positive regulation of Fc receptor mediated stimulatory signaling pathway, biological_process},
   {{LYN}}}}, GO:0061847 → {{0.00202189, 0.0130219, True},
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GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of mast cell proliferation, biological_process}, {{LYN}}}},
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GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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  {{establishment of RNA localization to telomere, biological_process}, {{ATM}}}},
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  {{establishment of protein-containing complex localization to telomere, biological_process}, {{ATM}}}},
GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of single strand break repair, biological_process}, {{PARP1}}}},
GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
  {{ATP binding, molecular_function}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {LYN}, {ATM}, {IRAK4}}}},
GO:0016301 → {{0.00292933, 0.0149088, True}, {20, 80, 19774, 2},
  {{kinase activity, molecular_function}, {{CSNK2A1}, {LYN}}}},
GO:0002331 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{tolerance induction to self antigen, biological_process}, {{LYN}}}},
GO:0002553 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{histamine secretion by mast cell, biological_process}, {{LYN}}}},
GO:0002762 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002902 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0004677 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0008384 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0010956 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of calcidiol 1-monooxygenase activity, biological_process}, {{NFKB1}}}},
GO:0030592 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{DNA ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0035663 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{Toll-like receptor 2 binding, molecular_function}, {{TIRAP}}}},
GO:0070447 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of oligodendrocyte progenitor proliferation, biological_process}, {{LYN}}}},
GO:0071500 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{cellular response to nitrosative stress, biological_process}, {{ATM}}}},
GO:0099091 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{postsynaptic specialization, intracellular component, cellular_component}, {{LYN}}}},
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GO:0140031 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{phosphorylation-dependent protein binding, molecular_function}, {{LYN}}}},
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GO:1902174 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of keratinocyte apoptotic process, biological_process}, {{PIAS4}}}},
GO:1904044 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{response to aldosterone, biological_process}, {{PARP1}}}},
GO:2000630 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of miRNA metabolic process, biological_process}, {{NFKB1}}}},
GO:2000670 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:2001170 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of ATP biosynthetic process, biological_process}, {{PARP1}}}},
GO:0000724 → {{0.00314887, 0.0153472, True}, {20, 83, 19774, 2},
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GO:0010957 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0032648 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0048305 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0071359 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{cellular response to dsRNA, biological_process}, {{NFKB1}}}},
GO:0090330 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:1900127 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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  {{signaling receptor binding, molecular_function}, {{TNFSF13B}, {CSNK2B}, {LYN}}}},
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GO:0032042 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0043208 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0048273 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0000784 → {{0.00536146, 0.0202836, True}, {20, 109, 19774, 2},
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GO:0070431 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0010008 → {{0.0188076, 0.0374078, True}, {20, 210, 19774, 2},
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196568, 0.0385302, True}, {20, 215, 19774, 2},
  {{regulation of apoptotic process, biological_process}, {{MALT1}, {ATM}}}},
GO:0002756 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{macrophage differentiation, biological_process}, {{PARP1}}}},
GO:0032991 → {{0.0204617, 0.0395348, True}, {20, 588, 19774, 3},
  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
 {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1}, {{aorta development, biological_process}, {{TAB1}}}},
GO:0042098 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{T cell proliferation, biological_process}, {{MALT1}}}},
GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
```

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```
    {{TAB1}}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
   {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
   {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
  {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
   {{cellular response to virus, biological_process}, {{CHUK}}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
   {{cellular response to zinc ion, biological_process}, {{PARP1}}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
   {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
   {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
   {{protein ADP-ribosylation, biological_process}, {{PARP1}}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
   {{male meiotic nuclear division, biological_process}, {{ATM}}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
   {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
   {{oligodendrocyte development, biological_process}, {{LYN}}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
   {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
   {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
   {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
   {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
   {{skeletal muscle contraction, biological_process}, {{CHUK}}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
   {{gamma-tubulin binding, molecular_function}, {{LYN}}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
   {{coronary vasculature development, biological_process}, {{TAB1}}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
   {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
   {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}}, GO:0001816 →
  {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
   {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
   {{response to gamma radiation, biological_process}, {{PARP1}}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
   {{protein kinase activator activity, molecular_function}, {{TAB1}}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
   {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}}, GO:0042113 →
  {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
   {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
   {{ephrin receptor binding, molecular_function}, {{LYN}}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
   {{response to axon injury, biological_process}, {{LYN}}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
   {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
   {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
   {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
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```
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
  {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{DNA damage checkpoint, biological_process}, {{ATM}}}},
GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

We now check again the ConstantGeneDictionary to notice that the previous ConstantGeneDictionary has now been replaced with a new default one.

In[6]:=
```
ConstantGeneDictionary
```

Out[6]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1, uc001aaq.2, uc001aar.2, uc001aau.3,
    uc021oeh.1, uc009vjk.2, ··· 121565 ···, uc022cff.1, uc022cfk.1, uc031tkn.1, uc022cgh.1,
    uc022cha.1, uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, ... → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

AugmentDictionary is best used in advanced applications, especially when utilizing/analyzing data from multiple species.

BackgroundSet (1)

In[1]:=
```
Needs["MathIOmica`"]
```

BackgroundSet provides a list of IDs (e.g. gene accessions) that should be considered as the background for the calculation.

By default the BackgroundSet is set to All:

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```
In[2]:= goExample1 = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
          "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
          "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, BackgroundSet → All]

Out[2]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
          {{positive regulation of NF-kappaB transcription factor activity, biological_process},
           {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
        GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
          {{interleukin-1-mediated signaling pathway, biological_process},
           {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
        GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
          {{stimulatory C-type lectin receptor signaling pathway, biological_process},
           {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
        GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
          {{tumor necrosis factor-mediated signaling pathway, biological_process},
           {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
        GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
          {{Fc-epsilon receptor signaling pathway, biological_process},
           {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
         {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
           {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
        GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
          {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
           {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
        GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
          {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
        GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
          {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
        GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
          {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
        GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
          {{protein serine/threonine kinase activity, molecular_function},
           {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
        GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
          {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
        GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
          {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
        GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
          {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
        GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
          {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
        GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
          {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
         {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
           {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
        GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
          {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
           {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
          {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
        GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
          {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
        GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
          {{regulation of signal transduction by p53 class mediator, biological_process},
           {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
          {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
           {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
         {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
           {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
            {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
        GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
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  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
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GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
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GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
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GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
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GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
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GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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   {{LYN}}}}, GO:0061847 → {{0.00202189, 0.0130219, True},
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GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0070668 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of RNA localization to telomere, biological_process}, {{ATM}}}},
GO:0097695 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
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GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
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GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
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GO:0016301 → {{0.00292933, 0.0149088, True}, {20, 80, 19774, 2},
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GO:0002331 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0030592 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0071500 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0099091 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0140031 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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  {{Toll-like receptor 4 binding, molecular_function}, {{TIRAP}}}},
GO:0042159 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0043208 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0006954 → {{0.00567463, 0.0211305, True}, {20, 366, 19774, 3},
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GO:0000785 → {{0.00584929, 0.0211305, True}, {20, 114, 19774, 2},
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GO:0016032 → {{0.00593612, 0.0211305, True}, {20, 372, 19774, 3},
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GO:1990266 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
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GO:0007143 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
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GO:0033235 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
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GO:0051901 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
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GO:0071481 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{cellular response to X-ray, biological_process}, {{ATM}}}},
GO:1902741 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
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  {{plasminogen activation, biological_process}, {{PLAU}}}},
GO:0035631 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{CD40 receptor complex, cellular_component}, {{CHUK}}}},
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GO:0050855 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
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GO:0046982 → {{0.0123921, 0.0295335, True}, {20, 487, 19774, 3},
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  {{blood coagulation, biological_process}, {{LYN}, {PLAU}}}},
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GO:0051146 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
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GO:0060397 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
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  {{growth hormone receptor signaling pathway via JAK-STAT, biological_process}, {{LYN}}}},
GO:0000729 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
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GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
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GO:0045638 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
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GO:1903827 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
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GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
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GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
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GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
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GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
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GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
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GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
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GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
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GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
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GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
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GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
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    {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|⟩
```

In a rather specialized example, let's limit the background to be the following list of genes (relating to KEGG "NFKB" pathway), e.g. from conducting an experiment using an array with only these probes included.

```
In[3]:= backgroundExample = {"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
    "CSNK2A2", "CSNK2B", "TICAM1", "TAB2", "DDX58", "LY96", "TAB3", "LAT", "CXCL2", "BLNK", "BIRC2",
    "BIRC3", "XIAP", "ICAM1", "TICAM2", "IKBKB", "IL1B", "IL1R1", "IL8", "IRAK1", "CCL4L2",
    "LBP", "LCK", "LTA", "LTB", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
    "NFKBIA", "IRAK4", "PIAS4", "PLAU", "PLCG1", "PLCG2", "PIDD", "PRKCB", "PRKCQ", "PTGS2",
    "BCL2", "BCL2A1", "RELA", "RELB", "BCL2L1", "CCL4", "CCL13", "CCL19", "CCL21", "CXCL12",
    "SYK", "MAP3K7", "BTK", "TLR4", "TNF", "TNFAIP3", "TNFRSF1A", "TRAF1", "TRAF2", "TRAF3",
    "TRAF5", "TRAF6", "UBE2I", "VCAM1", "ZAP70", "TRIM25", "CARD11", "IKBKG", "TNFSF11", "TRADD",
    "RIPK1", "TNFSF14", "TNFRSF11A", "CFLAR", "BCL10", "MAP3K14", "CD14", "CD40", "CD40LG"};
```

We need to first convert these to UniProt IDs, since the MathIOmica GO annotation is based on UniProt IDs. We can use

```
In[4]:= backgroundExampleUniprot = Query[Values /* Flatten /* Union] @
    GeneTranslation[backgroundExample, "UniProt ID", ConstantGeneDictionary, InputID → {"Gene Symbol"}]

Out[4]= {A1L159, A2A284, A6NHG8, B0QYN7, B1AMX9, B3KRB7, B3KWW1, B4DF52, B4DIR9, B4DU08, B4DUJ4, B4DWM0, B4E0A2,
  B5M0B5, B7WPI0, B8ZZW4, C7C5T6, C9JCG6, C9JHD5, C9JK38, D3DR86, D3DWY2, D3YTB5, E5RJJ7, E7ESM2,
  E7ESS4, E7ET53, E9PAP3, E9PDD1, F5GXE7, F5H061, F5H1P7, F5H5W6, F8W9A9, G5E9K3, H0YDU7, H3BQQ9,
  H7BYN8, I4EC36, I4EC38, I4EC39, J3KPU4, J3KQ87, J3KQJ6, O00206, O00463, O00585, O14788, O14920,
  O14920-2, O14920-4, O15111, O15519, O15519-11, O15519-12, O15519-2, O15519-3, O15519-4, O15519-7,
  O15519-8, O43318, O43318-2, O43318-3, O43318-4, O43557, O43557-2, O43561, O43561-2, O75293,
  O95786, O95786-2, O95999, P00749, P00749-2, P01374, P01375, P01584, P05362, P05771, P05771-2,
  P06239, P06239-3, P07948, P07948-2, P08571, P09874, P10145, P10415, P13236, P14778, P16885,
  P18428, P19174, P19320, P19320-2, P19438, P19438-3, P19784, P19838, P19838-2, P19838-3, P19875,
  P21580, P25942, P25942-2, P25963, P29965, P35354, P36941, P43403, P43403-3, P43405, P43405-2,
  P48061, P48061-3, P48061-4, P51617, P51617-2, P51617-4, P58753, P58753-2, P63279, P67870, P68400,
  P98170, Q00653, Q00653-4, Q01201, Q04206, Q04206-4, Q04759, Q04759-2, Q06187, Q06643, Q06643-2,
  Q07817, Q12933, Q12933-3, Q12933-4, Q13077, Q13114, Q13114-2, Q13315, Q13489, Q13490, Q13546,
  Q13546-2, Q14258, Q15628, Q15750, Q15750-2, Q16548, Q16548-2, Q2MD49, Q2MD54, Q2MD59, Q2TAM5,
  Q32ND9, Q3L8U2, Q3MS96, Q45NE6, Q572P5, Q573B4, Q59FT7, Q59GL9, Q5JY90, Q5TE63, Q68DE6, Q6P7P1,
  Q6ZMZ1, Q86XR7, Q8IUC6, Q8N2W9, Q8N5C8, Q8N5C8-2, Q8NHW4, Q8WV28, Q8WV28-2, Q96RJ3, Q99558, Q99616,
  Q99731, Q99836-3, Q99836-4, Q9BXL7, Q9HB75, Q9HB75-2, Q9HB75-3, Q9HB75-5, Q9NWZ3, Q9NYJ8, Q9P0L3,
  Q9UDY8, Q9UDY8-2, Q9UG54, Q9Y275, Q9Y275-2, Q9Y4K3, Q9Y6K9, Q9Y6K9-2, Q9Y6K9-3, Q9Y6Q6, Q9Y6Y9}
```

We see that by using the background, since the set is already enriched in NFKB pathway genes the significant result list is no longer available:

```
In[5]:= goExampleBackground = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C",
    "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1",
    "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, BackgroundSet → backgroundExampleUniprot]

Out[5]= <| |>
```

FilterSignificant (1)

```
In[1]:= Needs["MathIOmica`"]
```

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`FilterSignificant` is an option, which is by default set to True, and filters data based on whether the enrichment analysis is statistically significant or not.

```
In[2]:= goExampleFilterSignificantOn =
  GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
    "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM",
    "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, FilterSignificant → True]

Out[2]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
  GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
  GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
    {{protein serine/threonine kinase activity, molecular_function},
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
  GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
    {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
  GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
    {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
   {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
     {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
  GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
    {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
     {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
    {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
    {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
  GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
    {{regulation of signal transduction by p53 class mediator, biological_process},
     {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
    {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
```

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```
    {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
  {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
  {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
    {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
    {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
    {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
     {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
     {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
    {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
```

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GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
  {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{B-1 B cell differentiation, biological_process}, {{MALT1}}}},
GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of Fc receptor mediated stimulatory signaling pathway, biological_process},
   {{LYN}}}}, GO:0061847 → {{0.00202189, 0.0130219, True},
  {20, 2, 19774, 1}, {{response to cholecystokinin, biological_process}, {{CHUK}}}},
GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0070668 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{cellular response to bacterial lipopeptide, biological_process}, {{TIRAP}}}},
GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of RNA localization to telomere, biological_process}, {{ATM}}}},
GO:0097695 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of protein-containing complex localization to telomere, biological_process}, {{ATM}}}},
GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
```

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GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of single strand break repair, biological_process}, {{PARP1}}}},
GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
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  {{negative regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKBIA}}}}, GO:0044030 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{regulation of DNA methylation, biological_process}, {{PARP1}}}}, GO:0048599 →
 {{0.013073, 0.0302244, True}, {20, 13, 19774, 1}, {{oocyte development, biological_process}, {{ATM}}}},
GO:0050777 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{negative regulation of immune response, biological_process}, {{LYN}}}},
GO:0051279 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{regulation of release of sequestered calcium ion into cytosol, biological_process}, {{LYN}}}},
GO:0005149 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{interleukin-1 receptor binding, molecular_function}, {{IRAK4}}}}, GO:0016580 →
 {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1}, {{Sin3 complex, cellular_component}, {{CSNK2A1}}}},
GO:0032743 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{positive regulation of interleukin-2 production, biological_process}, {{MALT1}}}},
GO:0036092 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
```

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```
  {{phosphatidylinositol-3-phosphate biosynthetic process, biological_process}, {{ATM}}}},
GO:0045078 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{positive regulation of interferon-gamma biosynthetic process, biological_process}, {{TNFRSF13C}}}},
GO:0051146 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{striated muscle cell differentiation, biological_process}, {{CHUK}}}},
GO:0060397 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{growth hormone receptor signaling pathway via JAK-STAT, biological_process}, {{LYN}}}},
GO:0000729 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{DNA double-strand break processing, biological_process}, {{ATM}}}},
GO:0005161 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{platelet-derived growth factor receptor binding, molecular_function}, {{LYN}}}}, GO:0016581 →
 {{0.0150698, 0.032874, True}, {20, 15, 19774, 1}, {{NuRD complex, cellular_component}, {{CSNK2A1}}}},
GO:0032731 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of interleukin-1 beta production, biological_process}, {{MALT1}}}},
GO:0045410 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of interleukin-6 biosynthetic process, biological_process}, {{TIRAP}}}},
GO:0060252 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of glial cell proliferation, biological_process}, {{LYN}}}},
GO:0071044 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{histone mRNA catabolic process, biological_process}, {{ATM}}}},
GO:0010744 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKB1}}}}, GO:0010875 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cholesterol efflux, biological_process}, {{NFKBIA}}}},
GO:0016540 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein autoprocessing, biological_process}, {{PARP1}}}},
GO:0019789 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{SUMO transferase activity, molecular_function}, {{PIAS4}}}},
GO:0032270 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cellular protein metabolic process, biological_process}, {{NFKBIA}}}},
GO:0034142 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{toll-like receptor 4 signaling pathway, biological_process}, {{NFKBIA}}}},
GO:0071354 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{cellular response to interleukin-6, biological_process}, {{NFKB1}}}},
GO:1901222 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{regulation of NIK/NF-kappaB signaling, biological_process}, {{NFKBIA}}}},
GO:1990404 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein ADP-ribosylase activity, molecular_function}, {{PARP1}}}},
GO:2000679 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of transcription regulatory region DNA binding, biological_process}, {{PARP1}}}},
GO:0042493 → {{0.0163579, 0.0341685, True}, {20, 195, 19774, 2},
  {{response to drug, biological_process}, {{CHUK}, {LYN}}}},
GO:0004724 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{magnesium-dependent protein serine/threonine phosphatase activity, molecular_function}, {{TAB1}}}},
GO:0008340 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{determination of adult lifespan, biological_process}, {{ATM}}}},
GO:0034162 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{toll-like receptor 9 signaling pathway, biological_process}, {{IRAK4}}}},
GO:1903146 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{regulation of autophagy of mitochondrion, biological_process}, {{CSNK2A2}}}},
GO:0010469 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of signaling receptor activity, biological_process}, {{PLAU}}}},
GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid cell differentiation, biological_process}, {{TIRAP}}}},
GO:0031668 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{cellular response to extracellular stimulus, biological_process}, {{LYN}}}},
GO:0043011 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid dendritic cell differentiation, biological_process}, {{LTBR}}}},
GO:0043537 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of blood vessel endothelial cell migration, biological_process}, {{CSNK2B}}}},
GO:0045638 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
```

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```
  {{negative regulation of myeloid cell differentiation, biological_process}, {{NFKBIA}}}}, GO:0090734 →
 {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1}, {{site of DNA damage, cellular_component}, {{PARP1}}}},
GO:1903827 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of cellular protein localization, biological_process}, {{PARP1}}}},
GO:0010008 → {{0.0188076, 0.0374078, True}, {20, 210, 19774, 2},
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196568, 0.0385302, True}, {20, 215, 19774, 2},
  {{regulation of apoptotic process, biological_process}, {{MALT1}, {ATM}}}},
GO:0002756 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{macrophage differentiation, biological_process}, {{PARP1}}}},
GO:0032991 → {{0.0204617, 0.0395348, True}, {20, 588, 19774, 3},
  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
 {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1}, {{aorta development, biological_process}, {{TAB1}}}},
GO:0042098 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{T cell proliferation, biological_process}, {{MALT1}}}},
GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
 {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
```

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```
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
```

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```
GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
  {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{DNA damage checkpoint, biological_process}, {{ATM}}}},
GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

We can see for example the last 5 members of the list are all computed to have statistical significance:

```
In[3]:= goExampleFilterSignificantOn[[-5 ;;]]
```

```
Out[3]= <|GO:0000077 → {{0.0309063, 0.0491774, True},
  {20, 31, 19774, 1}, {{DNA damage checkpoint, biological_process}, {{ATM}}}},
GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

We now repeat the computation and setting the `FilterSignificant` to False

```
In[4]:= goExampleFilterSignificantOff =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
   "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM",
   "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, FilterSignificant → False]
```

```
Out[4]= <|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
   {{positive regulation of NF-kappaB transcription factor activity, biological_process},
    {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}}, ··· 539 ···, GO:0046872 → {··· 1 ···}|>
```

large output | show less | show more | show all | set size limit...

We can look at again the last 5 members of the list, and see that non-significant results are also included:

```
In[5]:= goExampleFilterSignificantOff[[-5 ;;]]
```

```
Out[5]= <|GO:0006357 → {{0.702027, 0.707257, False}, {20, 1161, 19774, 1},
   {{regulation of transcription by RNA polymerase II, biological_process}, {{PIAS4}}}},
GO:0016021 → {{0.759743, 0.763979, False}, {20, 3747, 19774, 3},
   {{integral component of membrane, cellular_component}, {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}},
GO:0003723 → {{0.766648, 0.769492, False}, {20, 1387, 19774, 1},
   {{RNA binding, molecular_function}, {{PARP1}}}}, GO:0016020 →
  {{0.878088, 0.879714, False}, {20, 1974, 19774, 1}, {{membrane, cellular_component}, {{PARP1}}}},
GO:0046872 → {{0.915878, 0.915878, False}, {20, 2301, 19774, 1},
   {{metal ion binding, molecular_function}, {{CSNK2B}}}}|>
```

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GeneDictionary (1)

In[1]:=
```
Needs["MathIOmica`"]
```

GeneDictionary takes values that point to an existing variable to be used as a gene dictionary in annotations. By default, it is set to None and the default ConstantGeneDictionary is used.

In[2]:=
```
goExample1 = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, GeneDictionary → None]
```

Out[2]=
```
<|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
  GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
  GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
    {{protein serine/threonine kinase activity, molecular_function},
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
  GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
    {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
  GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
    {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
   {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
     {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
  GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
    {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
     {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
    {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
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  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
  {{regulation of signal transduction by p53 class mediator, biological_process},
   {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
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GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
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GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
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  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
  {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{B-1 B cell differentiation, biological_process}, {{MALT1}}}},
GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of Fc receptor mediated stimulatory signaling pathway, biological_process},
   {{LYN}}}}, GO:0061847 → {{0.00202189, 0.0130219, True},
  {20, 2, 19774, 1}, {{response to cholecystokinin, biological_process}, {{CHUK}}}},
GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0070668 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{cellular response to bacterial lipopeptide, biological_process}, {{TIRAP}}}},
GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of RNA localization to telomere, biological_process}, {{ATM}}}},
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GO:0097695 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of protein-containing complex localization to telomere, biological_process}, {{ATM}}}},
GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of single strand break repair, biological_process}, {{PARP1}}}},
GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
  {{ATP binding, molecular_function}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {LYN}, {ATM}, {IRAK4}}}},
GO:0016301 → {{0.00292933, 0.0149088, True}, {20, 80, 19774, 2},
  {{kinase activity, molecular_function}, {{CSNK2A1}, {LYN}}}},
GO:0002331 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002553 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002762 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002774 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002902 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0008384 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{IkappaB kinase activity, molecular_function}, {{CHUK}}}},
GO:0010956 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of calcidiol 1-monooxygenase activity, biological_process}, {{NFKB1}}}},
GO:0030592 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{DNA ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0035663 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{Toll-like receptor 2 binding, molecular_function}, {{TIRAP}}}},
GO:0070447 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of oligodendrocyte progenitor proliferation, biological_process}, {{LYN}}}},
GO:0071500 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{cellular response to nitrosative stress, biological_process}, {{ATM}}}},
GO:0099091 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{postsynaptic specialization, intracellular component, cellular_component}, {{LYN}}}},
GO:0140031 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0140294 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{NAD DNA ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:1902174 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of keratinocyte apoptotic process, biological_process}, {{PIAS4}}}},
GO:1904044 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{response to aldosterone, biological_process}, {{PARP1}}}},
GO:2000630 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of miRNA metabolic process, biological_process}, {{NFKB1}}}},
GO:2000670 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of dendritic cell apoptotic process, biological_process}, {{LYN}}}},
GO:2001170 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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  {{negative regulation of ATP biosynthetic process, biological_process}, {{PARP1}}}},
GO:0000724 → {{0.00314887, 0.0153472, True}, {20, 83, 19774, 2},
  {{double-strand break repair via homologous recombination, biological_process}, {{PARP1}, {ATM}}}},
GO:0010957 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{negative regulation of vitamin D biosynthetic process, biological_process}, {{NFKB1}}}},
GO:0018312 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0032375 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0032648 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{regulation of interferon-beta production, biological_process}, {{TIRAP}}}},
GO:0048305 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{immunoglobulin secretion, biological_process}, {{TNFSF13B}}}},
GO:0071359 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{cellular response to dsRNA, biological_process}, {{NFKB1}}}},
GO:0090330 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{regulation of platelet aggregation, biological_process}, {{LYN}}}},
GO:1900127 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:1903978 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{regulation of microglial cell activation, biological_process}, {{ATM}}}},
GO:1990234 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{transferase complex, cellular_component}, {{PIAS4}}}},
GO:1990966 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{ATP generation from poly-ADP-D-ribose, biological_process}, {{PARP1}}}},
GO:2000321 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{positive regulation of T-helper 17 cell differentiation, biological_process}, {{MALT1}}}},
GO:0005102 → {{0.00432566, 0.0187215, True}, {20, 332, 19774, 3},
  {{signaling receptor binding, molecular_function}, {{TNFSF13B}, {CSNK2B}, {LYN}}}},
GO:0007179 → {{0.00444549, 0.0190874, True}, {20, 99, 19774, 2},
  {{transforming growth factor beta receptor signaling pathway, biological_process}, {{TAB1}, {PARP1}}}},
GO:0014910 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{regulation of smooth muscle cell migration, biological_process}, {{PLAU}}}},
GO:0032042 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{mitochondrial DNA metabolic process, biological_process}, {{PARP1}}}},
GO:0032269 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{negative regulation of cellular protein metabolic process, biological_process}, {{NFKB1}}}},
GO:0034136 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{negative regulation of toll-like receptor 2 signaling pathway, biological_process}, {{LYN}}}},
GO:0035662 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{Toll-like receptor 4 binding, molecular_function}, {{TIRAP}}}},
GO:0042159 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{lipoprotein catabolic process, biological_process}, {{ATM}}}},
GO:0043208 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0043504 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{mitochondrial DNA repair, biological_process}, {{PARP1}}}},
GO:0048273 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{mitogen-activated protein kinase p38 binding, molecular_function}, {{TAB1}}}},
GO:0050856 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{regulation of T cell receptor signaling pathway, biological_process}, {{MALT1}}}},
GO:0061041 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{regulation of wound healing, biological_process}, {{PLAU}}}},
GO:1904354 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{negative regulation of telomere capping, biological_process}, {{ATM}}}},
GO:1904358 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
 {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
```

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```
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
```

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```
    {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
  GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
  GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
    {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
  GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{DNA damage checkpoint, biological_process}, {{ATM}}}},
  GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
  GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
  GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
  GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

We can instead use a variable as a gene dictionary. For example suppose we have a rather restricted dictionary:

```
In[3]:= geneDictionaryExample =
  <|"human" → <|"UniProt ID" → {"P19838", "B4DUJ4", "O15111", "Q9NWZ3", "P19838", "J3KQ87", "P58753-2",
        "P67870", "P19838", "Q9NWZ3", "O15111", Missing[], "P68400", "Q99836-3", "B4DUJ4", "Q9NWZ3",
        "P67870", "Q9NWZ3", "P19838", "Q9Y275", "B4DUJ4", Missing[], "B4DUJ4", "Q15750", "O15111",
        "P67870", Missing[], "P19838-3", "O15111", "F5GXE7", "P25963", "P19838-2", "Q9NWZ3",
        "P07948", "Q6P7P1", "B4DUJ4", Missing[], "Q9NWZ3", "O15111", Missing[], "P67870", "J3KQJ6",
        "P25963", "Q99836-3", "H0YDU7", "D3DR86", "B4DUJ4", "Q9NWZ3", "P19838-3", "O15111",
        Missing[], "H0YDU7", "P25963", "B4DUJ4", "B4DUJ4", "B4DUJ4", "Q99836-4", "P68400", "B4DUJ4",
        Missing[], "P19838", Missing[], "B4DUJ4", "O15111", "P19838", "P68400", Missing[],
        "Q9NWZ3", "P19838-3", "O75293", "O15111", "Q9NWZ3", Missing[], "P67870", "P58753",
        "O75293", "Q96RJ3", "P67870", "B4DUJ4", "O15111", "P19838", "P19838", "P25963", "Q9NWZ3",
        "P19838-2", "O15111", "P25963", "Q9NWZ3", Missing[], Missing[], "P19838-2", "B4DUJ4",
        "Q9NWZ3", "O15111", "J3KQJ6", "Q15750-2", Missing[], "P68400", "B4DUJ4", "P19838-3"},
      "Gene Symbol" → {"NFKB1", "CSNK2B", "CHUK", "IRAK4", "NFKB1", "MYD88", "TIRAP", "CSNK2B",
        "NFKB1", "IRAK4", "CHUK", "CSNK2B", "CSNK2A1", "MYD88", "CSNK2B", "IRAK4", "CSNK2B", "IRAK4",
        "NFKB1", "TNFSF13B", "CSNK2B", "CSNK2B", "CSNK2B", "TAB1", "CHUK", "CSNK2B", "ATM", "NFKB1",
        "CHUK", "LTBR", "NFKBIA", "NFKB1", "IRAK4", "LYN", "ATM", "CSNK2B", "ATM", "IRAK4", "CHUK",
        "CSNK2B", "CSNK2B", "MYD88", "NFKBIA", "MYD88", "ATM", "NFKB2", "CSNK2B", "IRAK4", "NFKB1", "CHUK",
        "CSNK2B", "ATM", "NFKBIA", "CSNK2B", "CSNK2B", "CSNK2B", "MYD88", "CSNK2A1", "CSNK2B", "ATM",
        "NFKB1", "CSNK2B", "CSNK2B", "CHUK", "NFKB1", "CSNK2A1", "CSNK2A2", "IRAK4", "NFKB1", "GADD45B",
        "CHUK", "IRAK4", "TNFSF13B", "CSNK2B", "TIRAP", "GADD45B", "TNFRSF13C", "CSNK2B", "CSNK2B",
        "CHUK", "NFKB1", "NFKB1", "NFKBIA", "IRAK4", "NFKB1", "CHUK", "NFKBIA", "IRAK4", "CSNK2A2",
        "ATM", "NFKB1", "CSNK2B", "IRAK4", "CHUK", "MYD88", "TAB1", "ATM", "CSNK2A1", "CSNK2B", "NFKB1"},
      "KEGG Gene ID" → {"4790", "1460", "1147", "51135", "4790", "4615", "114609", "1460", "4790",
        "51135", "1147", "1460", "1457", "4615", "1460", "51135", "1460", "51135", "4790", "10673",
        "1460", "1460", "1460", "10454", "1147", "1460", "472", "4790", "1147", "4055", "4792", "4790",
        "51135", "4067", "472", "1460", "472", "51135", "1147", "1460", "1460", "4615", "4792",
        "4615", "472", "4791", "1460", "51135", "4790", "1147", "1460", "472", "4792", "1460", "1460",
        "1460", "4615", "1457", "1460", "472", "4790", "1460", "1460", "1147", "4790", "1457", "1459",
        "51135", "4790", "4616", "1147", "51135", "10673", "1460", "114609", "4616", "115650", "1460",
        "1460", "1147", "4790", "4790", "4792", "51135", "4790", "1147", "4792", "51135", "1459",
        "472", "4790", "1460", "51135", "1147", "4615", "10454", "472", "1457", "1460", "4790"}|>|>;

In[4]:= goExampleGeneDictionary =
  GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
    "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA",
    "IRAK4", "PIAS4", "PLAU"}, GeneDictionary → geneDictionaryExample]

Out[4]= <|GO:0070498 → {{1.77453×10^-9, 6.12212×10^-7, True},
    {12, 95, 19774, 5}, {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0051092 → {{1.84309×10^-8, 3.17932×10^-6, True}, {12, 151, 19774, 5},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {TIRAP}, {CHUK}, {NFKB1}, {IRAK4}}}},
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GO:0001782 → {{2.25703×10^-7, 0.0000259559, True}, {12, 21, 19774, 3},
  {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
GO:0033256 → {{3.37603×10^-7, 0.0000291183, True}, {12, 2, 19774, 2},
  {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
GO:0002223 → {{4.66133×10^-7, 0.0000298053, True}, {12, 112, 19774, 4},
  {{stimulatory C-type lectin receptor signaling pathway, biological_process},
   {{TAB1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0033209 → {{5.18353×10^-7, 0.0000298053, True},
  {12, 115, 19774, 4}, {{tumor necrosis factor-mediated signaling pathway, biological_process},
   {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {NFKBIA}}}},
GO:0002755 → {{9.22105×10^-7, 0.0000349302, True}, {12, 33, 19774, 3},
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
   {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0002636 → {{1.01247×10^-6, 0.0000349302, True}, {12, 3, 19774, 2},
  {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0005956 → {{1.01247×10^-6, 0.0000349302, True}, {12, 3, 19774, 2},
  {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031296 → {{1.01247×10^-6, 0.0000349302, True}, {12, 3, 19774, 2},
  {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0030890 → {{1.7967×10^-6, 0.0000563511, True}, {12, 41, 19774, 3},
  {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}},
GO:0038095 → {{2.53199×10^-6, 0.0000727946, True}, {12, 171, 19774, 4},
  {{Fc-epsilon receptor signaling pathway, biological_process}, {{TAB1}, {CHUK}, {LYN}, {NFKB1}}}},
GO:0031295 → {{3.93221×10^-6, 0.000104355, True}, {12, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
GO:0007249 → {{7.30196×10^-6, 0.000179941, True}, {12, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000185119, 0.000425774, True}, {12, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0035994 → {{0.0000352933, 0.000761012, True}, {12, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0004674 → {{0.0000502742, 0.00102027, True}, {12, 365, 19774, 4},
  {{protein serine/threonine kinase activity, molecular_function},
   {{CHUK}, {CSNK2A1}, {CSNK2B}, {IRAK4}}}}, GO:0031519 → {{0.000117504, 0.00213363, True},
  {12, 27, 19774, 2}, {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0051403 → {{0.000117504, 0.00213363, True}, {12, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0043123 → {{0.000151116, 0.0024935, True}, {12, 179, 19774, 3},
  {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
   {{TIRAP}, {CHUK}, {IRAK4}}}},
GO:0005737 → {{0.000160429, 0.0024935, True}, {12, 4436, 19774, 9}, {{cytoplasm, cellular_component},
   {{TNFSF13B}, {TIRAP}, {CHUK}, {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
GO:0043200 → {{0.000165766, 0.0024935, True}, {12, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045087 → {{0.000166233, 0.0024935, True}, {12, 497, 19774, 4},
  {{innate immune response, biological_process}, {{TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0006656 → {{0.000176401, 0.00253576, True}, {12, 33, 19774, 2},
  {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031663 → {{0.000187363, 0.00258561, True}, {12, 34, 19774, 2},
  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{LYN}, {NFKBIA}}}},
GO:0042802 → {{0.00024638, 0.0031562, True}, {12, 1054, 19774, 5},
  {{identical protein binding, molecular_function}, {{TIRAP}, {CSNK2A1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:0006915 → {{0.000247007, 0.0031562, True}, {12, 551, 19774, 4},
  {{apoptotic process, biological_process}, {{CSNK2A1}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
GO:0007254 → {{0.000374955, 0.00461998, True}, {12, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}},
GO:0005829 → {{0.000452699, 0.00538556, True}, {12, 5035, 19774, 9}, {{cytosol, cellular_component},
   {{TAB1}, {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2B}, {LYN}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
GO:0042102 → {{0.000585985, 0.00673883, True}, {12, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0009636 → {{0.000687455, 0.00765071, True}, {12, 65, 19774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
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GO:0008134 → {{0.000914036, 0.00843196, True}, {12, 331, 19 774, 3},
  {{transcription factor binding, molecular_function}, {{CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:0005102 → {{0.000922054, 0.00843196, True}, {12, 332, 19 774, 3},
  {{signaling receptor binding, molecular_function}, {{TNFSF13B}, {CSNK2B}, {LYN}}}},
GO:0018107 → {{0.000988173, 0.00843196, True}, {12, 78, 19 774, 2},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2B}}}},
GO:0032088 → {{0.000988173, 0.00843196, True}, {12, 78, 19 774, 2},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}}}}, GO:0016301 → {{0.00103914, 0.00843196, True},
  {12, 80, 19 774, 2}, {{kinase activity, molecular_function}, {{CSNK2A1}, {LYN}}}},
GO:0046330 → {{0.00103914, 0.00843196, True}, {12, 80, 19 774, 2},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {GADD45B}}}},
GO:0002431 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0060369 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{positive regulation of Fc receptor mediated stimulatory signaling pathway, biological_process},
   {{LYN}}}}, GO:0061847 → {{0.00121338, 0.00843196, True},
  {12, 2, 19 774, 1}, {{response to cholecystokinin, biological_process}, {{CHUK}}}},
GO:0070427 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{negative regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0070668 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{positive regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0071221 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{cellular response to bacterial lipopeptide, biological_process}, {{TIRAP}}}},
GO:1902532 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
GO:1905818 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{regulation of chromosome separation, biological_process}, {{CSNK2A1}}}},
GO:2000340 → {{0.00121338, 0.00843196, True}, {12, 2, 19 774, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0006954 → {{0.00122202, 0.00843196, True}, {12, 366, 19 774, 3},
  {{inflammatory response, biological_process}, {{TIRAP}, {CHUK}, {NFKB1}}}},
GO:0016236 → {{0.00146087, 0.00951134, True}, {12, 95, 19 774, 2},
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  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.016865, 0.029838, True}, {12, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0002250 → {{0.0169779, 0.0298846, True}, {12, 336, 19774, 2},
  {{adaptive immune response, biological_process}, {{TNFRSF13C}, {LYN}}}},
GO:0010803 → {{0.0174624, 0.0301227, True}, {12, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0174624, 0.0301227, True}, {12, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0174624, 0.0301227, True}, {12, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0174624, 0.0301227, True}, {12, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0033574 → {{0.0180596, 0.0306924, True}, {12, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0180596, 0.0306924, True}, {12, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0097421 → {{0.0180596, 0.0306924, True}, {12, 30, 19774, 1},
  {{liver regeneration, biological_process}, {{CSNK2B}}}},
GO:0005164 → {{0.0186564, 0.0313973, True}, {12, 31, 19774, 1},
  {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
GO:0043330 → {{0.0186564, 0.0313973, True}, {12, 31, 19774, 1},
  {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
GO:0038083 → {{0.0192528, 0.0319338, True}, {12, 32, 19774, 1},
  {{peptidyl-tyrosine autophosphorylation, biological_process}, {{LYN}}}},
GO:0043021 → {{0.0192528, 0.0319338, True}, {12, 32, 19774, 1},
  {{ribonucleoprotein complex binding, molecular_function}, {{CSNK2B}}}},
GO:0043392 → {{0.0192528, 0.0319338, True}, {12, 32, 19774, 1},
  {{negative regulation of DNA binding, biological_process}, {{NFKBIA}}}},
GO:0034614 → {{0.0204448, 0.0337486, True}, {12, 34, 19774, 1},
  {{cellular response to reactive oxygen species, biological_process}, {{CHUK}}}},
GO:0016032 → {{0.0205663, 0.0337874, True}, {12, 372, 19774, 2},
  {{viral process, biological_process}, {{LYN}, {NFKBIA}}}},
GO:0051219 → {{0.0210403, 0.0344023, True}, {12, 35, 19774, 1},
  {{phosphoprotein binding, molecular_function}, {{LYN}}}},
GO:0035556 → {{0.0215096, 0.0350038, True}, {12, 381, 19774, 2},
  {{intracellular signal transduction, biological_process}, {{LYN}, {IRAK4}}}},
GO:0030177 → {{0.0216354, 0.0350432, True}, {12, 36, 19774, 1},
  {{positive regulation of Wnt signaling pathway, biological_process}, {{CSNK2A1}}}},
GO:0003682 → {{0.0223633, 0.036053, True}, {12, 389, 19774, 2},
  {{chromatin binding, molecular_function}, {{CSNK2B}, {NFKB1}}}},
GO:0008285 → {{0.0226871, 0.0361216, True}, {12, 392, 19774, 2},
  {{negative regulation of cell population proliferation, biological_process}, {{CSNK2B}, {LYN}}}},
GO:0003007 → {{0.0228247, 0.0361216, True}, {12, 38, 19774, 1},
  {{heart morphogenesis, biological_process}, {{TAB1}}}},
GO:0043407 → {{0.0228247, 0.0361216, True}, {12, 38, 19774, 1},
  {{negative regulation of MAP kinase activity, biological_process}, {{LYN}}}},
GO:0071276 → {{0.0228247, 0.0361216, True}, {12, 38, 19774, 1},
  {{cellular response to cadmium ion, biological_process}, {{CHUK}}}},
GO:0045746 → {{0.0246061, 0.0385869, True}, {12, 41, 19774, 1},
  {{negative regulation of Notch signaling pathway, biological_process}, {{NFKBIA}}}},
GO:0051879 → {{0.0246061, 0.0385869, True}, {12, 41, 19774, 1},
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```
    {{Hsp90 protein binding, molecular_function}, {{CSNK2A1}}}},
  GO:0001932 → {{0.0251993, 0.0393383, True}, {12, 42, 19 774, 1},
    {{regulation of protein phosphorylation, biological_process}, {{LYN}}}},
  GO:0000186 → {{0.0257921, 0.0399026, True}, {12, 43, 19 774, 1},
    {{activation of MAPKK activity, biological_process}, {{GADD45B}}}}, GO:0009725 →
   {{0.0257921, 0.0399026, True}, {12, 43, 19 774, 1}, {{response to hormone, biological_process}, {{LYN}}}},
  GO:0002224 → {{0.0263846, 0.040637, True}, {12, 44, 19 774, 1},
    {{toll-like receptor signaling pathway, biological_process}, {{IRAK4}}}},
  GO:0030218 → {{0.0269768, 0.0413644, True}, {12, 45, 19 774, 1},
    {{erythrocyte differentiation, biological_process}, {{LYN}}}},
  GO:0004715 → {{0.0275686, 0.0418994, True}, {12, 46, 19 774, 1},
    {{non-membrane spanning protein tyrosine kinase activity, molecular_function}, {{LYN}}}},
  GO:0014070 → {{0.0275686, 0.0418994, True}, {12, 46, 19 774, 1},
    {{response to organic cyclic compound, biological_process}, {{LYN}}}},
  GO:0045944 → {{0.0280291, 0.0423779, True}, {12, 1134, 19 774, 3},
    {{positive regulation of transcription by RNA polymerase II, biological_process},
     {{CHUK}, {NFKB1}, {NFKBIA}}}}, GO:0008047 → {{0.0281601, 0.0423779, True},
    {12, 47, 19 774, 1}, {{enzyme activator activity, molecular_function}, {{TAB1}}}},
  GO:0006955 → {{0.0282519, 0.0423779, True}, {12, 441, 19 774, 2},
    {{immune response, biological_process}, {{TNFSF13B}, {CHUK}}}},
  GO:0010862 → {{0.0287513, 0.0429402, True}, {12, 48, 19 774, 1},
    {{positive regulation of pathway-restricted SMAD protein phosphorylation, biological_process},
     {{CSNK2B}}}}, GO:0005654 → {{0.0300759, 0.0447249, True}, {12, 3142, 19 774, 5},
    {{nucleoplasm, cellular_component}, {{CHUK}, {CSNK2A1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
  GO:0032481 → {{0.0305228, 0.0450016, True}, {12, 51, 19 774, 1},
    {{positive regulation of type I interferon production, biological_process}, {{NFKB1}}}},
  GO:0032760 → {{0.0305228, 0.0450016, True}, {12, 51, 19 774, 1},
    {{positive regulation of tumor necrosis factor production, biological_process}, {{TIRAP}}}},
  GO:0005080 → {{0.0317022, 0.0463443, True}, {12, 53, 19 774, 1},
    {{protein kinase C binding, molecular_function}, {{TIRAP}}}},
  GO:0009898 → {{0.0317022, 0.0463443, True}, {12, 53, 19 774, 1},
    {{cytoplasmic side of plasma membrane, cellular_component}, {{CHUK}}}},
  GO:0043312 → {{0.0331666, 0.0482805, True}, {12, 481, 19 774, 2},
    {{neutrophil degranulation, biological_process}, {{CSNK2B}, {NFKB1}}}},
  GO:0043066 → {{0.0336758, 0.0488157, True}, {12, 485, 19 774, 2},
    {{negative regulation of apoptotic process, biological_process}, {{NFKB1}, {NFKBIA}}}},
  GO:0048661 → {{0.034057, 0.0491618, True}, {12, 57, 19 774, 1},
    {{positive regulation of smooth muscle cell proliferation, biological_process}, {{IRAK4}}}},
  GO:0008284 → {{0.0345744, 0.0495954, True}, {12, 492, 19 774, 2},
    {{positive regulation of cell population proliferation, biological_process}, {{CSNK2A1}, {LYN}}}},
  GO:0030139 → {{0.0346449, 0.0495954, True}, {12, 58, 19 774, 1},
    {{endocytic vesicle, cellular_component}, {{TIRAP}}}}|>
```

GetGeneDictionaryOptions (1)

```
In[1]:= Needs["MathIOmica`"]
```

GetGeneDictionaryOptions values specify a list of options that will be passed to the internal GetGeneDictionary function. For example, we can re-import the gene dictionary from online:

```
In[2]:= goExampleGetGeneDictionaryOptions =
         GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
           "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
           "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, GetGeneDictionaryOptions → {ImportDirectly → True}]

Out[2]= <|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19 774, 7},
           {{positive regulation of NF-kappaB transcription factor activity, biological_process},
            {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
         GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19 774, 5},
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```
  {{interleukin-1-mediated signaling pathway, biological_process},
   {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
  {{stimulatory C-type lectin receptor signaling pathway, biological_process},
   {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
  {{tumor necrosis factor-mediated signaling pathway, biological_process},
   {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
  {{Fc-epsilon receptor signaling pathway, biological_process},
   {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
 {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
   {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
  {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
   {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
  {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
  {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
  {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
  {{protein serine/threonine kinase activity, molecular_function},
   {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
  {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
  {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
 {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
   {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
   {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
  {{regulation of signal transduction by p53 class mediator, biological_process},
   {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
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  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
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GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
  {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{B-1 B cell differentiation, biological_process}, {{MALT1}}}},
GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0097028 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
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GO:0046982 → {{0.0123921, 0.0295335, True}, {20, 487, 19774, 3},
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GO:0007596 → {{0.0126116, 0.029925, True}, {20, 170, 19774, 2},
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GO:0046777 → {{0.0128955, 0.0302244, True}, {20, 172, 19774, 2},
  {{protein autophosphorylation, biological_process}, {{LYN}, {ATM}}}},
GO:0010745 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
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  {{DNA double-strand break processing, biological_process}, {{ATM}}}},
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  {{positive regulation of interleukin-1 beta production, biological_process}, {{MALT1}}}},
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GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
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GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
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  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
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GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
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GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
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  {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
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GOAnalysisAssignerOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The GOAnalysisAssignerOptions option values specify a list of options that will be passed to the internal GOAnalysisAssigner function. These options supersede any other applicable options used internally by GOAnalysisAssigner. For example, we can restrict the GO terms to be included, to have at least 3 members each.

In[2]:=
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goExampleGoAnalysisAssignerOptions =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
   "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
   "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, GOAnalysisAssignerOptions → {LengthFilter → 3}]
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   {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
 GO:0047485 → {{3.53895×10^-6, 0.0001317, True}, {20, 106, 19772, 4},
   {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
 GO:0042802 → {{4.50137×10^-6, 0.000145154, True}, {20, 1054, 19772, 8}, {{identical protein binding,
      molecular_function}, {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
 GO:0002755 → {{4.7363×10^-6, 0.000145154, True}, {20, 33, 19772, 3},
   {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
    {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.7363×10^-6, 0.000145154, True}, {20, 33, 19772, 3},
   {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
 GO:0031663 → {{5.1913×10^-6, 0.000150259, True}, {20, 34, 19772, 3},
   {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
 GO:1901796 → {{8.21256×10^-6, 0.000225197, True}, {20, 131, 19772, 4},
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  {{regulation of signal transduction by p53 class mediator, biological_process},
   {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}},
GO:0030890 → {{9.20621×10^-6, 0.000239822, True}, {20, 41, 19772, 3},
  {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.000012325, 0.000305776, True}, {20, 9629, 19772, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180869, 0.00042833, True}, {20, 160, 19772, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200752, 0.000454747, True}, {20, 53, 19772, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309507, 0.000666269, True}, {20, 977, 19772, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319707, 0.000666269, True}, {20, 185, 19772, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371435, 0.000744298, True}, {20, 65, 19772, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531734, 0.00102605, True}, {20, 11, 19772, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641514, 0.00115251, True}, {20, 78, 19772, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641514, 0.00115251, True}, {20, 78, 19772, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691924, 0.00120164, True}, {20, 80, 19772, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.000075318, 0.00126583, True}, {20, 13, 19772, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101267, 0.00164875, True}, {20, 15, 19772, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.000111543, 0.0016739, True}, {20, 497, 19772, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115446, 0.0016739, True}, {20, 95, 19772, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.000115663, 0.0016739, True}, {20, 16, 19772, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.000115663, 0.0016739, True}, {20, 16, 19772, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.00014275, 0.00201007, True}, {20, 5639, 19772, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147292, 0.00201945, True}, {20, 18, 19772, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000180063, 0.00240546, True}, {20, 289, 19772, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.00023049, 0.00300214, True}, {20, 120, 19772, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.000302296, 0.00384137, True}, {20, 331, 19772, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311359, 0.00386234, True}, {20, 26, 19772, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321573, 0.00389088, True}, {20, 4436, 19772, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000333073, 0.00389088, True}, {20, 136, 19772, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000336064, 0.00389088, True}, {20, 27, 19772, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.00039996, 0.00452998, True}, {20, 3142, 19772, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415733, 0.00460844, True}, {20, 30, 19772, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
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GO:0006457 → {{0.00042671, 0.00463158, True}, {20, 148, 19 772, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473456, 0.0050341, True}, {20, 32, 19 772, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678544, 0.00707043, True}, {20, 1134, 19 772, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718793, 0.00734296, True}, {20, 177, 19 772, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896457, 0.00898181, True}, {20, 44, 19 772, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106634, 0.0104823, True}, {20, 48, 19 772, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00111033, 0.0107126, True}, {20, 5035, 19 772, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120311, 0.0113967, True}, {20, 51, 19 772, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131673, 0.0122502, True}, {20, 490, 19 772, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134786, 0.0123199, True}, {20, 54, 19 772, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.0014004, 0.0125794, True}, {20, 223, 19 772, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166112, 0.0146685, True}, {20, 60, 19 772, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174899, 0.0151391, True}, {20, 241, 19 772, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177253, 0.0151391, True}, {20, 62, 19 772, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00187046, 0.0157179, True}, {20, 4532, 19 772, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194614, 0.0160943, True}, {20, 65, 19 772, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200575, 0.016328, True}, {20, 66, 19 772, 2},
  {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
GO:0071300 → {{0.00218972, 0.0175501, True}, {20, 69, 19 772, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285839, 0.0175501, True}, {20, 79, 19 772, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.0029031, 0.0175501, True}, {20, 1501, 19 772, 6},
  {{ATP binding, molecular_function}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {LYN}, {ATM}, {IRAK4}}}},
GO:0016301 → {{0.00292991, 0.0175501, True}, {20, 80, 19 772, 2},
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GO:0002331 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
GO:0002513 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{tolerance induction to self antigen, biological_process}, {{LYN}}}},
GO:0002553 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{histamine secretion by mast cell, biological_process}, {{LYN}}}},
GO:0002762 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{negative regulation of myeloid leukocyte differentiation, biological_process}, {{LYN}}}},
GO:0002774 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{Fc receptor mediated inhibitory signaling pathway, biological_process}, {{LYN}}}},
GO:0002902 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{regulation of B cell apoptotic process, biological_process}, {{LYN}}}},
GO:0004677 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{DNA-dependent protein kinase activity, molecular_function}, {{ATM}}}},
GO:0008384 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{IkappaB kinase activity, molecular_function}, {{CHUK}}}},
GO:0010956 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
  {{negative regulation of calcidiol 1-monooxygenase activity, biological_process}, {{NFKB1}}}},
GO:0030592 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
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  {{DNA ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0034666 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{integrin alpha2-beta1 complex, cellular_component}, {{LYN}}}},
GO:0035663 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{Toll-like receptor 2 binding, molecular_function}, {{TIRAP}}}},
GO:0070447 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{positive regulation of oligodendrocyte progenitor proliferation, biological_process}, {{LYN}}}},
GO:0071500 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{cellular response to nitrosative stress, biological_process}, {{ATM}}}},
GO:0099091 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{postsynaptic specialization, intracellular component, cellular_component}, {{LYN}}}},
GO:0140031 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{phosphorylation-dependent protein binding, molecular_function}, {{LYN}}}},
GO:0140294 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{NAD DNA ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:1902174 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{positive regulation of keratinocyte apoptotic process, biological_process}, {{PIAS4}}}},
GO:1904044 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{response to aldosterone, biological_process}, {{PARP1}}}},
GO:2000630 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{positive regulation of miRNA metabolic process, biological_process}, {{NFKB1}}}},
GO:2000670 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{positive regulation of dendritic cell apoptotic process, biological_process}, {{LYN}}}},
GO:2001170 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{negative regulation of ATP biosynthetic process, biological_process}, {{PARP1}}}},
GO:0000724 → {{0.00314949, 0.0180317, True}, {20, 83, 19772, 2},
  {{double-strand break repair via homologous recombination, biological_process}, {{PARP1}, {ATM}}}},
GO:0010957 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{negative regulation of vitamin D biosynthetic process, biological_process}, {{NFKB1}}}},
GO:0018312 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{peptidyl-serine ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0032375 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{negative regulation of cholesterol transport, biological_process}, {{NFKB1}}}}, GO:0032449 →
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GO:0032648 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{regulation of interferon-beta production, biological_process}, {{TIRAP}}}},
GO:0048305 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{immunoglobulin secretion, biological_process}, {{TNFSF13B}}}},
GO:0071359 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{cellular response to dsRNA, biological_process}, {{NFKB1}}}},
GO:0090330 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{regulation of platelet aggregation, biological_process}, {{LYN}}}},
GO:1900127 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{positive regulation of hyaluronan biosynthetic process, biological_process}, {{NFKB1}}}},
GO:1903978 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{regulation of microglial cell activation, biological_process}, {{ATM}}}}, GO:1990234 →
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GO:1990966 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{ATP generation from poly-ADP-D-ribose, biological_process}, {{PARP1}}}},
GO:2000321 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{positive regulation of T-helper 17 cell differentiation, biological_process}, {{MALT1}}}},
GO:0005102 → {{0.00432688, 0.0214696, True}, {20, 332, 19772, 3},
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GO:0007179 → {{0.00444637, 0.0217354, True}, {20, 99, 19772, 2},
  {{transforming growth factor beta receptor signaling pathway, biological_process}, {{TAB1}, {PARP1}}}},
GO:0014910 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
  {{regulation of smooth muscle cell migration, biological_process}, {{PLAU}}}},
GO:0032042 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
  {{mitochondrial DNA metabolic process, biological_process}, {{PARP1}}}},
GO:0032269 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
  {{negative regulation of cellular protein metabolic process, biological_process}, {{NFKB1}}}},
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GO:0034136 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
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GO:0035662 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
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GO:0042159 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
  {{lipoprotein catabolic process, biological_process}, {{ATM}}}},
GO:0043208 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
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GO:0043504 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
  {{mitochondrial DNA repair, biological_process}, {{PARP1}}}},
GO:0048273 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
  {{mitogen-activated protein kinase p38 binding, molecular_function}, {{TAB1}}}},
GO:0050856 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
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GO:0061041 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
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GO:1904354 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
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GO:1904358 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
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GO:1990391 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
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GO:2000343 → {{0.00504795, 0.0217354, True}, {20, 5, 19772, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 2 production, biological_process}, {{TIRAP}}}},
GO:0000784 → {{0.00536251, 0.0227144, True}, {20, 109, 19772, 2},
  {{nuclear chromosome, telomeric region, cellular_component}, {{PARP1}, {ATM}}}},
GO:0016363 → {{0.00536251, 0.0227144, True}, {20, 109, 19772, 2},
  {{nuclear matrix, cellular_component}, {{CSNK2B}, {PIAS4}}}},
GO:0006954 → {{0.00567622, 0.0233664, True}, {20, 366, 19772, 3},
  {{inflammatory response, biological_process}, {{TIRAP}, {CHUK}, {NFKB1}}}},
GO:0000785 → {{0.00585043, 0.0233664, True}, {20, 114, 19772, 2},
  {{chromatin, cellular_component}, {{CSNK2A2}, {CSNK2B}}}},
GO:0016032 → {{0.00593778, 0.0233664, True}, {20, 372, 19772, 3},
  {{viral process, biological_process}, {{LTBR}, {LYN}, {NFKBIA}}}},
GO:0034774 → {{0.00595038, 0.0233664, True}, {20, 115, 19772, 2},
  {{secretory granule lumen, cellular_component}, {{CSNK2B}, {NFKB1}}}},
GO:0002768 → {{0.00605463, 0.0233664, True}, {20, 6, 19772, 1},
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GO:0009620 → {{0.00605463, 0.0233664, True}, {20, 6, 19772, 1},
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GO:0034137 → {{0.00605463, 0.0233664, True}, {20, 6, 19772, 1},
  {{positive regulation of toll-like receptor 2 signaling pathway, biological_process}, {{TIRAP}}}},
GO:0045646 → {{0.00605463, 0.0233664, True}, {20, 6, 19772, 1},
  {{regulation of erythrocyte differentiation, biological_process}, {{LYN}}}},
GO:0051972 → {{0.00605463, 0.0233664, True}, {20, 6, 19772, 1},
  {{regulation of telomerase activity, biological_process}, {{ATM}}}},
GO:1902231 → {{0.00605463, 0.0233664, True}, {20, 6, 19772, 1},
  {{positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage,
    biological_process}, {{PIAS4}}}}, GO:0071356 → {{0.00699277, 0.0250234, True}, {20, 125, 19772, 2},
  {{cellular response to tumor necrosis factor, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0007253 → {{0.00706034, 0.0250234, True}, {20, 7, 19772, 1},
  {{cytoplasmic sequestering of NF-kappaB, biological_process}, {{NFKBIA}}}},
GO:0014909 → {{0.00706034, 0.0250234, True}, {20, 7, 19772, 1},
  {{smooth muscle cell migration, biological_process}, {{PLAU}}}},
GO:0032210 → {{0.00706034, 0.0250234, True}, {20, 7, 19772, 1},
  {{regulation of telomere maintenance via telomerase, biological_process}, {{ATM}}}},
GO:0032927 → {{0.00706034, 0.0250234, True}, {20, 7, 19772, 1},
  {{positive regulation of activin receptor signaling pathway, biological_process}, {{CSNK2B}}}},
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GO:0033211 → {{0.00706034, 0.0250234, True}, {20, 7, 19772, 1},
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GO:0034141 → {{0.00706034, 0.0250234, True}, {20, 7, 19772, 1},
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GO:0043015 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}},
GO:0001816 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
```

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```
GO:1900745 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279583, 0.0480735, True}, {20, 28, 19772, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279583, 0.0480735, True}, {20, 28, 19772, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279583, 0.0480735, True}, {20, 28, 19772, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286065, 0.0486428, True}, {20, 263, 19772, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288075, 0.0486428, True}, {20, 264, 19772, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.028943, 0.0486428, True}, {20, 29, 19772, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.028943, 0.0486428, True}, {20, 29, 19772, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.028943, 0.0486428, True}, {20, 29, 19772, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.028943, 0.0486428, True}, {20, 29, 19772, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.028943, 0.0486428, True}, {20, 29, 19772, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298215, 0.0496554, True}, {20, 269, 19772, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299267, 0.0496554, True}, {20, 30, 19772, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299267, 0.0496554, True}, {20, 30, 19772, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299267, 0.0496554, True}, {20, 30, 19772, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}}|>
```

HypothesisFunction (1)

```
In[1]:= Needs["MathIOmica`"]
```

The `HypothesisFunction` option takes as values a function to implement multiple hypothesis testing. The default is using the BenjaminiHochbergFDR function. Any function f with three inputs can be used, of the form f[#1,#2,#3] where the inputs refer to:

#1 is the p-value list,

#2 is a significance cutoff,

#3 is the number of GO associations overall being tested.

The function f must output a list of 3 values: {original p-value, adjusted p-value, True or False based on whether this value is considered statistically significant or not respectively}.

We can implement a Bonferroni correction. We can define for example:

```
In[2]:= bonferroni[pValueList_, cutoff_, numberTested_] :=
  {#, #*numberTested, #*numberTested ≤ cutoff} & /@ pValueList
```

We set the `HypothesisFunction` value to our function above:

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In[3]:=
```
goExampleHypothesisFunction =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
   "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
   "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, HypothesisFunction → bonferroni]
```

Out[3]=
```
⟨|GO:0051092 → {{9.39025×10^-11, 1.21829×10^-6, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 0.000437198, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.00100142, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.00114348, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.00825902, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.00921315, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0103553, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0126093, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0126093, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
  GO:0001782 → {{1.16318×10^-6, 0.0150911, True}, {20, 21, 19774, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
  GO:0004674 → {{1.18238×10^-6, 0.0153402, True}, {20, 365, 19774, 6},
    {{protein serine/threonine kinase activity, molecular_function},
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
  GO:0031519 → {{2.54824×10^-6, 0.0330609, True}, {20, 27, 19774, 3},
    {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0002636 → {{2.9139×10^-6, 0.0378049, True}, {20, 3, 19774, 2},
    {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0005956 → {{2.9139×10^-6, 0.0378049, True}, {20, 3, 19774, 2},
    {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
  GO:0031296 → {{2.9139×10^-6, 0.0378049, True}, {20, 3, 19774, 2},
    {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0047485 → {{3.53754×10^-6, 0.0458961, True}, {20, 106, 19774, 4},
    {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}|⟩
```

InputID (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The InputID option specifies a list of the kind of identifiers/accessions to be used as input. The default is set to {"UniProt ID", "Gene Symbol"}.

For example if we already know we are using official Gene Symbol as an identifier we may specify this directly:

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```
In[2]:= goExampleInputID = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
          "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
          "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, InputID → {"Gene Symbol"}]

Out[2]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
          {{positive regulation of NF-kappaB transcription factor activity, biological_process},
           {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
        GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
          {{interleukin-1-mediated signaling pathway, biological_process},
           {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
        GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
          {{stimulatory C-type lectin receptor signaling pathway, biological_process},
           {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
        GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
          {{tumor necrosis factor-mediated signaling pathway, biological_process},
           {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
        GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
          {{Fc-epsilon receptor signaling pathway, biological_process},
           {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
         {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
           {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
        GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
          {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
           {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
        GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
          {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
        GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
          {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
        GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
          {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
        GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
          {{protein serine/threonine kinase activity, molecular_function},
           {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
        GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
          {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
        GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
          {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
        GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
          {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
        GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
          {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
        GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
          {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
         {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
           {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
        GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
          {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
           {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
          {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
        GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
          {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
        GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
          {{regulation of signal transduction by p53 class mediator, biological_process},
           {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
          {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
           {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
         {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
           {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
            {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
        GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
```

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```
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
```

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```
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
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GO:0090073 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{positive regulation of protein homodimerization activity, biological_process}, {{TIRAP}}}},
GO:1904385 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{cellular response to angiotensin, biological_process}, {{NFKB1}}}},
GO:0043312 → {{0.0119849, 0.0290293, True}, {20, 481, 19774, 3},
  {{neutrophil degranulation, biological_process}, {{CSNK2B}, {NFKB1}, {PLAU}}}},
GO:0001666 → {{0.0120525, 0.0290293, True}, {20, 166, 19774, 2},
  {{response to hypoxia, biological_process}, {{ATM}, {PLAU}}}},
GO:0007252 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{I-kappaB phosphorylation, biological_process}, {{CHUK}}}},
GO:0016572 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{histone phosphorylation, biological_process}, {{ATM}}}},
GO:0032495 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{response to muramyl dipeptide, biological_process}, {{NFKBIA}}}},
GO:0033148 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of intracellular estrogen receptor signaling pathway, biological_process},
   {{PARP1}}}}, GO:0042359 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{vitamin D metabolic process, biological_process}, {{PIAS4}}}}, GO:0042805 →
 {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1}, {{actinin binding, molecular_function}, {{NFKB1}}}},
GO:0043517 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of DNA damage response, signal transduction by p53 class mediator,
    biological_process}, {{ATM}}}}, GO:0051168 →
 {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1}, {{nuclear export, biological_process}, {{MALT1}}}},
GO:0060391 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of SMAD protein signal transduction, biological_process}, {{PARP1}}}},
GO:0090399 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{replicative senescence, biological_process}, {{ATM}}}},
GO:0097028 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{dendritic cell differentiation, biological_process}, {{LYN}}}},
GO:0043066 → {{0.0122555, 0.0293372, True}, {20, 485, 19774, 3},
  {{negative regulation of apoptotic process, biological_process}, {{MALT1}, {NFKB1}, {NFKBIA}}}},
GO:0046982 → {{0.0123921, 0.0295335, True}, {20, 487, 19774, 3},
  {{protein heterodimerization activity, molecular_function}, {{TIRAP}, {CHUK}, {NFKB1}}}},
GO:0007596 → {{0.0126116, 0.029925, True}, {20, 170, 19774, 2},
  {{blood coagulation, biological_process}, {{LYN}, {PLAU}}}},
GO:0046777 → {{0.0128955, 0.0302244, True}, {20, 172, 19774, 2},
  {{protein autophosphorylation, biological_process}, {{LYN}, {ATM}}}},
GO:0010745 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{negative regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKBIA}}}}, GO:0044030 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{regulation of DNA methylation, biological_process}, {{PARP1}}}}, GO:0048599 →
 {{0.013073, 0.0302244, True}, {20, 13, 19774, 1}, {{oocyte development, biological_process}, {{ATM}}}},
GO:0050777 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{negative regulation of immune response, biological_process}, {{LYN}}}},
GO:0051279 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{regulation of release of sequestered calcium ion into cytosol, biological_process}, {{LYN}}}},
GO:0005149 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{interleukin-1 receptor binding, molecular_function}, {{IRAK4}}}}, GO:0016580 →
 {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1}, {{Sin3 complex, cellular_component}, {{CSNK2A1}}}},
GO:0032743 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{positive regulation of interleukin-2 production, biological_process}, {{MALT1}}}},
GO:0036092 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{phosphatidylinositol-3-phosphate biosynthetic process, biological_process}, {{ATM}}}},
GO:0045078 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{positive regulation of interferon-gamma biosynthetic process, biological_process}, {{TNFRSF13C}}}},
GO:0051146 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{striated muscle cell differentiation, biological_process}, {{CHUK}}}},
GO:0060397 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
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  {{growth hormone receptor signaling pathway via JAK-STAT, biological_process}, {{LYN}}}},
GO:0000729 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{DNA double-strand break processing, biological_process}, {{ATM}}}},
GO:0005161 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{platelet-derived growth factor receptor binding, molecular_function}, {{LYN}}}}, GO:0016581 →
 {{0.0150698, 0.032874, True}, {20, 15, 19774, 1}, {{NuRD complex, cellular_component}, {{CSNK2A1}}}},
GO:0032731 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of interleukin-1 beta production, biological_process}, {{MALT1}}}},
GO:0045410 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of interleukin-6 biosynthetic process, biological_process}, {{TIRAP}}}},
GO:0060252 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of glial cell proliferation, biological_process}, {{LYN}}}},
GO:0071044 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{histone mRNA catabolic process, biological_process}, {{ATM}}}},
GO:0010744 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKB1}}}}, GO:0010875 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cholesterol efflux, biological_process}, {{NFKBIA}}}},
GO:0016540 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein autoprocessing, biological_process}, {{PARP1}}}},
GO:0019789 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{SUMO transferase activity, molecular_function}, {{PIAS4}}}},
GO:0032270 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cellular protein metabolic process, biological_process}, {{NFKBIA}}}},
GO:0034142 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{toll-like receptor 4 signaling pathway, biological_process}, {{NFKBIA}}}},
GO:0071354 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{cellular response to interleukin-6, biological_process}, {{NFKB1}}}},
GO:1901222 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{regulation of NIK/NF-kappaB signaling, biological_process}, {{NFKBIA}}}},
GO:1990404 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein ADP-ribosylase activity, molecular_function}, {{PARP1}}}},
GO:2000679 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of transcription regulatory region DNA binding, biological_process}, {{PARP1}}}},
GO:0042493 → {{0.0163579, 0.0341685, True}, {20, 195, 19774, 2},
  {{response to drug, biological_process}, {{CHUK}, {LYN}}}},
GO:0004724 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{magnesium-dependent protein serine/threonine phosphatase activity, molecular_function}, {{TAB1}}}},
GO:0008340 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{determination of adult lifespan, biological_process}, {{ATM}}}},
GO:0034162 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{toll-like receptor 9 signaling pathway, biological_process}, {{IRAK4}}}},
GO:1903146 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{regulation of autophagy of mitochondrion, biological_process}, {{CSNK2A2}}}},
GO:0010469 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of signaling receptor activity, biological_process}, {{PLAU}}}},
GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid cell differentiation, biological_process}, {{TIRAP}}}},
GO:0031668 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{cellular response to extracellular stimulus, biological_process}, {{LYN}}}},
GO:0043011 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid dendritic cell differentiation, biological_process}, {{LTBR}}}},
GO:0043537 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of blood vessel endothelial cell migration, biological_process}, {{CSNK2B}}}},
GO:0045638 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of myeloid cell differentiation, biological_process}, {{NFKBIA}}}}, GO:0090734 →
 {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1}, {{site of DNA damage, cellular_component}, {{PARP1}}}},
GO:1903827 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of cellular protein localization, biological_process}, {{PARP1}}}},
GO:0010008 → {{0.0188076, 0.0374078, True}, {20, 210, 19774, 2},
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
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GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196568, 0.0385302, True}, {20, 215, 19774, 2},
  {{regulation of apoptotic process, biological_process}, {{MALT1}, {ATM}}}},
GO:0002756 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{macrophage differentiation, biological_process}, {{PARP1}}}},
GO:0032991 → {{0.0204617, 0.0395348, True}, {20, 588, 19774, 3},
  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
 {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1}, {{aorta development, biological_process}, {{TAB1}}}},
GO:0042098 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{T cell proliferation, biological_process}, {{MALT1}}}},
GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
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GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
 {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
```

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```
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
  {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{DNA damage checkpoint, biological_process}, {{ATM}}}},
GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
```

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```
GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|⟩
```

GO annotation by default will use input IDs converted to UniProt IDs or as set by the option `OutputID`.

MultipleList (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`MultipleList` values can be set to True (default is False) to specify whether the input accessions list constituted a multi-omics list input that is annotated so. In such an annotation, each input list ID should have the form {ID,"Omics Type Label"}, e.g. {"NFKB1","Protein"}, and the different omics type are treated as different for each ID. If MultipleList is set to False, and labeled IDs are provided, labels corresponding to the same ID are treated as equivalent to avoid over-counting.

The data can be mixed, e.g. proteins and RNA with different labels. If MultipleList is set to False (default) then IDs with different label e.g ({NFKB1,Protein},{NFKB1,RNA}) are treated as equivalent, and reported together:

In[2]:=
```
analysisGOMultipleListFalse =
 GOAnalysis[{{"TAB1", "Protein"}, {"TAB1", "RNA"}, {"TNFSF13B", "Protein"}, {"MALT1", "RNA"},
   {"TIRAP", "RNA"}, {"CHUK", "Protein"}, {"TNFRSF13C", "Protein"}, {"PARP1", "RNA"},
   {"CSNK2A1", "RNA"}, {"CSNK2A2", "RNA"}, {"CSNK2B", "RNA"}, {"LTBR", "Protein"}, {"LTBR", "RNA"},
   {"LYN", "RNA"}, {"MYD88", "Protein"}, {"GADD45B", "Protein"} {"ATM", "RNA"}, {"NFKB1", "Protein"},
   {"NFKB1", "RNA"}, {"NFKB2", "Protein"}, {"NFKBIA", "RNA"}, {"NFKBIA", "Protein"},
   {"IRAK4", "RNA"}, {"PIAS4", "RNA"}, {"PLAU", "Protein"}}, MultipleList → False]
```

Out[2]=
```
⟨|GO:0051092 → {{3.90453×10^-11, 1.86246×10^-8, True}, {18, 151, 19774, 7},
   {{positive regulation of NF-kappaB transcription factor activity, biological_process},
    {{{TAB1, Protein}, {TAB1, RNA}}, {{MALT1, RNA}}, ⋯ 4 ⋯, {{IRAK4, RNA}}}}},
 ⋯ 299 ⋯, GO:0051219 → {⋯ 1 ⋯}|⟩
```

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We can instead treat the data as different by setting the `MultipleList` option to True. In this case IDs with different label e.g ({NFKB1,Protein},{NFKB1,RNA}) are treated as different and counted as such:

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In[3]:=
```
analysisGOMultipleListTrue =
 GOAnalysis[{{"TAB1", "Protein"}, {"TAB1", "RNA"}, {"TNFSF13B", "Protein"}, {"MALT1", "RNA"},
   {"TIRAP", "RNA"}, {"CHUK", "Protein"}, {"TNFRSF13C", "Protein"}, {"PARP1", "RNA"},
   {"CSNK2A1", "RNA"}, {"CSNK2A2", "RNA"}, {"CSNK2B", "RNA"}, {"LTBR", "Protein"}, {"LTBR", "RNA"},
   {"LYN", "RNA"}, {"MYD88", "Protein"}, {"GADD45B", "Protein"} {"ATM", "RNA"}, {"NFKB1", "Protein"},
   {"NFKB1", "RNA"}, {"NFKB2", "Protein"}, {"NFKBIA", "RNA"}, {"NFKBIA", "Protein"},
   {"IRAK4", "RNA"}, {"PIAS4", "RNA"}, {"PLAU", "Protein"}}, MultipleList → True]
```

Out[3]=
```
<|GO:0033256 → {{0., 0., True}, {22, 2, 19774, 4}, {{I-kappaB/NF-kappaB complex, cellular_component},
    {{{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
  ⋯317⋯, GO:0043552 → {{0.032868, 0.0491474, True}, {⋯1⋯}, {{⋯, ⋯20⋯}, ⋯1⋯}}|>
```

large output | show less | show more | show all | set size limit...

We using the `MultipleList` option as True we should consider also whether to add a `MultipleListCorrection` option.

MultipleListCorrection (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MultipleListCorrection is an option whether or not to correct for multi-omics analysis. The choices are the None (default), or Automatic, or a custom number. This essentially enlarges the population by this factor to account for additional IDs being considered as the result of a multi-omics cluster analysis. If the value is set to Automatic the number of unique ID labels is used to make the correction. This option is used in conjunction to setting `MultipleList → True`.

In[2]:=
```
analysisGOMultipleListTrue =
 GOAnalysis[{{"TAB1", "Protein"}, {"TAB1", "RNA"}, {"TNFSF13B", "Protein"}, {"MALT1", "RNA"},
   {"TIRAP", "RNA"}, {"CHUK", "Protein"}, {"TNFRSF13C", "Protein"}, {"PARP1", "RNA"},
   {"CSNK2A1", "RNA"}, {"CSNK2A2", "RNA"}, {"CSNK2B", "RNA"}, {"LTBR", "Protein"}, {"LTBR", "RNA"},
   {"LYN", "RNA"}, {"MYD88", "Protein"}, {"GADD45B", "Protein"}, {"ATM", "RNA"}, {"NFKB1", "Protein"},
   {"NFKB1", "RNA"}, {"NFKB2", "Protein"}, {"NFKBIA", "RNA"}, {"NFKBIA", "Protein"}, {"IRAK4", "RNA"},
   {"PIAS4", "RNA"}, {"PLAU", "Protein"}}, MultipleList → True, MultipleListCorrection → Automatic]
```

Out[2]=
```
<|GO:0051092 → {{9.26699×10^-14, 2.82044×10^-11, True}, {24, 302, 39548, 9},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{{TAB1, Protein}}, {{TAB1, RNA}}, ⋯5⋯, {{NFKB2, Protein}}, {{IRAK4, RNA}}}}}},
  ⋯341⋯, GO:0070911 → ⋯1⋯|>
```

large output | show less | show more | show all | set size limit...

OBOGODictionaryOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`OBOGODictionaryOptions` values specify a list of options to be passed to the internal OBOGODictionary function that provides the GO annotations. For example, we may want to update the OBO information by reimporting the data.

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```
In[2]:= goExampleOBOGODictionaryOpts =
         GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
           "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
           "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, OBOGODictionaryOptions → {ImportDirectly → True}]

Out[2]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
           {{positive regulation of NF-kappaB transcription factor activity, biological_process},
            {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
         GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
           {{interleukin-1-mediated signaling pathway, biological_process},
            {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
         GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
           {{stimulatory C-type lectin receptor signaling pathway, biological_process},
            {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
         GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
           {{tumor necrosis factor-mediated signaling pathway, biological_process},
            {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
         GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
           {{Fc-epsilon receptor signaling pathway, biological_process},
            {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
          {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
            {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
         GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
           {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
            {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
         GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
           {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
         GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
           {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
         GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
           {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
         GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
           {{protein serine/threonine kinase activity, molecular_function},
            {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
         GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
           {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
         GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
           {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
         GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
           {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
         GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
           {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
         GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
           {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
          {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
            {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
         GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
           {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
            {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
           {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
         GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
           {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
         GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
           {{regulation of signal transduction by p53 class mediator, biological_process},
            {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
           {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
            {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
          {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
            {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
             {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
```

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```
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
```

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```
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
  {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{B-1 B cell differentiation, biological_process}, {{MALT1}}}},
GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of Fc receptor mediated stimulatory signaling pathway, biological_process},
   {{LYN}}}}, GO:0061847 → {{0.00202189, 0.0130219, True},
  {20, 2, 19774, 1}, {{response to cholecystokinin, biological_process}, {{CHUK}}}},
GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0070668 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{cellular response to bacterial lipopeptide, biological_process}, {{TIRAP}}}},
GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of RNA localization to telomere, biological_process}, {{ATM}}}},
GO:0097695 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of protein-containing complex localization to telomere, biological_process}, {{ATM}}}},
GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of single strand break repair, biological_process}, {{PARP1}}}},
GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
```

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```
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
  {{ATP binding, molecular_function}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {LYN}, {ATM}, {IRAK4}}}},
GO:0016301 → {{0.00292933, 0.0149088, True}, {20, 80, 19774, 2},
  {{kinase activity, molecular_function}, {{CSNK2A1}, {LYN}}}},
GO:0002331 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{tolerance induction to self antigen, biological_process}, {{LYN}}}},
GO:0002553 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{histamine secretion by mast cell, biological_process}, {{LYN}}}},
GO:0002762 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of myeloid leukocyte differentiation, biological_process}, {{LYN}}}},
GO:0002774 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{Fc receptor mediated inhibitory signaling pathway, biological_process}, {{LYN}}}},
GO:0002902 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{regulation of B cell apoptotic process, biological_process}, {{LYN}}}},
GO:0004677 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{DNA-dependent protein kinase activity, molecular_function}, {{ATM}}}},
GO:0008384 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{IkappaB kinase activity, molecular_function}, {{CHUK}}}},
GO:0010956 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of calcidiol 1-monooxygenase activity, biological_process}, {{NFKB1}}}},
GO:0030592 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{DNA ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{integrin alpha2-beta1 complex, cellular_component}, {{LYN}}}},
GO:0035663 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{Toll-like receptor 2 binding, molecular_function}, {{TIRAP}}}},
GO:0070447 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of oligodendrocyte progenitor proliferation, biological_process}, {{LYN}}}},
GO:0071500 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{cellular response to nitrosative stress, biological_process}, {{ATM}}}},
GO:0099091 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{postsynaptic specialization, intracellular component, cellular_component}, {{LYN}}}},
GO:0140031 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{phosphorylation-dependent protein binding, molecular_function}, {{LYN}}}},
GO:0140294 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{NAD DNA ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:1902174 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of keratinocyte apoptotic process, biological_process}, {{PIAS4}}}},
GO:1904044 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{response to aldosterone, biological_process}, {{PARP1}}}},
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  {{SUMO transferase activity, molecular_function}, {{PIAS4}}}},
GO:0032270 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cellular protein metabolic process, biological_process}, {{NFKBIA}}}},
GO:0034142 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{toll-like receptor 4 signaling pathway, biological_process}, {{NFKBIA}}}},
GO:0071354 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{cellular response to interleukin-6, biological_process}, {{NFKB1}}}},
GO:1901222 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{regulation of NIK/NF-kappaB signaling, biological_process}, {{NFKBIA}}}},
GO:1990404 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein ADP-ribosylase activity, molecular_function}, {{PARP1}}}},
GO:2000679 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of transcription regulatory region DNA binding, biological_process}, {{PARP1}}}},
GO:0042493 → {{0.0163579, 0.0341685, True}, {20, 195, 19774, 2},
  {{response to drug, biological_process}, {{CHUK}, {LYN}}}},
GO:0004724 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{magnesium-dependent protein serine/threonine phosphatase activity, molecular_function}, {{TAB1}}}},
GO:0008340 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{determination of adult lifespan, biological_process}, {{ATM}}}},
GO:0034162 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{toll-like receptor 9 signaling pathway, biological_process}, {{IRAK4}}}},
GO:1903146 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{regulation of autophagy of mitochondrion, biological_process}, {{CSNK2A2}}}},
GO:0010469 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of signaling receptor activity, biological_process}, {{PLAU}}}},
GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid cell differentiation, biological_process}, {{TIRAP}}}},
GO:0031668 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{cellular response to extracellular stimulus, biological_process}, {{LYN}}}},
GO:0043011 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid dendritic cell differentiation, biological_process}, {{LTBR}}}},
GO:0043537 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of blood vessel endothelial cell migration, biological_process}, {{CSNK2B}}}},
GO:0045638 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of myeloid cell differentiation, biological_process}, {{NFKBIA}}}}, GO:0090734 →
 {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1}, {{site of DNA damage, cellular_component}, {{PARP1}}}},
GO:1903827 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of cellular protein localization, biological_process}, {{PARP1}}}},
GO:0010008 → {{0.0188076, 0.0374078, True}, {20, 210, 19774, 2},
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```
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196568, 0.0385302, True}, {20, 215, 19774, 2},
  {{regulation of apoptotic process, biological_process}, {{MALT1}, {ATM}}}},
GO:0002756 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{macrophage differentiation, biological_process}, {{PARP1}}}},
GO:0032991 → {{0.0204617, 0.0395348, True}, {20, 588, 19774, 3},
  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
 {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1}, {{aorta development, biological_process}, {{TAB1}}}},
GO:0042098 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{T cell proliferation, biological_process}, {{MALT1}}}},
GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
 {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
```

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GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
  {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{DNA damage checkpoint, biological_process}, {{ATM}}}},
GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
```

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```
    {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
  GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
  GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
  GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|⟩
```

OBODictionaryVariable (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`OBODictionaryVariable` values point to an alternative GO annotation variable. By defaut the value is set to None, and OBOGODictionary will be used to automatically generate the default GO annotation.

For example we create the OBO dictionary directly:

In[2]:=
```
oboVar = OBOGODictionary[]
```

Out[2]=
```
⟨|GO:0000001 → {mitochondrion inheritance, biological_process},
 GO:0000002 → {mitochondrial genome maintenance, biological_process},
 ⋯ 47397 ⋯, GO:2001316 → {kojic acid metabolic process, biological_process},
 GO:2001317 → {kojic acid biosynthetic process, biological_process}|⟩
```

large output | show less | show more | show all | set size limit...

In[3]:=
```
goExampleOBOGODictionaryVar =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
   "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
   "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, OBODictionaryVariable → oboVar]
```

Out[3]=
```
⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
```

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```
GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
  {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
  {{protein serine/threonine kinase activity, molecular_function},
   {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
  {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
  {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
 {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
   {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
   {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
  {{regulation of signal transduction by p53 class mediator, biological_process},
   {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
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    {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
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     {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
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GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
   {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
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GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
   {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
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GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
   {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
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GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
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GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
    {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
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GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
   {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
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GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
   {{positive regulation of transcription by RNA polymerase II, biological_process},
    {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
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GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
   {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
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     {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
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GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
   {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
   {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
   {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
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GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
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GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
   {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
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GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
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GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
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GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
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  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
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GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
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GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
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GO:0002774 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:2000670 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:2001170 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0000724 → {{0.00314887, 0.0153472, True}, {20, 83, 19774, 2},
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GO:0032648 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0034136 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0016363 → {{0.00536146, 0.0202836, True}, {20, 109, 19774, 2},
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GO:0006954 → {{0.00567463, 0.0211305, True}, {20, 366, 19774, 3},
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GO:0034774 → {{0.00594922, 0.0211305, True}, {20, 115, 19774, 2},
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GO:0051972 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
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GO:1902231 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
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GO:0007253 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0014909 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0032210 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0033211 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:1990266 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
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GO:0042127 → {{0.00881826, 0.0259564, True}, {20, 141, 19774, 2},
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  GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
    {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
  GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
    {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
  GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
    {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
  GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
    {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
  GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
    {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
  GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
    {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
  GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
    {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
   {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
  GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
    {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
  GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{response to testosterone, biological_process}, {{CSNK2B}}}},
  GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
  GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
  GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
    {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
  GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{DNA damage checkpoint, biological_process}, {{ATM}}}},
  GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
  GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
  GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
  GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

OntologyLengthFilter (1)

```
In[1]:= Needs["MathIOmica`"]
```

`OntologyLengthFilter` can be used to set the value for which terms to consider in the computation, by excluding GO terms that have fewer items compared to the OntologyLengthFilter value (the default is to exclude terms with single memberships, i.e. `OntologyLengthFilter → 2`. It is used by the internal GOAnalysisAssigner function (and if no other `GOAnalysisAssignerOptions` are assigned).

In this example we set the `OntologyLengthFilter` to 3:

```
In[2]:= goExampleOntologyLengthFilter =
  GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
    "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM",
    "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, OntologyLengthFilter → 3]
```

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```
Out[2]= ⟨|GO:0051092 → {{9.39682×10^-11, 4.89574×10^-8, True}, {20, 151, 19772, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.37149×10^-8, 8.78272×10^-6, True}, {20, 95, 19772, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.72254×10^-8, 0.0000114855, True}, {20, 112, 19772, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81803×10^-8, 0.0000114855, True}, {20, 115, 19772, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36898×10^-7, 0.0000594349, True}, {20, 171, 19772, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10604×10^-7, 0.0000594349, True}, {20, 551, 19772, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.9855×10^-7, 0.0000594349, True}, {20, 179, 19772, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0001782 → {{1.16353×10^-6, 0.0000684867, True}, {20, 21, 19772, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
  GO:0004674 → {{1.18307×10^-6, 0.0000684867, True}, {20, 365, 19772, 6},
    {{protein serine/threonine kinase activity, molecular_function},
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
  GO:0031519 → {{2.54901×10^-6, 0.000116804, True}, {20, 27, 19772, 3},
    {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0002636 → {{2.91449×10^-6, 0.000116804, True}, {20, 3, 19772, 2},
    {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0005956 → {{2.91449×10^-6, 0.000116804, True}, {20, 3, 19772, 2},
    {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
  GO:0031296 → {{2.91449×10^-6, 0.000116804, True}, {20, 3, 19772, 2},
    {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0047485 → {{3.53895×10^-6, 0.0001317, True}, {20, 106, 19772, 4},
    {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
  GO:0042802 → {{4.50137×10^-6, 0.000145154, True}, {20, 1054, 19772, 8}, {{identical protein binding,
      molecular_function}, {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
  GO:0002755 → {{4.7363×10^-6, 0.000145154, True}, {20, 33, 19772, 3},
    {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
     {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.7363×10^-6, 0.000145154, True}, {20, 33, 19772, 3},
    {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0031663 → {{5.1913×10^-6, 0.000150259, True}, {20, 34, 19772, 3},
    {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
  GO:1901796 → {{8.21256×10^-6, 0.000225197, True}, {20, 131, 19772, 4},
    {{regulation of signal transduction by p53 class mediator, biological_process},
     {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}},
  GO:0030890 → {{9.20621×10^-6, 0.000239822, True}, {20, 41, 19772, 3},
    {{positive regulation of B cell proliferation, biological_process},
     {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
   {{0.000012325, 0.000305776, True}, {20, 9629, 19772, 19}, {{protein binding, molecular_function},
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  GO:0018105 → {{0.0000180869, 0.00042833, True}, {20, 160, 19772, 4},
    {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
  GO:0031295 → {{0.0000200752, 0.000454747, True}, {20, 53, 19772, 3},
    {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
   {{0.0000309507, 0.000666269, True}, {20, 977, 19772, 7}, {{signal transduction, biological_process},
     {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
  GO:0016055 → {{0.0000319707, 0.000666269, True}, {20, 185, 19772, 4},
    {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
```

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```
GO:0007249 → {{0.0000371435, 0.000744298, True}, {20, 65, 19 772, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531734, 0.00102605, True}, {20, 11, 19 772, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641514, 0.00115251, True}, {20, 78, 19 772, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641514, 0.00115251, True}, {20, 78, 19 772, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691924, 0.00120164, True}, {20, 80, 19 772, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.000075318, 0.00126583, True}, {20, 13, 19 772, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101267, 0.00164875, True}, {20, 15, 19 772, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.000111543, 0.0016739, True}, {20, 497, 19 772, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115446, 0.0016739, True}, {20, 95, 19 772, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.000115663, 0.0016739, True}, {20, 16, 19 772, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.000115663, 0.0016739, True}, {20, 16, 19 772, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.00014275, 0.00201007, True}, {20, 5639, 19 772, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147292, 0.00201945, True}, {20, 18, 19 772, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000180063, 0.00240546, True}, {20, 289, 19 772, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.00023049, 0.00300214, True}, {20, 120, 19 772, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.000302296, 0.00384137, True}, {20, 331, 19 772, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311359, 0.00386234, True}, {20, 26, 19 772, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321573, 0.00389088, True}, {20, 4436, 19 772, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000333073, 0.00389088, True}, {20, 136, 19 772, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000336064, 0.00389088, True}, {20, 27, 19 772, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.00039996, 0.00452998, True}, {20, 3142, 19 772, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415733, 0.00460844, True}, {20, 30, 19 772, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.00042671, 0.00463158, True}, {20, 148, 19 772, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473456, 0.0050341, True}, {20, 32, 19 772, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678544, 0.00707043, True}, {20, 1134, 19 772, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718793, 0.00734296, True}, {20, 177, 19 772, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896457, 0.00898181, True}, {20, 44, 19 772, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106634, 0.0104823, True}, {20, 48, 19 772, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00111033, 0.0107126, True}, {20, 5035, 19 772, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120311, 0.0113967, True}, {20, 51, 19 772, 2},
```

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```
    {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
  GO:0006468 → {{0.00131673, 0.0122502, True}, {20, 490, 19 772, 4},
    {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
  GO:0006303 → {{0.00134786, 0.0123199, True}, {20, 54, 19 772, 2},
    {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
  GO:0030335 → {{0.0014004, 0.0125794, True}, {20, 223, 19 772, 3},
    {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
  GO:0042102 → {{0.00166112, 0.0146685, True}, {20, 60, 19 772, 2},
    {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0006974 → {{0.00174899, 0.0151391, True}, {20, 241, 19 772, 3},
    {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
  GO:0038061 → {{0.00177253, 0.0151391, True}, {20, 62, 19 772, 2},
    {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
  GO:0005886 → {{0.00187046, 0.0157179, True}, {20, 4532, 19 772, 11},
    {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
      {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
  GO:0009636 → {{0.00194614, 0.0160943, True}, {20, 65, 19 772, 2},
    {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
  GO:0048511 → {{0.00200575, 0.016328, True}, {20, 66, 19 772, 2},
    {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
  GO:0071300 → {{0.00218972, 0.0175501, True}, {20, 69, 19 772, 2},
    {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
  GO:0071260 → {{0.00285839, 0.0175501, True}, {20, 79, 19 772, 2},
    {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
  GO:0005524 → {{0.0029031, 0.0175501, True}, {20, 1501, 19 772, 6},
    {{ATP binding, molecular_function}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {LYN}, {ATM}, {IRAK4}}}},
  GO:0016301 → {{0.00292991, 0.0175501, True}, {20, 80, 19 772, 2},
    {{kinase activity, molecular_function}, {{CSNK2A1}, {LYN}}}},
  GO:0002331 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
  GO:0002513 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{tolerance induction to self antigen, biological_process}, {{LYN}}}},
  GO:0002553 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{histamine secretion by mast cell, biological_process}, {{LYN}}}},
  GO:0002762 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{negative regulation of myeloid leukocyte differentiation, biological_process}, {{LYN}}}},
  GO:0002774 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{Fc receptor mediated inhibitory signaling pathway, biological_process}, {{LYN}}}},
  GO:0002902 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{regulation of B cell apoptotic process, biological_process}, {{LYN}}}},
  GO:0004677 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{DNA-dependent protein kinase activity, molecular_function}, {{ATM}}}},
  GO:0008384 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{IkappaB kinase activity, molecular_function}, {{CHUK}}}},
  GO:0010956 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{negative regulation of calcidiol 1-monooxygenase activity, biological_process}, {{NFKB1}}}},
  GO:0030592 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{DNA ADP-ribosylation, biological_process}, {{PARP1}}}},
  GO:0034666 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{integrin alpha2-beta1 complex, cellular_component}, {{LYN}}}},
  GO:0035663 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{Toll-like receptor 2 binding, molecular_function}, {{TIRAP}}}},
  GO:0070447 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{positive regulation of oligodendrocyte progenitor proliferation, biological_process}, {{LYN}}}},
  GO:0071500 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{cellular response to nitrosative stress, biological_process}, {{ATM}}}},
  GO:0099091 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{postsynaptic specialization, intracellular component, cellular_component}, {{LYN}}}},
  GO:0140031 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{phosphorylation-dependent protein binding, molecular_function}, {{LYN}}}},
  GO:0140294 → {{0.00303168, 0.0175501, True}, {20, 3, 19 772, 1},
    {{NAD DNA ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
```

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GO:1902174 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{positive regulation of keratinocyte apoptotic process, biological_process}, {{PIAS4}}}},
GO:1904044 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{response to aldosterone, biological_process}, {{PARP1}}}},
GO:2000630 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{positive regulation of miRNA metabolic process, biological_process}, {{NFKB1}}}},
GO:2000670 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{positive regulation of dendritic cell apoptotic process, biological_process}, {{LYN}}}},
GO:2001170 → {{0.00303168, 0.0175501, True}, {20, 3, 19772, 1},
  {{negative regulation of ATP biosynthetic process, biological_process}, {{PARP1}}}},
GO:0000724 → {{0.00314949, 0.0180317, True}, {20, 83, 19772, 2},
  {{double-strand break repair via homologous recombination, biological_process}, {{PARP1}, {ATM}}}},
GO:0010957 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{negative regulation of vitamin D biosynthetic process, biological_process}, {{NFKB1}}}},
GO:0018312 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{peptidyl-serine ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0032375 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{negative regulation of cholesterol transport, biological_process}, {{NFKB1}}}}, GO:0032449 →
 {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1}, {{CBM complex, cellular_component}, {{MALT1}}}},
GO:0032648 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{regulation of interferon-beta production, biological_process}, {{TIRAP}}}},
GO:0048305 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{immunoglobulin secretion, biological_process}, {{TNFSF13B}}}},
GO:0071359 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{cellular response to dsRNA, biological_process}, {{NFKB1}}}},
GO:0090330 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{regulation of platelet aggregation, biological_process}, {{LYN}}}},
GO:1900127 → {{0.0040403, 0.0202403, True}, {20, 4, 19772, 1},
  {{positive regulation of hyaluronan biosynthetic process, biological_process}, {{NFKB1}}}},
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  {{cellular response to extracellular stimulus, biological_process}, {{LYN}}}},
GO:0043011 → {{0.0180596, 0.0374862, True}, {20, 18, 19772, 1},
  {{myeloid dendritic cell differentiation, biological_process}, {{LTBR}}}},
GO:0043537 → {{0.0180596, 0.0374862, True}, {20, 18, 19772, 1},
  {{negative regulation of blood vessel endothelial cell migration, biological_process}, {{CSNK2B}}}},
GO:0045638 → {{0.0180596, 0.0374862, True}, {20, 18, 19772, 1},
  {{negative regulation of myeloid cell differentiation, biological_process}, {{NFKBIA}}}}, GO:0090734 →
 {{0.0180596, 0.0374862, True}, {20, 18, 19772, 1}, {{site of DNA damage, cellular_component}, {{PARP1}}}},
GO:1903827 → {{0.0180596, 0.0374862, True}, {20, 18, 19772, 1},
  {{regulation of cellular protein localization, biological_process}, {{PARP1}}}},
GO:0010008 → {{0.0188112, 0.0388914, True}, {20, 210, 19772, 2},
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
GO:0031293 → {{0.0190537, 0.0389294, True}, {20, 19, 19772, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190537, 0.0389294, True}, {20, 19, 19772, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190537, 0.0389294, True}, {20, 19, 19772, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196606, 0.0400123, True}, {20, 215, 19772, 2},
  {{regulation of apoptotic process, biological_process}, {{MALT1}, {ATM}}}},
GO:0002756 → {{0.0200469, 0.0403261, True}, {20, 20, 19772, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200469, 0.0403261, True}, {20, 20, 19772, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200469, 0.0403261, True}, {20, 20, 19772, 1},
  {{macrophage differentiation, biological_process}, {{PARP1}}}},
GO:0032991 → {{0.0204671, 0.0410129, True}, {20, 588, 19772, 3},
  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210392, 0.041054, True}, {20, 21, 19772, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210392, 0.041054, True}, {20, 21, 19772, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210392, 0.041054, True}, {20, 21, 19772, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
 {{0.0210392, 0.041054, True}, {20, 21, 19772, 1}, {{aorta development, biological_process}, {{TAB1}}}},
GO:0042098 → {{0.0210392, 0.041054, True}, {20, 21, 19772, 1},
  {{T cell proliferation, biological_process}, {{MALT1}}}},
GO:0045088 → {{0.0210392, 0.041054, True}, {20, 21, 19772, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210392, 0.041054, True}, {20, 21, 19772, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220305, 0.0420436, True}, {20, 22, 19772, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220305, 0.0420436, True}, {20, 22, 19772, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220305, 0.0420436, True}, {20, 22, 19772, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220305, 0.0420436, True}, {20, 22, 19772, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220305, 0.0420436, True}, {20, 22, 19772, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220305, 0.0420436, True}, {20, 22, 19772, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230208, 0.0432991, True}, {20, 23, 19772, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230208, 0.0432991, True}, {20, 23, 19772, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
```

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```
 {{0.0230208, 0.0432991, True}, {20, 23, 19772, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230208, 0.0432991, True}, {20, 23, 19772, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240102, 0.0448363, True}, {20, 24, 19772, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240102, 0.0448363, True}, {20, 24, 19772, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241446, 0.0449262, True}, {20, 240, 19772, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249987, 0.0453809, True}, {20, 25, 19772, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249987, 0.0453809, True}, {20, 25, 19772, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249987, 0.0453809, True}, {20, 25, 19772, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249987, 0.0453809, True}, {20, 25, 19772, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249987, 0.0453809, True}, {20, 25, 19772, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249987, 0.0453809, True}, {20, 25, 19772, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249987, 0.0453809, True}, {20, 25, 19772, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258531, 0.0462075, True}, {20, 249, 19772, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259862, 0.0462075, True}, {20, 26, 19772, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}},
GO:0001816 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.0269727, 0.0468426, True}, {20, 27, 19772, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279583, 0.0480735, True}, {20, 28, 19772, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279583, 0.0480735, True}, {20, 28, 19772, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279583, 0.0480735, True}, {20, 28, 19772, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286065, 0.0486428, True}, {20, 263, 19772, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288075, 0.0486428, True}, {20, 264, 19772, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.028943, 0.0486428, True}, {20, 29, 19772, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.028943, 0.0486428, True}, {20, 29, 19772, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
```

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```
GO:0035666 → {{0.028943, 0.0486428, True}, {20, 29, 19772, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.028943, 0.0486428, True}, {20, 29, 19772, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.028943, 0.0486428, True}, {20, 29, 19772, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298215, 0.0496554, True}, {20, 269, 19772, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299267, 0.0496554, True}, {20, 30, 19772, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299267, 0.0496554, True}, {20, 30, 19772, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299267, 0.0496554, True}, {20, 30, 19772, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}}|>
```

OutputID (1)

```
In[1]:= Needs["MathIOmica`"]
```

The OutputID option string specifies what kind of IDs/accessions to convert the input IDs to compute the GO enrichment. GO annotation by default will use input IDs converted to "UniProt ID" (default value). This setting is to be used/modified in applications where other identifiers are required, e.g. modifying the GOAnalysisAssigner with a `GOFileColumns` option when importing new information.

In this example we set the OutputID to "UniProt ID" for the purposes of illustrating usage:

```
In[2]:= goExampleOutputID = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, OutputID → "UniProt ID"]

Out[2]= <|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
   {{positive regulation of NF-kappaB transcription factor activity, biological_process},
    {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
 GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
   {{interleukin-1-mediated signaling pathway, biological_process},
    {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
   {{stimulatory C-type lectin receptor signaling pathway, biological_process},
    {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
 GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
   {{tumor necrosis factor-mediated signaling pathway, biological_process},
    {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
 GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
   {{Fc-epsilon receptor signaling pathway, biological_process},
    {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
  {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
    {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
 GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
   {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
    {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
 GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
   {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
 GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
   {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
 GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
   {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
 GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
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```
  {{protein serine/threonine kinase activity, molecular_function},
   {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
  {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
  {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
 {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
   {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
   {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
  {{regulation of signal transduction by p53 class mediator, biological_process},
   {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
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GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
  {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{B-1 B cell differentiation, biological_process}, {{MALT1}}}},
GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
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GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of Fc receptor mediated stimulatory signaling pathway, biological_process},
   {{LYN}}}}, GO:0061847 → {{0.00202189, 0.0130219, True},
  {20, 2, 19774, 1}, {{response to cholecystokinin, biological_process}, {{CHUK}}}},
GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0070668 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{cellular response to bacterial lipopeptide, biological_process}, {{TIRAP}}}},
GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of RNA localization to telomere, biological_process}, {{ATM}}}},
GO:0097695 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{establishment of protein-containing complex localization to telomere, biological_process}, {{ATM}}}},
GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of single strand break repair, biological_process}, {{PARP1}}}},
GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
  {{ATP binding, molecular_function}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {LYN}, {ATM}, {IRAK4}}}},
GO:0016301 → {{0.00292933, 0.0149088, True}, {20, 80, 19774, 2},
  {{kinase activity, molecular_function}, {{CSNK2A1}, {LYN}}}},
GO:0002331 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{tolerance induction to self antigen, biological_process}, {{LYN}}}},
GO:0002553 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{histamine secretion by mast cell, biological_process}, {{LYN}}}},
GO:0002762 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of myeloid leukocyte differentiation, biological_process}, {{LYN}}}},
GO:0002774 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{Fc receptor mediated inhibitory signaling pathway, biological_process}, {{LYN}}}},
GO:0002902 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{regulation of B cell apoptotic process, biological_process}, {{LYN}}}},
GO:0004677 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{DNA-dependent protein kinase activity, molecular_function}, {{ATM}}}},
GO:0008384 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{IkappaB kinase activity, molecular_function}, {{CHUK}}}},
GO:0010956 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of calcidiol 1-monooxygenase activity, biological_process}, {{NFKB1}}}},
GO:0030592 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{DNA ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{integrin alpha2-beta1 complex, cellular_component}, {{LYN}}}},
GO:0035663 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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  {{Toll-like receptor 2 binding, molecular_function}, {{TIRAP}}}},
GO:0070447 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of oligodendrocyte progenitor proliferation, biological_process}, {{LYN}}}},
GO:0071500 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{cellular response to nitrosative stress, biological_process}, {{ATM}}}},
GO:0099091 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{postsynaptic specialization, intracellular component, cellular_component}, {{LYN}}}},
GO:0140031 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{phosphorylation-dependent protein binding, molecular_function}, {{LYN}}}},
GO:0140294 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{NAD DNA ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:1902174 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of keratinocyte apoptotic process, biological_process}, {{PIAS4}}}},
GO:1904044 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{response to aldosterone, biological_process}, {{PARP1}}}},
GO:2000630 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of miRNA metabolic process, biological_process}, {{NFKB1}}}},
GO:2000670 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of dendritic cell apoptotic process, biological_process}, {{LYN}}}},
GO:2001170 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of ATP biosynthetic process, biological_process}, {{PARP1}}}},
GO:0000724 → {{0.00314887, 0.0153472, True}, {20, 83, 19774, 2},
  {{double-strand break repair via homologous recombination, biological_process}, {{PARP1}, {ATM}}}},
GO:0010957 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{negative regulation of vitamin D biosynthetic process, biological_process}, {{NFKB1}}}},
GO:0018312 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0032375 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{negative regulation of cholesterol transport, biological_process}, {{NFKB1}}}}, GO:0032449 →
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GO:0032648 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{regulation of interferon-beta production, biological_process}, {{TIRAP}}}},
GO:0048305 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{immunoglobulin secretion, biological_process}, {{TNFSF13B}}}},
GO:0071359 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{cellular response to dsRNA, biological_process}, {{NFKB1}}}},
GO:0090330 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{regulation of platelet aggregation, biological_process}, {{LYN}}}},
GO:1900127 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{positive regulation of hyaluronan biosynthetic process, biological_process}, {{NFKB1}}}},
GO:1903978 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{regulation of microglial cell activation, biological_process}, {{ATM}}}},
GO:1990234 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{transferase complex, cellular_component}, {{PIAS4}}}},
GO:1990966 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{ATP generation from poly-ADP-D-ribose, biological_process}, {{PARP1}}}},
GO:2000321 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{positive regulation of T-helper 17 cell differentiation, biological_process}, {{MALT1}}}},
GO:0005102 → {{0.00432566, 0.0187215, True}, {20, 332, 19774, 3},
  {{signaling receptor binding, molecular_function}, {{TNFSF13B}, {CSNK2B}, {LYN}}}},
GO:0007179 → {{0.00444549, 0.0190874, True}, {20, 99, 19774, 2},
  {{transforming growth factor beta receptor signaling pathway, biological_process}, {{TAB1}, {PARP1}}}},
GO:0014910 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{regulation of smooth muscle cell migration, biological_process}, {{PLAU}}}},
GO:0032042 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{mitochondrial DNA metabolic process, biological_process}, {{PARP1}}}},
GO:0032269 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{negative regulation of cellular protein metabolic process, biological_process}, {{NFKB1}}}},
GO:0034136 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{negative regulation of toll-like receptor 2 signaling pathway, biological_process}, {{LYN}}}},
GO:0035662 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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  {{Toll-like receptor 4 binding, molecular_function}, {{TIRAP}}}},
GO:0042159 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{lipoprotein catabolic process, biological_process}, {{ATM}}}},
GO:0043208 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{glycosphingolipid binding, molecular_function}, {{LYN}}}},
GO:0043504 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{mitochondrial DNA repair, biological_process}, {{PARP1}}}},
GO:0048273 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{mitogen-activated protein kinase p38 binding, molecular_function}, {{TAB1}}}},
GO:0050856 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{regulation of T cell receptor signaling pathway, biological_process}, {{MALT1}}}},
GO:0061041 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{regulation of wound healing, biological_process}, {{PLAU}}}},
GO:1904354 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{negative regulation of telomere capping, biological_process}, {{ATM}}}},
GO:1904358 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{positive regulation of telomere maintenance via telomere lengthening, biological_process}, {{ATM}}}},
GO:1990391 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{DNA repair complex, cellular_component}, {{ATM}}}},
GO:2000343 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0000784 → {{0.00536146, 0.0202836, True}, {20, 109, 19774, 2},
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GO:0016363 → {{0.00536146, 0.0202836, True}, {20, 109, 19774, 2},
  {{nuclear matrix, cellular_component}, {{CSNK2B}, {PIAS4}}}},
GO:0006954 → {{0.00567463, 0.0211305, True}, {20, 366, 19774, 3},
  {{inflammatory response, biological_process}, {{TIRAP}, {CHUK}, {NFKB1}}}},
GO:0000785 → {{0.00584929, 0.0211305, True}, {20, 114, 19774, 2},
  {{chromatin, cellular_component}, {{CSNK2A2}, {CSNK2B}}}},
GO:0016032 → {{0.00593612, 0.0211305, True}, {20, 372, 19774, 3},
  {{viral process, biological_process}, {{LTBR}, {LYN}, {NFKBIA}}}},
GO:0034774 → {{0.00594922, 0.0211305, True}, {20, 115, 19774, 2},
  {{secretory granule lumen, cellular_component}, {{CSNK2B}, {NFKB1}}}},
GO:0002768 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{immune response-regulating cell surface receptor signaling pathway, biological_process}, {{LYN}}}},
GO:0009620 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{response to fungus, biological_process}, {{MALT1}}}},
GO:0019209 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{kinase activator activity, molecular_function}, {{MALT1}}}}, GO:0030061 →
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GO:0034137 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{positive regulation of toll-like receptor 2 signaling pathway, biological_process}, {{TIRAP}}}},
GO:0045646 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{regulation of erythrocyte differentiation, biological_process}, {{LYN}}}},
GO:0051972 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{regulation of telomerase activity, biological_process}, {{ATM}}}},
GO:1902231 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage,
    biological_process}, {{PIAS4}}}}, GO:0071356 → {{0.00699141, 0.0228698, True}, {20, 125, 19774, 2},
  {{cellular response to tumor necrosis factor, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0007253 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{cytoplasmic sequestering of NF-kappaB, biological_process}, {{NFKBIA}}}},
GO:0014909 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{smooth muscle cell migration, biological_process}, {{PLAU}}}},
GO:0032210 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{regulation of telomere maintenance via telomerase, biological_process}, {{ATM}}}},
GO:0032927 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{positive regulation of activin receptor signaling pathway, biological_process}, {{CSNK2B}}}},
GO:0033211 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{adiponectin-activated signaling pathway, biological_process}, {{CSNK2B}}}},
GO:0034141 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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  {{positive regulation of toll-like receptor 3 signaling pathway, biological_process}, {{TIRAP}}}},
GO:0050707 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{regulation of cytokine secretion, biological_process}, {{LYN}}}},
GO:0051101 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{regulation of DNA binding, biological_process}, {{CSNK2B}}}},
GO:0061154 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{endothelial tube morphogenesis, biological_process}, {{CSNK2B}}}},
GO:0070431 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{nucleotide-binding oligomerization domain containing 2 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:1902961 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{positive regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein
      catabolic process, biological_process}, {{LYN}}}}, GO:0002446 → {{0.00806427, 0.0250734, True},
  {20, 8, 19774, 1}, {{neutrophil mediated immunity, biological_process}, {{IRAK4}}}},
GO:0002467 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
  {{germinal center formation, biological_process}, {{NFKB2}}}},
GO:0006975 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
  {{DNA damage induced protein phosphorylation, biological_process}, {{ATM}}}},
GO:0010888 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
  {{negative regulation of lipid storage, biological_process}, {{NFKBIA}}}},
GO:0033129 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
  {{positive regulation of histone phosphorylation, biological_process}, {{ATM}}}},
GO:0036289 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
  {{peptidyl-serine autophosphorylation, biological_process}, {{ATM}}}},
GO:1990266 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
  {{neutrophil migration, biological_process}, {{IRAK4}}}},
GO:0042127 → {{0.00881826, 0.0259564, True}, {20, 141, 19774, 2},
  {{regulation of cell population proliferation, biological_process}, {{NFKBIA}, {PLAU}}}},
GO:0002726 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{positive regulation of T cell cytokine production, biological_process}, {{MALT1}}}},
GO:0007143 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{female meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008385 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{IkappaB kinase complex, cellular_component}, {{CHUK}}}},
GO:0034144 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{negative regulation of toll-like receptor 4 signaling pathway, biological_process}, {{LYN}}}},
GO:0034145 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{positive regulation of toll-like receptor 4 signaling pathway, biological_process}, {{TIRAP}}}},
GO:0043304 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{regulation of mast cell degranulation, biological_process}, {{LYN}}}},
GO:0045141 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{meiotic telomere clustering, biological_process}, {{ATM}}}}, GO:0050663 →
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GO:0061665 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{SUMO ligase activity, molecular_function}, {{PIAS4}}}},
GO:0070212 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{protein poly-ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0070417 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{cellular response to cold, biological_process}, {{NFKBIA}}}},
GO:0071316 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{cellular response to nicotine, biological_process}, {{NFKB1}}}},
GO:1904357 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{negative regulation of telomere maintenance via telomere lengthening, biological_process},
   {{PARP1}}}}, GO:1905168 → {{0.00906795, 0.0259564, True}, {20, 9, 19774, 1},
  {{positive regulation of double-strand break repair via homologous recombination, biological_process},
   {{PARP1}}}}, GO:0006955 → {{0.00947213, 0.0268386, True}, {20, 441, 19774, 3},
  {{immune response, biological_process}, {{TNFSF13B}, {CHUK}, {LTBR}}}},
GO:0001228 → {{0.00958954, 0.0268386, True}, {20, 443, 19774, 3},
  {{DNA-binding transcription activator activity, RNA polymerase II-specific, molecular_function},
   {{PARP1}, {NFKB1}, {NFKB2}}}}, GO:0003279 → {{0.0100707, 0.0268386, True},
  {20, 10, 19774, 1}, {{cardiac septum development, biological_process}, {{TAB1}}}},
GO:0009743 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{response to carbohydrate, biological_process}, {{LYN}}}},
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GO:0016303 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{1-phosphatidylinositol-3-kinase activity, molecular_function}, {{ATM}}}},
GO:0019887 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{protein kinase regulator activity, molecular_function}, {{CSNK2B}}}}, GO:0033151 →
 {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1}, {{V(D)J recombination, biological_process}, {{ATM}}}},
GO:0033194 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{response to hydroperoxide, biological_process}, {{CHUK}}}},
GO:0033235 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{positive regulation of protein sumoylation, biological_process}, {{PIAS4}}}},
GO:0051272 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{positive regulation of cellular component movement, biological_process}, {{LYN}}}},
GO:0051901 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{positive regulation of mitochondrial depolarization, biological_process}, {{PARP1}}}},
GO:0071223 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{cellular response to lipoteichoic acid, biological_process}, {{TIRAP}}}},
GO:0071481 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{cellular response to X-ray, biological_process}, {{ATM}}}},
GO:1902741 → {{0.0100707, 0.0268386, True}, {20, 10, 19774, 1},
  {{positive regulation of interferon-alpha secretion, biological_process}, {{CHUK}}}},
GO:0001817 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{regulation of cytokine production, biological_process}, {{LYN}}}},
GO:0010884 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{positive regulation of lipid storage, biological_process}, {{NFKB1}}}},
GO:0031639 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{plasminogen activation, biological_process}, {{PLAU}}}},
GO:0035631 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{CD40 receptor complex, cellular_component}, {{CHUK}}}},
GO:0042994 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{cytoplasmic sequestering of transcription factor, biological_process}, {{NFKBIA}}}},
GO:0050855 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{regulation of B cell receptor signaling pathway, biological_process}, {{LYN}}}},
GO:0070213 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{protein auto-ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0090073 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{positive regulation of protein homodimerization activity, biological_process}, {{TIRAP}}}},
GO:1904385 → {{0.0110724, 0.0282555, True}, {20, 11, 19774, 1},
  {{cellular response to angiotensin, biological_process}, {{NFKB1}}}},
GO:0043312 → {{0.0119849, 0.0290293, True}, {20, 481, 19774, 3},
  {{neutrophil degranulation, biological_process}, {{CSNK2B}, {NFKB1}, {PLAU}}}},
GO:0001666 → {{0.0120525, 0.0290293, True}, {20, 166, 19774, 2},
  {{response to hypoxia, biological_process}, {{ATM}, {PLAU}}}},
GO:0007252 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{I-kappaB phosphorylation, biological_process}, {{CHUK}}}},
GO:0016572 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{histone phosphorylation, biological_process}, {{ATM}}}},
GO:0032495 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{response to muramyl dipeptide, biological_process}, {{NFKBIA}}}},
GO:0033148 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of intracellular estrogen receptor signaling pathway, biological_process},
   {{PARP1}}}}, GO:0042359 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{vitamin D metabolic process, biological_process}, {{PIAS4}}}}, GO:0042805 →
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GO:0043517 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of DNA damage response, signal transduction by p53 class mediator,
    biological_process}, {{ATM}}}}, GO:0051168 →
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GO:0060391 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{positive regulation of SMAD protein signal transduction, biological_process}, {{PARP1}}}},
GO:0090399 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{replicative senescence, biological_process}, {{ATM}}}},
GO:0097028 → {{0.0120732, 0.0290293, True}, {20, 12, 19774, 1},
  {{dendritic cell differentiation, biological_process}, {{LYN}}}},
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GO:0043066 → {{0.0122555, 0.0293372, True}, {20, 485, 19774, 3},
  {{negative regulation of apoptotic process, biological_process}, {{MALT1}, {NFKB1}, {NFKBIA}}}},
GO:0046982 → {{0.0123921, 0.0295335, True}, {20, 487, 19774, 3},
  {{protein heterodimerization activity, molecular_function}, {{TIRAP}, {CHUK}, {NFKB1}}}},
GO:0007596 → {{0.0126116, 0.029925, True}, {20, 170, 19774, 2},
  {{blood coagulation, biological_process}, {{LYN}, {PLAU}}}},
GO:0046777 → {{0.0128955, 0.0302244, True}, {20, 172, 19774, 2},
  {{protein autophosphorylation, biological_process}, {{LYN}, {ATM}}}},
GO:0010745 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{negative regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKBIA}}}}, GO:0044030 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{regulation of DNA methylation, biological_process}, {{PARP1}}}}, GO:0048599 →
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GO:0050777 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{negative regulation of immune response, biological_process}, {{LYN}}}},
GO:0051279 → {{0.013073, 0.0302244, True}, {20, 13, 19774, 1},
  {{regulation of release of sequestered calcium ion into cytosol, biological_process}, {{LYN}}}},
GO:0005149 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
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GO:0032743 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{positive regulation of interleukin-2 production, biological_process}, {{MALT1}}}},
GO:0036092 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{phosphatidylinositol-3-phosphate biosynthetic process, biological_process}, {{ATM}}}},
GO:0045078 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{positive regulation of interferon-gamma biosynthetic process, biological_process}, {{TNFRSF13C}}}},
GO:0051146 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{striated muscle cell differentiation, biological_process}, {{CHUK}}}},
GO:0060397 → {{0.0140719, 0.0315888, True}, {20, 14, 19774, 1},
  {{growth hormone receptor signaling pathway via JAK-STAT, biological_process}, {{LYN}}}},
GO:0000729 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{DNA double-strand break processing, biological_process}, {{ATM}}}},
GO:0005161 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{platelet-derived growth factor receptor binding, molecular_function}, {{LYN}}}}, GO:0016581 →
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  {{positive regulation of interleukin-1 beta production, biological_process}, {{MALT1}}}},
GO:0045410 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of interleukin-6 biosynthetic process, biological_process}, {{TIRAP}}}},
GO:0060252 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{positive regulation of glial cell proliferation, biological_process}, {{LYN}}}},
GO:0071044 → {{0.0150698, 0.032874, True}, {20, 15, 19774, 1},
  {{histone mRNA catabolic process, biological_process}, {{ATM}}}},
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  {{positive regulation of macrophage derived foam cell differentiation, biological_process},
   {{NFKB1}}}}, GO:0010875 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cholesterol efflux, biological_process}, {{NFKBIA}}}},
GO:0016540 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
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GO:0032270 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{positive regulation of cellular protein metabolic process, biological_process}, {{NFKBIA}}}},
GO:0034142 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{toll-like receptor 4 signaling pathway, biological_process}, {{NFKBIA}}}},
GO:0071354 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{cellular response to interleukin-6, biological_process}, {{NFKB1}}}},
GO:1901222 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{regulation of NIK/NF-kappaB signaling, biological_process}, {{NFKBIA}}}},
GO:1990404 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
  {{protein ADP-ribosylase activity, molecular_function}, {{PARP1}}}},
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GO:2000679 → {{0.0160667, 0.0336903, True}, {20, 16, 19774, 1},
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GO:0042493 → {{0.0163579, 0.0341685, True}, {20, 195, 19774, 2},
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GO:0004724 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
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  {{determination of adult lifespan, biological_process}, {{ATM}}}},
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GO:1903146 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{regulation of autophagy of mitochondrion, biological_process}, {{CSNK2A2}}}},
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  {{regulation of signaling receptor activity, biological_process}, {{PLAU}}}},
GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
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  {{myeloid dendritic cell differentiation, biological_process}, {{LTBR}}}},
GO:0043537 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of blood vessel endothelial cell migration, biological_process}, {{CSNK2B}}}},
GO:0045638 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of myeloid cell differentiation, biological_process}, {{NFKBIA}}}}, GO:0090734 →
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GO:1903827 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of cellular protein localization, biological_process}, {{PARP1}}}},
GO:0010008 → {{0.0188076, 0.0374078, True}, {20, 210, 19774, 2},
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196568, 0.0385302, True}, {20, 215, 19774, 2},
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GO:0002756 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
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  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
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GO:0042098 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
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GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
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  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
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GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
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  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
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GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
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  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
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GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
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GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
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GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
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GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
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GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
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GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
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  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
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GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
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GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
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  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
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GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
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GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
  {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{DNA damage checkpoint, biological_process}, {{ATM}}}},
GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|⟩
```

pValueCutoff (1)

```
In[1]:= Needs["MathIOmica`"]
```

pValueCutoff provides a cutoff p-value for adjusted p-values to assess statistical significance. The default is 0.05. In this example we manually set the cutoff to to 10^{-6}:

```
In[2]:= goExamplePValue = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, pValueCutoff → 10^-6]

Out[2]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
   {{positive regulation of NF-kappaB transcription factor activity, biological_process},
    {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}}|⟩
```

ReportFilter (1)

```
In[1]:= Needs["MathIOmica`"]
```

ReportFilter provides a cutoff for membership in ontologies in selecting which

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terms/categories to return. It is used in conjunction with `ReportFilterFunction`. The default is 1.

We first consider the data

```
In[2]:= goExampleReportFilter1 = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP",
    "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88",
    "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, ReportFilter → 1]

Out[2]= ⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
  GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
    {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
  GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
    {{protein serine/threonine kinase activity, molecular_function},
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
  GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
    {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
  GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
    {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
  GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
    {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
   {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
     {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
  GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
    {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
     {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
    {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
    {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
  GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
    {{regulation of signal transduction by p53 class mediator, biological_process},
     {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
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```
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
  {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
    {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
  {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
  {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
  {{transcription factor binding, molecular_function}, {{PARP1}, {CSNK2B}, {NFKB1}, {NFKBIA}}}},
GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
  {{negative regulation of apoptotic signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
    {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
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  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19 774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19 774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19 774, 2},
  {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19 774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19 774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19 774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19 774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19 774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19 774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19 774, 2},
  {{positive regulation of T cell proliferation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19 774, 3},
  {{cellular response to DNA damage stimulus, biological_process}, {{PARP1}, {LYN}, {ATM}}}},
GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19 774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19 774, 11},
  {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
    {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}},
GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19 774, 2},
  {{response to toxic substance, biological_process}, {{CHUK}, {LYN}}}},
GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19 774, 2},
  {{rhythmic process, biological_process}, {{CSNK2A1}, {NFKB2}}}},
GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{B-1 B cell differentiation, biological_process}, {{MALT1}}}},
GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
GO:0002431 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{positive regulation of Fc receptor mediated stimulatory signaling pathway, biological_process},
   {{LYN}}}}, GO:0061847 → {{0.00202189, 0.0130219, True},
  {20, 2, 19 774, 1}, {{response to cholecystokinin, biological_process}, {{CHUK}}}},
GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{negative regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0070668 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{positive regulation of mast cell proliferation, biological_process}, {{LYN}}}},
GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{cellular response to bacterial lipopeptide, biological_process}, {{TIRAP}}}},
GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{establishment of RNA localization to telomere, biological_process}, {{ATM}}}},
GO:0097695 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
  {{establishment of protein-containing complex localization to telomere, biological_process}, {{ATM}}}},
GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19 774, 1},
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    {{negative regulation of intracellular signal transduction, biological_process}, {{LYN}}}},
  GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
    {{positive regulation of single strand break repair, biological_process}, {{PARP1}}}},
  GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
    {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
  GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
    {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
  GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
    {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
  GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
    {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
  GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
    {{ATP binding, molecular_function}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {LYN}, {ATM}, {IRAK4}}}},
  GO:0016301 → {{0.00292933, 0.0149088, True}, {20, 80, 19774, 2},
    {{kinase activity, molecular_function}, {{CSNK2A1}, {LYN}}}},
  GO:0002331 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
  GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{tolerance induction to self antigen, biological_process}, {{LYN}}}},
  GO:0002553 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{histamine secretion by mast cell, biological_process}, {{LYN}}}},
  GO:0002762 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{negative regulation of myeloid leukocyte differentiation, biological_process}, {{LYN}}}},
  GO:0002774 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{Fc receptor mediated inhibitory signaling pathway, biological_process}, {{LYN}}}},
  GO:0002902 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{regulation of B cell apoptotic process, biological_process}, {{LYN}}}},
  GO:0004677 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{DNA-dependent protein kinase activity, molecular_function}, {{ATM}}}},
  GO:0008384 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{IkappaB kinase activity, molecular_function}, {{CHUK}}}},
  GO:0010956 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{negative regulation of calcidiol 1-monooxygenase activity, biological_process}, {{NFKB1}}}},
  GO:0030592 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{DNA ADP-ribosylation, biological_process}, {{PARP1}}}},
  GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{integrin alpha2-beta1 complex, cellular_component}, {{LYN}}}},
  GO:0035663 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{Toll-like receptor 2 binding, molecular_function}, {{TIRAP}}}},
  GO:0070447 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{positive regulation of oligodendrocyte progenitor proliferation, biological_process}, {{LYN}}}},
  GO:0071500 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{cellular response to nitrosative stress, biological_process}, {{ATM}}}},
  GO:0099091 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{postsynaptic specialization, intracellular component, cellular_component}, {{LYN}}}},
  GO:0140031 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{phosphorylation-dependent protein binding, molecular_function}, {{LYN}}}},
  GO:0140294 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{NAD DNA ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
  GO:1902174 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{positive regulation of keratinocyte apoptotic process, biological_process}, {{PIAS4}}}},
  GO:1904044 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{response to aldosterone, biological_process}, {{PARP1}}}},
  GO:2000630 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{positive regulation of miRNA metabolic process, biological_process}, {{NFKB1}}}},
  GO:2000670 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{positive regulation of dendritic cell apoptotic process, biological_process}, {{LYN}}}},
  GO:2001170 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
    {{negative regulation of ATP biosynthetic process, biological_process}, {{PARP1}}}},
  GO:0000724 → {{0.00314887, 0.0153472, True}, {20, 83, 19774, 2},
    {{double-strand break repair via homologous recombination, biological_process}, {{PARP1}, {ATM}}}},
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GO:0010957 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{negative regulation of vitamin D biosynthetic process, biological_process}, {{NFKB1}}}},
GO:0018312 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{peptidyl-serine ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0032375 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{negative regulation of cholesterol transport, biological_process}, {{NFKB1}}}}, GO:0032449 →
 {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1}, {{CBM complex, cellular_component}, {{MALT1}}}},
GO:0032648 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
  {{regulation of interferon-beta production, biological_process}, {{TIRAP}}}},
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  {{toll-like receptor 9 signaling pathway, biological_process}, {{IRAK4}}}},
GO:1903146 → {{0.0170627, 0.0350986, True}, {20, 17, 19774, 1},
  {{regulation of autophagy of mitochondrion, biological_process}, {{CSNK2A2}}}},
GO:0010469 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of signaling receptor activity, biological_process}, {{PLAU}}}},
GO:0030099 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid cell differentiation, biological_process}, {{TIRAP}}}},
GO:0031668 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{cellular response to extracellular stimulus, biological_process}, {{LYN}}}},
GO:0043011 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{myeloid dendritic cell differentiation, biological_process}, {{LTBR}}}},
GO:0043537 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of blood vessel endothelial cell migration, biological_process}, {{CSNK2B}}}},
```

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```
GO:0045638 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{negative regulation of myeloid cell differentiation, biological_process}, {{NFKBIA}}}}, GO:0090734 →
 {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1}, {{site of DNA damage, cellular_component}, {{PARP1}}}},
GO:1903827 → {{0.0180577, 0.0360489, True}, {20, 18, 19774, 1},
  {{regulation of cellular protein localization, biological_process}, {{PARP1}}}},
GO:0010008 → {{0.0188076, 0.0374078, True}, {20, 210, 19774, 2},
  {{endosome membrane, cellular_component}, {{TAB1}, {IRAK4}}}},
GO:0031293 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{membrane protein intracellular domain proteolysis, biological_process}, {{NFKB1}}}},
GO:0070935 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{3'-UTR-mediated mRNA stabilization, biological_process}, {{TIRAP}}}},
GO:1904262 → {{0.0190518, 0.0374801, True}, {20, 19, 19774, 1},
  {{negative regulation of TORC1 signaling, biological_process}, {{ATM}}}},
GO:0042981 → {{0.0196568, 0.0385302, True}, {20, 215, 19774, 2},
  {{regulation of apoptotic process, biological_process}, {{MALT1}, {ATM}}}},
GO:0002756 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{MyD88-independent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0023019 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{signal transduction involved in regulation of gene expression, biological_process}, {{PARP1}}}},
GO:0030225 → {{0.0200449, 0.0388685, True}, {20, 20, 19774, 1},
  {{macrophage differentiation, biological_process}, {{PARP1}}}},
GO:0032991 → {{0.0204617, 0.0395348, True}, {20, 588, 19774, 3},
  {{protein-containing complex, cellular_component}, {{TAB1}, {MALT1}, {PARP1}}}},
GO:0006293 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{nucleotide-excision repair, preincision complex stabilization, biological_process}, {{PARP1}}}},
GO:0010804 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{negative regulation of tumor necrosis factor-mediated signaling pathway, biological_process},
   {{PIAS4}}}}, GO:0034622 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{cellular protein-containing complex assembly, biological_process}, {{CSNK2B}}}}, GO:0035904 →
 {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1}, {{aorta development, biological_process}, {{TAB1}}}},
GO:0042098 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{T cell proliferation, biological_process}, {{MALT1}}}},
GO:0045088 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of innate immune response, biological_process}, {{TIRAP}}}},
GO:0045859 → {{0.0210371, 0.0396553, True}, {20, 21, 19774, 1},
  {{regulation of protein kinase activity, biological_process}, {{CSNK2B}}}},
GO:0000717 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA duplex unwinding, biological_process}, {{PARP1}}}},
GO:0006295 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-excision repair, DNA incision, 3'-to lesion, biological_process}, {{PARP1}}}},
GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
 {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
```

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```
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
```

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```
    {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
  GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
    {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
  GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{DNA damage checkpoint, biological_process}, {{ATM}}}},
  GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
  GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
  GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
  GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

We now set a report filter. We may be interested in categories with at least 10 members in each result reported:

```
In[3]:= goExampleReportFilter10 = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP",
          "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88",
          "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, ReportFilter → 10]

Out[3]= <|GO:0005515 →
    {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
      {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
       {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
    {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
      {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
  GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
    {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
      {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
  GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
      {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
  GO:0005829 → {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12},
    {{cytosol, cellular_component}, {{TAB1}, {MALT1}, {TIRAP}, {CHUK},
      {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
  GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
    {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
      {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}}|>
```

ReportFilterFunction (1)

```
In[1]:= Needs["MathIOmica`"]
```

`ReportFilterFunction` specifies what function will be used to compare against `ReportFilter` option value in selecting which terms/categories to return. The default value is GreaterEqualThan.

We first consider data filtering results with more than or equal to 11 members:

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In[2]:=
```
goExampleReportFilterFn1 =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
   "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
  ReportFilter → 11, ReportFilterFunction → GreaterEqualThan]
```

Out[2]=
```
⟨|GO:0005515 →
  {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
 GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
   {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
     {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
 GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
   {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
     {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
 GO:0005829 → {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12},
   {{cytosol, cellular_component}, {{TAB1}, {MALT1}, {TIRAP}, {CHUK},
     {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
 GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
   {{plasma membrane, cellular_component}, {{TNFSF13B}, {TIRAP}, {TNFRSF13C},
     {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN}, {NFKBIA}, {IRAK4}, {PLAU}}}}|⟩
```

For an example we change this to look at groups strictly having more than 11 members

In[3]:=
```
goExampleReportFilterFn2 =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
   "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
  ReportFilter → 11, ReportFilterFunction → GreaterThan]
```

Out[3]=
```
⟨|GO:0005515 →
  {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
 GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
   {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
     {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
 GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
   {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
     {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
 GO:0005829 → {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12},
   {{cytosol, cellular_component}, {{TAB1}, {MALT1}, {TIRAP}, {CHUK},
     {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}}|⟩
```

Species (2)

In[1]:=
```
Needs["MathIOmica`"]
```

The `Species` option specifies the species considered in the calculation. The default implementation is "human":

In[2]:=
```
goExampleSpecies = GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, Species → "human"]
```

Out[2]=
```
⟨|GO:0051092 → {{9.39025×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
   {{positive regulation of NF-kappaB transcription factor activity, biological_process},
    {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
 GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
   {{interleukin-1-mediated signaling pathway, biological_process},
    {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
   {{stimulatory C-type lectin receptor signaling pathway, biological_process},
```

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```
    {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
  {{tumor necrosis factor-mediated signaling pathway, biological_process},
    {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
  {{Fc-epsilon receptor signaling pathway, biological_process},
    {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
 {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
    {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
  {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
    {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
  {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
  {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
  {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
  {{protein serine/threonine kinase activity, molecular_function},
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
  {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
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GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
  {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
 {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
    {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
    {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
  {{regulation of signal transduction by p53 class mediator, biological_process},
    {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
    {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
    {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
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GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
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  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19 774, 3},
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   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19 774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19 774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19 774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19 774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
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GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19 774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19 774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
   {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19 774, 14},
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GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19 774, 4},
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GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19 774, 3},
  {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19 774, 4},
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GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19 774, 2},
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GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19 774, 12},
  {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
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  {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19 774, 2},
  {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19 774, 10}, {{nucleoplasm, cellular_component},
   {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19 774, 2},
  {{liver regeneration, biological_process}, {{CSNK2A2}, {CSNK2B}}}},
GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19 774, 3},
  {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19 774, 2},
  {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19 774, 6},
  {{positive regulation of transcription by RNA polymerase II, biological_process},
   {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19 774, 3},
  {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19 774, 2},
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GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19 774, 2},
  {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
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    {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19 774, 2},
  {{positive regulation of type I interferon production, biological_process}, {{NFKB1}, {NFKB2}}}},
GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19 774, 4},
  {{protein phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {LYN}, {ATM}}}},
GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19 774, 2},
  {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
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GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
  {{positive regulation of cell migration, biological_process}, {{LYN}, {ATM}, {PLAU}}}},
GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
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GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
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GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
  {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
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GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
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GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
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GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
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  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
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  {{pre-B cell allelic exclusion, biological_process}, {{ATM}}}},
GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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  {{tolerance induction to self antigen, biological_process}, {{LYN}}}},
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  {{histamine secretion by mast cell, biological_process}, {{LYN}}}},
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GO:0010956 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0030592 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0099091 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:2000630 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0032648 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0048305 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0071359 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0090330 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:1900127 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:1903978 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0014910 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0032269 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0034136 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0042159 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0043208 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0043504 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0048273 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:1904358 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:2000343 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0016363 → {{0.00536146, 0.0202836, True}, {20, 109, 19774, 2},
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GO:0010613 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{positive regulation of cardiac muscle hypertrophy, biological_process}, {{PARP1}}}},
GO:0042629 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{mast cell granule, cellular_component}, {{LYN}}}}, GO:0042730 →
 {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1}, {{fibrinolysis, biological_process}, {{PLAU}}}},
GO:0070423 → {{0.0220283, 0.0406734, True}, {20, 22, 19774, 1},
  {{nucleotide-binding oligomerization domain containing signaling pathway, biological_process},
   {{TAB1}}}}, GO:0000715 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{nucleotide-excision repair, DNA damage recognition, biological_process}, {{PARP1}}}},
GO:0007094 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{mitotic spindle assembly checkpoint, biological_process}, {{ATM}}}}, GO:0070412 →
 {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1}, {{R-SMAD binding, molecular_function}, {{PARP1}}}},
GO:0098586 → {{0.0230185, 0.0419294, True}, {20, 23, 19774, 1},
  {{cellular response to virus, biological_process}, {{CHUK}}}},
GO:0071294 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{cellular response to zinc ion, biological_process}, {{PARP1}}}},
GO:0090023 → {{0.0240078, 0.0434389, True}, {20, 24, 19774, 1},
  {{positive regulation of neutrophil chemotaxis, biological_process}, {{TIRAP}}}},
GO:0004672 → {{0.0241401, 0.0435326, True}, {20, 240, 19774, 2},
  {{protein kinase activity, molecular_function}, {{CHUK}, {IRAK4}}}},
GO:0006471 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{protein ADP-ribosylation, biological_process}, {{PARP1}}}},
GO:0007140 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{male meiotic nuclear division, biological_process}, {{ATM}}}},
GO:0008139 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{nuclear localization sequence binding, molecular_function}, {{NFKBIA}}}},
GO:0014003 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{oligodendrocyte development, biological_process}, {{LYN}}}},
GO:0032735 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of interleukin-12 production, biological_process}, {{TIRAP}}}},
GO:1900182 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of protein localization to nucleus, biological_process}, {{PARP1}}}},
GO:2001238 → {{0.0249962, 0.0440487, True}, {20, 25, 19774, 1},
  {{positive regulation of extrinsic apoptotic signaling pathway, biological_process}, {{LTBR}}}},
GO:0007049 → {{0.0258482, 0.0449109, True}, {20, 249, 19774, 2},
  {{cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
GO:0003009 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{skeletal muscle contraction, biological_process}, {{CHUK}}}},
GO:0043015 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{gamma-tubulin binding, molecular_function}, {{LYN}}}},
```

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```
GO:0060976 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{coronary vasculature development, biological_process}, {{TAB1}}}},
GO:0061077 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{chaperone-mediated protein folding, biological_process}, {{CSNK2A1}}}},
GO:0070911 → {{0.0259836, 0.0449109, True}, {20, 26, 19774, 1},
  {{global genome nucleotide-excision repair, biological_process}, {{PARP1}}}}, GO:0001816 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{cytokine production, biological_process}, {{IRAK4}}}},
GO:0003950 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{NAD+ ADP-ribosyltransferase activity, molecular_function}, {{PARP1}}}},
GO:0010332 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{response to gamma radiation, biological_process}, {{PARP1}}}},
GO:0030295 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{protein kinase activator activity, molecular_function}, {{TAB1}}}},
GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{ephrin receptor binding, molecular_function}, {{LYN}}}},
GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{response to axon injury, biological_process}, {{LYN}}}},
GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
  {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
  {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
  {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
  {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
 {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
  {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{response to testosterone, biological_process}, {{CSNK2B}}}},
GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
  {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
  {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{DNA damage checkpoint, biological_process}, {{ATM}}}},
GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
  {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

In[1]:=
```
Needs["MathIOmica`"]
```

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For an advanced example we consider an Arabidopsis GO analysis. We create a dictionary, and by invoking GOAnalysisAssigner also memberships to GO associations:

In[2]:=
```
tairDictionary = Association@
  {"TAIR" → Query[All, "IDToGO", Keys]@GOAnalysisAssigner[Species → "TAIR", GOFileName → "tair.gaf.gz",
     ImportDirectly → True, GOFileColumns → {3, 5}]}
```

Out[2]=
```
<|TAIR →
  <|TAIR → {ENO1, ENOC, LOS2, AT1G25260, TUN, ALG3, APTG1, ATG12A, APG12B, ATG13, ALATS, CTEXP, TRM1a,
     ··· 31 417 ···, At3g59850, At3g11230, At1g15790, At3g17365, At4g28030, C7A10.720,
     At1g76720, At1g01570, At1g52510, At1g07480, At3g50210, At5g42100, DIT1}|>|>
```

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We can now perform GO analysis:

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```
In[3]:= GOAnalysis[{"RAD50", "GR1", "ENO1", "ENOC", "LOS2", "SAC52", "RPL10B",
          "PRPL11", "RPL3B", "SAG24", "MDN1", "RPL24A", "RPL23AA", "RPL16A", "ATL5", "STV1"},
         GeneDictionary → tairDictionary, Species → "TAIR", InputID → {"TAIR"}, OutputID → "TAIR", ReportFilter → 3]

Out[3]= ⟨|GO:0000027 → {{0., 0., True}, {16, 41, 31440, 10}, {{ribosomal large subunit assembly, biological_process},
            {{SAC52}, {RPL10B}, {PRPL11}, {RPL3B}, {SAG24}, {RPL24A}, {RPL23AA}, {RPL16A}, {ATL5}, {STV1}}}},
          GO:0003735 → {{0., 0., True}, {16, 325, 31440, 10},
            {{structural constituent of ribosome, molecular_function}, {{SAC52}, {RPL10B}, {PRPL11},
              {RPL3B}, {SAG24}, {RPL24A}, {RPL23AA}, {RPL16A}, {ATL5}, {STV1}}}}, GO:0022625 →
           {{0., 0., True}, {16, 160, 31440, 10}, {{cytosolic large ribosomal subunit, cellular_component},
            {{SAC52}, {RPL10B}, {PRPL11}, {RPL3B}, {SAG24}, {RPL24A}, {RPL23AA}, {RPL16A}, {ATL5}, {STV1}}}},
          GO:0006412 → {{5.47906×10^-12, 1.39716×10^-10, True}, {16, 978, 31440, 10},
            {{translation, biological_process},
             {{SAC52}, {RPL10B}, {PRPL11}, {RPL3B}, {SAG24}, {RPL24A}, {RPL23AA}, {RPL16A}, {ATL5}, {STV1}}}},
          GO:0000015 → {{1.08127×10^-10, 1.83815×10^-9, True}, {16, 3, 31440, 3},
            {{phosphopyruvate hydratase complex, cellular_component}, {{ENO1}, {ENOC}, {LOS2}}}},
          GO:0004634 → {{1.08127×10^-10, 1.83815×10^-9, True}, {16, 3, 31440, 3},
            {{phosphopyruvate hydratase activity, molecular_function}, {{ENO1}, {ENOC}, {LOS2}}}},
          GO:0005737 → {{4.3423×10^-9, 6.32736×10^-8, True}, {16, 4547, 31440, 13},
            {{cytoplasm, cellular_component}, {{RAD50}, {GR1}, {ENOC}, {LOS2}, {SAC52},
              {RPL10B}, {RPL3B}, {SAG24}, {RPL24A}, {RPL23AA}, {RPL16A}, {ATL5}, {STV1}}}},
          GO:0022626 → {{3.51135×10^-8, 4.47697×10^-7, True}, {16, 194, 31440, 5},
            {{cytosolic ribosome, cellular_component}, {{SAC52}, {PRPL11}, {SAG24}, {RPL23AA}, {ATL5}}}},
          GO:0005829 → {{8.08172×10^-8, 9.15929×10^-7, True}, {16, 3495, 31440, 11}, {{cytosol, cellular_component},
             {{GR1}, {ENOC}, {LOS2}, {SAC52}, {RPL10B}, {SAG24}, {RPL24A}, {RPL23AA}, {RPL16A}, {ATL5}, {STV1}}}},
          GO:0005840 → {{8.89655×10^-7, 9.07448×10^-6, True}, {16, 151, 31440, 4},
            {{ribosome, cellular_component}, {{SAC52}, {RPL10B}, {SAG24}, {ATL5}}}},
          GO:0005730 → {{2.56244×10^-6, 0.0000217807, True}, {16, 462, 31440, 5},
            {{nucleolus, cellular_component}, {{SAC52}, {RPL23AA}, {RPL16A}, {ATL5}, {STV1}}}},
          GO:0006096 → {{4.85211×10^-6, 0.0000353511, True}, {16, 66, 31440, 3},
            {{glycolytic process, biological_process}, {{ENO1}, {ENOC}, {LOS2}}}},
          GO:0032502 → {{4.85211×10^-6, 0.0000353511, True}, {16, 66, 31440, 3},
            {{developmental process, biological_process}, {{SAC52}, {RPL10B}, {SAG24}}}},
          GO:0019843 → {{7.72995×10^-6, 0.0000492784, True}, {16, 77, 31440, 3},
            {{rRNA binding, molecular_function}, {{PRPL11}, {RPL23AA}, {RPL16A}}}},
          GO:0005794 → {{0.000029775, 0.000168725, True}, {16, 1317, 31440, 6},
            {{Golgi apparatus, cellular_component}, {{SAC52}, {RPL10B}, {SAG24}, {RPL23AA}, {RPL16A}, {ATL5}}}},
          GO:0000287 → {{0.0000315255, 0.000169242, True}, {16, 123, 31440, 3},
            {{magnesium ion binding, molecular_function}, {{ENO1}, {ENOC}, {LOS2}}}},
          GO:0005773 → {{0.000308507, 0.00149846, True}, {16, 673, 31440, 4},
            {{vacuole, cellular_component}, {{SAC52}, {SAG24}, {RPL16A}, {ATL5}}}},
          GO:0009506 → {{0.00122269, 0.00461904, True}, {16, 971, 31440, 4},
            {{plasmodesma, cellular_component}, {{LOS2}, {MDN1}, {RPL23AA}, {RPL16A}}}},
          GO:0009941 → {{0.00281154, 0.00896178, True}, {16, 572, 31440, 3},
            {{chloroplast envelope, cellular_component}, {{RPL10B}, {PRPL11}, {MDN1}}}},
          GO:0005634 → {{0.00488504, 0.0118637, True}, {16, 10711, 31440, 11}, {{nucleus, cellular_component},
             {{RAD50}, {GR1}, {ENOC}, {LOS2}, {SAC52}, {RPL10B}, {PRPL11}, {RPL3B}, {SAG24}, {MDN1}, {ATL5}}}}|⟩
```

Also we note that the current computation ConstantGeneDictionary function has also been augmented as expected:

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In[4]:=
```
ConstantGeneDictionary
```

Out[4]=
```
<|human → <| ··· 1 ··· |>,
 TAIR → <|TAIR → {ENO1, ENOC, LOS2, AT1G25260, TUN, ALG3, APTG1, ATG12A, APG12B, ATG13,
     ALATS, ··· 31421 ···, At1g15790, At3g17365, At4g28030, C7A10.720, At1g76720,
     At1g01570, At1g52510, At1g07480, At3g50210, At5g42100, DIT1}|>|>
```

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TestFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The TestFunction option provides a function for calculating the raw p-values for the enrichment of each term. It must be a function of four inputs, f[#1,#2,#3,#4]. The default is using a hypergeometric distribution CDF, CDF[HypergeometricDistribution[#1,#2,#3],#4-1]] . The four inputs refer to:

#1 is number of draws (members in group being tested),

#2 is number of successes for category in population,

#3 is total number of members in population,

#4 is number of successes (or more) in current group being tested for specific category.

The output must be a p-value (real positive number ≤ 1).

In[2]:=
```
goExampleTestFunction =
 GOAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
   "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
  TestFunction → ((1 - N[CDF[HypergeometricDistribution[#1, #2, #3], #4 - 1]]) &)]
```

Out[2]=
```
<|GO:0051092 → {{9.39023×10^-11, 5.08012×10^-8, True}, {20, 151, 19774, 7},
    {{positive regulation of NF-kappaB transcription factor activity, biological_process},
     {{TAB1}, {MALT1}, {TIRAP}, {CHUK}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  GO:0070498 → {{3.3698×10^-8, 9.11531×10^-6, True}, {20, 95, 19774, 5},
    {{interleukin-1-mediated signaling pathway, biological_process},
     {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  GO:0002223 → {{7.71869×10^-8, 0.0000119204, True}, {20, 112, 19774, 5},
    {{stimulatory C-type lectin receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}},
  GO:0033209 → {{8.81364×10^-8, 0.0000119204, True}, {20, 115, 19774, 5},
    {{tumor necrosis factor-mediated signaling pathway, biological_process},
     {{TNFSF13B}, {CHUK}, {TNFRSF13C}, {LTBR}, {NFKBIA}}}},
  GO:0038095 → {{6.36582×10^-7, 0.0000581516, True}, {20, 171, 19774, 5},
    {{Fc-epsilon receptor signaling pathway, biological_process},
     {{TAB1}, {MALT1}, {CHUK}, {LYN}, {NFKB1}}}}, GO:0006915 →
   {{7.10124×10^-7, 0.0000581516, True}, {20, 551, 19774, 7}, {{apoptotic process, biological_process},
     {{PARP1}, {CSNK2A1}, {CSNK2A2}, {LTBR}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  GO:0043123 → {{7.98155×10^-7, 0.0000581516, True}, {20, 179, 19774, 5},
    {{positive regulation of I-kappaB kinase/NF-kappaB signaling, biological_process},
     {{MALT1}, {TIRAP}, {CHUK}, {LTBR}, {IRAK4}}}},
  GO:0033256 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{I-kappaB/NF-kappaB complex, cellular_component}, {{NFKB1}, {NFKBIA}}}},
  GO:1905818 → {{9.71889×10^-7, 0.0000581516, True}, {20, 2, 19774, 2},
    {{regulation of chromosome separation, biological_process}, {{CSNK2A1}, {CSNK2A2}}}},
```

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```
GO:0001782 → {{1.16318×10^-6, 0.0000581516, True}, {20, 21, 19774, 3},
  {{B cell homeostasis, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}},
GO:0004674 → {{1.18238×10^-6, 0.0000581516, True}, {20, 365, 19774, 6},
  {{protein serine/threonine kinase activity, molecular_function},
   {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {IRAK4}}}},
GO:0031519 → {{2.54824×10^-6, 0.000105095, True}, {20, 27, 19774, 3},
  {{PcG protein complex, cellular_component}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0002636 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{positive regulation of germinal center formation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0005956 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{protein kinase CK2 complex, cellular_component}, {{CSNK2A1}, {CSNK2B}}}},
GO:0031296 → {{2.9139×10^-6, 0.000105095, True}, {20, 3, 19774, 2},
  {{B cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}}}},
GO:0047485 → {{3.53754×10^-6, 0.000119613, True}, {20, 106, 19774, 4},
  {{protein N-terminus binding, molecular_function}, {{PARP1}, {CSNK2A1}, {CSNK2A2}, {ATM}}}}, GO:0042802 →
 {{4.498×10^-6, 0.000134819, True}, {20, 1054, 19774, 8}, {{identical protein binding, molecular_function},
   {{MALT1}, {TIRAP}, {PARP1}, {CSNK2A1}, {CSNK2B}, {LTBR}, {NFKB1}, {NFKBIA}}}},
GO:0002755 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{MyD88-dependent toll-like receptor signaling pathway, biological_process},
   {{TAB1}, {TIRAP}, {IRAK4}}}}, GO:0006656 → {{4.73487×10^-6, 0.000134819, True}, {20, 33, 19774, 3},
  {{phosphatidylcholine biosynthetic process, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0031663 → {{5.18974×10^-6, 0.000140382, True}, {20, 34, 19774, 3},
  {{lipopolysaccharide-mediated signaling pathway, biological_process}, {{MALT1}, {LYN}, {NFKBIA}}}},
GO:1901796 → {{8.20931×10^-6, 0.000211487, True}, {20, 131, 19774, 4},
  {{regulation of signal transduction by p53 class mediator, biological_process},
   {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}}}}, GO:0030890 → {{9.20344×10^-6, 0.000226321, True},
  {20, 41, 19774, 3}, {{positive regulation of B cell proliferation, biological_process},
   {{TNFSF13B}, {TIRAP}, {TNFRSF13C}}}}, GO:0005515 →
 {{0.0000123024, 0.000289373, True}, {20, 9629, 19774, 19}, {{protein binding, molecular_function},
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
GO:0018105 → {{0.0000180797, 0.000407547, True}, {20, 160, 19774, 4},
  {{peptidyl-serine phosphorylation, biological_process}, {{CHUK}, {CSNK2A1}, {CSNK2A2}, {ATM}}}},
GO:0031295 → {{0.0000200692, 0.000434297, True}, {20, 53, 19774, 3},
  {{T cell costimulation, biological_process}, {{TNFSF13B}, {TNFRSF13C}, {LYN}}}}, GO:0007165 →
 {{0.0000309306, 0.000640346, True}, {20, 977, 19774, 7}, {{signal transduction, biological_process},
   {{TNFSF13B}, {CSNK2A1}, {CSNK2B}, {LTBR}, {LYN}, {ATM}, {PLAU}}}},
GO:0016055 → {{0.0000319581, 0.000640346, True}, {20, 185, 19774, 4},
  {{Wnt signaling pathway, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}, {PIAS4}}}},
GO:0007249 → {{0.0000371324, 0.00071745, True}, {20, 65, 19774, 3},
  {{I-kappaB kinase/NF-kappaB signaling, biological_process}, {{TAB1}, {CHUK}, {NFKBIA}}}},
GO:0000185 → {{0.0000531626, 0.000991758, True}, {20, 11, 19774, 2},
  {{activation of MAPKKK activity, biological_process}, {{TAB1}, {GADD45B}}}},
GO:0018107 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{peptidyl-threonine phosphorylation, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0032088 → {{0.0000641322, 0.00111921, True}, {20, 78, 19774, 3},
  {{negative regulation of NF-kappaB transcription factor activity, biological_process},
   {{CHUK}, {NFKBIA}, {PIAS4}}}}, GO:0046330 → {{0.0000691718, 0.00116944, True}, {20, 80, 19774, 3},
  {{positive regulation of JNK cascade, biological_process}, {{TIRAP}, {LTBR}, {GADD45B}}}},
GO:0033628 → {{0.0000753028, 0.00123451, True}, {20, 13, 19774, 2},
  {{regulation of cell adhesion mediated by integrin, biological_process}, {{LYN}, {PLAU}}}},
GO:0035994 → {{0.000101246, 0.00161101, True}, {20, 15, 19774, 2},
  {{response to muscle stretch, biological_process}, {{NFKB1}, {NFKBIA}}}},
GO:0045087 → {{0.00011149, 0.00164635, True}, {20, 497, 19774, 5},
  {{innate immune response, biological_process}, {{MALT1}, {TIRAP}, {CHUK}, {LYN}, {IRAK4}}}},
GO:0016236 → {{0.000115412, 0.00164635, True}, {20, 95, 19774, 3},
  {{macroautophagy, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0030889 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of B cell proliferation, biological_process}, {{LYN}, {ATM}}}},
GO:2000059 → {{0.00011564, 0.00164635, True}, {20, 16, 19774, 2},
  {{negative regulation of ubiquitin-dependent protein catabolic process, biological_process},
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    {{CSNK2A1}, {CSNK2A2}}}}, GO:0005634 → {{0.000142579, 0.00197782, True}, {20, 5639, 19774, 14},
   {{nucleus, cellular_component}, {{TAB1}, {MALT1}, {PARP1}, {CSNK2A1}, {CSNK2A2},
     {CSNK2B}, {LYN}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0007250 → {{0.000147262, 0.00199172, True}, {20, 18, 19774, 2},
   {{activation of NF-kappaB-inducing kinase activity, biological_process}, {{MALT1}, {TIRAP}}}},
GO:0031625 → {{0.000179994, 0.00237504, True}, {20, 289, 19774, 4},
   {{ubiquitin protein ligase binding, molecular_function}, {{LTBR}, {LYN}, {NFKBIA}, {PIAS4}}}},
GO:0051726 → {{0.000230422, 0.00296806, True}, {20, 120, 19774, 3},
   {{regulation of cell cycle, biological_process}, {{CSNK2A1}, {CSNK2A2}, {GADD45B}}}},
GO:0008134 → {{0.00030218, 0.00380184, True}, {20, 331, 19774, 4},
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GO:2001234 → {{0.000311297, 0.00382754, True}, {20, 26, 19774, 2},
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GO:0005737 → {{0.000321249, 0.00386213, True}, {20, 4436, 19774, 12},
   {{cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {TIRAP}, {CHUK},
     {CSNK2B}, {LYN}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}}}},
GO:0032496 → {{0.000332974, 0.00386754, True}, {20, 136, 19774, 3},
   {{response to lipopolysaccharide, biological_process}, {{TIRAP}, {CHUK}, {NFKB2}}}},
GO:0051403 → {{0.000335997, 0.00386754, True}, {20, 27, 19774, 2},
   {{stress-activated MAPK cascade, biological_process}, {{CHUK}, {NFKB1}}}},
GO:0005654 → {{0.000399623, 0.00450408, True}, {20, 3142, 19774, 10}, {{nucleoplasm, cellular_component},
    {{CHUK}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {PIAS4}}}},
GO:0097421 → {{0.000415649, 0.00458911, True}, {20, 30, 19774, 2},
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GO:0006457 → {{0.000426584, 0.00461564, True}, {20, 148, 19774, 3},
   {{protein folding, biological_process}, {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
GO:0043200 → {{0.000473361, 0.00502134, True}, {20, 32, 19774, 2},
   {{response to amino acid, biological_process}, {{CHUK}, {LYN}}}},
GO:0045944 → {{0.000678181, 0.00705569, True}, {20, 1134, 19774, 6},
   {{positive regulation of transcription by RNA polymerase II, biological_process},
    {{CHUK}, {PARP1}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
GO:0050852 → {{0.000718583, 0.00733497, True}, {20, 177, 19774, 3},
   {{T cell receptor signaling pathway, biological_process}, {{MALT1}, {CHUK}, {NFKB1}}}},
GO:0000723 → {{0.000896278, 0.00897937, True}, {20, 44, 19774, 2},
   {{telomere maintenance, biological_process}, {{PARP1}, {ATM}}}},
GO:0007254 → {{0.00106612, 0.0104868, True}, {20, 48, 19774, 2},
   {{JNK cascade, biological_process}, {{TAB1}, {IRAK4}}}}, GO:0005829 →
 {{0.00110925, 0.0107162, True}, {20, 5035, 19774, 12}, {{cytosol, cellular_component}, {{TAB1}, {MALT1},
     {TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
GO:0032481 → {{0.00120287, 0.0114167, True}, {20, 51, 19774, 2},
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GO:0006468 → {{0.00131624, 0.0122773, True}, {20, 490, 19774, 4},
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GO:0006303 → {{0.00134759, 0.0123568, True}, {20, 54, 19774, 2},
   {{double-strand break repair via nonhomologous end joining, biological_process}, {{ATM}, {PIAS4}}}},
GO:0030335 → {{0.00139999, 0.0126232, True}, {20, 223, 19774, 3},
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GO:0042102 → {{0.00166079, 0.0130219, True}, {20, 60, 19774, 2},
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GO:0006974 → {{0.00174849, 0.0130219, True}, {20, 241, 19774, 3},
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GO:0038061 → {{0.00177217, 0.0130219, True}, {20, 62, 19774, 2},
   {{NIK/NF-kappaB signaling, biological_process}, {{CHUK}, {NFKB2}}}},
GO:0005886 → {{0.00186882, 0.0130219, True}, {20, 4532, 19774, 11},
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GO:0009636 → {{0.00194576, 0.0130219, True}, {20, 65, 19774, 2},
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GO:0048511 → {{0.00200535, 0.0130219, True}, {20, 66, 19774, 2},
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GO:0001923 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0002268 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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  {{follicular dendritic cell differentiation, biological_process}, {{NFKB2}}}},
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  {{Fc receptor mediated stimulatory signaling pathway, biological_process}, {{LYN}}}},
GO:0006991 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{response to sterol depletion, biological_process}, {{LYN}}}},
GO:0033003 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{regulation of mast cell activation, biological_process}, {{LYN}}}},
GO:0033257 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{Bcl3/NF-kappaB2 complex, cellular_component}, {{NFKB2}}}},
GO:0060369 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0070427 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{nucleotide-binding oligomerization domain containing 1 signaling pathway, biological_process},
   {{NFKBIA}}}}, GO:0070667 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0070668 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0071221 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:0097694 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:1902532 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
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GO:1903518 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of single strand break repair, biological_process}, {{PARP1}}}},
GO:1904884 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of telomerase catalytic core complex assembly, biological_process}, {{ATM}}}},
GO:2000340 → {{0.00202189, 0.0130219, True}, {20, 2, 19774, 1},
  {{positive regulation of chemokine (C-X-C motif) ligand 1 production, biological_process}, {{TIRAP}}}},
GO:0071300 → {{0.00218928, 0.0139341, True}, {20, 69, 19774, 2},
  {{cellular response to retinoic acid, biological_process}, {{LYN}, {ATM}}}},
GO:0071260 → {{0.00285783, 0.0149088, True}, {20, 79, 19774, 2},
  {{cellular response to mechanical stimulus, biological_process}, {{LTBR}, {NFKB1}}}},
GO:0005524 → {{0.00290162, 0.0149088, True}, {20, 1501, 19774, 6},
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GO:0002513 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002553 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002762 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0002774 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0004677 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0008384 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{IkappaB kinase activity, molecular_function}, {{CHUK}}}},
GO:0010956 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0034666 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{integrin alpha2-beta1 complex, cellular_component}, {{LYN}}}},
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GO:0070447 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{positive regulation of oligodendrocyte progenitor proliferation, biological_process}, {{LYN}}}},
GO:0071500 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0099091 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0140031 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:0140294 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:1902174 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:1904044 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:2000630 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:2000670 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
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GO:2001170 → {{0.00303137, 0.0149088, True}, {20, 3, 19774, 1},
  {{negative regulation of ATP biosynthetic process, biological_process}, {{PARP1}}}},
GO:0000724 → {{0.00314887, 0.0153472, True}, {20, 83, 19774, 2},
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GO:0010957 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0018312 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0032648 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0048305 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0071359 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0090330 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:1900127 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:1990234 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:2000321 → {{0.00403989, 0.0176256, True}, {20, 4, 19774, 1},
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GO:0005102 → {{0.00432566, 0.0187215, True}, {20, 332, 19774, 3},
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GO:0007179 → {{0.00444549, 0.0190874, True}, {20, 99, 19774, 2},
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GO:0014910 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0032042 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0032269 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
  {{negative regulation of cellular protein metabolic process, biological_process}, {{NFKB1}}}},
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GO:0034136 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0035662 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0042159 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0043208 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:2000343 → {{0.00504744, 0.0193664, True}, {20, 5, 19774, 1},
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GO:0000784 → {{0.00536146, 0.0202836, True}, {20, 109, 19774, 2},
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GO:0016363 → {{0.00536146, 0.0202836, True}, {20, 109, 19774, 2},
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GO:0006954 → {{0.00567463, 0.0211305, True}, {20, 366, 19774, 3},
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GO:0000785 → {{0.00584929, 0.0211305, True}, {20, 114, 19774, 2},
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GO:0016032 → {{0.00593612, 0.0211305, True}, {20, 372, 19774, 3},
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GO:0034774 → {{0.00594922, 0.0211305, True}, {20, 115, 19774, 2},
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GO:0051972 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{regulation of telomerase activity, biological_process}, {{ATM}}}},
GO:1902231 → {{0.00605401, 0.0211305, True}, {20, 6, 19774, 1},
  {{positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage,
    biological_process}, {{PIAS4}}}}, GO:0071356 → {{0.00699141, 0.0228698, True}, {20, 125, 19774, 2},
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GO:0007253 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0014909 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0032210 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0032927 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
  {{positive regulation of activin receptor signaling pathway, biological_process}, {{CSNK2B}}}},
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GO:0033211 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0051101 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0070431 → {{0.00705963, 0.0228698, True}, {20, 7, 19774, 1},
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GO:0002467 → {{0.00806427, 0.0250734, True}, {20, 8, 19774, 1},
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GO:0032757 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
  {{positive regulation of interleukin-8 production, biological_process}, {{TIRAP}}}}, GO:0042113 →
 {{0.02697, 0.0455962, True}, {20, 27, 19774, 1}, {{B cell activation, biological_process}, {{MALT1}}}},
GO:1900745 → {{0.02697, 0.0455962, True}, {20, 27, 19774, 1},
```

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```
    {{positive regulation of p38MAPK cascade, biological_process}, {{GADD45B}}}},
  GO:0046875 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
    {{ephrin receptor binding, molecular_function}, {{LYN}}}},
  GO:0048678 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
    {{response to axon injury, biological_process}, {{LYN}}}},
  GO:0070372 → {{0.0279555, 0.0468233, True}, {20, 28, 19774, 1},
    {{regulation of ERK1 and ERK2 cascade, biological_process}, {{LYN}}}},
  GO:0044877 → {{0.0286011, 0.0474442, True}, {20, 263, 19774, 2},
    {{protein-containing complex binding, molecular_function}, {{TAB1}, {ATM}}}},
  GO:0016579 → {{0.0288022, 0.0474442, True}, {20, 264, 19774, 2},
    {{protein deubiquitination, biological_process}, {{TAB1}, {NFKBIA}}}},
  GO:0006294 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
    {{nucleotide-excision repair, preincision complex assembly, biological_process}, {{PARP1}}}},
  GO:0010803 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
    {{regulation of tumor necrosis factor-mediated signaling pathway, biological_process}, {{CHUK}}}},
  GO:0035666 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
    {{TRIF-dependent toll-like receptor signaling pathway, biological_process}, {{CHUK}}}},
  GO:0046579 → {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1},
    {{positive regulation of Ras protein signal transduction, biological_process}, {{LYN}}}}, GO:0051059 →
   {{0.0289401, 0.0474442, True}, {20, 29, 19774, 1}, {{NF-kappaB binding, molecular_function}, {{NFKBIA}}}},
  GO:0006366 → {{0.0298159, 0.0484692, True}, {20, 269, 19774, 2},
    {{transcription by RNA polymerase II, biological_process}, {{PARP1}, {NFKB1}}}},
  GO:0033574 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{response to testosterone, biological_process}, {{CSNK2B}}}},
  GO:0043552 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{positive regulation of phosphatidylinositol 3-kinase activity, biological_process}, {{LYN}}}},
  GO:0071480 → {{0.0299237, 0.0484692, True}, {20, 30, 19774, 1},
    {{cellular response to gamma radiation, biological_process}, {{ATM}}}},
  GO:0048471 → {{0.030532, 0.0491774, True}, {20, 686, 19774, 3},
    {{perinuclear region of cytoplasm, cellular_component}, {{TNFSF13B}, {MALT1}, {LYN}}}},
  GO:0000077 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{DNA damage checkpoint, biological_process}, {{ATM}}}},
  GO:0005164 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{tumor necrosis factor receptor binding, molecular_function}, {{TNFSF13B}}}},
  GO:0007131 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{reciprocal meiotic recombination, biological_process}, {{ATM}}}},
  GO:0043330 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{response to exogenous dsRNA, biological_process}, {{NFKBIA}}}},
  GO:1903955 → {{0.0309063, 0.0491774, True}, {20, 31, 19774, 1},
    {{positive regulation of protein targeting to mitochondrion, biological_process}, {{CSNK2A2}}}}|>
```

Specifically:

```
In[3]:= 1 - N[CDF[HypergeometricDistribution[#1, #2, #3], #4 - 1]] &[20, 151, 19774, 7]
Out[3]= 9.39023×10^-11
```

See Also

BenjaminiHochbergFDR ▪ **EnrichmentReportExport** ▪ **GeneTranslation** ▪ **GetGeneDictionary** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGAnalysisAssigner** ▪ **KEGGPathwayVisual** ▪

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OBOGODictionary ▪ TimeSeriesClusters ▪ UCSCBrowserSQL

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾ URL ▾

GOAnalysisAssigner

GOAnalysisAssigner[]
creates identifier to gene ontology (GO) accession associations, restricted to required background set, downloading the data if necessary.

Details

- GOAnalysisAssigner[] creates identifier to gene ontology (GO) accession associations, restricted to required background set, downloading the data if necessary.
- The form of the output is for n member IDs and m GO categories:
- output = <Species → <"IDToGO" → <|ID_1 → {GO categories associated to ID_1},
  ID_2 → {GO categories associated to ID_2}, ..., ID_n → {GO categories associated to ID_n}|>,
  "GOToID" → <| GO : $Accession_1$ → {IDs associated to GO : $Accession_1$},
  GO : $Accession_2$ → {IDs associated to GO : $Accession_2$}, ..., GO : $Accession_m$ → {IDs associated to GO : $Accession_m$}|>|>
- If multiple species are considered in user applications the form above can easily be extended to accomodate more species as keys of the outer association, and provide the "IDToGO" and "GOToID" associations for each species accordingly.
- The following options can be given:

BackgroundSet	All	The BackgroundSet option allows the selection of what members to use as a background (e.g. genes), or to use All genes as background.
GOFileColumns	{2, 5}	Columns to use for IDs and GO:accessions respectively from the downloaded GO annotation file, used when ImportDirectly is set to True to obtain a new GO association file. The default corresponds to UniProt accessions in the second column.
GOFileName	None	Name for specific GO file to download from the GOURL if option ImportDirectly is set to True. If GOFileName is set to None then the species option is used to specify the file to download as "goa_" <> OptionValue[Species] <> ".gaf"<>".gz" from the GOURL.

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GOURL	"http://current.geneontology.org/annotations/"	The GOURL option provides the location (base URL) where the GO association annotation files are downloaded from.
ImportDirectly	False	ImportDirectly gives the option to import a new version of GO annotation file directly from the Gene Ontology consortium site to either replace the current version of the ID/term associations in the MathIOmica package data directory or add a new one (e.g. for a different species).
LengthFilter	None	LengthFilter gives the option to select how many members each GO category can have, as restricted by the LengthFilterFunction.
LengthFilterFunction	GreaterEqualThan	LengthFilterFunction is an option regarding which function to use to filter the number of members a reported GO category has compared to the number provided by LengthFilter.
MathIOmicaDataDirectory	If[!DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]/MathIOmicaData	MathIOmicaDataDirectory option specifies the directory where the default MathIOmica package data are stored. By default the option is set to create the standard directory if it does not exist already.
Species	"human"	The option Species provides a string indicating which species is being used.

Examples (9)

Basic Examples (1)

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First we need to load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

- We can now run GOAnalysisAssigner to create a dictionary between UniProt IDs and GO accessions, and similarly GO accession to UniProt IDs:

In[2]:=
```
assignmentsGO = GOAnalysisAssigner[]
```

Out[2]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A075B6H9 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     A0A075B6I0 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ··· 19 769 ···, Q9NVA4 → {GO:0016021}, Q6B9Z1 → {GO:0005102, GO:0005615},
     I3L0E3 → {GO:0005763}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

- The assignment has two Keys for the "human" set:

In[3]:=
```
Query[All, Keys]@assignmentsGO
```

Out[3]=
```
<|human → {IDToGO, GOToID}|>
```

- For example for accession "P19838" corresponding to NFKB1 we have:

In[4]:=
```
accessionsGO = Query["human", "IDToGO", "P19838"]@assignmentsGO
```

Out[4]=
```
{GO:0000122, GO:0000976, GO:0000977, GO:0000980, GO:0000981, GO:0001227, GO:0001228,
 GO:0002223, GO:0003682, GO:0003700, GO:0005515, GO:0005576, GO:0005634, GO:0005654,
 GO:0005737, GO:0005739, GO:0005829, GO:0006366, GO:0006915, GO:0006954, GO:0008134,
 GO:0010629, GO:0010744, GO:0010884, GO:0010956, GO:0010957, GO:0031293, GO:0032269, GO:0032375,
 GO:0032481, GO:0033256, GO:0034774, GO:0035580, GO:0035994, GO:0038095, GO:0042802, GO:0042803,
 GO:0042805, GO:0043066, GO:0043312, GO:0044212, GO:0045083, GO:0045893, GO:0045944, GO:0046982,
 GO:0050728, GO:0050852, GO:0051092, GO:0051403, GO:0070498, GO:0071222, GO:0071260, GO:0071316,
 GO:0071347, GO:0071354, GO:0071356, GO:0071359, GO:0090263, GO:1900127, GO:1904385, GO:2000630}
```

- We can see what all these terms' annotations are by using the OBOGODictionary function

In[5]:=
```
goAnnotationExample = OBOGODictionary[]
```

Out[5]=
```
<|GO:0000001 → {mitochondrion inheritance, biological_process},
 GO:0000002 → {mitochondrial genome maintenance, biological_process},
 GO:0000003 → {reproduction, biological_process}, ··· 47 395 ···, GO:2001315 →
  {UDP-4-deoxy-4-formamido-beta-L-arabinopyranose biosynthetic process, biological_process},
 GO:2001316 → {kojic acid metabolic process, biological_process},
 GO:2001317 → {kojic acid biosynthetic process, biological_process}|>
```

large output | show less | show more | show all | set size limit...

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In[6]:=
```
Query[accessionsGO]@goAnnotationExample
```

Out[6]=
```
<|GO:0000122 → {negative regulation of transcription by RNA polymerase II, biological_process},
 GO:0000976 → {transcription regulatory region sequence-specific DNA binding, molecular_function},
 GO:0000977 → {RNA polymerase II regulatory region sequence-specific DNA binding, molecular_function},
 GO:0000980 → {RNA polymerase II distal enhancer sequence-specific DNA binding, molecular_function},
 GO:0000981 → {DNA-binding transcription factor activity, RNA polymerase II-specific, molecular_function},
 GO:0001227 → {DNA-binding transcription repressor activity, RNA polymerase II-specific,
   molecular_function}, GO:0001228 →
  {DNA-binding transcription activator activity, RNA polymerase II-specific, molecular_function},
 GO:0002223 → {stimulatory C-type lectin receptor signaling pathway, biological_process},
 GO:0003682 → {chromatin binding, molecular_function},
 GO:0003700 → {DNA-binding transcription factor activity, molecular_function},
 GO:0005515 → {protein binding, molecular_function},
 GO:0005576 → {extracellular region, cellular_component}, GO:0005634 → {nucleus, cellular_component},
 GO:0005654 → {nucleoplasm, cellular_component}, GO:0005737 → {cytoplasm, cellular_component},
 GO:0005739 → {mitochondrion, cellular_component}, GO:0005829 → {cytosol, cellular_component},
 GO:0006366 → {transcription by RNA polymerase II, biological_process},
 GO:0006915 → {apoptotic process, biological_process},
 GO:0006954 → {inflammatory response, biological_process},
 GO:0008134 → {transcription factor binding, molecular_function},
 GO:0010629 → {negative regulation of gene expression, biological_process},
 GO:0010744 → {positive regulation of macrophage derived foam cell differentiation, biological_process},
 GO:0010884 → {positive regulation of lipid storage, biological_process},
 GO:0010956 → {negative regulation of calcidiol 1-monooxygenase activity, biological_process},
 GO:0010957 → {negative regulation of vitamin D biosynthetic process, biological_process},
 GO:0031293 → {membrane protein intracellular domain proteolysis, biological_process},
 GO:0032269 → {negative regulation of cellular protein metabolic process, biological_process},
 GO:0032375 → {negative regulation of cholesterol transport, biological_process},
 GO:0032481 → {positive regulation of type I interferon production, biological_process},
 GO:0033256 → {I-kappaB/NF-kappaB complex, cellular_component},
 GO:0034774 → {secretory granule lumen, cellular_component},
 GO:0035580 → {specific granule lumen, cellular_component},
 GO:0035994 → {response to muscle stretch, biological_process},
 GO:0038095 → {Fc-epsilon receptor signaling pathway, biological_process},
 GO:0042802 → {identical protein binding, molecular_function},
 GO:0042803 → {protein homodimerization activity, molecular_function},
 GO:0042805 → {actinin binding, molecular_function},
 GO:0043066 → {negative regulation of apoptotic process, biological_process},
 GO:0043312 → {neutrophil degranulation, biological_process},
 GO:0044212 → {transcription regulatory region DNA binding, molecular_function},
 GO:0045083 → {negative regulation of interleukin-12 biosynthetic process, biological_process},
 GO:0045893 → {positive regulation of transcription, DNA-templated, biological_process},
 GO:0045944 → {positive regulation of transcription by RNA polymerase II, biological_process},
 GO:0046982 → {protein heterodimerization activity, molecular_function},
 GO:0050728 → {negative regulation of inflammatory response, biological_process},
 GO:0050852 → {T cell receptor signaling pathway, biological_process},
 GO:0051092 → {positive regulation of NF-kappaB transcription factor activity, biological_process},
 GO:0051403 → {stress-activated MAPK cascade, biological_process},
 GO:0070498 → {interleukin-1-mediated signaling pathway, biological_process},
 GO:0071222 → {cellular response to lipopolysaccharide, biological_process},
 GO:0071260 → {cellular response to mechanical stimulus, biological_process},
 GO:0071316 → {cellular response to nicotine, biological_process},
 GO:0071347 → {cellular response to interleukin-1, biological_process},
 GO:0071354 → {cellular response to interleukin-6, biological_process},
 GO:0071356 → {cellular response to tumor necrosis factor, biological_process},
 GO:0071359 → {cellular response to dsRNA, biological_process},
 GO:0090263 → {positive regulation of canonical Wnt signaling pathway, biological_process},
 GO:1900127 → {positive regulation of hyaluronan biosynthetic process, biological_process},
 GO:1904385 → {cellular response to angiotensin, biological_process},
 GO:2000630 → {positive regulation of miRNA metabolic process, biological_process}|>
```

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- We can also query the members of a given GO term, e.g. "GO:0033256" (term for "I-kappaB/NF-kappaB complex"):

```
In[7]:= identitiesGO = Query["human", "GOToID", "GO:0033256"]@assignmentsGO
Out[7]= {P19838, P25963}
```

Options (8)

BackgroundSet (1)

```
In[1]:= Needs["MathIOmica`"]
```

The `BackgroundSet` option allows the selection of what members (IDs) to use as a background (e.g. genes), or to use All genes as background. In effect this restricts the reported dictionary to only these members.

As an example, we limit the set to the following IDs {P19838,P25963}:

```
In[2]:= GOAnalysisAssigner[BackgroundSet → {"P19838", "P25963"}]
Out[2]= <|human →
    <|IDToGO → <|P19838 → {GO:0000122, GO:0000976, GO:0000977, GO:0000980, GO:0000981, GO:0001227, GO:0001228,
          GO:0002223, GO:0003682, GO:0003700, GO:0005515, GO:0005576, GO:0005634, GO:0005654, GO:0005737,
          GO:0005739, GO:0005829, GO:0006366, GO:0006915, GO:0006954, GO:0008134, GO:0010629, GO:0010744,
          GO:0010884, GO:0010956, GO:0010957, GO:0031293, GO:0032269, GO:0032375, GO:0032481, GO:0033256,
          GO:0034774, GO:0035580, GO:0035994, GO:0038095, GO:0042802, GO:0042803, GO:0042805, GO:0043066,
          GO:0043312, GO:0044212, GO:0045083, GO:0045893, GO:0045944, GO:0046982, GO:0050728, GO:0050852,
          GO:0051092, GO:0051403, GO:0070498, GO:0071222, GO:0071260, GO:0071316, GO:0071347,
          GO:0071354, GO:0071356, GO:0071359, GO:0090263, GO:1900127, GO:1904385, GO:2000630},
        P25963 → {GO:0005515, GO:0005634, GO:0005654, GO:0005737, GO:0005829, GO:0005886, GO:0006606,
          GO:0006915, GO:0007249, GO:0007253, GO:0008134, GO:0008139, GO:0010745, GO:0010875, GO:0010888,
          GO:0016032, GO:0016579, GO:0019899, GO:0031625, GO:0031663, GO:0032088, GO:0032270,
          GO:0032495, GO:0033209, GO:0033256, GO:0034142, GO:0035994, GO:0042127, GO:0042802,
          GO:0042994, GO:0043066, GO:0043330, GO:0043392, GO:0045638, GO:0045746, GO:0045944,
          GO:0050729, GO:0051059, GO:0070417, GO:0070427, GO:0070431, GO:0070498, GO:1901222}|>,
     GOToID → <|GO:0000122 → {P19838}, GO:0000976 → {P19838}, GO:0000977 → {P19838},
        GO:0000980 → {P19838}, GO:0000981 → {P19838}, GO:0001227 → {P19838},
        GO:0001228 → {P19838}, GO:0002223 → {P19838}, GO:0003682 → {P19838}, GO:0003700 → {P19838},
        GO:0005515 → {P19838, P25963}, GO:0005576 → {P19838}, GO:0005634 → {P19838, P25963},
        GO:0005654 → {P19838, P25963}, GO:0005737 → {P19838, P25963}, GO:0005739 → {P19838},
        GO:0005829 → {P19838, P25963}, GO:0006366 → {P19838}, GO:0006915 → {P19838, P25963},
        GO:0006954 → {P19838}, GO:0008134 → {P19838, P25963}, GO:0010629 → {P19838},
        GO:0010744 → {P19838}, GO:0010884 → {P19838}, GO:0010956 → {P19838}, GO:0010957 → {P19838},
        GO:0031293 → {P19838}, GO:0032269 → {P19838}, GO:0032375 → {P19838}, GO:0032481 → {P19838},
        GO:0033256 → {P19838, P25963}, GO:0034774 → {P19838}, GO:0035580 → {P19838},
        GO:0035994 → {P19838, P25963}, GO:0038095 → {P19838}, GO:0042802 → {P19838, P25963},
        GO:0042803 → {P19838}, GO:0042805 → {P19838}, GO:0043066 → {P19838, P25963},
        GO:0043312 → {P19838}, GO:0044212 → {P19838}, GO:0045083 → {P19838}, GO:0045893 → {P19838},
        GO:0045944 → {P19838, P25963}, GO:0046982 → {P19838}, GO:0050728 → {P19838}, GO:0050852 → {P19838},
        GO:0051092 → {P19838}, GO:0051403 → {P19838}, GO:0070498 → {P19838, P25963}, GO:0071222 → {P19838},
        GO:0071260 → {P19838}, GO:0071316 → {P19838}, GO:0071347 → {P19838}, GO:0071354 → {P19838},
        GO:0071356 → {P19838}, GO:0071359 → {P19838}, GO:0090263 → {P19838}, GO:1900127 → {P19838},
        GO:1904385 → {P19838}, GO:2000630 → {P19838}, GO:0005886 → {P25963}, GO:0006606 → {P25963},
        GO:0007249 → {P25963}, GO:0007253 → {P25963}, GO:0008139 → {P25963}, GO:0010745 → {P25963},
        GO:0010875 → {P25963}, GO:0010888 → {P25963}, GO:0016032 → {P25963}, GO:0016579 → {P25963},
        GO:0019899 → {P25963}, GO:0031625 → {P25963}, GO:0031663 → {P25963}, GO:0032088 → {P25963},
        GO:0032270 → {P25963}, GO:0032495 → {P25963}, GO:0033209 → {P25963}, GO:0034142 → {P25963},
        GO:0042127 → {P25963}, GO:0042994 → {P25963}, GO:0043330 → {P25963}, GO:0043392 → {P25963},
        GO:0045638 → {P25963}, GO:0045746 → {P25963}, GO:0050729 → {P25963}, GO:0051059 → {P25963},
        GO:0070417 → {P25963}, GO:0070427 → {P25963}, GO:0070431 → {P25963}, GO:1901222 → {P25963}|>|>|>
```

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Setting `BackgroundSet` to All retrieves all the ID/GO term associations:

In[3]:=
```
GOAnalysisAssigner[BackgroundSet → All]
```

Out[3]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A075B6H9 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     A0A075B6I0 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ··· 19 769 ···, Q9NVA4 → {GO:0016021}, Q6B9Z1 → {GO:0005102, GO:0005615},
     I3L0E3 → {GO:0005763}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

GOFileColumns (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`GOFileColumns` specifies a list of which two column positions to use for IDs and GO:accessions respectively from the downloaded GO annotation file, used when `ImportDirectly` is set to True to obtain a new GO association file. The default corresponds to UniProt accessions, found in the second column of the corresponding online GO file.

In[2]:=
```
GOAnalysisAssigner[GOFileColumns → {2, 5}, ImportDirectly → True]
```

Out[2]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A075B6H9 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     A0A075B6I0 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ··· 19 769 ···, Q9NVA4 → {GO:0016021}, Q6B9Z1 → {GO:0005102, GO:0005615},
     I3L0E3 → {GO:0005763}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

For example, we can change this to using the 3rd column, which corresponds to gene names (please note that running the example below will replace the file in place in the MathIOmica package data directory and affect your results/annotations)

In[3]:=
```
GOAnalysisAssigner[GOFileColumns → {3, 5}, ImportDirectly → True]
```

Out[3]=
```
<|human → <|IDToGO → <|NUDT4B → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     IGLV4-69 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     IGLV8-61 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ··· 19 669 ···, TMEM184C → {GO:0016021}, IGFL4 → {GO:0005102, GO:0005615},
     hCG_1984214 → {GO:0005763}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

To restore the default standard file (using default {2,5} for the GOFileColumns option) we

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can simply call:

In[4]:=
```
GOAnalysisAssigner[ImportDirectly → True]
```

Out[4]=
```
⟨| human →
  ⟨| IDToGO → ⟨| A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A075B6H9 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     A0A075B6I0 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ⋯ 19 769 ⋯, Q9NVA4 → {GO:0016021}, Q6B9Z1 → {GO:0005102, GO:0005615},
     I3L0E3 → {GO:0005763} |⟩, GOToID → ⟨| ⋯ 1 ⋯ |⟩ |⟩ |⟩
```

large output | show less | show more | show all | set size limit...

GOFileName (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`GOFileName` provides the name for the specific GO annotation file to download from the `GOURL` specified website, when `ImprortDirectly` is set to True. If set to None (default) then the species option is used to specify the file to download as "goa_" <> OptionValue[Species] <> ".gz" from the `GOURL`. For example, we can download the human isoform annotation file:

In[2]:=
```
GOAnalysisAssigner[GOFileName → "goa_human_isoform.gaf.gz" , ImportDirectly → True]
```

Out[2]=
```
⟨| human →
  ⟨| IDToGO → ⟨| A0A087WTH5 → {GO:0005249, GO:0016021, GO:0071805}, A0A087WUV0 → {GO:0003676, GO:0006355},
     A0A087WVI0 → {GO:0006891, GO:0017119}, A0A087WX78 → {GO:0006357, GO:0070449},
     ⋯ 10 637 ⋯, U3KQF4 → {GO:0005654, GO:0005829, GO:0016567, GO:0061630}, U3KQK1 →
      {GO:0000398, GO:0000956, GO:0003723, GO:0005681}, V9GXZ4 → {GO:0016772} |⟩, GOToID → ⟨| ⋯ 1 ⋯ |⟩ |⟩ |⟩
```

large output | show less | show more | show all | set size limit...

ImportDirectly (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`ImportDirectly` gives the option to import a new version of GO annotation file directly from the Gene Ontology consortium site (or specified website through option `GOURL`) and either replace the current version of the ID/term associations in the MathIOmica package data directory or add a new one (e.g. for a different species).

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In[2]:=
```
GOAnalysisAssigner[ImportDirectly → True]
```

Out[2]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A075B6H9 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     A0A075B6I0 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ··· 19 769 ···, Q9NVA4 → {GO:0016021}, Q6B9Z1 → {GO:0005102, GO:0005615},
     I3L0E3 → {GO:0005763}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

LengthFilter (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`LengthFilter` gives the option to select how many members each GO category can have, as restricted by the `LengthFilterFunction`, the default is number of members in each GO category
`number of members in each GO category ≥ OptionValue[LengthFilter]`. By default LengthFilter is set to None, i.e. no filtering is performed:

In[2]:=
```
assignmentsGO = GOAnalysisAssigner[LengthFilter → None]
```

Out[2]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A075B6H9 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     A0A075B6I0 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ··· 19 769 ···, Q9NVA4 → {GO:0016021}, Q6B9Z1 → {GO:0005102, GO:0005615},
     I3L0E3 → {GO:0005763}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

The number of "GOToID" entries are:

In[3]:=
```
Query["human", "GOToID", Length[#] &]@assignmentsGO
```

Out[3]= 18 176

We can calculate the minimum length of these term lists:

In[4]:=
```
Query["human", "GOToID", All /* Min, Length[#] &]@assignmentsGO
```

Out[4]= 1

We now restrict the terms to have length greater than 3

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In[5]:=
```
assignmentsLengthFilter = GOAnalysisAssigner[LengthFilter → 3]
```

Out[5]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A0G2JNQ3 → {GO:0003723}, A0A0G2JPF8 → {GO:0003723, GO:0005634}, A0A2R8Y4L2 → {GO:0003723},
     A0A3B3IRV3 → {GO:0003723, GO:0005737}, ··· 19 762 ···, Q17RN3 → {GO:0072669}, Q8N8M0 → {GO:0016747},
     Q9P1F3 → {GO:0032970}, A6NJ78 → {GO:0070475}, P0C7V9 → {GO:0070475}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

We see that this restricts the number of terms compared to no filter:

In[6]:=
```
Query["human", "GOToID", Length[#] &]@assignmentsLengthFilter
```

Out[6]= 10 092

As expected the smallest list of IDs for a given GO term is 3:

In[7]:=
```
Query["human", "GOToID", All /* Min, Length[#] &]@assignmentsLengthFilter
```

Out[7]= 3

LengthFilterFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`LengthFilterFunction` is an option regarding which function to use to filter the number of members a reported GO category has compared to the number provided by `LengthFilter`. If `LengthFilter` is set to None no filtering is implemented. The default comparison function is GreaterEqualThan

For example we can create the IDs/Go term dictionaries listing only the IDs/GO terms, for which for all GO terms have at least 3 IDs associated to them.

In[2]:=
```
assignmentsFilterGreater = GOAnalysisAssigner[LengthFilterFunction → GreaterEqualThan, LengthFilter → 3]
```

Out[2]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A0G2JNQ3 → {GO:0003723}, A0A0G2JPF8 → {GO:0003723, GO:0005634}, A0A2R8Y4L2 → {GO:0003723},
     A0A3B3IRV3 → {GO:0003723, GO:0005737}, ··· 19 762 ···, Q17RN3 → {GO:0072669}, Q8N8M0 → {GO:0016747},
     Q9P1F3 → {GO:0032970}, A6NJ78 → {GO:0070475}, P0C7V9 → {GO:0070475}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

We see that the maximum number of IDs associated to a GO term is high:

In[3]:=
```
Query["human", "GOToID", All /* Max, Length[#] &]@assignmentsFilterGreater
```

Out[3]= 9629

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Instead, we can look at all GO terms that have less than 3 IDs associated to them:

In[4]:=
```
assignmentsFilterLess = GOAnalysisAssigner[LengthFilterFunction → LessThan, LengthFilter → 3]
```

Out[4]=
```
<|human → <|IDToGO →
    <|A0A087WXM9 → {GO:0010789}, A0A087WZV9 → {GO:0051499}, A0A0C5B5G6 → {GO:0043610, GO:0072522},
     P42345 → {GO:0014736, GO:0043610, GO:0099547, GO:1903691, GO:1904056, GO:1904193, GO:1904197,
       GO:1904206, GO:1904213, GO:1904690}, A0A0J9YVX5 → {GO:0043004}, ··· 5147 ···, Q03403 → {GO:0031723},
     O95456 → {GO:0080129}, P01303 → {GO:0031841}, Q7Z4H3 → {GO:0002953}|>, GOToID → <| ··· 1 ··· |> |> |>
```

large output | show less | show more | show all | set size limit...

We can now see that the maximum number of IDs associated to a GO term is 2, as we have restricted the possibilities:

In[5]:=
```
Query["human", "GOToID", All /* Max, Length[#] &]@assignmentsFilterLess
```

Out[5]= 2

MathIOmicaDataDirectory (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value point to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

In[2]:=
```
GOAnalysisAssigner[MathIOmicaDataDirectory → FileNameJoin[
   Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]
```

Out[2]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A075B6H9 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     A0A075B6I0 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ··· 19 769 ···, Q9NVA4 → {GO:0016021}, Q6B9Z1 → {GO:0005102, GO:0005615},
     I3L0E3 → {GO:0005763}|>, GOToID → <| ··· 1 ··· |> |> |>
```

large output | show less | show more | show all | set size limit...

Species (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The option `Species` provides a string indicating which species is being used. The default setting is "human":

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In[2]:=
```
GOAnalysisAssigner[Species → "human"]
```

Out[2]=
```
<|human →
  <|IDToGO → <|A0A024RBG1 → {GO:0003723, GO:0005829, GO:0008486, GO:0046872, GO:0052840, GO:0052842},
     A0A075B6H9 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     A0A075B6I0 → {GO:0002250, GO:0002377, GO:0005615, GO:0005886, GO:0006955, GO:0019814},
     ··· 19 769 ···, Q9NVA4 → {GO:0016021}, Q6B9Z1 → {GO:0005102, GO:0005615},
     I3L0E3 → {GO:0005763}|>, GOToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

We note here that the `Species` option may be used in conjunction when option `GOFileName` is set to None to specify the file to download when option `ImportDirectly` is set to True. The file "gene_association.goa_" <> OptionValue[Species] <> ".gz" is downloaded from the GOURL and used in constructing the ID/association dictionaries.

See Also

GeneTranslation ▪ **GetGeneDictionary** ▪ **GOAnalysis** ▪ **KEGGAnalysis** ▪ **KEGGAnalysisAssigner** ▪ **OBOGODictionary** ▪ **UCSCBrowserSQL**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

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Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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URL ▾

GeneTranslation

GeneTranslation[*inputIDList*, *targetIDList*, *geneDictionary*]
uses *geneDictionary* to convert *inputIDList* IDs to different annotations as indicated by *targetIDList*.

Details

- GeneTranslation[inputIDList, targetIDList, geneDictionary]
uses geneDictionary to convert inputList IDs to different annotations as indicated by targetIDList. It takes the following inputs:

inputIDList	List of n IDs (strings) to be converted in the form $\{inputID_1, inputID_2, ..., inputID_n\}$
targetIDList	List of target identifier strings, as used in the gene geneDictionary, $\{target\ ID_1, targetID_2, ...\ target\ ID_k\}$, e.g. {"UniProt ID","Gene Symbol"}. Can also be provided as a single string for only one kind of IDs.

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geneDictionary	Gene dictionary to base translation on in the form generated by GetGeneDictionary. For i species, each having m_i possible annotations (kinds of IDs) for n_i entities each (e.g. corresponding to n_i genes) the format is schematically:

```
geneDictionary =
 <|Species_1 → <|Kind of ID_11 →
      {accessions list_11 of length n_1},
    Kind of ID_12 → {accessions
       list_12 of length n_1}, ...,
    Kind of ID_1 m_1→ {accessions
       list_1 m_1 of length n_1}|>,
   Species_2 → <|Kind of ID_21 →
      {accessions list_21 of length n_2},
    Kind of ID_22 → {accessions
       list_22 of length n_2}, ...,
    Kind of ID_2 m_2→ {accessions
       list_2 m_2 of length n_2}|>,
   ...,
   Species_i → <|Kind of ID_i1 →
      {accessions list_i2 of length n_i},
    Kind of ID_i2 → {accessions
       list_12 of length n_i}, ...,
    Kind of ID_im_i→ {accessions
       list_12 of length n_i}|>
   |>.
```

- The following options can be given:

InputID	None	InputID is a string or string list to indicate the kind of ID to use from the input gene dictionary inner association keys.
Species	"human"	Species indicates which of the species (i.e. key) to use from the input gene dictionary.

- The output has different possible forms depending on the form of the InputID options.

- For InputID set to None, the output includes all m possible kinds of IDs in the input gene dictionary, reported for each of k target IDs.

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```
output = <|target ID1 → <|Kind of ID1 → {list of target ID1 translations for inputIDlist ID1 type inputs,
        corresponding to and listed in same order as inputIDlist},
      Kind of ID2 → {list of target ID1 translations for inputIDlist ID2 type inputs,
        corresponding to and listed in same order as inputIDlist}, ...,
      Kind of IDm → {list of target ID1 translations for inputIDlist IDm type inputs,
        corresponding to and listed in same order as inputIDlist}|>,
    targetID2→ <|Kind of ID1 → {list of target ID2 translations for inputIDlist ID1 type inputs,
        corresponding to and listed in same order as inputIDlist},
      Kind of ID2 → {list of target ID2 translations for inputIDlist ID2 type inputs,
        corresponding to and listed in same order as inputIDlist}, ...,
      Kind of IDm → {list of target ID2 translations for inputIDlist IDm type inputs,
        corresponding to and listed in same order as inputIDlist}|>, ...,
    targetIDk→ <|Kind of ID1 → {list of target IDk translations for inputIDlist ID1 type inputs,
        corresponding to and listed in same order as inputIDlist},
      Kind of ID2 → {list of target IDk translations for inputIDlist ID2 type inputs,
        corresponding to and listed in same order as inputIDlist}, ...,
      Kind of IDm → {list of target IDk translations for inputIDlist IDm type inputs,
        corresponding to and listed in same order as inputIDlist}|>
  |>
```

- The translation list will contain {} if there was no match, and Missing[] if the database (e.g. UCSC) did not contain a corresponding identifier.

- For InputID set to a list of strings the output has the form:

```
output = <|target ID1 → <| inputID1 → {list of target ID1 translations for inputID1},
      inputID2 → {list of target ID1 translations for inputID2}, ...,
      inputIDn → {list of target ID1 translations for inputIDn}|>,
    target ID2 → <| inputID1 → {list of target ID2 translations for inputID1},
      inputID2 → {list of target ID2 translations for inputID2}, ...,
      inputIDn → {list of target ID2 translations for inputIDn}|>, ...,
    target IDk → <| inputID1 → {list of target IDk translations for inputID1}, inputID2 →
       {list of target IDk translations for inputID2}, ..., inputIDn → {list of target IDk translations for inputID1}|>
  |>
```

- If the input targetIDList is a single string no outer key is displayed, as only one kind or target ID is considered for all output.

Examples (3)

Basic Examples (1)

First we need to load the MathIOmica package:

```
In[1]:= Needs["MathIOmica`"]
```

Let's consider the following example of UniProt IDs that we would like to translate to official Gene Symbols and RefSeq IDs. We use GetGeneDictionary to get the default MathIOmica gene dictionary. The inputs we consider are:

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In[2]:=
```
uniProtExampleIDs = {"Q6ZRT9", "Q6NZ36", "H7C361", "Q6ZRT9", "A8MQT6", "Q9BUW7",
  "Q6NZ67", "Q6P582", "P39019", "E9PM41", "A8MTZ0", "A8MTZ0", "E9PRI7", "A8MTZ0",
  "Q9H6L5", "Q5H9J7", "Q5H9J7", "Q5H9J7", "P06454", "Q53S24", "B8ZZW7", "A0PJW6"};
targetIDs = {"Gene Symbol", "RefSeq ID"};
geneDictionaryExample = GetGeneDictionary[]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
      uc001aaq.2, uc001aar.2, uc001aau.3, ⋯ 121569 ⋯, uc031tkn.1, uc022cgh.1, uc022cha.1,
      uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ⋯ 6 ⋯, HGU13 … ix ID → ⋯ 1 ⋯|>|>
```

large output | show less | show more | show all | set size limit...

In[3]:=
```
translatedIDs =
 GeneTranslation[uniProtExampleIDs, targetIDs, geneDictionaryExample, InputID → {"UniProt ID"}]
```

Out[3]=
```
<|Gene Symbol →
  <|Q6ZRT9 → {C1orf86}, Q6NZ36 → {C1orf86}, H7C361 → {C1orf86}, A8MQT6 → {C1orf86}, Q9BUW7 → {C9orf16},
   Q6NZ67 → {MZT2B}, Q6P582 → {MZT2A}, P39019 → {RPS19}, E9PM41 → {BBIP1}, A8MTZ0 → {BBIP1}, E9PRI7 → {BBIP1},
   Q9H6L5 → {FAM134B}, Q5H9J7 → {BEX5}, P06454 → {PTMA}, Q53S24 → {PTMA}, B8ZZW7 → {PTMA}, A0PJW6 → {TMEM223}|>,
 RefSeq ID → <|Q6ZRT9 → {NM_001146310, NM_001256945}, Q6NZ36 → {NM_182533}, H7C361 → {NM_001256946},
   A8MQT6 → {NM_001256947}, Q9BUW7 → {NM_024112}, Q6NZ67 → {NM_025029}, Q6P582 → {NM_001085365},
   P39019 → {NM_001022}, E9PM41 → {NM_001195304}, A8MTZ0 → {NM_001195305, NM_001195306, NM_001243783},
   E9PRI7 → {NM_001195307}, Q9H6L5 → {NM_001034850}, Q5H9J7 → {NM_001012978, NM_001159560},
   P06454 → {NM_001099285}, Q53S24 → {NM_002823}, B8ZZW7 → {NM_002823}, A0PJW6 → {NM_001080501}|>|>
```

If we do not specify an input ID we get:

In[4]:=
```
translatedIDsNoInput = GeneTranslation[uniProtExampleIDs, targetIDs, geneDictionaryExample]
```

Out[4]=
```
<|Gene Symbol →
  <|UCSC ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   UniProt ID → {{{C1orf86}, {C1orf86}}, {{C1orf86}}, {{C1orf86}}, {{C1orf86}, {C1orf86}}, {{C1orf86}},
     {{C9orf16}}, {{MZT2B}}, {{MZT2A}}, {{RPS19}}, {{BBIP1}}, {{BBIP1}, {BBIP1}, {BBIP1}}, {{BBIP1},
      {BBIP1}, {BBIP1}}, {{BBIP1}}, {{BBIP1}, {BBIP1}, {BBIP1}}, {{FAM134B}}, {{BEX5}, {BEX5}, {BEX5}},
     {{BEX5}, {BEX5}, {BEX5}}, {{BEX5}, {BEX5}, {BEX5}}, {{PTMA}}, {{PTMA}}, {{PTMA}}, {{TMEM223}}},
   Gene Symbol → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   RefSeq ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   NCBI Protein Accession →
    {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   Ensembl ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   KEGG Gene ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   HGU133Plus2 Affymetrix ID →
    {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}}|>,
 RefSeq ID → <|UCSC ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   UniProt ID → {{{NM_001146310}, {NM_001256945}}, {{NM_182533}}, {{NM_001256946}},
     {{NM_001146310}, {NM_001256945}}, {{NM_001256947}}, {{NM_024112}}, {{NM_025029}}, {{NM_001085365}},
     {{NM_001022}}, {{NM_001195304}}, {{NM_001195305}, {NM_001195306}, {NM_001243783}},
     {{NM_001195305}, {NM_001195306}, {NM_001243783}}, {{NM_001195307}}, {{NM_001195305}, {NM_001195306},
      {NM_001243783}}, {{NM_001034850}}, {{NM_001159560}, {NM_001012978}, {NM_001159560}},
     {{NM_001159560}, {NM_001012978}, {NM_001159560}}, {{NM_001159560}, {NM_001012978}, {NM_001159560}},
     {{NM_001099285}}, {{NM_002823}}, {{NM_002823}}, {{NM_001080501}}},
   Gene Symbol → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   RefSeq ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   NCBI Protein Accession →
    {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   Ensembl ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   KEGG Gene ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
   HGU133Plus2 Affymetrix ID →
    {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}}|>|>
```

If the targetID is provided as a string, no outer association is generated (i.e. it is assumed a

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single target ID was requested). For the above example we translate to "Gene Symbol" only:

In[5]:=
```
translatedIDsGeneSymbol =
 GeneTranslation[uniProtExampleIDs, "Gene Symbol", geneDictionaryExample, InputID → {"UniProt ID"}]
```

Out[5]=
```
<|Q6ZRT9 → {C1orf86}, Q6NZ36 → {C1orf86}, H7C361 → {C1orf86}, A8MQT6 → {C1orf86}, Q9BUW7 → {C9orf16},
 Q6NZ67 → {MZT2B}, Q6P582 → {MZT2A}, P39019 → {RPS19}, E9PM41 → {BBIP1}, A8MTZ0 → {BBIP1}, E9PRI7 → {BBIP1},
 Q9H6L5 → {FAM134B}, Q5H9J7 → {BEX5}, P06454 → {PTMA}, Q53S24 → {PTMA}, B8ZZW7 → {PTMA}, A0PJW6 → {TMEM223}|>
```

Options (2)

InputID (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`InputID` option takes as values a a string or string list to indicate the kind of ID to use from the input gene dictionary inner association keys.

Let's consider the following example of mixed set of Gene Symbol and UniProt IDs that we would like to translate to RefSeq IDs. We use GetGeneDictionary to get the default MathIOmica gene dictionary. The inputs we need are:

In[2]:=
```
mixedExampleIDs = {"CD46", "DHX58", "HMGB3", "MAP3K5", "NFKB2", "NOS2", "PYCARD",
  "PYDC1", "SSC5D", "A8MTZ0", "Q9H6L5", "Q5H9J7", "Q5H9J7", "Q5H9J7", "P06454", "Q53S24"};
targetIDs = {"RefSeq ID"};
geneDictionaryExample = GetGeneDictionary[]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
     uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
     uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H ... ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

In[3]:=
```
translatedMixedIDs =
 GeneTranslation[mixedExampleIDs, targetIDs, geneDictionaryExample, InputID → {"UniProt ID", "Gene Symbol"}]
```

Out[3]=
```
<|RefSeq ID →
  <|CD46 → {NM_002389, NM_153826, NM_172350, NM_172351, NM_172352, NM_172353, NM_172359, NM_172361},
   DHX58 → {NM_024119}, HMGB3 → {NM_005342}, MAP3K5 → {NM_005923},
   NFKB2 → {NM_001077494, NM_001261403, NM_002502}, NOS2 → {NM_000625},
   PYCARD → {NM_013258, NM_145182}, PYDC1 → {NM_152901}, SSC5D → {NM_001144950, NM_001195267},
   A8MTZ0 → {NM_001195305, NM_001195306, NM_001243783}, Q9H6L5 → {NM_001034850},
   Q5H9J7 → {NM_001012978, NM_001159560}, P06454 → {NM_001099285}, Q53S24 → {NM_002823}|>|>
```

If no InputID is specified, the different possibilities are displayed for all possible target IDs.

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In[4]:=
```
translatedMixedIDsAll = GeneTranslation[mixedExampleIDs, targetIDs, geneDictionaryExample, InputID → None]
```

Out[4]=
```
<|RefSeq ID → <|UCSC ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}}, UniProt ID →
    {{}, {}, {}, {}, {}, {}, {}, {}, {}, {{NM_001195305}, {NM_001195306}, {NM_001243783}}, {{NM_001034850}},
     {{NM_001159560}, {NM_001012978}, {NM_001159560}}, {{NM_001159560}, {NM_001012978}, {NM_001159560}},
     {{NM_001159560}, {NM_001012978}, {NM_001159560}}, {{NM_001099285}}, {{NM_002823}}},
  Gene Symbol → {{{NM_002389}, {NM_172351}, {NM_172359}, {NM_153826}, {NM_172352},
     {NM_172353}, {NM_172350}, {NM_172361}}, {{NM_024119}, {Missing[]}, {NM_024119}},
     {{NM_005342}, {NM_005342}, {Missing[]}}, {{NM_005923}, {NM_005923}, {NM_005923},
     {NM_005923}, {NM_005923}, {NM_005923}, {Missing[]}, {Missing[]}, {Missing[]}, {NM_005923},
     {NM_005923}, {NM_005923}}, {{NM_001077494}, {NM_001077494}, {NM_002502}, {NM_002502},
     {NM_002502}, {NM_002502}, {NM_001261403}, {NM_001261403}, {NM_002502}, {NM_002502}},
     {{NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625},
     {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625},
     {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625}, {NM_000625},
     {NM_000625}, {NM_000625}, {NM_000625}}, {{NM_013258}, {NM_013258}, {NM_145182}, {NM_145182}},
     {{NM_152901}, {NM_152901}}, {{NM_001144950}, {NM_001195267}}, {}, {}, {}, {}, {}, {}, {}},
  RefSeq ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
  NCBI Protein Accession → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
  Ensembl ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
  KEGG Gene ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}},
  HGU133Plus2 Affymetrix ID → {{}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}, {}}|>|>
```

Species (1)

In[1]:=
```
Needs["MathIOmica`"]
```

Species option indicates which of the species (i.e. key) to use from the input gene dictionary. The default value is set to "human".

Let's consider the following example of UniProt IDs that we would like to translate to official "Gene Symbol". We use GetGeneDictionary to get the default MathIOmica gene dictionary. The inputs we consider are:

In[2]:=
```
uniProtExampleIDs = {"Q6ZRT9", "Q6NZ36", "H7C361", "Q6ZRT9", "A8MQT6", "Q9BUW7",
  "Q6NZ67", "Q6P582", "P39019", "E9PM41", "A8MTZ0", "A8MTZ0", "E9PRI7", "A8MTZ0",
  "Q9H6L5", "Q5H9J7", "Q5H9J7", "Q5H9J7", "P06454", "Q53S24", "B8ZZW7", "A0PJW6"};
targetIDs = {"Gene Symbol"};
geneDictionaryExample = GetGeneDictionary[]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
     uc001aaq.2, uc001aar.2, uc001aau.3, ⋯ 121 569 ⋯, uc031tkn.1, uc022cgh.1, uc022cha.1,
     uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ⋯ 6 ⋯, H ... ID → ⋯ 1 ⋯|>|>
```

large output | show less | show more | show all | set size limit...

We see that the gene dictionary has species "human" identifiers:

```
Keys[geneDictionaryExample]
```

Out[3]= {human}

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In[4]:=
```
translatedIDsHuman = GeneTranslation[uniProtExampleIDs,
  targetIDs, geneDictionaryExample, InputID → {"UniProt ID"}, Species → "human"]
```

Out[4]=
```
<|Gene Symbol → <|Q6ZRT9 → {C1orf86}, Q6NZ36 → {C1orf86}, H7C361 → {C1orf86},
   A8MQT6 → {C1orf86}, Q9BUW7 → {C9orf16}, Q6NZ67 → {MZT2B}, Q6P582 → {MZT2A},
   P39019 → {RPS19}, E9PM41 → {BBIP1}, A8MTZ0 → {BBIP1}, E9PRI7 → {BBIP1}, Q9H6L5 → {FAM134B},
   Q5H9J7 → {BEX5}, P06454 → {PTMA}, Q53S24 → {PTMA}, B8ZZW7 → {PTMA}, A0PJW6 → {TMEM223}|>|>
```

See Also

GetGeneDictionary ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGAnalysisAssigner** ▪ **KEGGPathwayVisual** ▪ **OBOGODictionary** ▪ **TimeSeriesClusters**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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GetGeneDictionary

```
GetGeneDictionary[]
```
creates an ID/accession dictionary from a UCSC table search – typically of gene annotations.

Details

- `GetGeneDictionary[]` creates an an ID/accession dictionary from a UCSC search - typically of gene annotations. For `i` species, each having m_i possible annotations (kinds of IDs) for n_i entities each (e.g. corresponding to n_i genes) the format is schematically:

- $$\begin{aligned}\text{output} = <|\,&\text{Species}_1 \to <|\text{Kind of ID}_{11} \to \{\text{accessions list}_{11} \text{ of length } n_1\},\\ &\quad \text{Kind of ID}_{12} \to \{\text{accessions list}_{12} \text{ of length } n_1\}, \ldots,\\ &\quad \text{Kind of ID}_{1\,m_1} \to \{\text{accessions list}_{1\,m_1} \text{ of length } n_1\}|>,\\ &\text{Species}_2 \to <|\text{Kind of ID}_{21} \to \{\text{accessions list}_{21} \text{ of length } n_2\},\\ &\quad \text{Kind of ID}_{22} \to \{\text{accessions list}_{22} \text{ of length } n_2\}, \ldots,\\ &\quad \text{Kind of ID}_{2\,m_2} \to \{\text{accessions list}_{2\,m_2} \text{ of length } n_2\}|>,\\ &\ldots,\\ &\text{Species}_i \to <|\text{Kind of ID}_{i1} \to \{\text{accessions list}_{i2} \text{ of length } n_i\},\\ &\quad \text{Kind of ID}_{i2} \to \{\text{accessions list}_{12} \text{ of length } n_i\}, \ldots,\\ &\quad \text{Kind of ID}_{i\,m_i} \to \{\text{accessions list}_{12} \text{ of length } n_i\}|>\\ |>\end{aligned}$$

- For each `i` species, the m_i possible annotations all have the same number of n_i entities sorted in the same order corresponding to the same entity (e.g. the same gene). In other words entry `j` across kinds of IDs corresponds to the same entity.

- `GetGeneDictionary` utilizes MathIOmica data. If the option `ImportDirectly` is invoked, the function will attempt to connect to the UCSC browser tables via a SQL connection to obtain "human" data. This will only be feasible if SQL is enabled on the host system (e.g. mySQL installed and configured, and firewalls allow communication).

- The following options can be given:

ImportDirectly	False	ImportDirectly gives the option to create a new version of the gene dictionary by directly importing form the UCSC Browser tables, using a SQL query provided by the UCSCSQLString option. The default False setting will use the MathIOmica supplied gene dictionary.
JavaGBs	8	The JavaGBs option assigns the value of GBs of memory to be used by Java by running an internal ReinstallJava command with option JVMArgurments–> "–Xmx" <> OptionValue[JavaGBs] <> "g". The default is to use 8 GBs of memory.

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KEGGUCSCSplit	{True, "KEGG Gene ID"}	KEGGUCSCSplit is a two component list, {True/False, label}. If the first component is set to True the initially imported KEGG IDs, identified by the second component label, are split on "+" string to fix nomenclature issues, retaining the string following "+".
MathIOmicaDataDirectory	If[! DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]	MathIOmicaDataDirectory option specifies the directory where the default MathIOmica package data are stored. By default the option is set to create the standard directory if it does not exist already.
Species	"human"	Species provides a label for the species associated to the gene dictionary which is used as an outer key in the association. If ImportDirectly is set to False (default), the MathIOmica data provided uses this label to identify the data file stored in the MathIOmicaDataDirectory as OptionValue[Species]<>"GeneUCSCTable ", i.e. the default beign "humanGeneUCSCTable". If ImportDirectly is set to True, the data will be imported (by default "human set) using the UCSCSQLString option, for which Species specifies the key to use.

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UCSCSQLString	<|"human" → "SELECT hg19.kgXref.kgID, hg19.kgXref.spID, hg19.kgXref.geneSymbol, hg19.kgXref.refseq, hg19.kgXref.protAcc, hg19.knownToEnsembl. value, hg19.knownToKeggEntrez. keggEntrez, hg19.knownToU133Plus2. value FROM hg19.kgXref LEFT JOIN hg19.knownToEnsembl ON hg19.kgXref.kgID = hg19.knownToEnsembl. name LEFT JOIN hg19.knownToKeggEntrez ON hg19.kgXref.kgID = hg19.knownToKeggEntrez. name LEFT JOIN hg19.knownToU133Plus2 ON hg19.kgXref.kgID = hg19.knownToU133Plus2. name"|>	UCSCSQLString provides an association to be used when ImportDirectly is set to True to obtain data from the UCSC Browser tables. The key of the association must match the Species option value used (default "human"). The value for the species corresponds to the actual SQL command used.
UCSCSQLSelectLabels	<|"human" → {"UCSC ID", "UniProt ID", "Gene Symbol", "RefSeq ID", "NCBI Protein Accession", "Ensembl ID", "KEGG Gene ID", "HGU133Plus2 Affymetrix ID"}|>	UCSCSQLSelectLabels provides an association to be used to assign key labels for the data improted from the UCSC Browser tables. The key of the association must match the Species option value used (default "human"). The value is a multi component string list corresponding to the matrices in the MathIOmica data file, or the tables used in the SQL query provided by UCSCSQLString.

Examples (8)

Basic Examples (1)

First we need to load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

`GetGeneDictionary` generates a gene translation reference dictionary using MathIOmica's data:

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In[2]:=
```
geneDictionaryExample = GetGeneDictionary[]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
    uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
    uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H … ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

The dictionary has multiple accessions, labeled as:

In[3]:=
```
Query[All, Keys]@geneDictionaryExample
```

Out[3]=
```
<|human → {UCSC ID, UniProt ID, Gene Symbol, RefSeq ID,
   NCBI Protein Accession, Ensembl ID, KEGG Gene ID, HGU133Plus2 Affymetrix ID}|>
```

For a given entry we can get all corresponding IDs. For example for entry 13152

In[4]:=
```
Query[All, All, 13 152]@geneDictionaryExample
```

Out[4]=
```
<|human → <|UCSC ID → uc001ktc.4, UniProt ID → B7Z3H4,
   Gene Symbol → BTRC, RefSeq ID → NM_001256856, NCBI Protein Accession → NP_001243785,
   Ensembl ID → ENST00000370187, KEGG Gene ID → 8945, HGU133Plus2 Affymetrix ID → 204901_at|>|>
```

Options (7)

ImportDirectly (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`ImportDirectly` gives the option to create a new version of the gene dictionary by directly importing form the UCSC Browser tables, using a SQL query (SQL must be enabled on the host system) provided by the UCSCSQLString option. The current version in the MathIOmica package data directory will be replaced. The default False setting will use the MathIOmica supplied gene dictionary.

In[2]:=
```
GetGeneDictionary[ImportDirectly → True]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
    uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
    uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, HGU … ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

JavaGBs (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The JavaGBs option assigns the value of GBs of memory to be used by Java by running an internal ReinstallJava command with option JVMArgurments-> "-Xmx" <> OptionValue[JavaGBs] <> "g". The default is to use 8 GBs of memory. This is used particularly when ImportDirectly is set to True.

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In[2]:=
```
GetGeneDictionary[ImportDirectly → True, JavaGBs → 12]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
    uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
    uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H ... ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

KEGGUCSCSplit (1)

In[1]:=
```
Needs["MathIOmica`"]
```

KEGGUCSCSplit is a two component list, {True/False, label}. If the first component is set to True the initially imported KEGG IDs, identified by the second component label, are split on "+" string to fix nomenclature issues, retaining the string following "+".

Let's set this to False, and look at the output:

In[2]:=
```
geneDictionaryKEGGUCSCSplitFalse = GetGeneDictionary[KEGGUCSCSplit → {False, "KEGG Gene ID"}]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
    uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
    uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H ... ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

The first few non-missing KEGG IDs show the format:

In[3]:=
```
DeleteMissing[Query["human", "KEGG Gene ID"]@geneDictionaryKEGGUCSCSplitFalse]
```

Out[3]=
```
{hsa04740+79501, hsa04622+9636, hsa04512+375790, hsa00532+126792, hsa00534+126792,
 hsa01100+126792, hsa04742+83756, ··· 58 059 ···, hsa04060+64109, hsa04630+64109,
 hsa04060+64109, hsa04630+64109, hsa04020+293, hsa05012+293, hsa05016+293}
```

large output | show less | show more | show all | set size limit...

Now we set the option to True (default):

In[4]:=
```
geneDictionaryKEGGUCSCSplitTrue = GetGeneDictionary[KEGGUCSCSplit → {True, "KEGG Gene ID"}]
```

Out[4]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
    uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
    uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H ... ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

The first few non-missing KEGG IDs show the updated trimmed format:

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In[5]:=
```
DeleteMissing[Query["human", "KEGG Gene ID"]@geneDictionaryKEGGUCSCSplitTrue]
```

Out[5]=
```
{79501, 9636, 375790, 126792, 126792, 126792, 83756, 163688, 163688,
 163688, 163688, 163688, 163688, 163688, 163688, ··· 58 043 ···, 3581, 3581, 3581,
 64109, 64109, 64109, 64109, 286530, 64109, 64109, 64109, 64109, 293, 293, 293}
```
large output | show less | show more | show all | set size limit...

MathIOmicaDataDirectory (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value points to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

In[2]:=
```
GetGeneDictionary[MathIOmicaDataDirectory → FileNameJoin[
   Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
      uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
      uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H ... ID → ··· 1 ···|>|>
```
large output | show less | show more | show all | set size limit...

Species (1)

In[1]:=
```
Needs["MathIOmica`"]
```

If `ImportDirectly` is set to False (default), the MathIOmica data provided uses this label to identify the data file stored in the MathIOmicaDataDirectory as `OptionValue[Species] <> "GeneUCSCTable"`, i.e. the default being "humanGeneUCSCTable". If ImportDirectly is set to True, the data will be imported (by default "human set) using the UCSCSQLString option, for which Species specifies the key to use.

In[2]:=
```
GetGeneDictionary[Species → "human"]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
      uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
      uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H ... ID → ··· 1 ···|>|>
```
large output | show less | show more | show all | set size limit...

UCSCSQLString (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`UCSCSQLString` provides an association to be used when `ImportDirectly` is set to True to obtain data from the UCSC Browser tables. The key of the association must match the Species option value used (default "human"). The value for the species corresponds to

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the actual SQL command used.

In[2]:=
```
GetGeneDictionary[UCSCSQLString → <|
   "human" → "SELECT hg19.kgXref.kgID, hg19.kgXref.spID, hg19.kgXref.geneSymbol, hg19.kgXref.refseq,
      hg19.kgXref.protAcc, hg19.knownToEnsembl.value, hg19.knownToKeggEntrez.keggEntrez,
      hg19.knownToU133Plus2.value FROM hg19.kgXref LEFT JOIN hg19.knownToEnsembl ON
      hg19.kgXref.kgID = hg19.knownToEnsembl.name LEFT JOIN hg19.knownToKeggEntrez ON
      hg19.kgXref.kgID = hg19.knownToKeggEntrez.name LEFT JOIN hg19.knownToU133Plus2
      ON hg19.kgXref.kgID = hg19.knownToU133Plus2.name"|>, ImportDirectly → True]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
     uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
     uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H … ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

UCSCSQLSelectLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`UCSCSQLSelectLabels` provides an association to be used to assign key labels for the data imported from the UCSC Browser tables. The key of the association must match the `Species` option value used (default "human"). The value is a multi component string list corresponding to the matrices in the MathIOmica data file, or the tables used in the SQL query provided by `UCSCSQLString`.

In[2]:=
```
geneDictionaryLabels =
 GetGeneDictionary[UCSCSQLSelectLabels → <|"human" → {"UCSC ID", "UniProt ID", "Gene Symbol", "RefSeq ID",
      "NCBI Protein Accession", "Ensembl ID", "KEGG Gene ID", "HGU133Plus2 Affymetrix ID"}|>]
```

Out[2]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
     uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
     uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H … ID → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

In[3]:=
```
Query[All, Keys]@geneDictionaryLabels
```

Out[3]=
```
<|human → {UCSC ID, UniProt ID, Gene Symbol, RefSeq ID,
   NCBI Protein Accession, Ensembl ID, KEGG Gene ID, HGU133Plus2 Affymetrix ID}|>
```

Let's assume we want to change these labels (note that this may affect functionality of other functions if appropriate modifications are not made to those as well).

In[4]:=
```
geneDictionaryLabelsChanged = GetGeneDictionary[UCSCSQLSelectLabels → <|
    "human" → {"UCSCID", "UniProt", "Gene", "RefSeq", "NCBI", "Ensembl", "KEGG Gene ID", "HGU133Plus2"}|>]
```

Out[4]=
```
<|human → <|UCSCID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
     uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
     uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, HGU133Plus2 → ··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

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```
In[5]:= Query[All, Keys]@geneDictionaryLabelsChanged
Out[5]= <|human → {UCSCID, UniProt, Gene, RefSeq, NCBI, Ensembl, KEGG Gene ID, HGU133Plus2}|>
```

See Also

GeneTranslation ▪ GOAnalysis ▪ GOAnalysisAssigner ▪ KEGGAnalysis ▪ KEGGDictionary ▪ KEGGPathwayVisual ▪ MassDictionary ▪ MassMatcher ▪ OBOGODictionary ▪ TimeSeriesClusters ▪ UCSCBrowserSQL

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- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

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- MathIOmica Guide

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- MathIOmicaGuide
- MathIOmicaOverview

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Heatmapper

`Heatmapper[data]`
produces a heamap of the input data.

Details

- `Heatmapper[data]` produces a heamap (array plot) of the input data. It is used as a helper function for MathIOmica's heatmap/dendrogram implementations.
- Heatmapper sets Missing[] values to gray, and "Empty" values as transparent.
- The following options can be given:

ColorBlending	{CMYKColor[1, 0, 1, 0], CMYKColor[0, 1, 1, 0]}	Color scheme for the plot. The color list is passed to an internal Blend function to create a ColorFunction for the internal ArrayPlot.
ScaleShift	1	Option to reset the blend of the colors used overall. The option is a real positive number, and is used as a multiplier for the internal Blend function's second argument.

Examples (4)

Basic Examples (1)

First we need to load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

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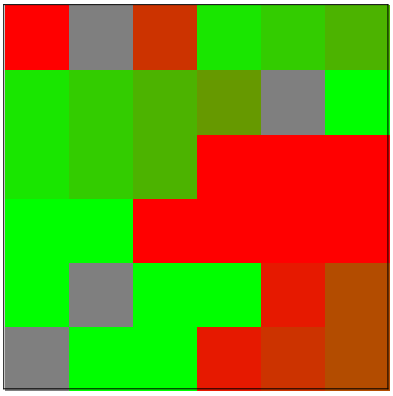
In[2]:=
```
Heatmapper[{{1, Missing[], 0.8, 0.1, 0.2, 0.3}, {0.1, 0.2, 0.3, 0.4, Missing[], 0}, {0.1, 0.2, 0.3, 1, 1, 1},
  {0, 0, 1, 1, 1, 1}, {0, Missing[], 0, 0, 0.9, 0.7}, {Missing[], 0, 0, 0.9, 0.8, 0.7}}]
```

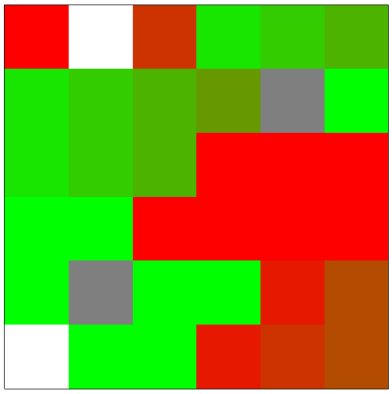
Out[2]=



Missing[] can be used, and will be marked as grey. "Empty" may be used to create transparent entries

In[3]:=
```
Heatmapper[{{1, "Empty", 0.8, 0.1, 0.2, 0.3}, {0.1, 0.2, 0.3, 0.4, Missing[], 0}, {0.1, 0.2, 0.3, 1, 1, 1},
  {0, 0, 1, 1, 1, 1}, {0, Missing[], 0, 0, 0.9, 0.7}, {"Empty", 0, 0, 0.9, 0.8, 0.7}}]
```

Out[3]=



Options (3)

ColorBlending (2)

In[1]:=
```
Needs["MathIOmica`"]
```

ColorBlending provides a list of colors to be used in the plot to create gradient effects. Named colors can be used as well.

In[2]:=
```
dataHeatmapper =
  {{1, Missing[], 0.8, 0.1, 0.2, 0.3}, {0.1, 0.2, 0.3, 0.4, Missing[], 0}, {0.1, 0.2, 0.3, 1, 1, 1},
   {0, 0, 1, 1, 1, 1}, {0, Missing[], 0, 0, 0.9, 0.7}, {Missing[], 0, 0, 0.9, 0.8, 0.7}};
```

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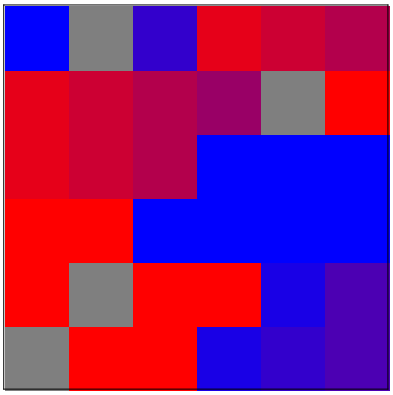
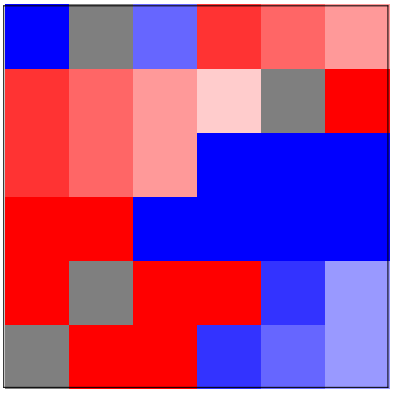
In[3]:=
```
Heatmapper[dataHeatmapper, ColorBlending → {Red, Blue}]
```

Out[3]=



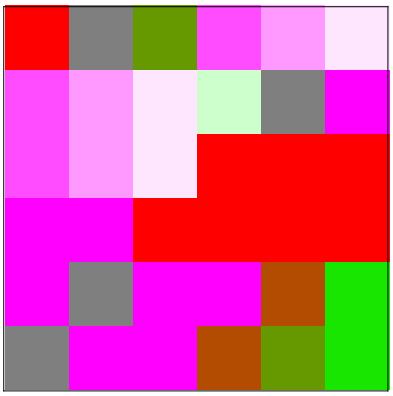
In[4]:=
```
Heatmapper[dataHeatmapper, ColorBlending → {Red, White, Blue}]
```

Out[4]=



In[5]:=
```
Heatmapper[dataHeatmapper,
 ColorBlending → {RGBColor[1, 0, 1], White, CMYKColor[1, 0, 1, 0], CMYKColor[0, 1, 1, 0]}]
```

Out[5]=



In[1]:=
```
Needs["MathIOmica`"]
```

All of Mathematica's color gradients can be used instead of a list:

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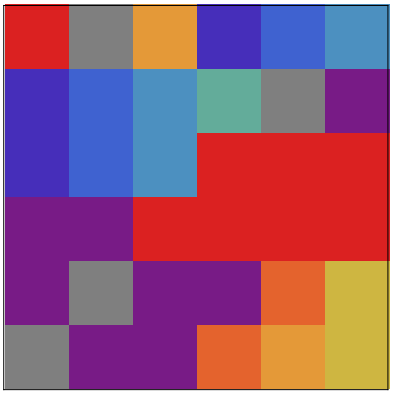
In[2]:=
```
ColorData["Gradients"]
```

Out[2]=
```
{AlpineColors, Aquamarine, ArmyColors, AtlanticColors, AuroraColors, AvocadoColors,
 BeachColors, BlueGreenYellow, BrassTones, BrightBands, BrownCyanTones, CandyColors, CherryTones,
 CMYKColors, CoffeeTones, DarkBands, DarkRainbow, DarkTerrain, DeepSeaColors, FallColors,
 FruitPunchColors, FuchsiaTones, GrayTones, GrayYellowTones, GreenBrownTerrain, GreenPinkTones,
 IslandColors, LakeColors, LightTemperatureMap, LightTerrain, MintColors, NeonColors, Pastel,
 PearlColors, PigeonTones, PlumColors, Rainbow, RedBlueTones, RedGreenSplit, RoseColors,
 RustTones, SandyTerrain, SiennaTones, SolarColors, SouthwestColors, StarryNightColors,
 SunsetColors, TemperatureMap, ThermometerColors, ValentineTones, WatermelonColors}
```

In[3]:=
```
dataHeatmapper =
  {{1, Missing[], 0.8, 0.1, 0.2, 0.3}, {0.1, 0.2, 0.3, 0.4, Missing[], 0}, {0.1, 0.2, 0.3, 1, 1, 1},
   {0, 0, 1, 1, 1, 1}, {0, Missing[], 0, 0, 0.9, 0.7}, {Missing[], 0, 0, 0.9, 0.8, 0.7}};
```

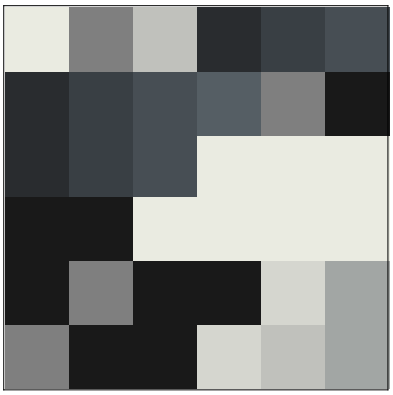
In[4]:=
```
Heatmapper[dataHeatmapper, ColorBlending → "Rainbow"]
```

Out[4]=



In[5]:=
```
Heatmapper[dataHeatmapper, ColorBlending → "GrayTones"]
```

Out[5]=



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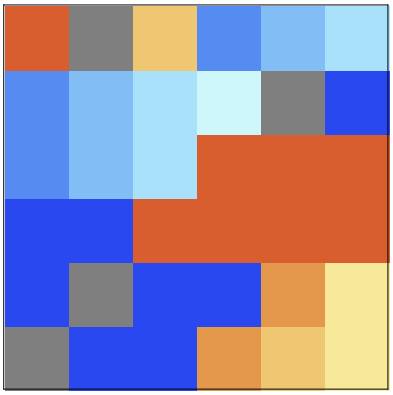
In[6]:=
```
Heatmapper[dataHeatmapper, ColorBlending → "LightTemperatureMap"]
```

Out[6]=



ScaleShift (1)

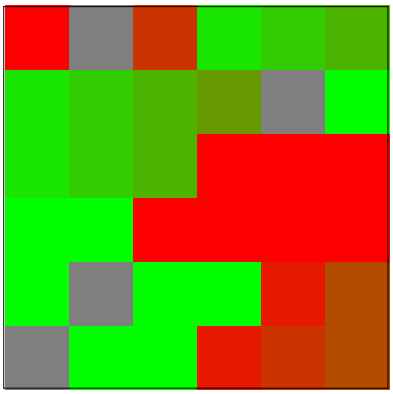
In[1]:=
```
Needs["MathIOmica`"]
```

ScaleShift provides a shift of overall color in a heatmap, allowing for overall adjustments if necessary:

In[2]:=
```
dataHeatmapper =
  {{1, Missing[], 0.8, 0.1, 0.2, 0.3}, {0.1, 0.2, 0.3, 0.4, Missing[], 0}, {0.1, 0.2, 0.3, 1, 1, 1},
   {0, 0, 1, 1, 1, 1}, {0, Missing[], 0, 0, 0.9, 0.7}, {Missing[], 0, 0, 0.9, 0.8, 0.7}};
```

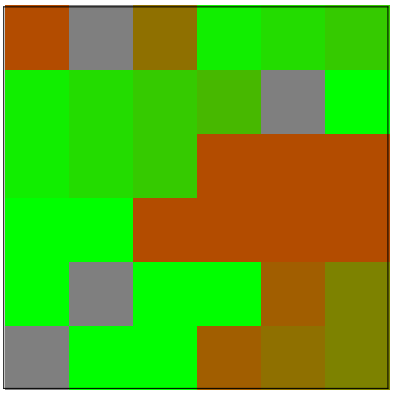
In[3]:=
```
Heatmapper[dataHeatmapper, ScaleShift → 1]
```

Out[3]=



In[4]:=
```
Heatmapper[dataHeatmapper, ScaleShift → 0.7]
```

Out[4]=



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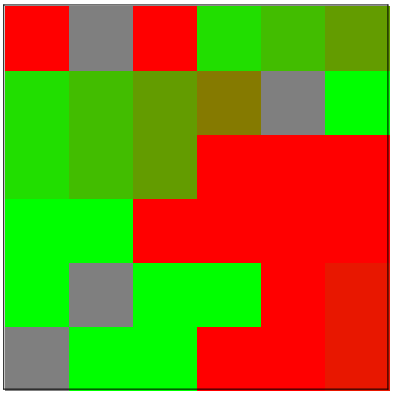
In[5]:=
```
Heatmapper[dataHeatmapper, ScaleShift → 1.3]
```

Out[5]=


See Also

MatrixClusters ▪ **MatrixDendrogramHeatmap** ▪ **MatrixDendrogramsHeatmaps** ▪ **TimeSeriesDendrogramHeatmap** ▪ **TimeSeriesDendrogramsHeatmaps** ▪ **TimeSeriesClusters** ▪ **TimeSeriesSingleClusters** ▪ **TimeSeriesSingleDendrogramHeatmap** ▪ **TimeSeriesSingleDendrogramsHeatmaps**

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HorizontalSelection

`HorizontalSelection`
is an option for varous MathIOmica functions, such as Applier, that allows for horizontal selection across components for a single level association with multi–list values.

Details

- HorizontalSelection an option that is set to True when selecting across Keys that have multi-list values in associations.

See Also

Applier ▪ **Returner**

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InverseAutocovariance

`InverseAutocovariance[data, setTimes]`
calculates the inverse Fourier transform of the autocovariance for a time series that runs over specified set times, using a Lomb–Scargle approach.

Details

- `InverseAutocovariance[data, setTimes]` calculates the inverse Fourier transform of the autocovariance for a time series that runs over specified set times, using a Lomb-Scargle approach. It takes as input:

data	Time series (data as a list; list may be the value of a single key in an association). The series may include Missing data points. Data may be entered as list of N signal intensities corresponding one–to–one to the N setTimes with Missing inserted appropriately if the data is absent, $\{X_1 = X(t_1), X_2 = X(t_2), \ldots, X_N = X(t_N)\}$. Alternatively, the data may be a list of pairs of values $\{\{t_1,X_1\},\{t_2,X_2\},\ldots,\{t_N,X_N\}\}$ for only existing measurements.
setTimes	A complete set of all possible N times during which data could have been collected in the window of the experiment, including times for which no data was collected, $\{t_1, t_2, \ldots, t_N\}$.

- InverseAutocovariance returns a list of {frequency list, intensity list} of the corresponding frequencies (oversampled as discussed below, typically by a factor of two) and intensities.
- The following options can be given:

UpperFrequencyFactor	1	Value ≥ 1, by which to scale the upper Nyquist cutoff frequency and increase spectral resolution.
PairReturn	True	Whether data should be returned as {frequency list,intensity list} or as pairs: {{frequency1,intensity1}, {frequency2, intensity2},...,{frequencyN,intensityN}.

Background

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The normalized autocorrelation calculation involves an inverse Fourier transform on the Lomb-Scargle periodogram. This function utilizes a slightly modified frequency list, as discussed below, compared to the Lomb-Scargle function and corresponding spectral output. To differentiate this new list of spectral outputs from the periodogram, it is called the Inverse Fourier Transformed Autocovariance $S_x(f)$. The complete time window of the experiment (set times) is defined by the range of $\{t_{complete}\}$, $t_{window} = \text{Max}[\{t_{complete}\}] - \text{Min}[\{t_{complete}\}]$. From this time window, the Nyquist frequency is defined to be $f_{Nyq} = \frac{N}{2}\frac{1}{t_{window}}$, and a given UpperFrequencyFactor factor ≥ 1 sets the cutoff frequency f_{cutoff} for calculation by $\frac{f_{cutoff}}{f_{Nyq}} = \text{UpperFrequencyFactor}$. It is recommended to set UpperFrequencyFactor close to 1 unless one has an explicit reason to do otherwise.

- The challenge is to determine a frequency mesh for $S_x(f)$. This mesh must be such that if one were to add an $f = 0$ element at the beginning, then the list would be *evenly-spaced* from $f = 0$ to the upper-cutoff frequency $f_c = \text{UpperFrequencyFactor} * f_{Nyq}. = \text{UpperFrequencyFactor} * \frac{N}{2} * f_0$. This requirement is necessary to perform the inverse Fourier transform for the calculation of the autocorrelation. The frequency mesh calculated in $P_x(f)$ above is not evenly spaced because the low-pass filter means that the difference between f_0 and 0, $f_0 - 0 = f_0$, is not equal to the spacing f_s between all the other frequencies, $f_0 \neq f_s$. The frequency mesh is set in the following manner: zero-pad in time space so that the sampling period is doubled, and thus the fundamental frequency is cut in half, $f_0 \to \frac{f_0}{2}$. This procedure prevents wrap-around. Then, set the spacing between frequencies to be equal to this halved fundamental frequency, $f_s = \frac{f_0}{2}$. Thus, $\{f_i\} = \{f_s, 2 f_s, \ldots, \text{Floor}(N * \text{UpperFrequencyFactor}) * f_s\}$, since the upper frequency cutoff is $f_c = \text{UpperFrequencyFactor} * \frac{N}{2} * f_0 = \text{UpperFrequencyFactor} * N * f_s$, . If UpperFrequencyFactor = 1, and one goes up to the smallest integer less than or equal to this then the floor is unnecessary. For a given time series $\{X_i\}$, the Autocorrelation $\rho_X(\tau)$ as a function of time lag τ is, in essence, an Inverse Fourier Transform of the corresponding InverseAutocovariance InverseAutocovariance S_X, normalized to unity at zero time lag, $\rho_X(0) = 1$.

References

- Lomb, N.R, *Least-squares frequency analysis of unequally spaced data*, Astrophysics and Space Science 39 (2) : 447–462 (1976). External link: http://dx.doi.org/10.1007/BF00648343.
- Scargle, J.D., *Studies in astronomical time series analysis II - Statistical aspects of spectral analysis of unevenly spaced data*, Astrophysical Journal 263 : 835 (1982). External link: http://dx.doi.org/10.1086/160554.
- Scargle, J.D., *Studies in astronomical time series analysis. III - Fourier transforms, autocorrelation functions, and cross-correlation functions of unevenly spaced data*, Astrophysical Journal 343 : 874 (1989). External link: http://dx.doi.org/10.1086/167757.

Examples (7)

Basic Examples (4)

Package Dependencies (1)

First we load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

General Example: Noisy Sinusoidal Data (1)

We consider the following noisy measurement:

In[1]:=
```
dataInverseAutocovarianceExample1 =
  Table[{n, Sin[0.1 * 2 π n] + Sin[0.25 * 2 π n] + RandomReal[{-1, 1}]}, {n, 0, 200}];
```

The data is pairs of values for the ith point $\{t_i, X_i\}$. A plot of the data looks like:

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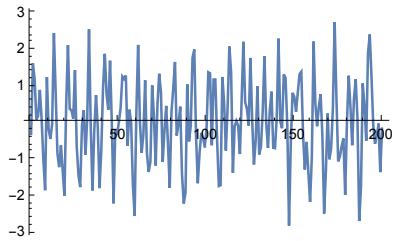
In[2]:=
```
ListLinePlot[dataInverseAutocovarianceExample1]
```

Out[2]=


We obtain a list of frequencies and intensities:

In[3]:=
```
dataInverseAutocovarianceSpectrum = InverseAutocovariance[dataInverseAutocovarianceExample1, Range[0, 200]]
```

Out[3]=
```
{{0.0025, 0.00186731}, {0.005, 0.123848}, {0.0075, 0.522926}, {0.01, 0.578724},
 {0.0125, 0.714593}, {0.015, 0.703048}, {0.0175, 0.0233578}, {0.02, 0.439924},
 {0.0225, 0.234689}, {0.025, 0.169702}, {0.0275, 0.644313}, {0.03, 0.135456},
 {0.0325, 0.00928521}, {0.035, 0.0578148}, {0.0375, 0.0226547},
```

If we plot the data we see peaks corresponding to the frequencies:

In[4]:=
```
ListLinePlot[dataInverseAutocovarianceSpectrum, PlotRange → Full]
```

Out[4]=

The InverseAutocovariance function can also take a list of data:

In[5]:=
```
dataInverseAutocovarianceExample2 =
  Table[Sin[0.15 * 2 π n ] + Sin[0.2 * 2 π n] + Sin[0.4 * 2 π n] + RandomReal[{-1, 1}], {n, 0, 200}];
```

In[6]:=
```
dataInverseAutocovarianceSpectrum2 =
  InverseAutocovariance[dataInverseAutocovarianceExample2, Range[0, 200]];
```

A plot the spectrum we see peaks corresponding to the frequencies corresponding to the example signal:

In[7]:=
```
ListLinePlot[dataInverseAutocovarianceSpectrum2, PlotRange → Full]
```

Out[7]=

Let's consider a sample with missing data. First we generate a data list:

In[8]:=
```
dataInverseAutocovarianceExample3a = Table[Cos[0.2 * 2 π n ] + Sin[0.1 * 2 π n], {n, 0, 100}];
```

We next introduce missing data at random integer positions, say 10 points missing :

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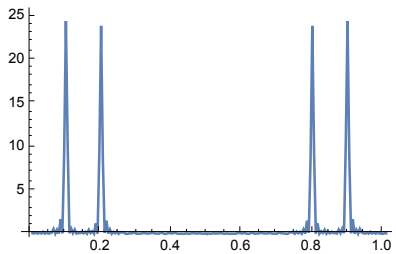
In[9]:=
```
dataInverseAutocovarianceExample3aMissing =
 Nest[ReplacePart[#, RandomInteger[{1, 100}] → Missing[]] &, dataInverseAutocovarianceExample3a, 10]
```

Out[9]=
```
{1., 0.896802, 0.14204, 0.14204, 0.896802, 1., -0.278768, -1.76007, -1.76007, -0.278768, 1., 0.896802,
 Missing[], 0.14204, 0.896802, 1., -0.278768, -1.76007, -1.76007, -0.278768, Missing[], 0.896802, 0.14204,
 Missing[], 0.896802, 1., -0.278768, -1.76007, -1.76007, -0.278768, 1., 0.896802, 0.14204, 0.14204,
 0.896802, 1., -0.278768, -1.76007, -1.76007, -0.278768, Missing[], 0.896802, 0.14204, 0.14204, 0.896802,
 1., -0.278768, -1.76007, -1.76007, -0.278768, 1., 0.896802, 0.14204, 0.14204, 0.896802, Missing[],
 -0.278768, -1.76007, -1.76007, Missing[], 1., 0.896802, 0.14204, 0.14204, 0.896802, 1., -0.278768,
 -1.76007, -1.76007, -0.278768, 1., 0.896802, 0.14204, 0.14204, Missing[], 1., Missing[], -1.76007,
 -1.76007, -0.278768, 1., 0.896802, 0.14204, 0.14204, 0.896802, 1., -0.278768, -1.76007, -1.76007,
 -0.278768, 1., 0.896802, 0.14204, Missing[], 0.896802, 1., -0.278768, -1.76007, -1.76007, -0.278768, 1.}
```

In[10]:=
```
dataInverseAutocovarianceSpectrum3a =
  InverseAutocovariance[dataInverseAutocovarianceExample3aMissing, Range[0, 100]];
```

In[11]:=
```
ListLinePlot[dataInverseAutocovarianceSpectrum3a, PlotRange → Full]
```

Out[11]=



Instead of data tagged Missing we may have an unevenly sampled dataset provided as pairs of data. We consider a similar example:

In[12]:=
```
dataInverseAutocovarianceExample3b = Table[{n, Cos[0.2 * 2 π n] + Sin[0.1 * 2 π n]}, {n, 0, 100}];
```

Let's sample 90 points:

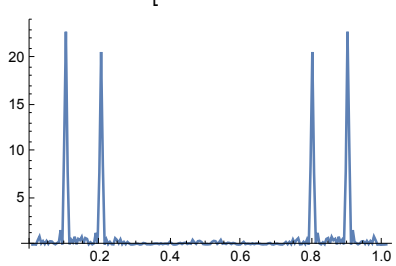
In[13]:=
```
dataInverseAutocovarianceExample3bUneven = RandomSample[dataInverseAutocovarianceExample3b, 90];
```

In[14]:=
```
dataInverseAutocovarianceSpectrum3b =
 InverseAutocovariance[dataInverseAutocovarianceExample3bUneven, Range[0, 100]]
```

Out[14]=
```
{{0.005, 0.00528973}, {0.01, 0.0222607}, {0.015, 0.000166558},
 {0.02, 0.460032}, {0.025, 0.866506}, {0.03, 0.132358}, {0.035, 0.376699},
 {0.04, 0.0667815}, {0.045, 0.389626}, {0.05, 0.0803389}, {0.055, 0.357866},
 {0.06, 0.334007}, {0.065, 0.13117}, {0.07, 0.0307772}, {0.075, 0.168579},
```

In[15]:=
```
ListLinePlot[dataInverseAutocovarianceSpectrum3b, PlotRange → Full]
```

Out[15]=



The data could also have been provided as an association

In[16]:=
```
dataInverseAutocovarianceExample3c = <|
   "Unevenly Sampled data" → dataInverseAutocovarianceExample3bUneven|>;
```

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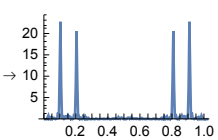
In[17]:=
```
dataInverseAutocovarianceSpectrum3c =
 InverseAutocovariance[dataInverseAutocovarianceExample3c, Range[0, 100]]
```

Out[17]=
```
<|Unevenly Sampled data → {{0.005, 0.00528973}, {0.01, 0.0222607}, {0.015, 0.000166558},
   {0.02, 0.460032}, {0.025, 0.866506}, {0.03, 0.132358}, {0.035, 0.376699}, {0.04, 0.0667815},
   {0.045, 0.389626}, {0.05, 0.0803389}, {0.055, 0.357866}, {0.06, 0.334007}, {0.065, 0.13117},
   {0.07, 0.0307772}, {0.075, 0.168579}, {0.08, 0.24088}, {0.085, 1.55527}, {0.09, 0.0185381},
   {0.095, 10.7387}, {0.1, 22.8949}, {0.105, 7.86187}, {0.11, 0.0273243}, {0.115, 0.528793},
   {0.12, 0.244904}, {0.125, 0.849659}, {0.13, 0.0257427}, {0.135, 0.613741}, {0.14, 0.470469},
   {0.145, 0.829159}, {0.15, 0.103059}, {0.155, 0.704324}, {0.16, 0.606842}, {0.165, 0.0457746},
   {0.17, 0.243167}, {0.175, 0.0283226}, {0.18, 0.142619}, {0.185, 1.25964}, {0.19, 0.0908412},
   {0.195, 7.70492}, {0.2, 20.7152}, {0.205, 8.52323}, {0.21, 0.00430506}, {0.215, 0.546743},
   {0.22, 0.050593}, {0.225, 0.292767}, {0.23, 0.043366}, {0.235, 0.0263529}, {0.24, 0.683261},
   {0.245, 0.493201}, {0.25, 0.149968}, {0.255, 0.551377}, {0.26, 0.0470436}, {0.265, 0.283641},
   {0.27, 0.0423873}, {0.275, 0.281035}, {0.28, 0.106912}, {0.285, 0.00561172},
   {0.29, 0.0117644}, {0.295, 0.0429548}, {0.3, 0.100768}, {0.305, 0.0814375}, {0.31, 0.00426515},
   {0.315, 0.0279961}, {0.32, 0.169433}, {0.325, 0.132908}, {0.33, 0.0291026}, {0.335, 0.0330566},
   {0.34, 0.0156497}, {0.345, 0.037149}, {0.35, 0.0960938}, {0.355, 0.113616}, {0.36, 0.112112},
   {0.365, 0.0404981}, {0.37, 0.130775}, {0.375, 0.0382609}, {0.38, 0.0916124}, {0.385, 0.101552},
   {0.39, 0.0490352}, {0.395, 0.2899}, {0.4, 0.141756}, {0.405, 0.0121063}, {0.41, 0.00120121},
   {0.415, 0.0292738}, {0.42, 0.128668}, {0.425, 0.175055}, {0.43, 0.0579558}, {0.435, 0.169995},
   {0.44, 0.200468}, {0.445, 0.0643765}, {0.45, 0.147827}, {0.455, 0.0963753}, {0.46, 0.50113},
   {0.465, 0.237216}, {0.47, 0.0784102}, {0.475, 0.362708}, {0.48, 0.396185}, {0.485, 0.284655},
   {0.49, 0.0526237}, {0.495, 0.0282934}, {0.5, 0.0496043}, {0.505, 0.0282934}, {0.51, 0.0526237},
   {0.515, 0.284655}, {0.52, 0.396185}, {0.525, 0.362708}, {0.53, 0.0784102}, {0.535, 0.237216},
   {0.54, 0.50113}, {0.545, 0.0963753}, {0.55, 0.147827}, {0.555, 0.0643765}, {0.56, 0.200468},
   {0.565, 0.169995}, {0.57, 0.0579558}, {0.575, 0.175055}, {0.58, 0.128668}, {0.585, 0.0292738},
   {0.59, 0.00120121}, {0.595, 0.0121063}, {0.6, 0.141756}, {0.605, 0.2899}, {0.61, 0.0490352},
   {0.615, 0.101552}, {0.62, 0.0916124}, {0.625, 0.0382609}, {0.63, 0.130775}, {0.635, 0.0404981},
   {0.64, 0.112112}, {0.645, 0.113616}, {0.65, 0.0960938}, {0.655, 0.037149}, {0.66, 0.0156497},
   {0.665, 0.0330566}, {0.67, 0.0291026}, {0.675, 0.132908}, {0.68, 0.169433}, {0.685, 0.0279961},
   {0.69, 0.00426515}, {0.695, 0.0814375}, {0.7, 0.100768}, {0.705, 0.0429548}, {0.71, 0.0117644},
   {0.715, 0.00561172}, {0.72, 0.106912}, {0.725, 0.281035}, {0.73, 0.0423873}, {0.735, 0.283641},
   {0.74, 0.0470436}, {0.745, 0.551377}, {0.75, 0.149968}, {0.755, 0.493201}, {0.76, 0.683261},
   {0.765, 0.0263529}, {0.77, 0.043366}, {0.775, 0.292767}, {0.78, 0.050593}, {0.785, 0.546743},
   {0.79, 0.00430506}, {0.795, 8.52323}, {0.8, 20.7152}, {0.805, 7.70492}, {0.81, 0.0908412},
   {0.815, 1.25964}, {0.82, 0.142619}, {0.825, 0.0283226}, {0.83, 0.243167}, {0.835, 0.0457746},
   {0.84, 0.606842}, {0.845, 0.704324}, {0.85, 0.103059}, {0.855, 0.829159}, {0.86, 0.470469},
   {0.865, 0.613741}, {0.87, 0.0257427}, {0.875, 0.849659}, {0.88, 0.244904}, {0.885, 0.528793},
   {0.89, 0.0273243}, {0.895, 7.86187}, {0.9, 22.8949}, {0.905, 10.7387}, {0.91, 0.0185381},
   {0.915, 1.55527}, {0.92, 0.24088}, {0.925, 0.168579}, {0.93, 0.0307772}, {0.935, 0.13117},
   {0.94, 0.334007}, {0.945, 0.357866}, {0.95, 0.0803389}, {0.955, 0.389626}, {0.96, 0.0667815},
   {0.965, 0.376699}, {0.97, 0.132358}, {0.975, 0.866506}, {0.98, 0.460032}, {0.985, 0.000166558},
   {0.99, 0.0222607}, {0.995, 0.00528973}, {1., 0.}, {1.005, 0.00528973}, {1.01, 0.0222607}}|>
```

In[18]:=
```
Query[All, ListLinePlot[#, PlotRange → Full] &]@dataInverseAutocovarianceSpectrum3c
```

Out[18]= ⟨|Unevenly Sampled data →



|⟩

Linear Signal Examples (1)

Below are some examples of the InverseAutocovariance for linear signal:

In[1]:=
```
timeSetLinear = Transpose[{Range[1, 100, 1], Range[1, 100, 1]}];
```

In[2]:=
```
lineLS = InverseAutocovariance[timeSetLinear, Range[1, 100, 1]];
```

Below are some examples of the InverseAutocovariance spectrum for linear signal:

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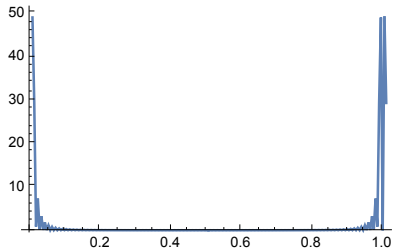
In[3]:=
```
ListLinePlot[lineLS, PlotRange → All]
```

Out[3]=



Here we create a function to generate some randomly sampled linear time series:

In[4]:=
```
timeSeriesLine[n_] := SortBy[RandomSample[Transpose[{Range[1, 100, 1], Range[1, 100, 1]}], n], First];
```

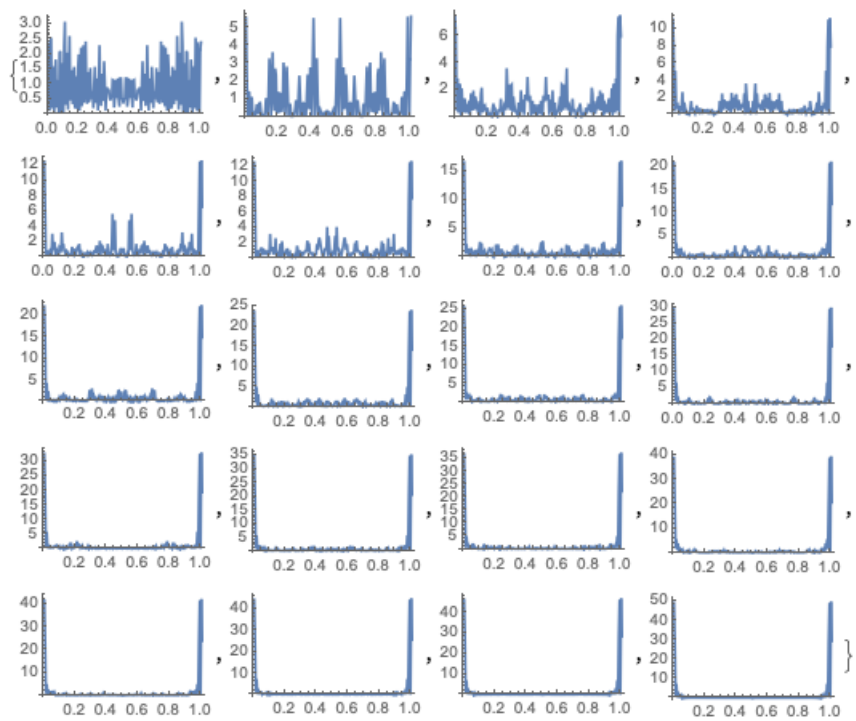
And also a function to generate the spectra pairs:

In[5]:=
```
lineUnevenLS[n_] := InverseAutocovariance[timeSeriesLine[n] , Range[1, 100, 1]] ;
```

Here is an assortment of randomly sampled spectral plots from a linear series:

In[6]:=
```
ListLinePlot[lineUnevenLS[#], PlotRange → All] & /@ Range[5, 100, 5]
```

Out[6]=



Random Noise Examples (1)

Below are some examples of the InverseAutocovariance power spectrum for random noise:

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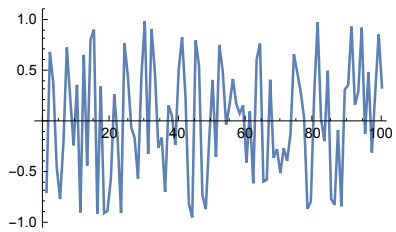
In[1]:=
```
randomListExample = RandomReal[{-1, 1}, 100]
```

Out[1]=
```
{-0.691476, 0.686992, 0.382344, -0.441555, -0.762457, -0.202333, 0.730608, 0.231497, -0.233407, 0.363399,
 -0.894012, 0.6579, -0.431069, 0.809825, 0.906123, -0.906177, 0.346161, -0.899944, -0.878233,
 -0.557465, 0.268824, -0.17577, -0.900237, 0.773774, 0.451525, -0.0533929, -0.15861, -0.560012,
 0.445204, 0.990657, -0.317285, 0.912852, 0.475407, -0.258521, -0.15684, -0.69228, 0.160151,
 0.0597643, -0.230539, 0.510113, 0.830979, 0.250776, -0.804419, -0.943189, 0.799253, 0.551547,
 -0.722788, -0.860553, -0.180595, 0.411345, -0.346708, 0.755954, 0.495727, -0.0278975, 0.163767,
 0.420959, 0.176141, 0.0814202, 0.160475, -0.402419, 0.10286, -0.607119, 0.613585, 0.768665,
 -0.589797, -0.571386, 0.412795, -0.355344, -0.271746, -0.506353, -0.261298, -0.386529, -0.116835,
 0.662397, 0.484919, 0.292202, 0.0374341, -0.858171, -0.78641, 0.279127, 0.978124, 0.0300489,
 -0.192017, 0.501608, -0.762557, -0.818982, -0.0834074, -0.833899, 0.314211, 0.360729, 0.937148,
 0.165061, 0.293022, 0.926109, -0.119184, 0.489506, -0.305156, 0.286883, 0.858035, 0.336654}
```

The data looks like :

In[2]:=
```
ListLinePlot[randomListExample]
```

Out[2]=

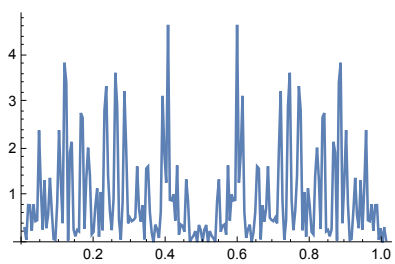


The InverseAutocovariance gives:

In[3]:=
```
randomListInverseAutocovariance =
  InverseAutocovariance[Transpose[{Range[1, 100], randomListExample}], Range[1, 100]];
```

In[4]:=
```
ListLinePlot[randomListInverseAutocovariance, PlotRange → All]
```

Out[4]=



We can also remove data to see how the periodogram performs with missing data/uneven sampling:

In[5]:=
```
timeSeriesRandomSample[n_] :=
  SortBy[RandomSample[Transpose[{Range[1, 100], randomListExample}], n], First];
```

In[6]:=
```
randomUnevenInverseAutocovariance[n_] :=
  InverseAutocovariance[timeSeriesRandomSample[n], Range[1, 100, 1]] ;
```

We plot the spectra with 50-100 points sampled in steps of 10:

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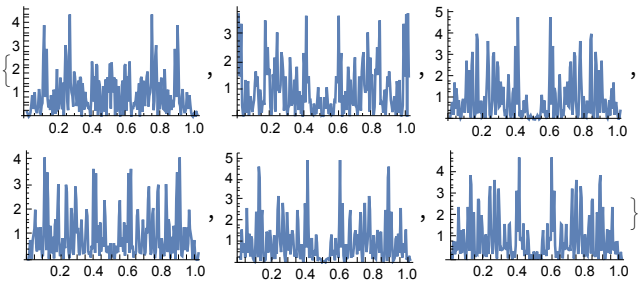
In[7]:=
```
ListLinePlot[randomUnevenInverseAutocovariance[#], PlotRange → All] & /@ Range[50, 100, 10]
```

Out[7]=



Options (2)

UpperFrequencyFactor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

UpperFrequencyFactor takes values ≥ 1, by which to scale the upper Nyquist cutoff frequency and increase spectral resolution. It is recommended to set UpperFrequencyFactor close to 1. The default value is 1.

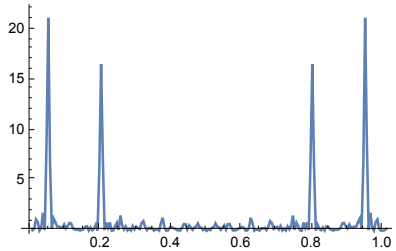
We consider the following example data

In[2]:=
```
dataInverseAutocovarianceExampleB =
 Table[{n, Cos[0.05 * 2 π n ] + Cos[0.2 * 2 π n] + RandomReal[{-1, 1}]}, {n, 0, 100}]
```

Out[2]=
```
{{0, 2.77466}, {1, 1.38445}, {2, -0.154635}, {3, -0.876294}, {4, 1.54662}, {5, 0.0158952},
 {6, -0.943448}, {7, -2.00292}, {8, -2.01808}, {9, -0.771209}, {10, -0.900748}, {11, -0.534676},
 {12, -2.58953}, {13, -0.910163}, {14, -0.440752}, {15, 0.470264}, {16, 1.16376}, {17, -0.338362},
 {18, -0.204161}, {19, 1.35585}, {20, 2.25718}, {21, 0.414278}, {22, 0.0727585}, {23, -0.225894},
 {24, 0.711218}, {25, 0.259149}, {26, -0.591443}, {27, -1.41903}, {28, -1.62983}, {29, 0.0450619},
 {30, 0.0729334}, {31, -0.792752}, {32, -0.718077}, {33, -1.62349}, {34, -0.315768},
 {35, 0.901024}, {36, 1.52399}, {37, -0.263403}, {38, 0.851587}, {39, 0.923275}, {40, 1.04222},
 {41, 1.95055}, {42, -0.895033}, {43, 0.0126117}, {44, 0.361121}, {45, 1.3568}, {46, 0.79415},
 {47, -0.635476}, {48, -0.94405}, {49, 0.295446}, {50, -0.583123}, {51, 0.0862633}, {52, -2.52688},
 {53, -1.47493}, {54, 0.47576}, {55, 1.58093}, {56, 1.18722}, {57, 0.286272}, {58, 0.0897782},
 {59, 1.71331}, {60, 1.61731}, {61, 0.688184}, {62, 0.215734}, {63, 0.0818077}, {64, 1.23823},
 {65, 0.056653}, {66, -0.0245681}, {67, -1.68007}, {68, -2.37635}, {69, -1.54598}, {70, 0.14262},
 {71, -1.47898}, {72, -2.60832}, {73, -1.13691}, {74, -0.1186}, {75, 1.61307}, {76, 1.19467},
 {77, -0.865498}, {78, -0.177018}, {79, 1.0341}, {80, 1.64289}, {81, 0.494644}, {82, 0.594532},
 {83, 0.291329}, {84, -0.219982}, {85, 0.299346}, {86, 0.884463}, {87, -0.637669}, {88, -1.18719},
 {89, -0.162324}, {90, -0.164941}, {91, -0.131999}, {92, -2.36468}, {93, -1.00532}, {94, 0.402805},
 {95, 0.0580306}, {96, -0.33899}, {97, 0.686104}, {98, -0.0214903}, {99, 1.71853}, {100, 1.1429}}
```

In[3]:=
```
ListLinePlot[InverseAutocovariance[dataInverseAutocovarianceExampleB,
  Range[0, 100], UpperFrequencyFactor → 1], PlotRange → All]
```

Out[3]=



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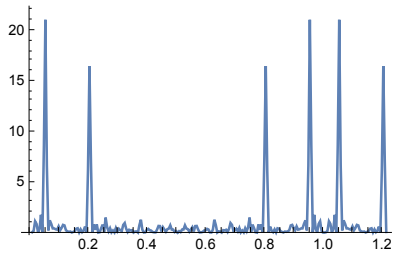
Changing the upper Nyquist frequency can have a drastic effect on the spectrum:

In[4]:=
```
ListLinePlot[InverseAutocovariance[dataInverseAutocovarianceExampleB,
  Range[0, 100], UpperFrequencyFactor → 1.2], PlotRange → All]
```

Out[4]=



PairReturn (1)

In[1]:=
```
Needs["MathIOmica`"]
```

PairReturn is an option that is by default set to True, of whether to return pairs of frequencies and intensities, or a list of frequencies and a corresponding list of intensities for a periodogram.

In[2]:=
```
dataInverseAutocovarianceExampleC = Table[Sin[0.05 * 2 π n], {n, 0, 100}]
```

Out[2]=
```
{0., 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785, 0.309017, 1.22465×10^-16,
 -0.309017, -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017,
 -2.44929×10^-16, 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785,
 0.309017, 3.67394×10^-16, -0.309017, -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017,
 -0.587785, -0.309017, -4.89859×10^-16, 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057,
 0.809017, 0.587785, 0.309017, 6.12323×10^-16, -0.309017, -0.587785, -0.809017, -0.951057, -1.,
 -0.951057, -0.809017, -0.587785, -0.309017, -7.34788×10^-16, 0.309017, 0.587785, 0.809017, 0.951057,
 1., 0.951057, 0.809017, 0.587785, 0.309017, 8.57253×10^-16, -0.309017, -0.587785, -0.809017,
 -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017, -9.79717×10^-16, 0.309017, 0.587785,
 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785, 0.309017, 1.10218×10^-15, -0.309017,
 -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017, -1.22465×10^-15}
```

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In[3]:=
```
InverseAutocovariance[dataInverseAutocovarianceExampleC, Range[0, 100], PairReturn → True]
```

Out[3]=
```
{{0.005, 0.801627}, {0.01, 0.}, {0.015, 0.950023}, {0.02, 0.}, {0.025, 1.40231}, {0.03, 0.}, {0.035, 3.04474},
 {0.04, 0.}, {0.045, 22.0538}, {0.05, 50.25}, {0.055, 18.1731}, {0.06, 0.}, {0.065, 1.69677},
 {0.07, 0.}, {0.075, 0.521837}, {0.08, 0.}, {0.085, 0.230699}, {0.09, 0.}, {0.095, 0.122429}, {0.1, 0.},
 {0.105, 0.0726843}, {0.11, 0.}, {0.115, 0.046602}, {0.12, 0.}, {0.125, 0.0316199}, {0.13, 0.},
 {0.135, 0.0224145}, {0.14, 0.}, {0.145, 0.0164567}, {0.15, 0.}, {0.155, 0.0124372}, {0.16, 0.},
 {0.165, 0.00963133}, {0.17, 0.}, {0.175, 0.0076161}, {0.18, 0.}, {0.185, 0.00613316}, {0.19, 0.},
 {0.195, 0.00501887}, {0.2, 0.}, {0.205, 0.00416618}, {0.21, 0.}, {0.215, 0.00350312}, {0.22, 0.},
 {0.225, 0.00298016}, {0.23, 0.}, {0.235, 0.00256243}, {0.24, 0.}, {0.245, 0.00222495}, {0.25, 0.},
 {0.255, 0.00194951}, {0.26, 0.}, {0.265, 0.00172263}, {0.27, 0.}, {0.275, 0.00153419}, {0.28, 0.},
 {0.285, 0.00137652}, {0.29, 0.}, {0.295, 0.0012437}, {0.3, 0.}, {0.305, 0.00113115}, {0.31, 0.},
 {0.315, 0.00103526}, {0.32, 0.}, {0.325, 0.000953189}, {0.33, 0.}, {0.335, 0.000882666}, {0.34, 0.},
 {0.345, 0.000821869}, {0.35, 0.}, {0.355, 0.000769321}, {0.36, 0.}, {0.365, 0.000723822}, {0.37, 0.},
 {0.375, 0.000684394}, {0.38, 0.}, {0.385, 0.000650229}, {0.39, 0.}, {0.395, 0.000620665}, {0.4, 0.},
 {0.405, 0.000595155}, {0.41, 0.}, {0.415, 0.000573246}, {0.42, 0.}, {0.425, 0.000554564}, {0.43, 0.},
 {0.435, 0.000538803}, {0.44, 0.}, {0.445, 0.000525711}, {0.45, 0.}, {0.455, 0.000515086}, {0.46, 0.},
 {0.465, 0.000506768}, {0.47, 0.}, {0.475, 0.000500633}, {0.48, 0.}, {0.485, 0.000496591}, {0.49, 0.},
 {0.495, 0.000494585}, {0.5, 0.}, {0.505, 0.000494585}, {0.51, 0.}, {0.515, 0.000496591}, {0.52, 0.},
 {0.525, 0.000500633}, {0.53, 0.}, {0.535, 0.000506768}, {0.54, 0.}, {0.545, 0.000515086}, {0.55, 0.},
 {0.555, 0.000525711}, {0.56, 0.}, {0.565, 0.000538803}, {0.57, 0.}, {0.575, 0.000554564}, {0.58, 0.},
 {0.585, 0.000573246}, {0.59, 0.}, {0.595, 0.000595155}, {0.6, 0.}, {0.605, 0.000620665}, {0.61, 0.},
 {0.615, 0.000650229}, {0.62, 0.}, {0.625, 0.000684394}, {0.63, 0.}, {0.635, 0.000723822}, {0.64, 0.},
 {0.645, 0.000769321}, {0.65, 0.}, {0.655, 0.000821869}, {0.66, 0.}, {0.665, 0.000882666}, {0.67, 0.},
 {0.675, 0.000953189}, {0.68, 0.}, {0.685, 0.00103526}, {0.69, 0.}, {0.695, 0.00113115}, {0.7, 0.},
 {0.705, 0.0012437}, {0.71, 0.}, {0.715, 0.00137652}, {0.72, 0.}, {0.725, 0.00153419}, {0.73, 0.},
 {0.735, 0.00172263}, {0.74, 0.}, {0.745, 0.00194951}, {0.75, 0.}, {0.755, 0.00222495}, {0.76, 0.},
 {0.765, 0.00256243}, {0.77, 0.}, {0.775, 0.00298016}, {0.78, 0.}, {0.785, 0.00350312}, {0.79, 0.},
 {0.795, 0.00416618}, {0.8, 0.}, {0.805, 0.00501887}, {0.81, 0.}, {0.815, 0.00613316}, {0.82, 0.},
 {0.825, 0.0076161}, {0.83, 0.}, {0.835, 0.00963133}, {0.84, 0.}, {0.845, 0.0124372}, {0.85, 0.},
 {0.855, 0.0164567}, {0.86, 0.}, {0.865, 0.0224145}, {0.87, 0.}, {0.875, 0.0316199}, {0.88, 0.},
 {0.885, 0.046602}, {0.89, 0.}, {0.895, 0.0726843}, {0.9, 0.}, {0.905, 0.122429}, {0.91, 0.},
 {0.915, 0.230699}, {0.92, 0.}, {0.925, 0.521837}, {0.93, 0.}, {0.935, 1.69677}, {0.94, 0.}, {0.945, 18.1731},
 {0.95, 50.25}, {0.955, 22.0538}, {0.96, 0.}, {0.965, 3.04474}, {0.97, 0.}, {0.975, 1.40231},
 {0.98, 0.}, {0.985, 0.950023}, {0.99, 0.}, {0.995, 0.801627}, {1., 0.}, {1.005, 0.801627}, {1.01, 0.}}
```

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In[4]:=
```
InverseAutocovariance[dataInverseAutocovarianceExampleC, Range[0, 100], PairReturn → False]
```

Out[4]=
```
{{0.005, 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.04, 0.045, 0.05, 0.055, 0.06, 0.065, 0.07, 0.075, 0.08,
  0.085, 0.09, 0.095, 0.1, 0.105, 0.11, 0.115, 0.12, 0.125, 0.13, 0.135, 0.14, 0.145, 0.15, 0.155, 0.16,
  0.165, 0.17, 0.175, 0.18, 0.185, 0.19, 0.195, 0.2, 0.205, 0.21, 0.215, 0.22, 0.225, 0.23, 0.235, 0.24,
  0.245, 0.25, 0.255, 0.26, 0.265, 0.27, 0.275, 0.28, 0.285, 0.29, 0.295, 0.3, 0.305, 0.31, 0.315, 0.32,
  0.325, 0.33, 0.335, 0.34, 0.345, 0.35, 0.355, 0.36, 0.365, 0.37, 0.375, 0.38, 0.385, 0.39, 0.395, 0.4,
  0.405, 0.41, 0.415, 0.42, 0.425, 0.43, 0.435, 0.44, 0.445, 0.45, 0.455, 0.46, 0.465, 0.47, 0.475,
  0.48, 0.485, 0.49, 0.495, 0.5, 0.505, 0.51, 0.515, 0.52, 0.525, 0.53, 0.535, 0.54, 0.545, 0.55, 0.555,
  0.56, 0.565, 0.57, 0.575, 0.58, 0.585, 0.59, 0.595, 0.6, 0.605, 0.61, 0.615, 0.62, 0.625, 0.63,
  0.635, 0.64, 0.645, 0.65, 0.655, 0.66, 0.665, 0.67, 0.675, 0.68, 0.685, 0.69, 0.695, 0.7, 0.705,
  0.71, 0.715, 0.72, 0.725, 0.73, 0.735, 0.74, 0.745, 0.75, 0.755, 0.76, 0.765, 0.77, 0.775, 0.78,
  0.785, 0.79, 0.795, 0.8, 0.805, 0.81, 0.815, 0.82, 0.825, 0.83, 0.835, 0.84, 0.845, 0.85, 0.855, 0.86,
  0.865, 0.87, 0.875, 0.88, 0.885, 0.89, 0.895, 0.9, 0.905, 0.91, 0.915, 0.92, 0.925, 0.93, 0.935,
  0.94, 0.945, 0.95, 0.955, 0.96, 0.965, 0.97, 0.975, 0.98, 0.985, 0.99, 0.995, 1., 1.005, 1.01},
 {0.801627, 0., 0.950023, 0., 1.40231, 0., 3.04474, 0., 22.0538, 50.25, 18.1731, 0., 1.69677, 0.,
  0.521837, 0., 0.230699, 0., 0.122429, 0., 0.0726843, 0., 0.046602, 0., 0.0316199, 0., 0.0224145, 0.,
  0.0164567, 0., 0.0124372, 0., 0.00963133, 0., 0.0076161, 0., 0.00613316, 0., 0.00501887, 0., 0.00416618,
  0., 0.00350312, 0., 0.00298016, 0., 0.00256243, 0., 0.00222495, 0., 0.00194951, 0., 0.00172263, 0.,
  0.00153419, 0., 0.00137652, 0., 0.0012437, 0., 0.00113115, 0., 0.00103526, 0., 0.000953189, 0.,
  0.000882666, 0., 0.000821869, 0., 0.000769321, 0., 0.000723822, 0., 0.000684394, 0., 0.000650229, 0.,
  0.000620665, 0., 0.000595155, 0., 0.000573246, 0., 0.000554564, 0., 0.000538803, 0., 0.000525711, 0.,
  0.000515086, 0., 0.000506768, 0., 0.000500633, 0., 0.000496591, 0., 0.000494585, 0., 0.000494585, 0.,
  0.000496591, 0., 0.000500633, 0., 0.000506768, 0., 0.000515086, 0., 0.000525711, 0., 0.000538803, 0.,
  0.000554564, 0., 0.000573246, 0., 0.000595155, 0., 0.000620665, 0., 0.000650229, 0., 0.000684394,
  0., 0.000723822, 0., 0.000769321, 0., 0.000821869, 0., 0.000882666, 0., 0.000953189, 0., 0.00103526,
  0., 0.00113115, 0., 0.0012437, 0., 0.00137652, 0., 0.00153419, 0., 0.00172263, 0., 0.00194951,
  0., 0.00222495, 0., 0.00256243, 0., 0.00298016, 0., 0.00350312, 0., 0.00416618, 0., 0.00501887,
  0., 0.00613316, 0., 0.0076161, 0., 0.00963133, 0., 0.0124372, 0., 0.0164567, 0., 0.0224145, 0.,
  0.0316199, 0., 0.046602, 0., 0.0726843, 0., 0.122429, 0., 0.230699, 0., 0.521837, 0., 1.69677, 0.,
  18.1731, 50.25, 22.0538, 0., 3.04474, 0., 1.40231, 0., 0.950023, 0., 0.801627, 0., 0.801627, 0.}}
```

Properties & Relations (1)

The LombScargle function can be used to calculate an appropriate periodogram in the original sense of the Lomb-Scargle transformation. The InverseAutocovariance is instead use when an Autocorrelation needs to be calculated and is a modified version of the LombScargle function as discussed in the function Details section.

See Also

Autocorrelation ▪ **LombScargle**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

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Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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JoinNestedAssociations

JoinNestedAssociations[*associationList*]
merges the nested associationList by joining the inner associations.

Details

- JoinNestedAssociations[*associationList*] is designed to work on data provided as an association of associations, to allow the user to merge outer associations while joining the internal associations for each matching key.

Examples (1)

Basic Examples (1)

We first load MathIOmica:

```
In[1]:= Needs["MathIOmica`"]
```

```
In[2]:= associationExampleA =
  <|"Class1" → <|"item1" → {{1, 1, 1}, {"a", "a", "b"}}, "item2" → {{1, 2, 1}, {"a", "b", "b"}}|>,
   "Class2" → <|"item3" → {{2, 3, 1}, {"b", "c", "b"}}, "item4" → {{2, 4, 1}, {"b", "d", "b"}}|>|>;
associationExampleB = <|"Class2" → <|"item3b" → {{2, 3, 1}, {"b", "c", "b"}},
     "item4b" → {{2, 4, 1}, {"b", "d", "b"}}|>,
   "Class3" → <|"item5b" → {{3, 5, 1}, {"c", "e", "b"}}, "item6b" → {{3, 6, 1}, {"c", "f", "b"}}|>|>;
associationExampleC = <|"Class2" → <|"item3c" → {{2, 3, 1}, {"a", "b", "c"}},
     "item4c" → {{4, 3, 4}, {"b", "c", "d"}}|>,
   "Class4" → <|"item7c" → {{1, 2, 3}, {"a", "b", "c"}}, "item8c" → {{2, 3, 4}, {"b", "c", "d"}}|>|>;
```

We can join these associations so that outer keys that are common have their inner associations enlarged to include members from both original associations:

```
In[3]:= JoinNestedAssociations[{associationExampleA, associationExampleB}]
```

```
Out[3]= <|Class1 → <|item1 → {{1, 1, 1}, {a, a, b}}, item2 → {{1, 2, 1}, {a, b, b}}|>,
 Class2 → <|item3 → {{2, 3, 1}, {b, c, b}}, item4 → {{2, 4, 1}, {b, d, b}},
   item3b → {{2, 3, 1}, {b, c, b}}, item4b → {{2, 4, 1}, {b, d, b}}|>,
 Class3 → <|item5b → {{3, 5, 1}, {c, e, b}}, item6b → {{3, 6, 1}, {c, f, b}}|>|>
```

The supplied list can include multiple associations:

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```
In[4]:= JoinNestedAssociations[{associationExampleA, associationExampleB, associationExampleC}]

Out[4]= <|Class1 → <|item1 → {{1, 1, 1}, {a, a, b}}, item2 → {{1, 2, 1}, {a, b, b}}|>,
  Class2 → <|item3 → {{2, 3, 1}, {b, c, b}}, item4 → {{2, 4, 1}, {b, d, b}}, item3b → {{2, 3, 1}, {b, c, b}},
    item4b → {{2, 4, 1}, {b, d, b}}, item3c → {{2, 3, 1}, {a, b, c}}, item4c → {{4, 3, 4}, {b, c, d}}|>,
  Class3 → <|item5b → {{3, 5, 1}, {c, e, b}}, item6b → {{3, 6, 1}, {c, f, b}}|>,
  Class4 → <|item7c → {{1, 2, 3}, {a, b, c}}, item8c → {{2, 3, 4}, {b, c, d}}|>|>
```

See Also

ConstantAssociator ▪ **DataImporter** ▪ **DataImporterDirect** ▪ **DataImporterDirectLabeled** ▪ **EnlargeInnerAssociation** ▪ **FileSelector** ▪ **OmicsObject** ▪ **OmicsObjectCreator**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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KEGGAnalysis

KEGGAnalysis[data]
calculates input data over–representation analysis for KEGG: Kyoto Encyclopedia of Genes and Genomes pathways.

Details

- KEGGAnalysis[*data*] calculates input data over-representation analysis (ORA) for KEGG: Kyoto Encyclopedia of Genes and Genomes pathways. We note that the function utilizes data obtained from the KEGG databases, and by default uses human data annotated by "KEGG Gene ID".
- The input data can be a single list of n genes in the form:
- data = {ID_1, ID_2, ..., ID_n}
- The IDs may be provided as ID strings, ID_j (e.g. "NFKB1") as strings enclosed in list brackets {ID_j}, (e.g. {"NFKB1"} or as labeled strings in the case of multiple omics being considered. Labeled IDs are typically provided as:
- {{ID_1, ... optional label $items_1$, $label_1$},
  {ID_2, ... optional label $items_2$, ..., $label_2$}, ... {ID_n, ..., optional label $items_n$, ..., $label_n$}}.
- The ID labels are typically a string, e.g. typically "RNA" or "Protein", (e.g. {"NFKB1","Protein"}) or for a molecular ID obtained from metabolomics experiments, can also contain other optional label items such as mass and retention time {"cpd:C00449", 276.133, 11.0041, "Meta"}. The main label must always be the last element in the list.
- The output has the following structures: for a single list input:
- listOutput = <|
  KEGG : $pathway_1$ → {{p - $value_1$, multiple hypothesis adjusted p - $value_1$, True / False for statistical significance},
    {{number of members in group being tested, number of successes for $term_1$ in population, total number of members in population, number of members (or more) in current group being tested associated to $pathway_1$},
    {KEGG $pathway_1$ description, {input IDs associated to $pathway_1$}}}},
  KEGG : $pathway_2$ → {{p - $value_2$, multiple hypothesis adjusted p - $value_2$, True / False for statistical significance},
    {{number of members in group being tested, number of successes for $term_2$ in population, total number of members in population, number of members (or more) in current group being tested associated to $pathway_2$},
    {KEGG $pathway_1$ description, {input IDs associated to $pathway_2$}}}}, ...,
  KEGG : $pathway_n$ → {{p - $value_n$, multiple hypothesis adjusted p - $value_n$, True / False for statistical significance},
    {{number of members in group being tested, number of successes for $term_n$ in population, total number of members in population, number of members (or more) in current group being tested associated to $pathway_n$},
    {KEGG $pathway_n$ description, {input IDs associated to $pathway_n$}}}}
  |>
- The input data can also be an association of multiple L groups to be tested:
- data = <|$Group_1$ → {ID_{11}, ID_{12}, ..., $ID_{1\,n_1}$},
  $Group_2$ → {ID_{21}, ID_{22}, ..., $ID_{2\,n2}$}, ...,
  $Group_L$ → {ID_{11}, ID_{12}, ..., $ID_{1\,n_L}$}|>.
- In this case the output for each group has the listOutput format described above:

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- `associationOutput = <|Group1 → listOutput1,`
  `Group2 → listOutput2, ...,`
  `GroupL → listOutputL|>`

- KEGGAnalysis can also take as input the output of clustering of time series classification data, e.g. TimeSeriesClusters or TimeSeriesSingleClusters association of associations. The groups for each class will then have keys labeled "GroupAssociations", that include the labels used in the clustering. The labels must correspond to protein or gene accessions/IDs. For each class and group the corresponding KEGGAnalysis enrichment is computed and returned.

- There are two types of analyses that are carried out, which can be set by the AnalysisType option value. The default "Genomic" analysis is based on input gene symbols. The "Molecular" analysis is based on molecular input accessions (e.g. compounds "cpd" databases). For multi-omic input the user may select to do All analyses. In this case an additional outer association is created with labels indicating each of "Genomic" or "Molecular" analysis carried out.

- The enrichment analysis is an over-representation calculation, using a hypergeometric test. For a given a given group (e.g. members of a cluster after classification), we try to identify which KEGG pathway terms are over-represented by membership of IDs to that cluster. The KEGGAnalysis function allows us to select the background, and hence address selection bias. Additionally a Benjamini-Hochberg procedure false discovery rate (FDR) may be calculated for each representation.

- We assume here we are considering a population (possible measurements) of N total identifiers (e.g. genes or compounds), and a given pathway term T has M_T identifiers/entries associated to it. For any group/cluster we are interested in (e.g. as differentially expressed), that contains a subset of $n_{group} < N$ identifiers, we can identify which x_T identifiers are associated to term T. Then we would like to calculate the probability, p_T, that at least x_T identifiers could have an association to term T randomly (i.e. more than x_T number of successes):

- $p_T\,(\text{at least } x \text{ successes}) = \sum_{i=x}^{n_{group}} \frac{\binom{M_T}{i}\binom{N-M_T}{n_{group}-i}}{\binom{N}{n_{group}}}$.

- Using this hypergeometric distribution calculation, we can choose a p-value cutoff, typically at 0.95, to consider any cluster/group's number of successes (for a specified pathway) to show enrichment in be enriched in a term T of interest.

- In practice, typically a database (such as KEGG, or GO) has annotated only a subset $N_a \subset N$ of these total identifiers. The calculation then is modified to reduce this bias, by performing the analysis on a subset of the identifiers of interest to the ones that belong to N_a, and effectively we also have $n_{group} \to n_{group,a} = \{j \in n_{group} : j \in N_a\}$.

- Additionally, there are cases when the overall measurements can be restricted to certain sets only, i.e. a different background or species, $N \to N_b \subset N$. Then the pathway/group terms are also restricted to the ones that belong to N_b, $M_{T,b} = \{k \in M_{T,b} : k \in N_b\}$.

- In the case that labeled multi-omics data is provided there are multiple choices. If no MultipleList options are invoked (see below), the identifiers are treated as equivalent and are simply grouped together. If the same identifier shows with the same label these identifiers are treated as equivalent (i.e. no overcounting). If the MultipleList and MultipleListCorrection are set, the population N is enlarged by a factor f_P and so is the membership of each term to accommodate the changes. In the case of two omics, the assumption is that they can each contribute equally to a term and the Automatic KEGGAnalysis function correction is a simple factor of $f_P = 2$.

- Finally, there is the need to address false discovery rates and account for multiple hypothesis testing. The default method is the computation of a Benjamini-Hochberg false discovery rate (FDR) using BenjaminiHochbergFDR .

- The following options can be given:

AdditionalFilter	None	AdditionalFilter provides additional filtering that may be applied to the standard output structure to be returned.

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AnalysisType	"Genomic"	AnalysisType provides a selection for the type of analysis to perform. "Genomic" analysis (default) uses gene identifier based analysis. "Molecular" analysis uses molecular analysis. Setting the option to All carries out all possible analysis types for the input data.
AugmentDictionary	True	AugmentDictionary provides a choice whether or not to augment the current ConstantGeneDictionary variable or create a new one.
BacgroundSet	All	BackgroundSet provides a list of IDs (e.g. gene accessions) that should be considered as the background for the calculation.
FilterSignificant	True	FilterSignificant can be set to True to filter data based on whether the enrichment analysis is statistically significant, or if set to False to return all membership computations.
GeneDictionary	None	GeneDictionary points to an existing variable to use as a gene dictionary in annotations. If set to None the default ConstantGeneDictionary will be used.
GetGeneDictionaryOptions	{}	The GetGeneDictionaryOptions option specifies a list of options that will be passed to the internal GetGeneDictionary function.

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HypothesisFunction	(Query["Results"][BenjaminiHochbergFDR[#1, SignificanceLevel –> #2]] &) &	The HypothesisFunction option allows us to chose a function to implement multiple hypothesis testing. The default is using the BenjaminiHochbergFDR function. The user can use any function f with three inputs, of the form f[#1,#2,#3] where the inputs refer to: #1 is the p–value list, #2 is a significance cutoff, #3 is the number of GO associations overall being tested. The function f must output a list of 3 values: {original p–value, adjusted p–value, True or False based on whether this value is considered statistically significant or not respectively}.
InputID	{"UniProt ID", "Gene Symbol"}	The InputID option specifies the kind of identifiers/accessions used as input.
KEGGAnalysisAssignerOptions	{}	The KEGGAnalysisAssignerOptions option specifies a list of options that will be passed to the internal KEGGAnalysisAssigner function.
KEGGDatabase	"pathway"	KEGGDatabase value indicates which KEGG database to use as the target database.
KEGGDictionaryOptions	{}	KEGGDictionaryOptions specifies a list of options to be passed to the internal KEGGDictionary function that provides the KEGG annotations.
KEGGDictionaryVariable	None	KEGGDictionaryVariable can provide a KEGG annotation variable. If set to None, KEGGDictionary will be used internally to automatically generate the default KEGG annotation.
KEGGMolecular	"cpd"	KEGGMolecular specifies which database to use for molecular analysis. The default is the compound database ("cpd").

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KEGGOrganism	"hsa"	KEGGOrganism indicates which organism (org) to use for "Genomic" type of analysis. The default is human analysis org="hsa".
MathIOmicaDataDirectory	If[! DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]	MathIOmicaDataDirectory option specifies the directory where the default MathIOmica package data are stored. By default the option is set to create the standard directory if it does not exist already.
MolecularInputID	{"cpd"}	MolecularInputID is a string list to indicate the kind of ID to use for the input molecule entries.
MolecularOutputID	"cpd"	MolecularOutputID is a string to indicate the kind of ID to convert input molecule entries. The default is "cpd" consistently with use of the "cpd" database as the default molecular analysis.
MolecularSpecies	"compound"	MolecularSpecies specifies the kind of molecular input.
MultipleList	False	MultipleList option specifies whether the input accessions list constituted a multi–omics list input that is annotated so. Each ID j input must be a list form, i.e. enclosed as $\{ID_j\}$. If this is the case, MultipleList is set to True and each input list ID should have the form {ID,"Omics Type Label"}, e.g. {"NFKB1","Protein"}, and the different omics type are treated as different for each ID. If MultipleList is set to False, and labeled IDs are provided, labels corresponding to the same ID are treated as equivalent to avoid overcounting.

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MultipleListCorrection	None	MultipleListCorrection is an option whether or not to correct for multi–omics analysis. The choices are None, Automatic, or a custom number. This essentially enlarges the population by this factor to account for additional IDs being considered as the result of a multi–omics cluster analysis. If the value is set to Automatic the number of unique ID labels is used to make the correction.
NonUCSC	False	NonUCSC option set to False assumes UCSC browser was used in determining an internal GeneDictionary used in ID translations where the KEGG identifiers for genes are number strings (e.g. 4790). The NonUCSC option can be set to True if standard KEGG accessions are used in a user provided GeneDictionary variable, in the form OptionValue[KEGGOrganism] <>":"<>"number string", e.g. "hsa:4790"
OutputID	"KEGG Gene ID"	OutputID is a string to indicate the kind of ID to convert input genomic analysis entries. The default is "KEGG Gene ID" consistently with use of the "pathway" database as the default genomic analysis.
PathwayLengthFilter	2	PathwayLengthFilter can be used to set the value for which terms to consider in the computation, by excluding KEGG pathways that have fewer items compared to the PathwayLengthFilter value. It is used by the internal KEGGAnalysisAssigner function.
pValueCutoff	0.05	pValueCutoff provides a cutoff p–value for adjusted p–values to assess statistical significance.
ReportFilter	1	ReportFilter provides a cutoff for membership in pathways in selecting which terms/pathways to return. It is used in conjunction with ReportFilterFunction.

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ReportFilterFunction	GreaterEqualThan	ReportFilterFunction specifies what operator form will be used to compare against ReportFilter option value in selecting which terms/pathways to return. The default is to use GreaterEqualThan
Species	"human"	The Species option specifies the species considered in the calculation.
TestFunction	(1 – N[CDF[HypergeometricDistribution[#1, #2, #3], #4 – 1]]) &	The TestFunction option calculates the p–values for the enrichment of each term. It can be a function of four inputs, f[#1,#2,#3,#4] (e.g. the default is using a hypergeometric distribution CDF, 1–N[CDF[HypergeometricDistribution[#1,#2,#3],#4–1]]]. The four inputs refer to: #1 is number of draws (members in group being tested), #2 is number of successes for category in population, #3 is total number of members in population, #4 is number of successes (or more) in current group being tested for specific category. The output is a p–value (real positive number ≤ 1).

- KEGGAnalysis generates a global ConstantGeneDictionary variable if one does not exist already.

Examples (42)

Basic Examples (7)

We first load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

Let's do a KEGG pathway analysis for a group of genes (most in the NFKB pathway), annotated with their "Gene Symbol":

In[2]:=
```
keggExample1 = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C",
   "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM",
   "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"}]
```

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```
Out[2]= ⟨|path:hsa04064 → {{1.97851×10^-37, 2.13679×10^-35, True},
    {25, 100, 7873, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05235 → {{1.79086×10^-10, 9.67067×10^-9, True}, {25, 89, 7873, 8},
    {PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
     {{TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05169 → {{5.52831×10^-9, 1.6516×10^-7, True}, {25, 201, 7873, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {LYN}, {MYD88}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
  path:hsa05162 → {{6.11703×10^-9, 1.6516×10^-7, True}, {25, 138, 7873, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04620 → {{2.26434×10^-8, 4.89098×10^-7, True}, {25, 104, 7873, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05161 → {{5.03513×10^-7, 9.06323×10^-6, True}, {25, 163, 7873, 7},
    {Hepatitis B - Homo sapiens (human), {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05145 → {{1.08499×10^-6, 0.0000167398, True}, {25, 113, 7873, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04623 → {{1.3115×10^-6, 0.0000177053, True}, {25, 63, 7873, 5},
    {Cytosolic DNA-sensing pathway - Homo sapiens (human),
     {{CHUK}, {NFKB1}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
  path:hsa05135 → {{1.62311×10^-6, 0.0000194774, True}, {25, 121, 7873, 6},
    {Yersinia infection - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05140 → {{2.93621×10^-6, 0.0000289479, True}, {25, 74, 7873, 5},
    {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05170 → {{2.95816×10^-6, 0.0000289479, True}, {25, 212, 7873, 7},
    {Human immunodeficiency virus 1 infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {MYD88}, {ATM}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{3.21643×10^-6, 0.0000289479, True}, {25, 136, 7873, 6},
    {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{3.67271×10^-6, 0.0000305118, True}, {25, 219, 7873, 7},
    {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
     {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04662 → {{4.88946×10^-6, 0.0000377187, True}, {25, 82, 7873, 5},
    {B cell receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000150012, 0.000099902, True}, {25, 103, 7873, 5},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
     {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04621 → {{0.0000152076, 0.000099902, True}, {25, 178, 7873, 6},
    {NOD-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04625 → {{0.0000157253, 0.000099902, True}, {25, 104, 7873, 5},
    {C-type lectin receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}, path:hsa04010 →
   {{0.0000259458, 0.000147729, True}, {25, 295, 7873, 7}, {MAPK signaling pathway - Homo sapiens (human),
     {{TAB1}, {CHUK}, {MYD88}, {GADD45B}, {NFKB1}, {NFKB2}, {IRAK4}}}},
  path:hsa05134 → {{0.0000259894, 0.000147729, True}, {25, 56, 7873, 4},
    {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04380 → {{0.0000429841, 0.000232114, True}, {25, 128, 7873, 5},
    {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05120 → {{0.0000629652, 0.000323821, True}, {25, 70, 7873, 4},
    {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
     {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05133 → {{0.000086981, 0.000408432, True},
    {25, 76, 7873, 4}, {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
  path:hsa05220 → {{0.000086981, 0.000408432, True}, {25, 76, 7873, 4},
    {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
  path:hsa05164 → {{0.000152329, 0.000685481, True}, {25, 167, 7873, 5},
    {Influenza A - Homo sapiens (human), {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05222 → {{0.000190876, 0.000824586, True}, {25, 93, 7873, 4},
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  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
path:hsa05152 → {{0.000210914, 0.000876104, True}, {25, 179, 7873, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05215 → {{0.000224582, 0.000898328, True}, {25, 97, 7873, 4},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}, {PLAU}}}},
path:hsa04660 → {{0.000282919, 0.00109126, True}, {25, 103, 7873, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000361486, 0.00134622, True}, {25, 201, 7873, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04668 → {{0.000389851, 0.00140347, True}, {25, 112, 7873, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04672 → {{0.000473279, 0.00164884, True}, {25, 49, 7873, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04137 → {{0.00108509, 0.00366217, True},
  {25, 65, 7873, 3}, {Mitophagy - animal - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05131 → {{0.00123718, 0.00404894, True}, {25, 68, 7873, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00129071, 0.00409989, True}, {25, 69, 7873, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00134568, 0.00415238, True}, {25, 70, 7873, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00146001, 0.00438004, True}, {25, 72, 7873, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05212 → {{0.0016427, 0.0047949, True}, {25, 75, 7873, 3},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}}}},
path:hsa05167 → {{0.00258637, 0.00716226, True}, {25, 186, 7873, 4},
  {Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05202 → {{0.00258637, 0.00716226, True}, {25, 186, 7873, 4},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{GADD45B}, {ATM}, {NFKB1}, {PLAU}}}},
path:hsa04062 → {{0.00279404, 0.00754391, True}, {25, 190, 7873, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa04658 → {{0.0029483, 0.00776626, True}, {25, 92, 7873, 3},
  {Th1 and Th2 cell differentiation - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04657 → {{0.00304021, 0.0078177, True}, {25, 93, 7873, 3},
  {IL-17 signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05168 → {{0.0036852, 0.00925585, True}, {25, 492, 7873, 6},
  {Herpes simplex virus 1 infection - Homo sapiens (human),
   {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa01523 → {{0.00425473, 0.010056, True}, {25, 31, 7873, 2},
  {Antifolate resistance - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa03020 → {{0.00425473, 0.010056, True}, {25, 31, 7873, 2},
  {RNA polymerase - Homo sapiens (human), {{POLR3B}, {POLR3A}}}},
path:hsa03008 → {{0.00428312, 0.010056, True}, {25, 105, 7873, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04659 → {{0.00451611, 0.0103774, True}, {25, 107, 7873, 3},
  {Th17 cell differentiation - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00607598, 0.013671, True}, {25, 119, 7873, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04068 → {{0.00809109, 0.0178334, True}, {25, 132, 7873, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa05418 → {{0.00932162, 0.0201347, True}, {25, 139, 7873, 3},
  {Fluid shear stress and atherosclerosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {PIAS4}}}},
path:hsa05160 → {{0.0125296, 0.0265332, True}, {25, 155, 7873, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04218 → {{0.0136471, 0.0277717, True}, {25, 160, 7873, 3},
  {Cellular senescence - Homo sapiens (human), {{GADD45B}, {ATM}, {NFKB1}}}},
path:hsa04310 → {{0.0136471, 0.0277717, True}, {25, 160, 7873, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa00240 → {{0.0138859, 0.0277717, True}, {25, 57, 7873, 2},
  {Pyrimidine metabolism - Homo sapiens (human), {{NME1}, {CTPS1}}}},
path:hsa05221 → {{0.0183406, 0.0360144, True}, {25, 66, 7873, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0216033, 0.0416634, True}, {25, 72, 7873, 2},
```

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```
    {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa05200 → {{0.0234256, 0.0443854, True}, {25, 530, 7873, 5},
    {Pathways in cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|⟩
```

We can obtain the results for any of the data:

```
In[3]:= Query[{1}]@keggExample1

Out[3]= ⟨|path:hsa04064 → {{1.97851×10^-37, 2.13679×10^-35, True},
    {25, 100, 7873, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}}|⟩
```

We see that the result is statistically significant. KEGG pathway path:hsa04064 is the ""NF-kappa B signaling pathway - Homo sapiens (human)"". 21 of the 25 input genes with KEGG annotation are associated to this term. The term has 93 entries associated to it.

```
In[1]:= Needs["MathIOmica`"]
```

The information can be computed for multiple groups, if these are provided as an association:

```
In[2]:= analysisKEGGAssociation = KEGGAnalysis[<|
    "Group1" → {"C6orf57", "CD46", "DHX58", "HMGB3", "MAP3K5", "NFKB2", "NOS2", "PYCARD", "PYDC1", "SSC5D"},
    "Group2" → {"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
      "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1",
      "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"}|>]

Out[2]= ⟨|Group1 → ⟨|path:hsa05134 → {{0.00102, 0.0334234, True},
      {7, 56, 7873, 2}, {Legionellosis - Homo sapiens (human), {{NFKB2}, {PYCARD}}}},
    path:hsa05133 → {{0.00187169, 0.0334234, True}, {7, 76, 7873, 2},
      {Pertussis - Homo sapiens (human), {{NOS2}, {PYCARD}}}},
    path:hsa05132 → {{0.00222823, 0.0334234, True}, {7, 83, 7873, 2},
      {Salmonella infection - Homo sapiens (human), {{NOS2}, {PYCARD}}}},
    path:hsa04625 → {{0.00347585, 0.0391033, True}, {7, 104, 7873, 2},
      {C-type lectin receptor signaling pathway - Homo sapiens (human), {{NFKB2}, {PYCARD}}}}|⟩,
  Group2 → ⟨|path:hsa04064 → {{0., 0., True}, {25, 100, 7873, 21},
      {NF-kappa B signaling pathway - Homo sapiens (human),
       {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
        {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
    path:hsa05235 → {{1.79087×10^-10, 9.67067×10^-9, True}, {25, 89, 7873, 8},
      {PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
       {{TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
    path:hsa05169 → {{5.52831×10^-9, 1.6516×10^-7, True}, {25, 201, 7873, 9},
      {Epstein-Barr virus infection - Homo sapiens (human),
       {{TAB1}, {CHUK}, {LYN}, {MYD88}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
    path:hsa05162 → {{6.11703×10^-9, 1.6516×10^-7, True}, {25, 138, 7873, 8}, {Measles - Homo sapiens (human),
       {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
    path:hsa04620 → {{2.26434×10^-8, 4.89098×10^-7, True}, {25, 104, 7873, 7},
      {Toll-like receptor signaling pathway - Homo sapiens (human),
       {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
    path:hsa05161 → {{5.03513×10^-7, 9.06323×10^-6, True}, {25, 163, 7873, 7},
      {Hepatitis B - Homo sapiens (human), {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
    path:hsa05145 → {{1.08499×10^-6, 0.0000167398, True}, {25, 113, 7873, 6},
      {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
    path:hsa04623 → {{1.3115×10^-6, 0.0000177053, True}, {25, 63, 7873, 5},
      {Cytosolic DNA-sensing pathway - Homo sapiens (human),
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    {{CHUK}, {NFKB1}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
path:hsa05135 → {{1.62311×10^-6, 0.0000194774, True}, {25, 121, 7873, 6},
  {Yersinia infection - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05140 → {{2.93621×10^-6, 0.0000289479, True}, {25, 74, 7873, 5},
  {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05170 → {{2.95816×10^-6, 0.0000289479, True}, {25, 212, 7873, 7},
  {Human immunodeficiency virus 1 infection - Homo sapiens (human),
   {{TAB1}, {CHUK}, {MYD88}, {ATM}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04210 → {{3.21643×10^-6, 0.0000289479, True}, {25, 136, 7873, 6},
  {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
path:hsa05166 → {{3.67271×10^-6, 0.0000305118, True}, {25, 219, 7873, 7},
  {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
   {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04662 → {{4.88946×10^-6, 0.0000377187, True}, {25, 82, 7873, 5},
  {B cell receptor signaling pathway - Homo sapiens (human),
   {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05142 → {{0.0000150012, 0.000099902, True}, {25, 103, 7873, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04621 → {{0.0000152076, 0.000099902, True}, {25, 178, 7873, 6},
  {NOD-like receptor signaling pathway - Homo sapiens (human),
   {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04625 → {{0.0000157253, 0.000099902, True}, {25, 104, 7873, 5},
  {C-type lectin receptor signaling pathway - Homo sapiens (human),
   {{MALT1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}, path:hsa04010 →
 {{0.0000259458, 0.000147729, True}, {25, 295, 7873, 7}, {MAPK signaling pathway - Homo sapiens (human),
   {{TAB1}, {CHUK}, {MYD88}, {GADD45B}, {NFKB1}, {NFKB2}, {IRAK4}}}},
path:hsa05134 → {{0.0000259894, 0.000147729, True}, {25, 56, 7873, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04380 → {{0.0000429841, 0.000232114, True}, {25, 128, 7873, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000629652, 0.000323821, True}, {25, 70, 7873, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05133 → {{0.000086981, 0.000408432, True},
  {25, 76, 7873, 4}, {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05220 → {{0.000086981, 0.000408432, True}, {25, 76, 7873, 4},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
path:hsa05164 → {{0.000152329, 0.000685481, True}, {25, 167, 7873, 5},
  {Influenza A - Homo sapiens (human), {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.000190876, 0.000824586, True}, {25, 93, 7873, 4},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
path:hsa05152 → {{0.000210914, 0.000876104, True}, {25, 179, 7873, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05215 → {{0.000224582, 0.000898328, True}, {25, 97, 7873, 4},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}, {PLAU}}}},
path:hsa04660 → {{0.000282919, 0.00109126, True}, {25, 103, 7873, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000361486, 0.00134622, True}, {25, 201, 7873, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04668 → {{0.000389851, 0.00140347, True}, {25, 112, 7873, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04672 → {{0.000473279, 0.00164884, True}, {25, 49, 7873, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04137 → {{0.00108509, 0.00366217, True},
  {25, 65, 7873, 3}, {Mitophagy - animal - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05131 → {{0.00123718, 0.00404894, True}, {25, 68, 7873, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00129071, 0.00409989, True}, {25, 69, 7873, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00134568, 0.00415238, True}, {25, 70, 7873, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00146001, 0.00438004, True}, {25, 72, 7873, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
```

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```
  path:hsa05212 → {{0.0016427, 0.0047949, True}, {25, 75, 7873, 3},
    {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}}}},
  path:hsa05167 → {{0.00258637, 0.00716226, True}, {25, 186, 7873, 4},
    {Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human),
     {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05202 → {{0.00258637, 0.00716226, True},
    {25, 186, 7873, 4}, {Transcriptional misregulation in cancer - Homo sapiens (human),
     {{GADD45B}, {ATM}, {NFKB1}, {PLAU}}}},
  path:hsa04062 → {{0.00279404, 0.00754391, True}, {25, 190, 7873, 4},
    {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa04658 → {{0.0029483, 0.00776626, True}, {25, 92, 7873, 3},
    {Th1 and Th2 cell differentiation - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04657 → {{0.00304021, 0.0078177, True}, {25, 93, 7873, 3},
    {IL-17 signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa05168 → {{0.0036852, 0.00925585, True}, {25, 492, 7873, 6},
    {Herpes simplex virus 1 infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa01523 → {{0.00425473, 0.010056, True}, {25, 31, 7873, 2},
    {Antifolate resistance - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa03020 → {{0.00425473, 0.010056, True}, {25, 31, 7873, 2},
    {RNA polymerase - Homo sapiens (human), {{POLR3B}, {POLR3A}}}},
  path:hsa03008 → {{0.00428312, 0.010056, True}, {25, 105, 7873, 3},
    {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa04659 → {{0.00451611, 0.0103774, True}, {25, 107, 7873, 3},
    {Th17 cell differentiation - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04722 → {{0.00607598, 0.013671, True}, {25, 119, 7873, 3},
    {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04068 → {{0.00809109, 0.0178334, True}, {25, 132, 7873, 3},
    {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
  path:hsa05418 → {{0.00932162, 0.0201347, True}, {25, 139, 7873, 3},
    {Fluid shear stress and atherosclerosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {PIAS4}}}},
  path:hsa05160 → {{0.0125296, 0.0265332, True}, {25, 155, 7873, 3},
    {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04218 → {{0.0136471, 0.0277717, True}, {25, 160, 7873, 3},
    {Cellular senescence - Homo sapiens (human), {{GADD45B}, {ATM}, {NFKB1}}}},
  path:hsa04310 → {{0.0136471, 0.0277717, True}, {25, 160, 7873, 3},
    {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa00240 → {{0.0138859, 0.0277717, True}, {25, 57, 7873, 2},
    {Pyrimidine metabolism - Homo sapiens (human), {{NME1}, {CTPS1}}}},
  path:hsa05221 → {{0.0183406, 0.0360144, True}, {25, 66, 7873, 2},
    {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa04115 → {{0.0216033, 0.0416634, True}, {25, 72, 7873, 2},
    {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa05200 → {{0.0234256, 0.0443854, True}, {25, 530, 7873, 5},
    {Pathways in cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>|>
```

We can obtain the results for any of the data. Let's look at the top (lowest p-value) two results in both groups:

```
In[3]:= Query[All, {1, 2}]@analysisKEGGAssociation

Out[3]= <|Group1 → <|path:hsa05134 → {{0.00102, 0.0334234, True},
      {7, 56, 7873, 2}, {Legionellosis - Homo sapiens (human), {{NFKB2}, {PYCARD}}}},
    path:hsa05133 → {{0.00187169, 0.0334234, True}, {7, 76, 7873, 2},
      {Pertussis - Homo sapiens (human), {{NOS2}, {PYCARD}}}}|>,
  Group2 → <|path:hsa04064 → {{0., 0., True}, {25, 100, 7873, 21},
      {NF-kappa B signaling pathway - Homo sapiens (human), {{TAB1}, {TNFSF13B}, {MALT1},
        {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LTBR}, {LYN},
        {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
    path:hsa05235 → {{1.79087×10^-10, 9.67067×10^-9, True}, {25, 89, 7873, 8},
      {PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
       {{TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}}|>|>
```

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```
In[1]:= Needs["MathIOmica`"]
```

The data can be computed with or without a label. If labeled, the gene ID must be the first element for each ID provided. The data is in the form {ID,label}:

```
In[2]:= analysisKEGGLabel = KEGGAnalysis[{{"C6orf57", "Protein"}, {"CD46", "Protein"},
          {"DHX58", "Protein"}, {"HMGB3", "Protein"}, {"MAP3K5", "Protein"}, {"NFKB2", "Protein"},
          {"NOS2", "Protein"}, {"PYCARD", "Protein"}, {"PYDC1", "Protein"}, {"SSC5D", "Protein"}}]

Out[2]= <|path:hsa05134 → {{0.00102, 0.0334234, True}, {7, 56, 7873, 2},
          {Legionellosis - Homo sapiens (human), {{{NFKB2, Protein}}, {{PYCARD, Protein}}}}}},
        path:hsa05133 → {{0.00187169, 0.0334234, True}, {7, 76, 7873, 2},
          {Pertussis - Homo sapiens (human), {{{NOS2, Protein}}, {{PYCARD, Protein}}}}}},
        path:hsa05132 → {{0.00222823, 0.0334234, True}, {7, 83, 7873, 2},
          {Salmonella infection - Homo sapiens (human), {{{NOS2, Protein}}, {{PYCARD, Protein}}}}}},
        path:hsa04625 → {{0.00347585, 0.0391033, True}, {7, 104, 7873, 2},
          {C-type lectin receptor signaling pathway - Homo sapiens (human),
           {{{NFKB2, Protein}}, {{PYCARD, Protein}}}}}}|>
```

The same result is obtained if IDs are enclosed in list brackets:

```
In[3]:= KEGGAnalysis[{{"C6orf57"}, {"CD46"}, {"DHX58"}, {"HMGB3"},
          {"MAP3K5"}, {"NFKB2"}, {"NOS2"}, {"PYCARD"}, {"PYDC1"}, {"SSC5D"}}]

Out[3]= <|path:hsa05134 → {{0.00102, 0.0334234, True},
          {7, 56, 7873, 2}, {Legionellosis - Homo sapiens (human), {{{NFKB2}}, {{PYCARD}}}}}},
        path:hsa05133 → {{0.00187169, 0.0334234, True}, {7, 76, 7873, 2},
          {Pertussis - Homo sapiens (human), {{{NOS2}}, {{PYCARD}}}}}},
        path:hsa05132 → {{0.00222823, 0.0334234, True}, {7, 83, 7873, 2},
          {Salmonella infection - Homo sapiens (human), {{{NOS2}}, {{PYCARD}}}}}},
        path:hsa04625 → {{0.00347585, 0.0391033, True}, {7, 104, 7873, 2},
          {C-type lectin receptor signaling pathway - Homo sapiens (human), {{{NFKB2}}, {{PYCARD}}}}}}|>
```

The same result is obtained if IDs are input as strings:

```
In[4]:= KEGGAnalysis[{"C6orf57", "CD46", "DHX58", "HMGB3", "MAP3K5", "NFKB2", "NOS2", "PYCARD", "PYDC1", "SSC5D"}]

Out[4]= <|path:hsa05134 → {{0.00102, 0.0334234, True}, {7, 56, 7873, 2},
          {Legionellosis - Homo sapiens (human), {{NFKB2}, {PYCARD}}}}}, path:hsa05133 →
         {{0.00187169, 0.0334234, True}, {7, 76, 7873, 2}, {Pertussis - Homo sapiens (human), {{NOS2}, {PYCARD}}}}},
        path:hsa05132 → {{0.00222823, 0.0334234, True}, {7, 83, 7873, 2},
          {Salmonella infection - Homo sapiens (human), {{NOS2}, {PYCARD}}}}},
        path:hsa04625 → {{0.00347585, 0.0391033, True}, {7, 104, 7873, 2},
          {C-type lectin receptor signaling pathway - Homo sapiens (human), {{NFKB2}, {PYCARD}}}}}|>
```

```
In[1]:= Needs["MathIOmica`"]
```

The data can be mixed, e.g. proteins and RNA with different labels:

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```
In[2]:= analysisKEGGMixed = KEGGAnalysis[{{"C6orf57", "Protein"}, {"CD46", "Protein"}, {"DHX58", "Protein"},
          {"HMGB3", "RNA"}, {"HMGB3", "Protein"}, {"MAP3K5", "Protein"}, {"NFKB2", "RNA"}, {"NFKB2", "Protein"},
          {"NOS2", "RNA"}, {"PYCARD", "RNA"}, {"PYDC1", "Protein"}, {"SSC5D", "Protein"}}]

Out[2]= <|path:hsa05134 → {{0.00102, 0.0334234, True}, {7, 56, 7873, 2},
          {Legionellosis - Homo sapiens (human), {{{NFKB2, Protein}, {NFKB2, RNA}}, {{PYCARD, RNA}}}}}},
        path:hsa05133 → {{0.00187169, 0.0334234, True}, {7, 76, 7873, 2},
          {Pertussis - Homo sapiens (human), {{{NOS2, RNA}}, {{PYCARD, RNA}}}}}},
        path:hsa05132 → {{0.00222823, 0.0334234, True}, {7, 83, 7873, 2},
          {Salmonella infection - Homo sapiens (human), {{{NOS2, RNA}}, {{PYCARD, RNA}}}}}},
        path:hsa04625 → {{0.00347585, 0.0391033, True}, {7, 104, 7873, 2},
          {C-type lectin receptor signaling pathway - Homo sapiens (human),
           {{{NFKB2, Protein}, {NFKB2, RNA}}, {{PYCARD, RNA}}}}}}|>
```

The data in this case treated as originating from a single population. Protein and RNA labeled data for the same identifier are treated as equivalent.

We can instead treat the data as different by setting the `MultipleList` and MultipleListCorrection options:

```
In[3]:= analysisKEGGMixedMulti =
         KEGGAnalysis[{{"C6orf57", "Protein"}, {"CD46", "Protein"}, {"DHX58", "Protein"}, {"HMGB3", "RNA"},
           {"HMGB3", "Protein"}, {"MAP3K5", "Protein"}, {"NFKB2", "RNA"}, {"NFKB2", "Protein"},
           {"NOS2", "RNA"}, {"PYCARD", "RNA"}, {"PYDC1", "Protein"}, {"SSC5D", "Protein"}},
          MultipleList → True, MultipleListCorrection → Automatic]

Out[3]= <|path:hsa05134 → {{0.0000191159, 0.000860216, True}, {8, 112, 15746, 3},
          {Legionellosis - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}, {{PYCARD, RNA}}}}}},
        path:hsa04625 → {{0.000121165, 0.0027262, True}, {8, 208, 15746, 3},
          {C-type lectin receptor signaling pathway - Homo sapiens (human),
           {{{NFKB2, RNA}}, {{NFKB2, Protein}}, {{PYCARD, RNA}}}}}},
        path:hsa05133 → {{0.00249513, 0.0267029, True}, {8, 152, 15746, 2},
          {Pertussis - Homo sapiens (human), {{{NOS2, RNA}}, {{PYCARD, RNA}}}}}}, path:hsa04010 →
         {{0.00254536, 0.0267029, True}, {8, 590, 15746, 3}, {MAPK signaling pathway - Homo sapiens (human),
           {{{MAP3K5, Protein}}, {{NFKB2, RNA}}, {{NFKB2, Protein}}}}}},
        path:hsa05132 → {{0.00296699, 0.0267029, True}, {8, 166, 15746, 2},
          {Salmonella infection - Homo sapiens (human), {{{NOS2, RNA}}, {{PYCARD, RNA}}}}}},
        path:hsa04064 → {{0.0042741, 0.0320558, True}, {8, 200, 15746, 2},
          {NF-kappa B signaling pathway - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}}}}},
        path:hsa04380 → {{0.00691099, 0.0444278, True}, {8, 256, 15746, 2},
          {Osteoclast differentiation - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}}}}}|>
```

```
In[1]:= Needs["MathIOmica`"]
```

Let's consider an example from real protein data. We will use already clustered data, from the MathIOmica proteomics examples. Let's import the data, which should be located at:

```
In[2]:= proteinExampleClusterFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "proteinClusteringExample"}

Out[2]= /Users/george/Library/Mathematica/Applications/MathIOmica/MathIOmicaData/ExampleData/
          proteinClusteringExample
```

We can now get the data :

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In[3]:=
```
proteinExampleClusters = Get[proteinExampleClusterFile]
```

Out[3]=
```
<|SpikeMax → <| ··· 1 ··· |>, ··· 4 ···, f7 → <|Cluster → Cluster[ ··· 1 ··· ],
   InitialSplitCluster → {Cluster[Cluster[ ··· 1 ··· ], Cluster[ ··· 1 ··· ], 0.362674, 11, 6], ··· 1 ···},
   ··· 2 ···, Data → { ··· 1 ··· }, GroupAssociations → <| ··· 1 ··· |> |> |>
```

large output | show less | show more | show all | set size limit...

We can calculate the KEGGAnalysis for each group in each class:

In[4]:=
```
enrichmentKEGGprotein = KEGGAnalysis[proteinExampleClusters]
```

Out[4]=
```
<|SpikeMax → <|G1S1 → <|path:hsa03050 →
      {{0.0000278892, 0.000920344, True}, {11, 45, 7873, 3}, {Proteasome - Homo sapiens (human),
        {{{P60900, Protein}}, {{P25788, Protein}}, {{P35998, Protein}}}}}}|>,
   G1S2 → <| |>, G2S1 → <| |>, G2S2 → <|path:hsa00020 → {{6.38195×10^-7, 0.0000274424, True},
      {19, 30, 7873, 4}, {Citrate cycle (TCA cycle) - Homo sapiens (human),
        {{{Q96I99, Protein}}, {{P10515, Protein}}, {{Q02218, Protein}}, {{Q99798, Protein}}}}}},
     path:hsa01200 → {{6.54994×10^-6, 0.000140824, True}, {19, 117, 7873, 5},
      {Carbon metabolism - Homo sapiens (human), {{{Q96I99, Protein}}, {{P10515, Protein}},
        {{Q02218, Protein}}, {{P40939, Protein}}, {{Q99798, Protein}}}}}}, path:hsa01100 →
      {{0.0000179583, 0.000257402, True}, {19, 1433, 7873, 12}, {Metabolic pathways - Homo sapiens (human),
        {{{P22695, Protein}}, {{Q96I99, Protein}}, {{P30519, Protein}}, {{P20674, Protein}},
        {{P10515, Protein}}, {{Q02218, Protein}}, {{P40939, Protein}}, {{P22307, Protein}},
        {{Q9HAN9, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}, {{Q99798, Protein}}}}}},
     path:hsa00190 → {{0.000247782, 0.00266366, True}, {19, 133, 7873, 4},
      {Oxidative phosphorylation - Homo sapiens (human),
        {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}},
     path:hsa05012 → {{0.000318481, 0.00273894, True}, {19, 142, 7873, 4},
      {Parkinson disease - Homo sapiens (human), {{{P22695, Protein}}},
        {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}}, path:hsa05010 →
      {{0.000645264, 0.00462439, True}, {19, 171, 7873, 4}, {Alzheimer disease - Homo sapiens (human),
        {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}},
     path:hsa05016 → {{0.00101639, 0.00624352, True}, {19, 193, 7873, 4},
      {Huntington disease - Homo sapiens (human), {{{P22695, Protein}}},
        {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}}, path:hsa04714 →
      {{0.00197759, 0.0106295, True}, {19, 231, 7873, 4}, {Thermogenesis - Homo sapiens (human),
        {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}, {{P06576, Protein}}}}}},
     path:hsa00640 → {{0.00295641, 0.0141251, True}, {19, 34, 7873, 2},
      {Propanoate metabolism - Homo sapiens (human), {{{Q96I99, Protein}}, {{P40939, Protein}}}}}},
     path:hsa00071 → {{0.00491423, 0.0201455, True}, {19, 44, 7873, 2},
      {Fatty acid degradation - Homo sapiens (human), {{{P42126, Protein}}, {{P40939, Protein}}}}}},
     path:hsa04932 → {{0.0051535, 0.0201455, True}, {19, 149, 7873, 3},
      {Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
        {{{P22695, Protein}}, {{P20674, Protein}}, {{P17568, Protein}}}}}},
     path:hsa05134 → {{0.00786334, 0.0269167, True}, {19, 56, 7873, 2},
      {Legionellosis - Homo sapiens (human), {{{P10809, Protein}}, {{O75396, Protein}}}}}},
     path:hsa01212 → {{0.0081376, 0.0269167, True}, {19, 57, 7873, 2},
      {Fatty acid metabolism - Homo sapiens (human), {{{P40939, Protein}}, {{P22307, Protein}}}}}},
     path:hsa03018 → {{0.0152219, 0.0467529, True}, {19, 79, 7873, 2},
      {RNA degradation - Homo sapiens (human), {{{P38646, Protein}}, {{P10809, Protein}}}}}}|>,
   G3S1 → <|path:hsa03018 → {{0.0100343, 0.0100343, True}, {1, 79, 7873, 1},
      {RNA degradation - Homo sapiens (human), {{{O75175, Protein}}}}}}|>|>,
  SpikeMin → <|G1S1 → <| |>, G1S2 → <| |>, G1S3 → <| |>|>,
  f1 →
   <|G1S1 → <| |>,
    G1S2 → <|path:hsa05416 → {{0.0151848, 0.0326546, True}, {2, 60, 7873, 1},
      {Viral myocarditis - Homo sapiens (human), {{{P08174, Protein}}}}}},
     path:hsa04610 → {{0.0199692, 0.0326546, True}, {2, 79, 7873, 1},
      {Complement and coagulation cascades - Homo sapiens (human), {{{P08174, Protein}}}}}},
```

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```
    path:hsa04640 → {{0.0244909, 0.0326546, True}, {2, 97, 7873, 1},
      {Hematopoietic cell lineage - Homo sapiens (human), {{{P08174, Protein}}}}},
    path:hsa04360 → {{0.0454542, 0.0454542, True}, {2, 181, 7873, 1},
      {Axon guidance - Homo sapiens (human), {{{O15031, Protein}}}}}|>, G2S1 → <| |>,
  G2S2 → <| |>, G3S1 → <|path:hsa03050 → {{0.000658782, 0.015152, True}, {7, 45, 7873, 2},
      {Proteasome - Homo sapiens (human), {{{P40306, Protein}}}, {{P55036, Protein}}}}}|>,
  G3S2 → <|path:hsa01200 → {{0.00212657, 0.0255189, True}, {5, 117, 7873, 2},
      {Carbon metabolism - Homo sapiens (human), {{{P23368, Protein}}}, {{Q96AT9, Protein}}}}}|>|>,
f5 → <|G1S1 → <|path:hsa04960 → {{0.00469961, 0.0266677, True}, {1, 37, 7873, 1},
      {Aldosterone-regulated sodium reabsorption - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa04973 → {{0.00558872, 0.0266677, True}, {1, 44, 7873, 1},
      {Carbohydrate digestion and absorption - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa04930 → {{0.00584275, 0.0266677, True}, {1, 46, 7873, 1},
      {Type II diabetes mellitus - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa04923 → {{0.0069859, 0.0266677, True}, {1, 55, 7873, 1},
      {Regulation of lipolysis in adipocytes - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa05213 → {{0.00736695, 0.0266677, True}, {1, 58, 7873, 1},
      {Endometrial cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa04370 → {{0.00749397, 0.0266677, True}, {1, 59, 7873, 1},
      {VEGF signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa04213 → {{0.00787502, 0.0266677, True}, {1, 62, 7873, 1},
      {Longevity regulating pathway - multiple species - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa05221 → {{0.00838308, 0.0266677, True}, {1, 66, 7873, 1},
      {Acute myeloid leukemia - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa05223 → {{0.00838308, 0.0266677, True}, {1, 66, 7873, 1},
      {Non-small cell lung cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa04664 → {{0.00863711, 0.0266677, True}, {1, 68, 7873, 1},
      {Fc epsilon RI signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa05211 → {{0.00876413, 0.0266677, True}, {1, 69, 7873, 1},
      {Renal cell carcinoma - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa05230 → {{0.00876413, 0.0266677, True}, {1, 69, 7873, 1},
      {Central carbon metabolism in cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa04917 → {{0.00889115, 0.0266677, True}, {1, 70, 7873, 1},
      {Prolactin signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa05218 → {{0.00914518, 0.0266677, True}, {1, 72, 7873, 1},
      {Melanoma - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa01524 → {{0.0092722, 0.0266677, True}, {1, 73, 7873, 1},
      {Platinum drug resistance - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa00562 → {{0.00939921, 0.0266677, True}, {1, 74, 7873, 1},
      {Inositol phosphate metabolism - Homo sapiens (human), {{{O00329, Protein}}}}},
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      {Bacterial invasion of epithelial cells - Homo sapiens (human), {{{O00329, Protein}}}}},
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    path:hsa05214 → {{0.00952623, 0.0266677, True}, {1, 75, 7873, 1},
      {Glioma - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa05220 → {{0.00965325, 0.0266677, True}, {1, 76, 7873, 1},
      {Chronic myeloid leukemia - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa01521 → {{0.0100343, 0.0266677, True}, {1, 79, 7873, 1},
      {EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human), {{{O00329, Protein}}}}},
    path:hsa04662 → {{0.0104153, 0.0266677, True}, {1, 82, 7873, 1},
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    path:hsa04012 → {{0.0107964, 0.0266677, True}, {1, 85, 7873, 1},
      {ErbB signaling pathway - Homo sapiens (human), {{{O00329, Protein}}}}},
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    path:hsa04211 → {{0.0113045, 0.0266677, True}, {1, 89, 7873, 1},
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    path:hsa05235 → {{0.0113045, 0.0266677, True}, {1, 89, 7873, 1},
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    path:hsa04666 → {{0.0119395, 0.0266677, True}, {1, 94, 7873, 1},
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    path:hsa05146 → {{0.0120666, 0.0266677, True}, {1, 95, 7873, 1},
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  {Amoebiasis - Homo sapiens (human), {{{O00329, Protein}}}}},
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path:hsa05231 → {{0.0125746, 0.0266677, True}, {1, 99, 7873, 1},
  {Choline metabolism in cancer - Homo sapiens (human), {{{O00329, Protein}}}}},
path:hsa04750 → {{0.0127016, 0.0266677, True}, {1, 100, 7873, 1},
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path:hsa04625 → {{0.0132097, 0.0266677, True}, {1, 104, 7873, 1},
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path:hsa04725 → {{0.0142258, 0.0266677, True}, {1, 112, 7873, 1},
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      {Human papillomavirus infection - Homo sapiens (human), {{{O00329, Protein}}}}}},
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    path:hsa04144 → {{0.030992, 0.030992, True}, {1, 244, 7873, 1},
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    path:hsa04721 → {{0.0197176, 0.0332332, True}, {2, 78, 7873, 1},
      {Synaptic vesicle cycle - Homo sapiens (human), {{{P50570, Protein}}}}},
    path:hsa04666 → {{0.023738, 0.0332332, True}, {2, 94, 7873, 1},
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  G1S2 → 〈|path:hsa03010 → {{7.49039×10^-8, 3.9699×10^-6, True}, {13, 153, 7873, 6},
      {Ribosome - Homo sapiens (human), {{{Q02543, Protein}}, {{P62888, Protein}},
        {{P27635, Protein}}, {{P61353, Protein}}, {{P26373, Protein}}, {{P35268, Protein}}}}}|〉,
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      {Complement and coagulation cascades - Homo sapiens (human), {{{P13987, Protein}}}}},
    path:hsa04640 → {{0.0244909, 0.0293891, True}, {2, 97, 7873, 1},
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  G1S2 → 〈|path:hsa00512 → {{0.00786001, 0.02358, True}, {2, 31, 7873, 1},
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    path:hsa04713 → {{0.0123206, 0.0331513, True}, {1, 97, 7873, 1},
      {Circadian entrainment - Homo sapiens (human), {{{P62879, Protein}}}}},
    path:hsa04725 → {{0.0142258, 0.0331513, True}, {1, 112, 7873, 1},
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    path:hsa04724 → {{0.0144799, 0.0331513, True}, {1, 114, 7873, 1},
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  {Glutamatergic synapse - Homo sapiens (human), {{{P62879, Protein}}}}},
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  {Relaxin signaling pathway - Homo sapiens (human), {{{P62879, Protein}}}}},
path:hsa04728 → {{0.0166391, 0.0331513, True}, {1, 131, 7873, 1},
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path:hsa04371 → {{0.0174012, 0.0331513, True}, {1, 137, 7873, 1},
  {Apelin signaling pathway - Homo sapiens (human), {{{P62879, Protein}}}}},
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  {Alcoholism - Homo sapiens (human), {{{P62879, Protein}}}}},
path:hsa05167 → {{0.023625, 0.0331513, True}, {1, 186, 7873, 1},
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path:hsa04062 → {{0.0241331, 0.0331513, True}, {1, 190, 7873, 1},
  {Chemokine signaling pathway - Homo sapiens (human), {{{P62879, Protein}}}}},
path:hsa05170 → {{0.0269275, 0.0331513, True}, {1, 212, 7873, 1},
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path:hsa05163 → {{0.0285787, 0.0331513, True}, {1, 225, 7873, 1},
  {Human cytomegalovirus infection - Homo sapiens (human), {{{P62879, Protein}}}}},
path:hsa04014 → {{0.0294678, 0.0331513, True}, {1, 232, 7873, 1},
  {Ras signaling pathway - Homo sapiens (human), {{{P62879, Protein}}}}},
path:hsa04151 → {{0.0449638, 0.0476087, True}, {1, 354, 7873, 1},
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The data has multiple clusters:

In[5]:=
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Query[All,Keys]@enrichmentKEGGprotein
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Out[5]=
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<|SpikeMax → {G1S1, G1S2, G2S1, G2S2, G3S1},
 SpikeMin → {G1S1, G1S2, G1S3}, f1 → {G1S1, G1S2, G2S1, G2S2, G3S1, G3S2},
 f5 → {G1S1, G1S2, G2S1, G2S2}, f6 → {G1S1, G1S2, G2S1}, f7 → {G1S1, G1S2, G2S1}|>
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Let's look at the top category in each group in each class:

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In[6]:=
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Query[All, All, {1}]@enrichmentKEGGprotein
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Out[6]=
```
⟨|SpikeMax → ⟨|G1S1 → ⟨|path:hsa03050 →
      {{0.0000278892, 0.000920344, True}, {11, 45, 7873, 3}, {Proteasome - Homo sapiens (human),
        {{{P60900, Protein}}, {{P25788, Protein}}, {{P35998, Protein}}}}}}|⟩,
    G1S2 → Missing[PartAbsent, {1}], G2S1 → Missing[PartAbsent, {1}],
    G2S2 → ⟨|path:hsa00020 → {{6.38195×10^-7, 0.0000274424, True},
      {19, 30, 7873, 4}, {Citrate cycle (TCA cycle) - Homo sapiens (human),
        {{{Q96I99, Protein}}, {{P10515, Protein}}, {{Q02218, Protein}}, {{Q99798, Protein}}}}}}|⟩,
    G3S1 → ⟨|path:hsa03018 → {{0.0100343, 0.0100343, True}, {1, 79, 7873, 1},
      {RNA degradation - Homo sapiens (human), {{{O75175, Protein}}}}}}|⟩|⟩,
  SpikeMin → ⟨|G1S1 → Missing[PartAbsent, {1}], G1S2 → Missing[PartAbsent, {1}],
    G1S3 → Missing[PartAbsent, {1}]|⟩,
  f1 → ⟨|G1S1 → Missing[PartAbsent, {1}], G1S2 → ⟨|path:hsa05416 → {{0.0151848, 0.0326546, True},
      {2, 60, 7873, 1}, {Viral myocarditis - Homo sapiens (human), {{{P08174, Protein}}}}}}|⟩,
    G2S1 → Missing[PartAbsent, {1}], G2S2 → Missing[PartAbsent, {1}],
    G3S1 → ⟨|path:hsa03050 → {{0.000658782, 0.015152, True}, {7, 45, 7873, 2},
      {Proteasome - Homo sapiens (human), {{{P40306, Protein}}, {{P55036, Protein}}}}}}|⟩,
    G3S2 → ⟨|path:hsa01200 → {{0.00212657, 0.0255189, True}, {5, 117, 7873, 2},
      {Carbon metabolism - Homo sapiens (human), {{{P23368, Protein}}, {{Q96AT9, Protein}}}}}}|⟩|⟩,
  f5 → ⟨|G1S1 → ⟨|path:hsa04960 → {{0.00469961, 0.0266677, True}, {1, 37, 7873, 1},
      {Aldosterone-regulated sodium reabsorption - Homo sapiens (human), {{{O00329, Protein}}}}}}|⟩,
    G1S2 → ⟨|path:hsa04110 → {{0.01575, 0.01575, True}, {1, 124, 7873, 1},
      {Cell cycle - Homo sapiens (human), {{{Q8N3U4, Protein}}}}}}|⟩,
    G2S1 → ⟨|path:hsa04961 → {{0.00635082, 0.0198146, True}, {1, 50, 7873, 1},
      {Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
        {{{O94973, Protein}}}}}}|⟩, G2S2 → Missing[PartAbsent, {1}]|⟩,
  f6 → ⟨|G1S1 → ⟨|path:hsa04144 → {{0.000956689, 0.00669682, True}, {2, 244, 7873, 2},
      {Endocytosis - Homo sapiens (human), {{{Q9Y371, Protein}}, {{P50570, Protein}}}}}}|⟩,
    G1S2 → ⟨|path:hsa03010 → {{7.49039×10^-8, 3.9699×10^-6, True}, {13, 153, 7873, 6},
      {Ribosome - Homo sapiens (human), {{{Q02543, Protein}}, {{P62888, Protein}},
        {{P27635, Protein}}, {{P61353, Protein}}, {{P26373, Protein}}, {{P35268, Protein}}}}}}|⟩,
    G2S1 → ⟨|path:hsa04966 → {{0.00342944, 0.023117, True}, {1, 27, 7873, 1},
      {Collecting duct acid secretion - Homo sapiens (human), {{{Q9Y5K8, Protein}}}}}}|⟩|⟩,
  f7 → ⟨|G1S1 → ⟨|path:hsa00052 → {{0.00786001, 0.0293891, True}, {2, 31, 7873, 1},
      {Galactose metabolism - Homo sapiens (human), {{{P07902, Protein}}}}}}|⟩,
    G1S2 → ⟨|path:hsa00512 → {{0.00786001, 0.02358, True}, {2, 31, 7873, 1},
      {Mucin type O-glycan biosynthesis - Homo sapiens (human), {{{Q10471, Protein}}}}}}|⟩,
    G2S1 → ⟨|path:hsa04727 → {{0.0113045, 0.0331513, True}, {1, 89, 7873, 1},
      {GABAergic synapse - Homo sapiens (human), {{{P62879, Protein}}}}}}|⟩|⟩|⟩
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can carry out a "Molecular" analysis for compound data. We consider the following metabolomics data, which has labels "Meta" and additional mass and retention time information in the form {`identifier, mass, retention time, label`}:

In[2]:=
```
compoundsExample =
  {{"cpd:C19691", 325.2075`, 10.677681`, "Meta"}, {"cpd:C17905", 594.2002`, 8.727458`, "Meta"},
   {"cpd:C09921", 204.0784`, 12.3909445`, "Meta"}, {"cpd:C18218", 272.2356`, 13.473582`, "Meta"},
   {"cpd:C14169", 235.1573`, 12.267084`, "Meta"}, {"cpd:C14245", 262.2296`, 13.545572`, "Meta"},
   {"cpd:C09137", 352.2615`, 14.0554285`, "Meta"}, {"cpd:C09674", 296.1624`, 12.147417`, "Meta"},
   {"cpd:C00449", 276.1334`, 11.004139`, "Meta"}, {"cpd:C02999", 364.1497`, 12.147243`, "Meta"},
   {"cpd:C07915", 309.194`, 7.3625283`, "Meta"}, {"cpd:C08760", 496.2309`, 8.7241125`, "Meta"},
   {"cpd:C14549", 276.0972`, 11.078914`, "Meta"}, {"cpd:C20533", 601.3378`, 12.75722`, "Meta"},
   {"cpd:C20790", 212.1051`, 7.127666`, "Meta"}, {"cpd:C09137", 352.2613`, 12.869867`, "Meta"},
   {"cpd:C17648", 400.2085`, 10.843841`, "Meta"}, {"cpd:C07807", 240.1471`, 0.48564285`, "Meta"},
   {"cpd:C08564", 324.0948`, 10.281`, "Meta"}, {"cpd:C19426", 338.2818`, 13.758765`, "Meta"},
   {"cpd:C02943", 468.3218`, 14.263261`, "Meta"}, {"cpd:C04882", 1193.342`, 14.707576`, "Meta"}};
```

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```
In[3]:= KEGGAnalysis[compoundsExample, FilterSignificant → True, AnalysisType → "Molecular"]
Out[3]= <|path:map00300 → {{0.00020774, 0.00186966, True}, {4, 35, 5841, 2}, {Lysine biosynthesis,
    {{{cpd:C00449, 276.133, 11.0041, Meta}}, {{cpd:C04882, 1193.34, 14.7076, Meta}}}}}|>
```

```
In[1]:= Needs["MathIOmica`"]
```

We can carry out multiomics data analysis. We consider the following simple example:

```
In[2]:= multiOmicsData = {{"C6orf57", "Protein"}, {"CD46", "Protein"}, {"DHX58", "Protein"}, {"HMGB3", "RNA"},
   {"HMGB3", "Protein"}, {"MAP3K5", "Protein"}, {"NFKB2", "RNA"}, {"NFKB2", "Protein"},
   {"NOS2", "RNA"}, {"PYCARD", "RNA"}, {"PYDC1", "Protein"}, {"SSC5D", "Protein"},
   {"cpd:C19691", 325.2075`, 10.677681`, "Meta"}, {"cpd:C17905", 594.2002`, 8.727458`, "Meta"},
   {"cpd:C09921", 204.0784`, 12.3909445`, "Meta"}, {"cpd:C18218", 272.2356`, 13.473582`, "Meta"},
   {"cpd:C14169", 235.1573`, 12.267084`, "Meta"}, {"cpd:C14245", 262.2296`, 13.545572`, "Meta"},
   {"cpd:C09137", 352.2615`, 14.0554285`, "Meta"}, {"cpd:C09674", 296.1624`, 12.147417`, "Meta"},
   {"cpd:C00449", 276.1334`, 11.004139`, "Meta"}, {"cpd:C02999", 364.1497`, 12.147243`, "Meta"},
   {"cpd:C07915", 309.194`, 7.3625283`, "Meta"}, {"cpd:C08760", 496.2309`, 8.7241125`, "Meta"},
   {"cpd:C14549", 276.0972`, 11.078914`, "Meta"}, {"cpd:C20533", 601.3378`, 12.75722`, "Meta"},
   {"cpd:C20790", 212.1051`, 7.127666`, "Meta"}, {"cpd:C09137", 352.2613`, 12.869867`, "Meta"},
   {"cpd:C17648", 400.2085`, 10.843841`, "Meta"}, {"cpd:C07807", 240.1471`, 0.48564285`, "Meta"},
   {"cpd:C08564", 324.0948`, 10.281`, "Meta"}, {"cpd:C19426", 338.2818`, 13.758765`, "Meta"},
   {"cpd:C02943", 468.3218`, 14.263261`, "Meta"}, {"cpd:C04882", 1193.342`, 14.707576`, "Meta"}};
```

We can carry out "Genomic" and "Molecular" analysis concurrently by setting `AnalysisType → All`:

```
In[3]:= KEGGAnalysis[multiOmicsData, AnalysisType → All, MultipleList → True, MultipleListCorrection → Automatic]
Out[3]= <|Molecular → <|path:map00300 → {{0.00020774, 0.00186966, True}, {4, 35, 5841, 2}, {Lysine biosynthesis,
        {{{cpd:C00449, 276.133, 11.0041, Meta}}, {{cpd:C04882, 1193.34, 14.7076, Meta}}}}}|>,
  Genomic → <|path:hsa05134 → {{0.0000192837, 0.000867768, True}, {8, 168, 23619, 3},
      {Legionellosis - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}, {{PYCARD, RNA}}}}}},
    path:hsa04625 → {{0.000121716, 0.00273861, True}, {8, 312, 23619, 3},
      {C-type lectin receptor signaling pathway - Homo sapiens (human),
       {{{NFKB2, RNA}}, {{NFKB2, Protein}}, {{PYCARD, RNA}}}}}},
    path:hsa05133 → {{0.00250017, 0.0267518, True}, {8, 228, 23619, 2},
      {Pertussis - Homo sapiens (human), {{{NOS2, RNA}}, {{PYCARD, RNA}}}}}}, path:hsa04010 →
     {{0.00254894, 0.0267518, True}, {8, 885, 23619, 3}, {MAPK signaling pathway - Homo sapiens (human),
       {{{MAP3K5, Protein}}, {{NFKB2, RNA}}, {{NFKB2, Protein}}}}}},
    path:hsa05132 → {{0.00297243, 0.0267518, True}, {8, 249, 23619, 2},
      {Salmonella infection - Homo sapiens (human), {{{NOS2, RNA}}, {{PYCARD, RNA}}}}}},
    path:hsa04064 → {{0.00428046, 0.0321034, True}, {8, 300, 23619, 2},
      {NF-kappa B signaling pathway - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}}}}},
    path:hsa04380 → {{0.00691874, 0.0444776, True}, {8, 384, 23619, 2},
      {Osteoclast differentiation - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}}}}}|>|>
```

Options (34)

AdditionalFilter (2)

```
In[1]:= Needs["MathIOmica`"]
```

AdditionalFilter provides additional filtering that may be applied to the standard output structure to be returned. This is typically implemented by a Select operator form statement.

Let's do a KEGG analysis for a group of genes, annotated with their "Gene Symbol":

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```
In[2]:= keggExample1 = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C",
          "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1",
          "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"}];
```

We can obtain the first 5 results for the data:

```
In[3]:= keggExample1[[1 ;; 5]]

Out[3]= ⟨|path:hsa04064 → {{3.27957×10^-37, 2.62366×10^-35, True},
          {25, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
           {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
            {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
        path:hsa05169 → {{2.69713×10^-11, 1.07885×10^-9, True}, {25, 204, 7086, 11},
          {Epstein-Barr virus infection - Homo sapiens (human), {{TAB1}, {CHUK}, {CSNK2A1},
           {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
        path:hsa05162 → {{1.23085×10^-8, 3.28226×10^-7, True}, {25, 136, 7086, 8}, {Measles - Homo sapiens (human),
           {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
        path:hsa04620 → {{5.28996×10^-8, 1.05799×10^-6, True}, {25, 106, 7086, 7},
          {Toll-like receptor signaling pathway - Homo sapiens (human),
           {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
         {{1.43121×10^-7, 2.28994×10^-6, True}, {25, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
           {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}}|⟩
```

Now let us apply a filter, to only select results for which "NFKB2" is included. In the output this would mean checking for membership in the 3rd list, 2nd sublist:

```
In[4]:= keggExample1Filtered =
         KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
           "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU",
           "POLR3B", "NME1", "CTPS1", "POLR3A"}, AdditionalFilter → Select[MemberQ[#[[3, 2]], {"NFKB2"}] &]]

Out[4]= ⟨|path:hsa04064 → {{3.27957×10^-37, 2.62366×10^-35, True},
          {25, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
           {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
            {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
        path:hsa05169 → {{2.69713×10^-11, 1.07885×10^-9, True}, {25, 204, 7086, 11},
          {Epstein-Barr virus infection - Homo sapiens (human), {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2},
           {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {POLR3B}, {POLR3A}}}}, path:hsa05166 →
         {{0.0000219498, 0.000159635, True}, {25, 259, 7086, 7}, {HTLV-I infection - Homo sapiens (human),
           {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
        path:hsa05134 → {{0.0000364135, 0.000224083, True}, {25, 55, 7086, 4},
          {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
        path:hsa04380 → {{0.0000818726, 0.000421518, True}, {25, 132, 7086, 5},
          {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
        path:hsa05203 → {{0.00063924, 0.00222344, True}, {25, 205, 7086, 5},
          {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
        path:hsa04010 → {{0.00170641, 0.00519202, True}, {25, 255, 7086, 5},
          {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}}|⟩
```

```
In[1]:= Needs["MathIOmica`"]
```

Now we apply a filter to only select results for which the pathway text includes the term "carcinogenesis". In the output this would mean checking for this pattern in the in the 3rd list, 1st sublist:

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```
In[2]:= keggExample1FilteredText =
         KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
           "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
           "NFKBIA", "IRAK4", "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"},
          AdditionalFilter → Select[StringMatchQ[#[[3, 1]], ___ ~~ "carcinogenesis" ~~ ___] &]]

Out[2]= <|path:hsa05203 → {{0.00063924, 0.00222344, True}, {25, 205, 7086, 5},
           {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

AnalysisType (3)

```
In[1]:= Needs["MathIOmica`"]
```

AnalysisType provides a selection for the type of analysis to perform. "Genomic" analysis (default) uses gene identifier based analysis. "Molecular" analysis uses molecular analysis. Setting the option to All carries out all possible analysis types for the input data.

```
In[2]:= analysisKEGGGenomic = KEGGAnalysis[<|
           "Group1" → {"C6orf57", "CD46", "DHX58", "HMGB3", "MAP3K5", "NFKB2", "NOS2", "PYCARD", "PYDC1", "SSC5D"},
           "Group2" → {"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
             "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA",
             "IRAK4", "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"}|>, AnalysisType → "Genomic"]

Out[2]= <|Group1 → <|path:hsa05134 → {{0.00121168, 0.0234184, True},
             {7, 55, 7086, 2}, {Legionellosis - Homo sapiens (human), {{NFKB2}, {PYCARD}}}},
           path:hsa04621 → {{0.00130102, 0.0234184, True}, {7, 57, 7086, 2},
             {NOD-like receptor signaling pathway - Homo sapiens (human), {{PYCARD}, {PYDC1}}}},
           path:hsa05133 → {{0.00224298, 0.0264506, True}, {7, 75, 7086, 2},
             {Pertussis - Homo sapiens (human), {{NOS2}, {PYCARD}}}},
           path:hsa05132 → {{0.00293895, 0.0264506, True}, {7, 86, 7086, 2},
             {Salmonella infection - Homo sapiens (human), {{NOS2}, {PYCARD}}}}|>,
         Group2 → <|path:hsa04064 → {{3.27957×10^-37, 2.62366×10^-35, True}, {25, 93, 7086, 21},
             {NF-kappa B signaling pathway - Homo sapiens (human),
              {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
               {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
           path:hsa05169 → {{2.69713×10^-11, 1.07885×10^-9, True}, {25, 204, 7086, 11},
             {Epstein-Barr virus infection - Homo sapiens (human), {{TAB1}, {CHUK}, {CSNK2A1},
               {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
           path:hsa05162 → {{1.23085×10^-8, 3.28226×10^-7, True}, {25, 136, 7086, 8}, {Measles - Homo sapiens (human),
              {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
           path:hsa04620 → {{5.28996×10^-8, 1.05799×10^-6, True}, {25, 106, 7086, 7},
             {Toll-like receptor signaling pathway - Homo sapiens (human),
              {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
           path:hsa05168 → {{1.43121×10^-7, 2.28994×10^-6, True}, {25, 186, 7086, 8},
             {Herpes simplex infection - Homo sapiens (human),
              {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
           path:hsa04623 → {{2.37065×10^-6, 0.0000308255, True}, {25, 64, 7086, 5},
             {Cytosolic DNA-sensing pathway - Homo sapiens (human),
              {{CHUK}, {NFKB1}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
           path:hsa05145 → {{2.69723×10^-6, 0.0000308255, True}, {25, 119, 7086, 6},
             {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
           path:hsa04662 → {{4.57186×10^-6, 0.0000434807, True}, {25, 73, 7086, 5},
             {B cell receptor signaling pathway - Homo sapiens (human),
              {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
           path:hsa05140 → {{4.89158×10^-6, 0.0000434807, True}, {25, 74, 7086, 5},
             {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
           path:hsa04210 → {{6.94486×10^-6, 0.0000555589, True}, {25, 140, 7086, 6},
             {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
           path:hsa05166 → {{0.0000219498, 0.000159635, True}, {25, 259, 7086, 7},
             {HTLV-I infection - Homo sapiens (human),
```

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```
    {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05142 → {{0.0000260113, 0.000173409, True}, {25, 104, 7086, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05134 → {{0.0000364135, 0.000224083, True}, {25, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{0.0000419741, 0.000239852, True}, {25, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000818726, 0.000421518, True}, {25, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000843036, 0.000421518, True}, {25, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05133 → {{0.000123744, 0.000582327, True},
  {25, 75, 7086, 4}, {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05161 → {{0.000132079, 0.000587018, True}, {25, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05152 → {{0.000342678, 0.00144285, True}, {25, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa00240 → {{0.000453162, 0.00172633, True}, {25, 105, 7086, 4},
  {Pyrimidine metabolism - Homo sapiens (human), {{POLR3B}, {NME1}, {CTPS1}, {POLR3A}}}},
path:hsa04660 → {{0.000453162, 0.00172633, True}, {25, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.000540824, 0.00196663, True}, {25, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.00063924, 0.00222344, True}, {25, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.000681647, 0.00227216, True}, {25, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa05131 → {{0.001467, 0.00469441, True},
  {25, 65, 7086, 3}, {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04010 → {{0.00170641, 0.00519202, True}, {25, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04622 → {{0.00181721, 0.00519202, True}, {25, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00181721, 0.00519202, True}, {25, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00205037, 0.00565621, True}, {25, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00213205, 0.00568546, True}, {25, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00309301, 0.00798195, True}, {25, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00327339, 0.00818346, True}, {25, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00360717, 0.00848745, True}, {25, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00360717, 0.00848745, True}, {25, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00384779, 0.00879494, True}, {25, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03020 → {{0.00555558, 0.0123457, True}, {25, 32, 7086, 2},
  {RNA polymerase - Homo sapiens (human), {{POLR3B}, {POLR3A}}}},
path:hsa04722 → {{0.00830127, 0.0179487, True}, {25, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0109938, 0.0230144, True}, {25, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.0112195, 0.0230144, True}, {25, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.0123888, 0.0247777, True}, {25, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.0133733, 0.0260942, True}, {25, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0169404, 0.0322673, True}, {25, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
```

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```
    path:hsa05212 → {{0.0223323, 0.0415485, True}, {25, 66, 7086, 2},
      {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
    path:hsa00230 → {{0.0231928, 0.0421686, True}, {25, 176, 7086, 3},
      {Purine metabolism - Homo sapiens (human), {{POLR3B}, {NME1}, {POLR3A}}}},
    path:hsa04115 → {{0.0242685, 0.0427679, True}, {25, 69, 7086, 2},
      {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
    path:hsa05202 → {{0.0245915, 0.0427679, True}, {25, 180, 7086, 3},
      {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}}|⟩|⟩
```

```
In[1]:= Needs["MathIOmica`"]
```

We can carry out a "Molecular" analysis for compound data. We consider the following metabolomics data, which has labels "Meta" and additional mass and retention time information in the form {`identifier, mass, retention time, label`}:

```
In[2]:= compoundsExample =
  {{"cpd:C19691", 325.2075`, 10.677681`, "Meta"}, {"cpd:C17905", 594.2002`, 8.727458`, "Meta"},
   {"cpd:C09921", 204.0784`, 12.3909445`, "Meta"}, {"cpd:C18218", 272.2356`, 13.473582`, "Meta"},
   {"cpd:C14169", 235.1573`, 12.267084`, "Meta"}, {"cpd:C14245", 262.2296`, 13.545572`, "Meta"},
   {"cpd:C09137", 352.2615`, 14.0554285`, "Meta"}, {"cpd:C09674", 296.1624`, 12.147417`, "Meta"},
   {"cpd:C00449", 276.1334`, 11.004139`, "Meta"}, {"cpd:C02999", 364.1497`, 12.147243`, "Meta"},
   {"cpd:C07915", 309.194`, 7.3625283`, "Meta"}, {"cpd:C08760", 496.2309`, 8.7241125`, "Meta"},
   {"cpd:C14549", 276.0972`, 11.078914`, "Meta"}, {"cpd:C20533", 601.3378`, 12.75722`, "Meta"},
   {"cpd:C20790", 212.1051`, 7.127666`, "Meta"}, {"cpd:C09137", 352.2613`, 12.869867`, "Meta"},
   {"cpd:C17648", 400.2085`, 10.843841`, "Meta"}, {"cpd:C07807", 240.1471`, 0.48564285`, "Meta"},
   {"cpd:C08564", 324.0948`, 10.281`, "Meta"}, {"cpd:C19426", 338.2818`, 13.758765`, "Meta"},
   {"cpd:C02943", 468.3218`, 14.263261`, "Meta"}, {"cpd:C04882", 1193.342`, 14.707576`, "Meta"}};

In[3]:= KEGGAnalysis[compoundsExample, FilterSignificant → True, AnalysisType → "Molecular"]

Out[3]= <|path:map00300 → {{0.00020774, 0.00186966, True}, {4, 35, 5841, 2}, {Lysine biosynthesis,
    {{{cpd:C00449, 276.133, 11.0041, Meta}}, {{cpd:C04882, 1193.34, 14.7076, Meta}}}}}|>
```

```
In[1]:= Needs["MathIOmica`"]
```

We can carry out multiomics data analysis. We consider the following simple example:

```
In[2]:= multiOmicsData = {{"C6orf57", "Protein"}, {"CD46", "Protein"}, {"DHX58", "Protein"}, {"HMGB3", "RNA"},
   {"HMGB3", "Protein"}, {"MAP3K5", "Protein"}, {"NFKB2", "RNA"}, {"NFKB2", "Protein"},
   {"NOS2", "RNA"}, {"PYCARD", "RNA"}, {"PYDC1", "Protein"}, {"SSC5D", "Protein"},
   {"cpd:C19691", 325.2075`, 10.677681`, "Meta"}, {"cpd:C17905", 594.2002`, 8.727458`, "Meta"},
   {"cpd:C09921", 204.0784`, 12.3909445`, "Meta"}, {"cpd:C18218", 272.2356`, 13.473582`, "Meta"},
   {"cpd:C14169", 235.1573`, 12.267084`, "Meta"}, {"cpd:C14245", 262.2296`, 13.545572`, "Meta"},
   {"cpd:C09137", 352.2615`, 14.0554285`, "Meta"}, {"cpd:C09674", 296.1624`, 12.147417`, "Meta"},
   {"cpd:C00449", 276.1334`, 11.004139`, "Meta"}, {"cpd:C02999", 364.1497`, 12.147243`, "Meta"},
   {"cpd:C07915", 309.194`, 7.3625283`, "Meta"}, {"cpd:C08760", 496.2309`, 8.7241125`, "Meta"},
   {"cpd:C14549", 276.0972`, 11.078914`, "Meta"}, {"cpd:C20533", 601.3378`, 12.75722`, "Meta"},
   {"cpd:C20790", 212.1051`, 7.127666`, "Meta"}, {"cpd:C09137", 352.2613`, 12.869867`, "Meta"},
   {"cpd:C17648", 400.2085`, 10.843841`, "Meta"}, {"cpd:C07807", 240.1471`, 0.48564285`, "Meta"},
   {"cpd:C08564", 324.0948`, 10.281`, "Meta"}, {"cpd:C19426", 338.2818`, 13.758765`, "Meta"},
   {"cpd:C02943", 468.3218`, 14.263261`, "Meta"}, {"cpd:C04882", 1193.342`, 14.707576`, "Meta"}};
```

We can carry out "Genomic" and "Molecular" analysis concurrently by setting `AnalysisType → All`:

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```
In[3]:= KEGGAnalysis[multiOmicsData, AnalysisType → All, MultipleList → True, MultipleListCorrection → Automatic]

Out[3]= ⟨|Molecular → ⟨|path:map00300 → {{0.00020774, 0.00186966, True}, {4, 35, 5841, 2}, {Lysine biosynthesis,
          {{{cpd:C00449, 276.133, 11.0041, Meta}}, {{cpd:C04882, 1193.34, 14.7076, Meta}}}}}|⟩,
        Genomic → ⟨|path:hsa05134 → {{0.0000249895, 0.000899622, True}, {8, 165, 21258, 3},
            {Legionellosis - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}, {{PYCARD, RNA}}}}},
          path:hsa04621 → {{0.00174483, 0.0269499, True}, {8, 171, 21258, 2},
            {NOD-like receptor signaling pathway - Homo sapiens (human), {{{PYCARD, RNA}}, {{PYDC1, Protein}}}}},
          path:hsa04010 → {{0.00226983, 0.0269499, True}, {8, 765, 21258, 3},
            {MAPK signaling pathway - Homo sapiens (human),
             {{{MAP3K5, Protein}}, {{NFKB2, RNA}}, {{NFKB2, Protein}}}}},
          path:hsa05133 → {{0.00299443, 0.0269499, True}, {8, 225, 21258, 2},
            {Pertussis - Homo sapiens (human), {{{NOS2, RNA}}, {{PYCARD, RNA}}}}},
          path:hsa05132 → {{0.003915, 0.0273689, True}, {8, 258, 21258, 2},
            {Salmonella infection - Homo sapiens (human), {{{NOS2, RNA}}, {{PYCARD, RNA}}}}},
          path:hsa04064 → {{0.00456148, 0.0273689, True}, {8, 279, 21258, 2},
            {NF-kappa B signaling pathway - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}}}},
          path:hsa05200 → {{0.00794118, 0.0404914, True}, {8, 1191, 21258, 3},
            {Pathways in cancer - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}, {{NOS2, RNA}}}}},
          path:hsa04380 → {{0.00899809, 0.0404914, True}, {8, 396, 21258, 2},
            {Osteoclast differentiation - Homo sapiens (human), {{{NFKB2, RNA}}, {{NFKB2, Protein}}}}}|⟩|⟩
```

AugmentDictionary (1)

```
In[1]:= Needs["MathIOmica`"]
```

AugmentDictionary provides a choice whether or not to augment the current ConstantGeneDictionary variable or create a new one. In the example below gene dictionary already exists, and set a simple dictionary as an example (please note that this will reset your variable if you have one already created, so use with caution):

```
In[2]:= ConstantGeneDictionary =
          ⟨|"humanExample" → ⟨|"UCSC ID" → {"uc001aaa.3", "uc010nxr.1", "uc010nxq.1", "uc001aal.1", "uc001aaq.2",
               "uc001aar.2", "uc001aau.3", "uc021oeh.1", "uc009vjk.2", "uc021oei.1", "uc010nxu.2", "uc001aax.1",
               "uc001abb.3", "uc001abp.2", "uc021oem.2", "uc009vjn.2", "uc009vjo.2", "uc031pjk.1", "uc031pjj.1",
               "uc001abu.1", "uc001abw.1", "uc031pjv.1", "uc031pkd.1", "uc031pkk.1", "uc031pkl.1"},
             "Gene Symbol" → {"DDX11L1", "DDX11L1", "DDX11L1", "OR4F5", "DQ597235", "DQ599768",
               "LOC100132062", "LOC100133331", "LOC100133331", "LOC388312", "OR4F29", "BC036251",
               "M37726", "LOC643837", "LOC643837", "LOC643837", "LOC643837", "LOC643837",
               "LOC643837", "AK056486", "SAMD11", "SAMD11", "SAMD11", "SAMD11", "SAMD11"}|⟩|⟩;
```

If we now run a standard analysis with the AugmentDictionary option set to True we have:

```
In[3]:= keggExampleAugmentTrue = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
          "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
          "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, AugmentDictionary → True]

Out[3]= ⟨|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
            {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
             {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
              {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
          path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
             {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
          path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
            {Epstein-Barr virus infection - Homo sapiens (human),
             {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
          path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
            {Toll-like receptor signaling pathway - Homo sapiens (human),
             {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
```

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```
 {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
   {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
  {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
  {B cell receptor signaling pathway - Homo sapiens (human),
   {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
  {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
  {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
  {HTLV-I infection - Homo sapiens (human),
   {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
```

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```
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

We now check again the ConstantGeneDictionary :

In[4]:=
```
ConstantGeneDictionary
```

Out[4]=
```
<|humanExample →
  <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1, uc001aaq.2, uc001aar.2, uc001aau.3,
     ⋯ 11 ⋯, uc031pjj.1, uc001abu.1, uc001abw.1, uc031pjv.1, uc031pkd.1,
     uc031pkk.1, uc031pkl.1}, ⋯ 1 ⋯|>, human → ⋯ 1 ⋯|>
```

large output | show less | show more | show all | set size limit...

We see that this has augmented the previous dictionary with the "human" annotation used in the example. We now repeat with `AugmentDictionary` set to False:

In[5]:=
```
keggExampleAugmentFalse =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
   "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
   "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, AugmentDictionary → False]
```

Out[5]=
```
<|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
  {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
   {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
  {Epstein-Barr virus infection - Homo sapiens (human),
   {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
  {Toll-like receptor signaling pathway - Homo sapiens (human),
   {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
 {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
   {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
```

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```
  {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
  {B cell receptor signaling pathway - Homo sapiens (human),
   {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
  {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
  {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
  {HTLV-I infection - Homo sapiens (human),
   {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
```

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```
  path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
    {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
    {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
  path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
    {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
    {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
    {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
  path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
    {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
    {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
    {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
  path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
    {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

We now check again the ConstantGeneDictionary to notice that the previous ConstantGeneDictionary has now been replaced with a new default one.

In[6]:=
```
ConstantGeneDictionary
```

Out[6]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1,
      uc001aaq.2, uc001aar.2, uc001aau.3, ··· 121 569 ···, uc031tkn.1, uc022cgh.1, uc022cha.1,
      uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ··· 6 ···, H ... ID → ··· 1 ···|>|>
```

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AugmentDictionary is best used in advanced applications, especially when utilizing/analyzing data from multiple species.

BackgroundSet (1)

In[1]:=
```
Needs["MathIOmica`"]
```

BackgroundSet provides a list of IDs (e.g. gene accessions/entries) that should be considered as the background for the calculation.

By default the BackgroundSet is set to All:

In[2]:=
```
keggExample1 = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
    "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
    "NFKBIA", "IRAK4", "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"}, BackgroundSet → All]
```

Out[2]=
```
<|path:hsa04064 → {{3.27957×10^-37, 2.62366×10^-35, True},
    {25, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05169 → {{2.69713×10^-11, 1.07885×10^-9, True}, {25, 204, 7086, 11},
    {Epstein-Barr virus infection - Homo sapiens (human), {{TAB1}, {CHUK}, {CSNK2A1},
      {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {POLR3B}, {POLR3A}}},
```

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```
path:hsa05162 → {{1.23085×10^-8, 3.28226×10^-7, True}, {25, 136, 7086, 8}, {Measles - Homo sapiens (human),
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04620 → {{5.28996×10^-8, 1.05799×10^-6, True}, {25, 106, 7086, 7},
  {Toll-like receptor signaling pathway - Homo sapiens (human),
    {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
 {{1.43121×10^-7, 2.28994×10^-6, True}, {25, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa04623 → {{2.37065×10^-6, 0.0000308255, True}, {25, 64, 7086, 5},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human),
    {{CHUK}, {NFKB1}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
path:hsa05145 → {{2.69723×10^-6, 0.0000308255, True}, {25, 119, 7086, 6},
  {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04662 → {{4.57186×10^-6, 0.0000434807, True}, {25, 73, 7086, 5},
  {B cell receptor signaling pathway - Homo sapiens (human),
    {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05140 → {{4.89158×10^-6, 0.0000434807, True}, {25, 74, 7086, 5},
  {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04210 → {{6.94486×10^-6, 0.0000555589, True}, {25, 140, 7086, 6},
  {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
path:hsa05166 → {{0.0000219498, 0.000159635, True}, {25, 259, 7086, 7},
  {HTLV-I infection - Homo sapiens (human),
    {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05142 → {{0.0000260113, 0.000173409, True}, {25, 104, 7086, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
    {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05134 → {{0.0000364135, 0.000224083, True}, {25, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{0.0000419741, 0.000239852, True}, {25, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000818726, 0.000421518, True}, {25, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000843036, 0.000421518, True}, {25, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
    {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05133 → {{0.000123744, 0.000582327, True},
  {25, 75, 7086, 4}, {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05161 → {{0.000132079, 0.000587018, True}, {25, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05152 → {{0.000342678, 0.00144285, True}, {25, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa00240 → {{0.000453162, 0.00172633, True}, {25, 105, 7086, 4},
  {Pyrimidine metabolism - Homo sapiens (human), {{POLR3B}, {NME1}, {CTPS1}, {POLR3A}}}},
path:hsa04660 → {{0.000453162, 0.00172633, True}, {25, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.000540824, 0.00196663, True}, {25, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.00063924, 0.00222344, True}, {25, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.000681647, 0.00227216, True}, {25, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
    {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa05131 → {{0.001467, 0.00469441, True},
  {25, 65, 7086, 3}, {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04010 → {{0.00170641, 0.00519202, True}, {25, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04622 → {{0.00181721, 0.00519202, True}, {25, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00181721, 0.00519202, True}, {25, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00205037, 0.00565621, True}, {25, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00213205, 0.00568546, True}, {25, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00309301, 0.00798195, True}, {25, 176, 7086, 4},
```

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```
    {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05222 → {{0.00327339, 0.00818346, True}, {25, 86, 7086, 3},
    {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa03008 → {{0.00360717, 0.00848745, True}, {25, 89, 7086, 3},
    {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa05215 → {{0.00360717, 0.00848745, True}, {25, 89, 7086, 3},
    {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04062 → {{0.00384779, 0.00879494, True}, {25, 187, 7086, 4},
    {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa03020 → {{0.00555558, 0.0123457, True}, {25, 32, 7086, 2},
    {RNA polymerase - Homo sapiens (human), {{POLR3B}, {POLR3A}}}},
  path:hsa04722 → {{0.00830127, 0.0179487, True}, {25, 120, 7086, 3},
    {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05160 → {{0.0109938, 0.0230144, True}, {25, 133, 7086, 3},
    {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04068 → {{0.0112195, 0.0230144, True}, {25, 134, 7086, 3},
    {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
  path:hsa04530 → {{0.0123888, 0.0247777, True}, {25, 139, 7086, 3},
    {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa04310 → {{0.0133733, 0.0260942, True}, {25, 143, 7086, 3},
    {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa05221 → {{0.0169404, 0.0322673, True}, {25, 57, 7086, 2},
    {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa05212 → {{0.0223323, 0.0415485, True}, {25, 66, 7086, 2},
    {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa00230 → {{0.0231928, 0.0421686, True}, {25, 176, 7086, 3},
    {Purine metabolism - Homo sapiens (human), {{POLR3B}, {NME1}, {POLR3A}}}},
  path:hsa04115 → {{0.0242685, 0.0427679, True}, {25, 69, 7086, 2},
    {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa05202 → {{0.0245915, 0.0427679, True}, {25, 180, 7086, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}}|>
```

In a rather specialized example, let's limit the background to be the following list of genes (relating to KEGG "NFKB" pathway), e.g. from conducting an experiment using an array with only these probes included.

```
In[3]:= backgroundExample = {"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
    "CSNK2A2", "CSNK2B", "TICAM1", "TAB2", "DDX58", "LY96", "TAB3", "LAT", "CXCL2", "BLNK", "BIRC2",
    "BIRC3", "XIAP", "ICAM1", "TICAM2", "IKBKB", "IL1B", "IL1R1", "IL8", "IRAK1", "CCL4L2",
    "LBP", "LCK", "LTA", "LTB", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
    "NFKBIA", "IRAK4", "PIAS4", "PLAU", "PLCG1", "PLCG2", "PIDD", "PRKCB", "PRKCQ", "PTGS2",
    "BCL2", "BCL2A1", "RELA", "RELB", "BCL2L1", "CCL4", "CCL13", "CCL19", "CCL21", "CXCL12",
    "SYK", "MAP3K7", "BTK", "TLR4", "TNF", "TNFAIP3", "TNFRSF1A", "TRAF1", "TRAF2", "TRAF3",
    "TRAF5", "TRAF6", "UBE2I", "VCAM1", "ZAP70", "TRIM25", "CARD11", "IKBKG", "TNFSF11", "TRADD",
    "RIPK1", "TNFSF14", "TNFRSF11A", "CFLAR", "BCL10", "MAP3K14", "CD14", "CD40", "CD40LG"};
```

We need to first convert these to "KEGG Gene IDs", since the MathIOmica GO annotation is based on UniProt IDs. We can use the inbuilt gene dictionary, adding "hsa:" to each numeric accession string (based on UCSC) to have standard KEGG accession nomenclature used by KEGGAnalysis pathways.

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```
In[4]:= backgroundExampleKEGG = "hsa:" <> # & /@ Query[Values /* Flatten /* Union] @
          GeneTranslation[backgroundExample, "KEGG Gene ID", ConstantGeneDictionary, InputID → {"Gene Symbol"}]

Out[4]= {hsa:10454, hsa:10673, hsa:10892, hsa:114609, hsa:1147, hsa:115650, hsa:142, hsa:1457, hsa:1459, hsa:1460,
         hsa:148022, hsa:23118, hsa:23586, hsa:23643, hsa:257397, hsa:27040, hsa:2920, hsa:29760, hsa:329,
         hsa:330, hsa:331, hsa:3383, hsa:353376, hsa:3551, hsa:3553, hsa:3554, hsa:3576, hsa:3654, hsa:388372,
         hsa:3929, hsa:3932, hsa:4049, hsa:4050, hsa:4055, hsa:4067, hsa:4615, hsa:4616, hsa:472, hsa:4790,
         hsa:4791, hsa:4792, hsa:51135, hsa:51588, hsa:5328, hsa:5335, hsa:5336, hsa:55367, hsa:5579, hsa:5588,
         hsa:5743, hsa:596, hsa:597, hsa:5970, hsa:5971, hsa:598, hsa:6351, hsa:6357, hsa:6363, hsa:6366,
         hsa:6387, hsa:6850, hsa:6885, hsa:695, hsa:7099, hsa:7124, hsa:7128, hsa:7132, hsa:7185, hsa:7186,
         hsa:7187, hsa:7188, hsa:7189, hsa:7329, hsa:7412, hsa:7535, hsa:7706, hsa:84433, hsa:8517, hsa:8600,
         hsa:8717, hsa:8737, hsa:8740, hsa:8792, hsa:8837, hsa:8915, hsa:9020, hsa:929, hsa:958, hsa:959}
```

We see that by using the background, since the set is already enriched in NFKB pathway genes the previous significant result list is now not significant any more:

```
In[5]:= KEGGExampleBackground =
         KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
           "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
          BackgroundSet → backgroundExampleKEGG, FilterSignificant → False]

Out[5]= <|path:hsa03008 → {{0.0117115, 0.730604, False}, {21, 3, 89, 3},
           {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
         path:hsa05162 → {{0.0252773, 0.730604, False}, {21, 18, 89, 8}, {Measles - Homo sapiens (human),
            {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
         path:hsa04068 → {{0.0394921, 0.730604, False}, {21, 4, 89, 3},
           {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
         path:hsa04520 → {{0.0394921, 0.730604, False}, {21, 4, 89, 3},
           {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}}, path:hsa04110 →
          {{0.0536261, 0.793667, False}, {21, 2, 89, 2}, {Cell cycle - Homo sapiens (human), {{GADD45B}, {ATM}}}},
         path:hsa04310 → {{0.0832875, 0.880468, False}, {21, 5, 89, 3},
           {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
         path:hsa04530 → {{0.0832875, 0.880468, False}, {21, 5, 89, 3},
           {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
         path:hsa04024 → {{0.137456, 0.93885, False}, {21, 3, 89, 2},
           {cAMP signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
         path:hsa04115 → {{0.137456, 0.93885, False}, {21, 3, 89, 2},
           {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
         path:hsa05203 → {{0.155143, 0.93885, False}, {21, 13, 89, 5}, {Viral carcinogenesis - Homo sapiens (human),
            {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}}, path:hsa05168 →
          {{0.185695, 0.93885, False}, {21, 25, 89, 8}, {Herpes simplex infection - Homo sapiens (human),
            {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
         path:hsa04672 → {{0.208009, 0.93885, False}, {21, 7, 89, 3},
           {Intestinal immune network for IgA production - Homo sapiens (human),
            {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa05131 → {{0.208009, 0.93885, False},
           {21, 7, 89, 3}, {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
         path:hsa05215 → {{0.208009, 0.93885, False}, {21, 7, 89, 3},
           {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
         path:hsa05220 → {{0.208009, 0.93885, False}, {21, 7, 89, 3},
           {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
         path:hsa05166 → {{0.221233, 0.93885, False}, {21, 22, 89, 7}, {HTLV-I infection - Homo sapiens (human),
            {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
         path:hsa05120 → {{0.238245, 0.93885, False}, {21, 11, 89, 4},
           {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
            {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05134 → {{0.238245, 0.93885, False}, {21, 11, 89, 4},
           {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}}, path:hsa04662 →
          {{0.253743, 0.93885, False}, {21, 15, 89, 5}, {B cell receptor signaling pathway - Homo sapiens (human),
            {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
         path:hsa05140 → {{0.253743, 0.93885, False}, {21, 15, 89, 5},
           {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05169 →
          {{0.307532, 0.979932, False}, {21, 32, 89, 9}, {Epstein-Barr virus infection - Homo sapiens (human),
            {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
         path:hsa05161 → {{0.308976, 0.979932, False}, {21, 16, 89, 5},
```

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```
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05221 → {{0.33684, 0.979932, False}, {21, 5, 89, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05142 → {{0.366479, 0.979932, False}, {21, 17, 89, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa04211 → {{0.418284, 0.979932, False},
  {21, 2, 89, 1}, {Longevity regulating pathway - Homo sapiens (human), {{NFKB1}}}},
path:hsa04730 → {{0.418284, 0.979932, False}, {21, 2, 89, 1},
  {Long-term depression - Homo sapiens (human), {{LYN}}}}, path:hsa05030 →
 {{0.418284, 0.979932, False}, {21, 2, 89, 1}, {Cocaine addiction - Homo sapiens (human), {{NFKB1}}}},
path:hsa05152 → {{0.424964, 0.979932, False}, {21, 18, 89, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04722 → {{0.434032, 0.979932, False}, {21, 10, 89, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05206 → {{0.434032, 0.979932, False}, {21, 10, 89, 3},
  {MicroRNAs in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.43494, 0.979932, False}, {21, 6, 89, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05133 → {{0.494168, 0.979932, False}, {21, 15, 89, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04623 → {{0.507453, 0.979932, False}, {21, 11, 89, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.507453, 0.979932, False}, {21, 11, 89, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05202 → {{0.507453, 0.979932, False}, {21, 11, 89, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa04620 → {{0.515623, 0.979932, False}, {21, 28, 89, 7},
  {Toll-like receptor signaling pathway - Homo sapiens (human),
   {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04210 → {{0.527063, 0.979932, False}, {21, 24, 89, 6},
  {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
path:hsa05145 → {{0.527063, 0.979932, False}, {21, 24, 89, 6},
  {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04010 → {{0.540133, 0.979932, False}, {21, 20, 89, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04062 → {{0.555899, 0.979932, False}, {21, 16, 89, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05164 → {{0.555899, 0.979932, False}, {21, 16, 89, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04630 → {{0.558698, 0.979932, False}, {21, 3, 89, 1},
  {Jak-STAT signaling pathway - Homo sapiens (human), {{PIAS4}}}},
path:hsa04066 → {{0.607076, 0.979932, False}, {21, 8, 89, 2},
  {HIF-1 signaling pathway - Homo sapiens (human), {{LTBR}, {NFKB1}}}},
path:hsa04931 → {{0.607076, 0.979932, False}, {21, 8, 89, 2},
  {Insulin resistance - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}}, path:hsa04611 →
 {{0.666458, 0.979932, False}, {21, 4, 89, 1}, {Platelet activation - Homo sapiens (human), {{LYN}}}},
path:hsa04917 → {{0.666458, 0.979932, False}, {21, 4, 89, 1},
  {Prolactin signaling pathway - Homo sapiens (human), {{NFKB1}}}},
path:hsa04621 → {{0.668244, 0.979932, False}, {21, 18, 89, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04660 → {{0.668244, 0.979932, False}, {21, 18, 89, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04151 → {{0.678251, 0.979932, False}, {21, 9, 89, 2},
  {PI3K-Akt signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}}}}, path:hsa04150 →
 {{0.748862, 0.979932, False}, {21, 5, 89, 1}, {mTOR signaling pathway - Homo sapiens (human), {{CHUK}}}},
path:hsa05321 → {{0.748862, 0.979932, False}, {21, 5, 89, 1},
  {Inflammatory bowel disease (IBD) - Homo sapiens (human), {{NFKB1}}}},
path:hsa04380 → {{0.778327, 0.979932, False}, {21, 25, 89, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04014 → {{0.790829, 0.979932, False}, {21, 11, 89, 2},
  {Ras signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05132 → {{0.790829, 0.979932, False}, {21, 11, 89, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa04622 → {{0.79227, 0.979932, False}, {21, 16, 89, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
```

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```
path:hsa05160 → {{0.79227, 0.979932, False}, {21, 16, 89, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}}, path:hsa01524 →
 {{0.811647, 0.979932, False}, {21, 6, 89, 1}, {Platinum drug resistance - Homo sapiens (human), {{ATM}}}},
path:hsa04120 → {{0.811647, 0.979932, False}, {21, 6, 89, 1},
  {Ubiquitin mediated proteolysis - Homo sapiens (human), {{PIAS4}}}},
path:hsa04666 → {{0.811647, 0.979932, False}, {21, 6, 89, 1},
  {Fc gamma R-mediated phagocytosis - Homo sapiens (human), {{LYN}}}},
path:hsa05143 → {{0.811647, 0.979932, False}, {21, 6, 89, 1},
  {African trypanosomiasis - Homo sapiens (human), {{MYD88}}}}, path:hsa05205 →
 {{0.811647, 0.979932, False}, {21, 6, 89, 1}, {Proteoglycans in cancer - Homo sapiens (human), {{PLAU}}}},
path:hsa05222 → {{0.830431, 0.979932, False}, {21, 17, 89, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04664 → {{0.859302, 0.979932, False}, {21, 7, 89, 1},
  {Fc epsilon RI signaling pathway - Homo sapiens (human), {{LYN}}}},
path:hsa05200 → {{0.865438, 0.979932, False}, {21, 23, 89, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04071 → {{0.895335, 0.979932, False}, {21, 8, 89, 1},
  {Sphingolipid signaling pathway - Homo sapiens (human), {{NFKB1}}}},
path:hsa04932 → {{0.895335, 0.979932, False}, {21, 8, 89, 1},
  {Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human), {{NFKB1}}}},
path:hsa05340 → {{0.895335, 0.979932, False}, {21, 8, 89, 1},
  {Primary immunodeficiency - Homo sapiens (human), {{TNFRSF13C}}}},
path:hsa05144 → {{0.92247, 0.979932, False}, {21, 9, 89, 1}, {Malaria - Homo sapiens (human), {{MYD88}}}},
path:hsa05146 →
 {{0.92247, 0.979932, False}, {21, 9, 89, 1}, {Amoebiasis - Homo sapiens (human), {{NFKB1}}}},
path:hsa05323 → {{0.942822, 0.979932, False}, {21, 10, 89, 1},
  {Rheumatoid arthritis - Homo sapiens (human), {{TNFSF13B}}}},
path:hsa04060 → {{0.946394, 0.979932, False}, {21, 22, 89, 3},
  {Cytokine-cytokine receptor interaction - Homo sapiens (human), {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}},
path:hsa04933 → {{0.958021, 0.979932, False}, {21, 11, 89, 1},
  {AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human), {{NFKB1}}}},
path:hsa04668 → {{0.96669, 0.979932, False}, {21, 29, 89, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04064 → {{1., 1., False}, {21, 89, 89, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}}|>
```

FilterSignificant (1)

```
In[1]:= Needs["MathIOmica`"]
```

`FilterSignificant` is an option, which is by default set to True, and filters data based on whether the enrichment analysis is statistically significant or not.

```
In[2]:= keggExampleFilterSignificantOn = KEGGAnalysis[{"C6orf57", "CD46", "DHX58", "HMGB3",
   "MAP3K5", "NFKB2", "NOS2", "PYCARD", "PYDC1", "SSC5D"}, FilterSignificant → True]

Out[2]= <|path:hsa05134 → {{0.00121168, 0.0234184, True},
   {7, 55, 7086, 2}, {Legionellosis - Homo sapiens (human), {{NFKB2}, {PYCARD}}}},
 path:hsa04621 → {{0.00130102, 0.0234184, True}, {7, 57, 7086, 2},
   {NOD-like receptor signaling pathway - Homo sapiens (human), {{PYCARD}, {PYDC1}}}}, path:hsa05133 →
  {{0.00224298, 0.0264506, True}, {7, 75, 7086, 2}, {Pertussis - Homo sapiens (human), {{NOS2}, {PYCARD}}}},
 path:hsa05132 → {{0.00293895, 0.0264506, True}, {7, 86, 7086, 2},
   {Salmonella infection - Homo sapiens (human), {{NOS2}, {PYCARD}}}}|>

In[3]:= Length[keggExampleFilterSignificantOn]

Out[3]= 4
```

We can see that the genes show enrichment in 4 pathways.

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We now repeat the computation to see all results, by setting the `FilterSignificant` to False:

In[4]:=
```
keggExampleFilterSignificantOff = KEGGAnalysis[{"C6orf57", "CD46", "DHX58", "HMGB3",
   "MAP3K5", "NFKB2", "NOS2", "PYCARD", "PYDC1", "SSC5D"}, FilterSignificant → False]
```

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```
Out[4]= <|path:hsa05134 → {{0.00121168, 0.0234184, True},
    {7, 55, 7086, 2}, {Legionellosis - Homo sapiens (human), {{NFKB2}, {PYCARD}}}},
  path:hsa04621 → {{0.00130102, 0.0234184, True}, {7, 57, 7086, 2},
    {NOD-like receptor signaling pathway - Homo sapiens (human), {{PYCARD}, {PYDC1}}}}, path:hsa05133 →
   {{0.00224298, 0.0264506, True}, {7, 75, 7086, 2}, {Pertussis - Homo sapiens (human), {{NOS2}, {PYCARD}}}},
  path:hsa05132 → {{0.00293895, 0.0264506, True}, {7, 86, 7086, 2},
    {Salmonella infection - Homo sapiens (human), {{NOS2}, {PYCARD}}}},
  path:hsa00220 → {{0.0205702, 0.144208, False}, {7, 21, 7086, 1},
    {Arginine biosynthesis - Homo sapiens (human), {{NOS2}}}},
  path:hsa04010 → {{0.0240347, 0.144208, False}, {7, 255, 7086, 2},
    {MAPK signaling pathway - Homo sapiens (human), {{MAP3K5}, {NFKB2}}}},
  path:hsa00330 → {{0.0483799, 0.170438, False}, {7, 50, 7086, 1},
    {Arginine and proline metabolism - Homo sapiens (human), {{NOS2}}}},
  path:hsa05014 → {{0.0493266, 0.170438, False}, {7, 51, 7086, 1},
    {Amyotrophic lateral sclerosis (ALS) - Homo sapiens (human), {{MAP3K5}}}},
  path:hsa05200 → {{0.0545134, 0.170438, False}, {7, 397, 7086, 2},
    {Pathways in cancer - Homo sapiens (human), {{NFKB2}, {NOS2}}}},
  path:hsa04623 → {{0.0615611, 0.170438, False}, {7, 64, 7086, 1},
    {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{PYCARD}}}},
  path:hsa04622 → {{0.0671621, 0.170438, False}, {7, 70, 7086, 1},
    {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{DHX58}}}}, path:hsa05140 →
   {{0.0708802, 0.170438, False}, {7, 74, 7086, 1}, {Leishmaniasis - Homo sapiens (human), {{NOS2}}}},
  path:hsa01524 → {{0.0718077, 0.170438, False}, {7, 75, 7086, 1},
    {Platinum drug resistance - Homo sapiens (human), {{MAP3K5}}}},
  path:hsa04610 → {{0.0755099, 0.170438, False}, {7, 79, 7086, 1},
    {Complement and coagulation cascades - Homo sapiens (human), {{CD46}}}}, path:hsa04146 →
   {{0.0791994, 0.170438, False}, {7, 83, 7086, 1}, {Peroxisome - Homo sapiens (human), {{NOS2}}}},
  path:hsa05222 → {{0.0819583, 0.170438, False}, {7, 86, 7086, 1},
    {Small cell lung cancer - Homo sapiens (human), {{NOS2}}}},
  path:hsa04064 → {{0.0883681, 0.170438, False}, {7, 93, 7086, 1},
    {NF-kappa B signaling pathway - Homo sapiens (human), {{NFKB2}}}}, path:hsa05146 →
   {{0.0947394, 0.170438, False}, {7, 100, 7086, 1}, {Amoebiasis - Homo sapiens (human), {{NOS2}}}},
  path:hsa04066 → {{0.0974583, 0.170438, False}, {7, 103, 7086, 1},
    {HIF-1 signaling pathway - Homo sapiens (human), {{NOS2}}}},
  path:hsa05142 → {{0.0983631, 0.170438, False}, {7, 104, 7086, 1},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human), {{NOS2}}}},
  path:hsa04668 → {{0.103775, 0.170438, False}, {7, 110, 7086, 1},
    {TNF signaling pathway - Homo sapiens (human), {{MAP3K5}}}}, path:hsa05145 →
   {{0.111841, 0.170438, False}, {7, 119, 7086, 1}, {Toxoplasmosis - Homo sapiens (human), {{NOS2}}}},
  path:hsa04722 → {{0.112734, 0.170438, False}, {7, 120, 7086, 1},
    {Neurotrophin signaling pathway - Homo sapiens (human), {{MAP3K5}}}},
  path:hsa04071 → {{0.113625, 0.170438, False}, {7, 121, 7086, 1},
    {Sphingolipid signaling pathway - Homo sapiens (human), {{MAP3K5}}}},
  path:hsa04380 → {{0.123382, 0.173894, False}, {7, 132, 7086, 1},
    {Osteoclast differentiation - Homo sapiens (human), {{NFKB2}}}}, path:hsa05162 →
   {{0.126907, 0.173894, False}, {7, 136, 7086, 1}, {Measles - Homo sapiens (human), {{CD46}}}},
  path:hsa04210 → {{0.13042, 0.173894, False}, {7, 140, 7086, 1},
    {Apoptosis - Homo sapiens (human), {{MAP3K5}}}}, path:hsa04932 → {{0.140018, 0.180024, False},
    {7, 151, 7086, 1}, {Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human), {{MAP3K5}}}},
  path:hsa04141 → {{0.15296, 0.1855, False}, {7, 166, 7086, 1},
    {Protein processing in endoplasmic reticulum - Homo sapiens (human), {{MAP3K5}}}},
  path:hsa05164 → {{0.161495, 0.1855, False}, {7, 176, 7086, 1},
    {Influenza A - Homo sapiens (human), {{PYCARD}}}}, path:hsa05152 →
   {{0.164041, 0.1855, False}, {7, 179, 7086, 1}, {Tuberculosis - Homo sapiens (human), {{NOS2}}}},
  path:hsa04020 → {{0.164889, 0.1855, False}, {7, 180, 7086, 1},
    {Calcium signaling pathway - Homo sapiens (human), {{NOS2}}}},
  path:hsa05169 → {{0.185002, 0.196762, False}, {7, 204, 7086, 1},
    {Epstein-Barr virus infection - Homo sapiens (human), {{NFKB2}}}},
  path:hsa05203 → {{0.185831, 0.196762, False}, {7, 205, 7086, 1},
    {Viral carcinogenesis - Homo sapiens (human), {{NFKB2}}}}, path:hsa05166 →
   {{0.229536, 0.236094, False}, {7, 259, 7086, 1}, {HTLV-I infection - Homo sapiens (human), {{NFKB2}}}},
  path:hsa01100 → {{0.740959, 0.740959, False}, {7, 1243, 7086, 1},
    {Metabolic pathways - Homo sapiens (human), {{NOS2}}}}|>
```

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In[5]:=
```
Length[keggExampleFilterSignificantOff]
```

Out[5]= 36

We can see that 36 pathways had gene membership, though only 4 showed as statistically significant based on our cutoffs.

GeneDictionary (1)

In[1]:=
```
Needs["MathIOmica`"]
```

GeneDictionary takes values that point to an existing variable to be used as a gene dictionary in annotations. By default, it is set to None and the default ConstantGeneDictionary is used.

In[2]:=
```
keggExampleDefaultGeneDictionary =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
   "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM",
   "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, GeneDictionary → None]
```

Out[2]=
```
<|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
   {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
   {Epstein-Barr virus infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
   {Toll-like receptor signaling pathway - Homo sapiens (human),
    {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
  {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
   {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
   {B cell receptor signaling pathway - Homo sapiens (human),
    {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
   {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
   {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
   {HTLV-I infection - Homo sapiens (human),
    {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
   {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
    {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
   {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
   {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
   {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
   {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
    {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
```

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```
path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

We can instead use a variable as a gene dictionary. For example suppose we have a rather

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restricted dictionary:

In[3]:=
```
geneDictionaryExample =
  <|"human" → <|"UniProt ID" → {"P19838", "B4DUJ4", "O15111", "Q9NWZ3", "P19838", "J3KQ87", "P58753-2",
        "P67870", "P19838", "Q9NWZ3", "O15111", Missing[], "P68400", "Q99836-3", "B4DUJ4", "Q9NWZ3",
        "P67870", "Q9NWZ3", "P19838", "Q9Y275", "B4DUJ4", Missing[], "B4DUJ4", "Q15750", "O15111",
        "P67870", Missing[], "P19838-3", "O15111", "F5GXE7", "P25963", "P19838-2", "Q9NWZ3",
        "P07948", "Q6P7P1", "B4DUJ4", Missing[], "Q9NWZ3", "O15111", Missing[], "P67870", "J3KQJ6",
        "P25963", "Q99836-3", "H0YDU7", "D3DR86", "B4DUJ4", "Q9NWZ3", "P19838-3", "O15111",
        Missing[], "H0YDU7", "P25963", "B4DUJ4", "B4DUJ4", "B4DUJ4", "Q99836-4", "P68400", "B4DUJ4",
        Missing[], "P19838", Missing[], "B4DUJ4", "O15111", "P19838", "P68400", Missing[],
        "Q9NWZ3", "P19838-3", "O75293", "O15111", "Q9NWZ3", Missing[], "P67870", "P58753",
        "O75293", "Q96RJ3", "P67870", "B4DUJ4", "O15111", "P19838", "P19838", "P25963", "Q9NWZ3",
        "P19838-2", "O15111", "P25963", "Q9NWZ3", Missing[], Missing[], "P19838-2", "B4DUJ4",
        "Q9NWZ3", "O15111", "J3KQJ6", "Q15750-2", Missing[], "P68400", "B4DUJ4", "P19838-3"},
      "Gene Symbol" → {"NFKB1", "CSNK2B", "CHUK", "IRAK4", "NFKB1", "MYD88", "TIRAP", "CSNK2B",
        "NFKB1", "IRAK4", "CHUK", "CSNK2B", "CSNK2A1", "MYD88", "CSNK2B", "IRAK4", "CSNK2B", "IRAK4",
        "NFKB1", "TNFSF13B", "CSNK2B", "CSNK2B", "CSNK2B", "TAB1", "CHUK", "CSNK2B", "ATM", "NFKB1",
        "CHUK", "LTBR", "NFKBIA", "NFKB1", "IRAK4", "LYN", "ATM", "CSNK2B", "ATM", "IRAK4", "CHUK",
        "CSNK2B", "CSNK2B", "MYD88", "NFKBIA", "MYD88", "ATM", "NFKB2", "CSNK2B", "IRAK4", "NFKB1", "CHUK",
        "CSNK2B", "ATM", "NFKBIA", "CSNK2B", "CSNK2B", "CSNK2B", "MYD88", "CSNK2A1", "CSNK2B", "ATM",
        "NFKB1", "CSNK2B", "CSNK2B", "CHUK", "NFKB1", "CSNK2A1", "CSNK2A2", "IRAK4", "NFKB1", "GADD45B",
        "CHUK", "IRAK4", "TNFSF13B", "CSNK2B", "TIRAP", "GADD45B", "TNFRSF13C", "CSNK2B", "CSNK2B",
        "CHUK", "NFKB1", "NFKB1", "NFKBIA", "IRAK4", "NFKB1", "CHUK", "NFKBIA", "IRAK4", "CSNK2A2",
        "ATM", "NFKB1", "CSNK2B", "IRAK4", "CHUK", "MYD88", "TAB1", "ATM", "CSNK2A1", "CSNK2B", "NFKB1"},
      "KEGG Gene ID" → {"4790", "1460", "1147", "51135", "4790", "4615", "114609", "1460", "4790",
        "51135", "1147", "1460", "1457", "4615", "1460", "51135", "1460", "51135", "4790", "10673",
        "1460", "1460", "1460", "10454", "1147", "1460", "472", "4790", "1147", "4055", "4792", "4790",
        "51135", "4067", "472", "1460", "472", "51135", "1147", "1460", "1460", "4615", "4792",
        "4615", "472", "4791", "1460", "51135", "4790", "1147", "1460", "472", "4792", "1460", "1460",
        "1460", "4615", "1457", "1460", "472", "4790", "1460", "1460", "1147", "4790", "1457", "1459",
        "51135", "4790", "4616", "1147", "51135", "10673", "1460", "114609", "4616", "115650", "1460",
        "1460", "1147", "4790", "4790", "4792", "51135", "4790", "1147", "4792", "51135", "1459",
        "472", "4790", "1460", "51135", "1147", "4615", "10454", "472", "1457", "1460", "4790"}|>|>;
```

In[4]:=
```
keggExampleGeneDictionary =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
   "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
   "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, GeneDictionary → geneDictionaryExample]
```

Out[4]=
```
<|path:hsa04064 → {{2.18446×10^-33, 1.55097×10^-31, True},
    {17, 93, 7086, 17}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {TIRAP}, {CHUK}, {TNFRSF13C}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
  path:hsa05169 → {{2.2705×10^-10, 7.45273×10^-9, True}, {17, 204, 7086, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05162 → {{3.14904×10^-10, 7.45273×10^-9, True}, {17, 136, 7086, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04620 → {{2.3615×10^-9, 4.19166×10^-8, True}, {17, 106, 7086, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
   {{3.85313×10^-9, 5.47145×10^-8, True}, {17, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05145 → {{2.10387×10^-7, 2.48958×10^-6, True}, {17, 119, 7086, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05140 → {{6.08045×10^-7, 6.16732×10^-6, True}, {17, 74, 7086, 5},
    {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05166 →
   {{1.14225×10^-6, 0.0000101375, True}, {17, 259, 7086, 7}, {HTLV-I infection - Homo sapiens (human),
     {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{3.3262×10^-6, 0.00002624, True}, {17, 104, 7086, 5},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
     {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
```

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```
path:hsa05134 → {{7.17431×10^-6, 0.0000509376, True}, {17, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{8.28483×10^-6, 0.0000534748, True}, {17, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000107499, 0.0000636035, True}, {17, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04210 → {{0.0000143264, 0.000078244, True}, {17, 140, 7086, 5},
  {Apoptosis - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
path:hsa05120 → {{0.0000168059, 0.0000831776, True}, {17, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05161 → {{0.0000175727, 0.0000831776, True}, {17, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa04662 → {{0.0000222962, 0.0000989392, True}, {17, 73, 7086, 4},
  {B cell receptor signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000248248, 0.00010368, True}, {17, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05203 → {{0.0000899197, 0.000354683, True}, {17, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04668 → {{0.000111974, 0.000418429, True}, {17, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04672 → {{0.000209704, 0.000744448, True}, {17, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}},
path:hsa04010 → {{0.000251628, 0.000850743, True}, {17, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000436601, 0.00140903, True}, {17, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000457048, 0.00141089, True}, {17, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.000568539, 0.00161465, True}, {17, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.000568539, 0.00161465, True}, {17, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.000643108, 0.00172304, True}, {17, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.000669287, 0.00172304, True}, {17, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00067951, 0.00172304, True}, {17, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05152 → {{0.00072423, 0.00177311, True}, {17, 179, 7086, 4},
  {Tuberculosis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04062 → {{0.000853703, 0.00202043, True}, {17, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05222 → {{0.00103797, 0.00237728, True}, {17, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00114668, 0.00246711, True}, {17, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00114668, 0.00246711, True}, {17, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04660 → {{0.00184839, 0.00385987, True}, {17, 105, 7086, 3},
  {T cell receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00270812, 0.00549361, True}, {17, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0036255, 0.00710581, True}, {17, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00370303, 0.00710581, True}, {17, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00410597, 0.00767167, True}, {17, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00444697, 0.00809576, True}, {17, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.00800175, 0.0142031, True}, {17, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
```

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```
  path:hsa05212 → {{0.010619, 0.0183889, True}, {17, 66, 7086, 2},
    {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa04115 → {{0.0115651, 0.0195506, True}, {17, 69, 7086, 2},
    {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa05200 → {{0.012898, 0.0212967, True}, {17, 397, 7086, 4},
    {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05132 → {{0.017593, 0.0283887, True}, {17, 86, 7086, 2},
    {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
  path:hsa04060 → {{0.0238402, 0.0376146, True}, {17, 265, 7086, 3},
    {Cytokine-cytokine receptor interaction - Homo sapiens (human), {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}},
  path:hsa04066 → {{0.024689, 0.038107, True}, {17, 103, 7086, 2},
    {HIF-1 signaling pathway - Homo sapiens (human), {{LTBR}, {NFKB1}}}},
  path:hsa04931 → {{0.0274325, 0.0414406, True}, {17, 109, 7086, 2},
    {Insulin resistance - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}}|>
```

GetGeneDictionaryOptions (1)

GetGeneDictionaryOptions values specify a list of options that will be passed to the internal GetGeneDictionary function. For example, we can re-import the gene dictionary from online:

```
In[1]:= keggExampleGetGeneDictionaryOptions =
  KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
    "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
    "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, GetGeneDictionaryOptions → {ImportDirectly → True}]

Out[1]= <|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
    {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
   {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
    {B cell receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
    {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
    {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
    {HTLV-I infection - Homo sapiens (human),
     {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
     {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
    {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
    {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
    {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
```

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```
path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

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HypothesisFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The HypothesisFunction option takes as values a function to implement multiple hypothesis testing. The default is using the BenjaminiHochbergFDR function. Any function f with three inputs can be used, of the form f[#1,#2,#3] where the inputs refer to:

#1 is the p-value list,

#2 is a significance cutoff,

#3 is the number of pathways/maps overall being tested.

The function f must output a list of 3 values: {original p-value, adjusted p-value, True or False based on whether this value is considered statistically significant or not respectively}.

We can implement a Bonferroni correction. We can define for example:

In[2]:=
```
bonferroni[pValueList_, cutoff_, numberTested_] :=
  {#, #*numberTested, #*numberTested ≤ cutoff} & /@ pValueList
```

We set the HypothesisFunction value to our function above:

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```
In[3]:= keggExampleHypothesisFunction =
         KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
           "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA",
           "IRAK4", "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"}, HypothesisFunction → bonferroni]

Out[3]= ⟨|path:hsa04064 → {{3.27957×10^-37, 9.96989×10^-35, True},
           {25, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
            {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
             {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
         path:hsa05169 → {{2.69713×10^-11, 8.19929×10^-9, True}, {25, 204, 7086, 11},
           {Epstein-Barr virus infection - Homo sapiens (human), {{TAB1}, {CHUK}, {CSNK2A1},
             {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
         path:hsa05162 → {{1.23085×10^-8, 3.74178×10^-6, True}, {25, 136, 7086, 8}, {Measles - Homo sapiens (human),
            {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
         path:hsa04620 → {{5.28996×10^-8, 0.0000160815, True}, {25, 106, 7086, 7},
           {Toll-like receptor signaling pathway - Homo sapiens (human),
            {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
          {{1.43121×10^-7, 0.0000435088, True}, {25, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
            {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
         path:hsa04623 → {{2.37065×10^-6, 0.000720676, True}, {25, 64, 7086, 5},
           {Cytosolic DNA-sensing pathway - Homo sapiens (human),
            {{CHUK}, {NFKB1}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
         path:hsa05145 → {{2.69723×10^-6, 0.000819959, True}, {25, 119, 7086, 6},
           {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
         path:hsa04662 → {{4.57186×10^-6, 0.00138985, True}, {25, 73, 7086, 5},
           {B cell receptor signaling pathway - Homo sapiens (human),
            {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
         path:hsa05140 → {{4.89158×10^-6, 0.00148704, True}, {25, 74, 7086, 5},
           {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
         path:hsa04210 → {{6.94486×10^-6, 0.00211124, True}, {25, 140, 7086, 6},
           {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
         path:hsa05166 → {{0.0000219498, 0.00667273, True}, {25, 259, 7086, 7},
           {HTLV-I infection - Homo sapiens (human),
            {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
         path:hsa05142 → {{0.0000260113, 0.00790744, True}, {25, 104, 7086, 5},
           {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
            {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
         path:hsa05134 → {{0.0000364135, 0.0110697, True}, {25, 55, 7086, 4},
           {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
         path:hsa04621 → {{0.0000419741, 0.0127601, True}, {25, 57, 7086, 4},
           {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
         path:hsa04380 → {{0.0000818726, 0.0248893, True}, {25, 132, 7086, 5},
           {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
         path:hsa05120 → {{0.0000843036, 0.0256283, True}, {25, 68, 7086, 4},
           {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
            {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05133 → {{0.000123744, 0.0376183, True},
           {25, 75, 7086, 4}, {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
         path:hsa05161 → {{0.000132079, 0.040152, True}, {25, 146, 7086, 5},
           {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}}|⟩
```

InputID (1)

```
In[1]:= Needs["MathIOmica`"]
```

The InputID option specifies a list of the kind of identifiers/accessions to be used as input. The default is set to {"UniProt ID", "Gene Symbol"}.

For example if we already know we are using official Gene Symbol as an identifier we may

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specify this directly:

In[2]:=
```
keggExampleInputID = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, InputID → {"Gene Symbol"}]
```

Out[2]=
```
<|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
   {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
   {Epstein-Barr virus infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
   {Toll-like receptor signaling pathway - Homo sapiens (human),
    {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
  {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
   {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
   {B cell receptor signaling pathway - Homo sapiens (human),
    {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
   {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
   {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
   {HTLV-I infection - Homo sapiens (human),
    {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
   {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
    {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
   {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
   {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
   {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
   {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
    {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
   {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
   {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
  path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
   {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
  path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
   {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
   {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
   {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
   {Intestinal immune network for IgA production - Homo sapiens (human),
    {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
   {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
  path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
   {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
```

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```
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

KEGG annotation by default will use input IDs converted to "KEGG Gene ID" or as set by the option `OutputID`.

KEGGAnalysisAssignerOptions (1)

```
In[1]:= Needs["MathIOmica`"]
```

The KEGGAnalysisAssignerOptions option specifies a list of options that will be passed to the internal KEGGAnalysisAssigner function. These options supersede any other applicable options used internally by KEGGAnalysisAssigner. For example, we can restrict the KEGG pathways/maps to be included, to have at least 100 members each:

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```
In[2]:= keggExampleKEGGAnalysisAssignerOptions =
  KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
    "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
    "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, KEGGAnalysisAssignerOptions → {LengthFilter → 100}]

Out[2]= ⟨|path:hsa05162 → {{1.34868×10^-8, 3.38071×10^-7, True}, {21, 136, 5695, 8}, {Measles - Homo sapiens (human),
      {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05169 → {{1.64913×10^-8, 3.38071×10^-7, True}, {21, 204, 5695, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
      {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04620 → {{5.95231×10^-8, 8.13483×10^-7, True}, {21, 106, 5695, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
      {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
   {{1.57564×10^-7, 1.61503×10^-6, True}, {21, 186, 5695, 8}, {Herpes simplex infection - Homo sapiens (human),
      {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05145 → {{3.08087×10^-6, 0.0000252631, True}, {21, 119, 5695, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{7.93795×10^-6, 0.0000542427, True}, {21, 140, 5695, 6},
    {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{0.0000249259, 0.000145995, True}, {21, 259, 5695, 7},
    {HTLV-I infection - Homo sapiens (human),
      {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000297409, 0.000152422, True}, {21, 104, 5695, 5},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
      {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04380 → {{0.0000936184, 0.000426484, True}, {21, 132, 5695, 5},
    {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05161 → {{0.00015103, 0.000619222, True}, {21, 146, 5695, 5},
    {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05152 → {{0.000391837, 0.00146048, True}, {21, 179, 5695, 5},
    {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
  path:hsa04660 → {{0.000512895, 0.00175239, True}, {21, 105, 5695, 4},
    {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04668 → {{0.000612037, 0.00193027, True}, {21, 110, 5695, 4},
    {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa05203 → {{0.00073089, 0.00214046, True}, {21, 205, 5695, 5},
    {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04010 → {{0.00195052, 0.00533143, True}, {21, 255, 5695, 5},
    {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
  path:hsa05164 → {{0.00349408, 0.00895358, True}, {21, 176, 5695, 4},
    {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04062 → {{0.00434533, 0.0104799, True}, {21, 187, 5695, 4},
    {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa04722 → {{0.00919858, 0.0209523, True}, {21, 120, 5695, 3},
    {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05160 → {{0.0121744, 0.0254687, True}, {21, 133, 5695, 3},
    {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04068 → {{0.0124238, 0.0254687, True}, {21, 134, 5695, 3},
    {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
  path:hsa04530 → {{0.0137152, 0.0267772, True}, {21, 139, 5695, 3},
    {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa04310 → {{0.014802, 0.0275856, True}, {21, 143, 5695, 3},
    {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa05202 → {{0.0271677, 0.0484293, True}, {21, 180, 5695, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}}|⟩
```

KEGGDatabase (1)

```
In[1]:= Needs["MathIOmica`"]
```

KEGGDatabase value indicates which KEGG database to use as the target database. The

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default is to use "pathway" database. This should only be changed in advanced applications.

```
In[2]:= keggExampleDatabasePathway =
  KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
    "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1",
    "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, KEGGDatabase → "pathway"]

Out[2]= ⟨|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
    {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}, path:hsa05168 →
   {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8}, {Herpes simplex infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
    {B cell receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
    {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
    {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
    {HTLV-I infection - Homo sapiens (human),
     {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
     {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
    {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
    {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
    {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
    {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
     {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
    {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
    {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
  path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
    {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
  path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
    {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
    {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
    {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
    {Intestinal immune network for IgA production - Homo sapiens (human),
     {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
    {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
  path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
    {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
```

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```
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

We can for example instead query disease membership. We also have to set KEGGDictionaryOptions if we would like to gett the proper definitions for the maps:

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In[3]:=
```
keggExampleDatabaseDisease =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
   "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
  KEGGDatabase → "disease", KEGGDictionaryOptions → {KEGGQuery1 → "disease", KEGGQuery2 → ""}]
```

Out[3]=
```
<|ds:H00095 → {{0.00341953, 0.0143252, True}, {4, 2, 2338, 1},
    {Ectodermal dysplasia associated immunodeficiency (EDA-ID), including the following two diseases:
       NF-kappa-B essential modulator (NEMO) defect; Inhibitor of kappa-B (I-kappa-B) defect,
     {{NFKBIA}}}}, ds:H00848 → {{0.00683029, 0.0143252, True}, {4, 4, 2338, 1},
    {Ataxia with ocular apraxia (AOA), including: Ataxia telangiectasia (AT);
       Ataxia telangiectasia like disorder (ATLD); Ataxia oculomotor apraxia
       type 1 (AOA1); Ataxia oculomotor apraxia type 2 (AOA2), {{ATM}}}}},
 ds:H00007 → {{0.0102323, 0.0143252, True}, {4, 6, 2338, 1}, {Hodgkin lymphoma, {{NFKBIA}}}},
 ds:H00088 →
  {{0.0102323, 0.0143252, True}, {4, 6, 2338, 1},
    {Common variable immunodeficiency (CVID), including the following four diseases: Inducible T Cell
       costimulator (ICOS) defect; TACI defect; CD19 defect; BAFFR defect; CD20 defect; CD81 defect,
     {{TNFRSF13C}}}}, ds:H00094 → {{0.0102323, 0.0143252, True}, {4, 6, 2338, 1},
    {Immunodeficiency associated with DNA repair defects, including the following six diseases: Ataxia
       telangiectasia (AT) [DS:H00064]; Ataxia-talangiectasia-like syndrome; Nijmegen syndrome
       [DS:H01344]; DNA ligase I deficiency; DNA ligase IV deficiency; Bloom syndrome [DS:H01346],
     {{ATM}}}}, ds:H00005 → {{0.01701, 0.019845, True}, {4, 10, 2338, 1},
    {Chronic lymphocytic leukemia (CLL), {{ATM}}}},
 ds:H00031 → {{0.0271113, 0.0271113, True}, {4, 16, 2338, 1},
    {Breast cancer, {{PLAU}}}}|>
```

KEGGDictionaryOptions (3)

In[1]:=
```
Needs["MathIOmica`"]
```

KEGGDictionaryOptions specifies a list of options to be passed to the internal KEGGDictionary function that provides the KEGG annotations. We may for example want to update the definitions by importing directly new ones:

In[2]:=
```
keggExampleDictionaryOpts1 =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
   "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
   "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, KEGGDictionaryOptions → {ImportDirectly → True}]
```

Out[2]=
```
<|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
    {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
 path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05168 → {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8},
    {Herpes simplex virus 1 infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
 path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
    {B cell receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
 path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
```

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```
  {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
  {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
  {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
   {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
```

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```
  path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
    {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
  path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
    {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
  path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
    {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
    {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
    {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
  path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
    {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

```
In[1]:= Needs["MathIOmica`"]
```

As another example we may be querying a database other than the standard "pathway" one. In this case we want to use a different KEGG dictionary to get the definitions for each map. For example we may want to query modules instead of pathways:

```
In[2]:= keggExampleDatabaseModule =
  KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
    "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
   KEGGDatabase → "module", KEGGDictionaryOptions → {KEGGQuery1 → "module", KEGGQuery2 → "hsa"}]

Out[2]= <|md:hsa_M00686 → {{7.92516×10^-12, 3.17007×10^-11, True}, {8, 15, 1528, 6},
    {Toll-like receptor signaling, {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}}|>
```

```
In[1]:= Needs["MathIOmica`"]
```

As another example we query the disease database

```
In[2]:= keggExampleDatabaseModule =
  KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
    "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
   KEGGDatabase → "disease", KEGGDictionaryOptions → {KEGGQuery1 → "disease", KEGGQuery2 → ""}]

Out[2]= <|ds:H00095 → {{0.00341953, 0.0143252, True}, {4, 2, 2338, 1},
    {Ectodermal dysplasia associated immunodeficiency (EDA-ID), including the following two diseases:
       NF-kappa-B essential modulator (NEMO) defect; Inhibitor of kappa-B (I-kappa-B) defect,
     {{NFKBIA}}}}, ds:H00848 → {{0.00683029, 0.0143252, True}, {4, 4, 2338, 1},
    {Ataxia with ocular apraxia (AOA), including: Ataxia telangiectasia (AT);
       Ataxia telangiectasia like disorder (ATLD); Ataxia oculomotor apraxia
       type 1 (AOA1); Ataxia oculomotor apraxia type 2 (AOA2), {{ATM}}}},
  ds:H00007 → {{0.0102323, 0.0143252, True}, {4, 6, 2338, 1}, {Hodgkin lymphoma, {{NFKBIA}}}},
  ds:H00088 →
   {{0.0102323, 0.0143252, True}, {4, 6, 2338, 1},
    {Common variable immunodeficiency (CVID), including the following four diseases: Inducible T Cell
       costimulator (ICOS) defect; TACI defect; CD19 defect; BAFFR defect; CD20 defect; CD81 defect,
     {{TNFRSF13C}}}}, ds:H00094 → {{0.0102323, 0.0143252, True}, {4, 6, 2338, 1},
    {Immunodeficiency associated with DNA repair defects, including the following six diseases: Ataxia
       telangiectasia (AT) [DS:H00064]; Ataxia-talangiectasia-like syndrome; Nijmegen syndrome
       [DS:H01344]; DNA ligase I deficiency; DNA ligase IV deficiency; Bloom syndrome [DS:H01346],
     {{ATM}}}}, ds:H00005 → {{0.01701, 0.019845, True}, {4, 10, 2338, 1},
    {Chronic lymphocytic leukemia (CLL), {{ATM}}}},
  ds:H00031 → {{0.0271113, 0.0271113, True}, {4, 16, 2338, 1},
    {Breast cancer, {{PLAU}}}}|>
```

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KEGGDictionaryVariable (1)

In[1]:=
```
Needs["MathIOmica`"]
```

KEGGDictionaryVariable can provide a KEGG annotation variable. If set to None, KEGGDictionary will be used internally to automatically generate the default KEGG annotation.

For example we create the KEGG dictionary directly:

In[2]:=
```
keggDictionaryVar = KEGGDictionary[]
```

Out[2]=
```
<|path:hsa00010 → Glycolysis / Gluconeogenesis - Homo sapiens (human),
 path:hsa00020 → Citrate cycle (TCA cycle) - Homo sapiens (human),
 path:hsa00030 → Pentose phosphate pathway - Homo sapiens (human),
 path:hsa00040 → Pentose and glucuronate interconversions - Homo sapiens (human),
 path:hsa00051 → Fructose and mannose metabolism - Homo sapiens (human),
 path:hsa00052 → Galactose metabolism - Homo sapiens (human),
 path:hsa00053 → Ascorbate and aldarate metabolism - Homo sapiens (human),
 path:hsa00061 → Fatty acid biosynthesis - Homo sapiens (human),
 path:hsa00062 → Fatty acid elongation - Homo sapiens (human),
 path:hsa00071 → Fatty acid degradation - Homo sapiens (human),
 path:hsa00072 → Synthesis and degradation of ketone bodies - Homo sapiens (human),
 path:hsa00100 → Steroid biosynthesis - Homo sapiens (human),
 path:hsa00120 → Primary bile acid biosynthesis - Homo sapiens (human),
 path:hsa00130 → Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human),
 path:hsa00140 → Steroid hormone biosynthesis - Homo sapiens (human),
 path:hsa00190 → Oxidative phosphorylation - Homo sapiens (human),
 path:hsa00220 → Arginine biosynthesis - Homo sapiens (human),
 path:hsa00230 → Purine metabolism - Homo sapiens (human),
 path:hsa00232 → Caffeine metabolism - Homo sapiens (human),
 path:hsa00240 → Pyrimidine metabolism - Homo sapiens (human),
 path:hsa00250 → Alanine, aspartate and glutamate metabolism - Homo sapiens (human),
 path:hsa00260 → Glycine, serine and threonine metabolism - Homo sapiens (human),
 path:hsa00270 → Cysteine and methionine metabolism - Homo sapiens (human),
 path:hsa00280 → Valine, leucine and isoleucine degradation - Homo sapiens (human),
 path:hsa00290 → Valine, leucine and isoleucine biosynthesis - Homo sapiens (human),
 path:hsa00310 → Lysine degradation - Homo sapiens (human),
 path:hsa00330 → Arginine and proline metabolism - Homo sapiens (human),
 path:hsa00340 → Histidine metabolism - Homo sapiens (human),
 path:hsa00350 → Tyrosine metabolism - Homo sapiens (human),
 path:hsa00360 → Phenylalanine metabolism - Homo sapiens (human),
 path:hsa00380 → Tryptophan metabolism - Homo sapiens (human),
 path:hsa00400 → Phenylalanine, tyrosine and tryptophan biosynthesis - Homo sapiens (human),
 path:hsa00410 → beta-Alanine metabolism - Homo sapiens (human),
 path:hsa00430 → Taurine and hypotaurine metabolism - Homo sapiens (human),
 path:hsa00440 → Phosphonate and phosphinate metabolism - Homo sapiens (human),
 path:hsa00450 → Selenocompound metabolism - Homo sapiens (human),
 path:hsa00471 → D-Glutamine and D-glutamate metabolism - Homo sapiens (human),
 path:hsa00472 → D-Arginine and D-ornithine metabolism - Homo sapiens (human),
 path:hsa00480 → Glutathione metabolism - Homo sapiens (human),
 path:hsa00500 → Starch and sucrose metabolism - Homo sapiens (human),
 path:hsa00510 → N-Glycan biosynthesis - Homo sapiens (human),
 path:hsa00511 → Other glycan degradation - Homo sapiens (human),
 path:hsa00512 → Mucin type O-glycan biosynthesis - Homo sapiens (human),
 path:hsa00514 → Other types of O-glycan biosynthesis - Homo sapiens (human),
 path:hsa00515 → Mannose type O-glycan biosynthesis - Homo sapiens (human),
 path:hsa00520 → Amino sugar and nucleotide sugar metabolism - Homo sapiens (human),
 path:hsa00524 → Neomycin, kanamycin and gentamicin biosynthesis - Homo sapiens (human),
 path:hsa00531 → Glycosaminoglycan degradation - Homo sapiens (human), path:hsa00532 →
  Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Homo sapiens (human),
 path:hsa00533 → Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human),
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path:hsa00534 → Glycosaminoglycan biosynthesis - heparan sulfate / heparin - Homo sapiens (human),
path:hsa00561 → Glycerolipid metabolism - Homo sapiens (human),
path:hsa00562 → Inositol phosphate metabolism - Homo sapiens (human),
path:hsa00563 → Glycosylphosphatidylinositol (GPI)-anchor biosynthesis - Homo sapiens (human),
path:hsa00564 → Glycerophospholipid metabolism - Homo sapiens (human),
path:hsa00565 → Ether lipid metabolism - Homo sapiens (human),
path:hsa00590 → Arachidonic acid metabolism - Homo sapiens (human),
path:hsa00591 → Linoleic acid metabolism - Homo sapiens (human),
path:hsa00592 → alpha-Linolenic acid metabolism - Homo sapiens (human),
path:hsa00600 → Sphingolipid metabolism - Homo sapiens (human),
path:hsa00601 → Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human),
path:hsa00603 → Glycosphingolipid biosynthesis - globo and isoglobo series - Homo sapiens (human),
path:hsa00604 → Glycosphingolipid biosynthesis - ganglio series - Homo sapiens (human),
path:hsa00620 → Pyruvate metabolism - Homo sapiens (human),
path:hsa00630 → Glyoxylate and dicarboxylate metabolism - Homo sapiens (human),
path:hsa00640 → Propanoate metabolism - Homo sapiens (human),
path:hsa00650 → Butanoate metabolism - Homo sapiens (human),
path:hsa00670 → One carbon pool by folate - Homo sapiens (human),
path:hsa00730 → Thiamine metabolism - Homo sapiens (human),
path:hsa00740 → Riboflavin metabolism - Homo sapiens (human),
path:hsa00750 → Vitamin B6 metabolism - Homo sapiens (human),
path:hsa00760 → Nicotinate and nicotinamide metabolism - Homo sapiens (human),
path:hsa00770 → Pantothenate and CoA biosynthesis - Homo sapiens (human),
path:hsa00780 → Biotin metabolism - Homo sapiens (human),
path:hsa00785 → Lipoic acid metabolism - Homo sapiens (human),
path:hsa00790 → Folate biosynthesis - Homo sapiens (human),
path:hsa00830 → Retinol metabolism - Homo sapiens (human),
path:hsa00860 → Porphyrin and chlorophyll metabolism - Homo sapiens (human),
path:hsa00900 → Terpenoid backbone biosynthesis - Homo sapiens (human),
path:hsa00910 → Nitrogen metabolism - Homo sapiens (human),
path:hsa00920 → Sulfur metabolism - Homo sapiens (human),
path:hsa00970 → Aminoacyl-tRNA biosynthesis - Homo sapiens (human),
path:hsa00980 → Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human),
path:hsa00982 → Drug metabolism - cytochrome P450 - Homo sapiens (human),
path:hsa00983 → Drug metabolism - other enzymes - Homo sapiens (human),
path:hsa01040 → Biosynthesis of unsaturated fatty acids - Homo sapiens (human),
path:hsa01100 → Metabolic pathways - Homo sapiens (human),
path:hsa01200 → Carbon metabolism - Homo sapiens (human),
path:hsa01210 → 2-Oxocarboxylic acid metabolism - Homo sapiens (human),
path:hsa01212 → Fatty acid metabolism - Homo sapiens (human),
path:hsa01230 → Biosynthesis of amino acids - Homo sapiens (human),
path:hsa01521 → EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human),
path:hsa01522 → Endocrine resistance - Homo sapiens (human),
path:hsa01523 → Antifolate resistance - Homo sapiens (human),
path:hsa01524 → Platinum drug resistance - Homo sapiens (human),
path:hsa02010 → ABC transporters - Homo sapiens (human),
path:hsa03008 → Ribosome biogenesis in eukaryotes - Homo sapiens (human),
path:hsa03010 → Ribosome - Homo sapiens (human), path:hsa03013 → RNA transport - Homo sapiens (human),
path:hsa03015 → mRNA surveillance pathway - Homo sapiens (human),
path:hsa03018 → RNA degradation - Homo sapiens (human),
path:hsa03020 → RNA polymerase - Homo sapiens (human),
path:hsa03022 → Basal transcription factors - Homo sapiens (human),
path:hsa03030 → DNA replication - Homo sapiens (human), path:hsa03040 → Spliceosome - Homo sapiens (human),
path:hsa03050 → Proteasome - Homo sapiens (human), path:hsa03060 → Protein export - Homo sapiens (human),
path:hsa03320 → PPAR signaling pathway - Homo sapiens (human),
path:hsa03410 → Base excision repair - Homo sapiens (human),
path:hsa03420 → Nucleotide excision repair - Homo sapiens (human),
path:hsa03430 → Mismatch repair - Homo sapiens (human),
path:hsa03440 → Homologous recombination - Homo sapiens (human),
path:hsa03450 → Non-homologous end-joining - Homo sapiens (human),
path:hsa03460 → Fanconi anemia pathway - Homo sapiens (human),
path:hsa04010 → MAPK signaling pathway - Homo sapiens (human),
path:hsa04012 → ErbB signaling pathway - Homo sapiens (human),
path:hsa04014 → Ras signaling pathway - Homo sapiens (human),
path:hsa04015 → Rap1 signaling pathway - Homo sapiens (human),
path:hsa04020 → Calcium signaling pathway - Homo sapiens (human),
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path:hsa04022 → cGMP-PKG signaling pathway - Homo sapiens (human),
path:hsa04024 → cAMP signaling pathway - Homo sapiens (human),
path:hsa04060 → Cytokine-cytokine receptor interaction - Homo sapiens (human),
path:hsa04061 → Viral protein interaction with cytokine and cytokine receptor - Homo sapiens (human),
path:hsa04062 → Chemokine signaling pathway - Homo sapiens (human),
path:hsa04064 → NF-kappa B signaling pathway - Homo sapiens (human),
path:hsa04066 → HIF-1 signaling pathway - Homo sapiens (human),
path:hsa04068 → FoxO signaling pathway - Homo sapiens (human),
path:hsa04070 → Phosphatidylinositol signaling system - Homo sapiens (human),
path:hsa04071 → Sphingolipid signaling pathway - Homo sapiens (human),
path:hsa04072 → Phospholipase D signaling pathway - Homo sapiens (human),
path:hsa04080 → Neuroactive ligand-receptor interaction - Homo sapiens (human),
path:hsa04110 → Cell cycle - Homo sapiens (human), path:hsa04114 → Oocyte meiosis - Homo sapiens (human),
path:hsa04115 → p53 signaling pathway - Homo sapiens (human),
path:hsa04120 → Ubiquitin mediated proteolysis - Homo sapiens (human),
path:hsa04122 → Sulfur relay system - Homo sapiens (human),
path:hsa04130 → SNARE interactions in vesicular transport - Homo sapiens (human),
path:hsa04136 → Autophagy - other - Homo sapiens (human),
path:hsa04137 → Mitophagy - animal - Homo sapiens (human),
path:hsa04140 → Autophagy - animal - Homo sapiens (human),
path:hsa04141 → Protein processing in endoplasmic reticulum - Homo sapiens (human),
path:hsa04142 → Lysosome - Homo sapiens (human), path:hsa04144 → Endocytosis - Homo sapiens (human),
path:hsa04145 → Phagosome - Homo sapiens (human), path:hsa04146 → Peroxisome - Homo sapiens (human),
path:hsa04150 → mTOR signaling pathway - Homo sapiens (human),
path:hsa04151 → PI3K-Akt signaling pathway - Homo sapiens (human),
path:hsa04152 → AMPK signaling pathway - Homo sapiens (human),
path:hsa04210 → Apoptosis - Homo sapiens (human),
path:hsa04211 → Longevity regulating pathway - Homo sapiens (human),
path:hsa04213 → Longevity regulating pathway - multiple species - Homo sapiens (human),
path:hsa04215 → Apoptosis - multiple species - Homo sapiens (human),
path:hsa04216 → Ferroptosis - Homo sapiens (human), path:hsa04217 → Necroptosis - Homo sapiens (human),
path:hsa04218 → Cellular senescence - Homo sapiens (human),
path:hsa04260 → Cardiac muscle contraction - Homo sapiens (human),
path:hsa04261 → Adrenergic signaling in cardiomyocytes - Homo sapiens (human),
path:hsa04270 → Vascular smooth muscle contraction - Homo sapiens (human),
path:hsa04310 → Wnt signaling pathway - Homo sapiens (human),
path:hsa04330 → Notch signaling pathway - Homo sapiens (human),
path:hsa04340 → Hedgehog signaling pathway - Homo sapiens (human),
path:hsa04350 → TGF-beta signaling pathway - Homo sapiens (human),
path:hsa04360 → Axon guidance - Homo sapiens (human),
path:hsa04370 → VEGF signaling pathway - Homo sapiens (human),
path:hsa04371 → Apelin signaling pathway - Homo sapiens (human),
path:hsa04380 → Osteoclast differentiation - Homo sapiens (human),
path:hsa04390 → Hippo signaling pathway - Homo sapiens (human),
path:hsa04392 → Hippo signaling pathway - multiple species - Homo sapiens (human),
path:hsa04510 → Focal adhesion - Homo sapiens (human),
path:hsa04512 → ECM-receptor interaction - Homo sapiens (human),
path:hsa04514 → Cell adhesion molecules (CAMs) - Homo sapiens (human),
path:hsa04520 → Adherens junction - Homo sapiens (human),
path:hsa04530 → Tight junction - Homo sapiens (human), path:hsa04540 → Gap junction - Homo sapiens (human),
path:hsa04550 → Signaling pathways regulating pluripotency of stem cells - Homo sapiens (human),
path:hsa04610 → Complement and coagulation cascades - Homo sapiens (human),
path:hsa04611 → Platelet activation - Homo sapiens (human),
path:hsa04612 → Antigen processing and presentation - Homo sapiens (human),
path:hsa04614 → Renin-angiotensin system - Homo sapiens (human),
path:hsa04620 → Toll-like receptor signaling pathway - Homo sapiens (human),
path:hsa04621 → NOD-like receptor signaling pathway - Homo sapiens (human),
path:hsa04622 → RIG-I-like receptor signaling pathway - Homo sapiens (human),
path:hsa04623 → Cytosolic DNA-sensing pathway - Homo sapiens (human),
path:hsa04625 → C-type lectin receptor signaling pathway - Homo sapiens (human),
path:hsa04630 → JAK-STAT signaling pathway - Homo sapiens (human),
path:hsa04640 → Hematopoietic cell lineage - Homo sapiens (human),
path:hsa04650 → Natural killer cell mediated cytotoxicity - Homo sapiens (human),
path:hsa04657 → IL-17 signaling pathway - Homo sapiens (human),
path:hsa04658 → Th1 and Th2 cell differentiation - Homo sapiens (human),
path:hsa04659 → Th17 cell differentiation - Homo sapiens (human),
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path:hsa04660 → T cell receptor signaling pathway - Homo sapiens (human),
path:hsa04662 → B cell receptor signaling pathway - Homo sapiens (human),
path:hsa04664 → Fc epsilon RI signaling pathway - Homo sapiens (human),
path:hsa04666 → Fc gamma R-mediated phagocytosis - Homo sapiens (human),
path:hsa04668 → TNF signaling pathway - Homo sapiens (human),
path:hsa04670 → Leukocyte transendothelial migration - Homo sapiens (human),
path:hsa04672 → Intestinal immune network for IgA production - Homo sapiens (human),
path:hsa04710 → Circadian rhythm - Homo sapiens (human),
path:hsa04713 → Circadian entrainment - Homo sapiens (human),
path:hsa04714 → Thermogenesis - Homo sapiens (human),
path:hsa04720 → Long-term potentiation - Homo sapiens (human),
path:hsa04721 → Synaptic vesicle cycle - Homo sapiens (human),
path:hsa04722 → Neurotrophin signaling pathway - Homo sapiens (human),
path:hsa04723 → Retrograde endocannabinoid signaling - Homo sapiens (human),
path:hsa04724 → Glutamatergic synapse - Homo sapiens (human),
path:hsa04725 → Cholinergic synapse - Homo sapiens (human),
path:hsa04726 → Serotonergic synapse - Homo sapiens (human),
path:hsa04727 → GABAergic synapse - Homo sapiens (human),
path:hsa04728 → Dopaminergic synapse - Homo sapiens (human),
path:hsa04730 → Long-term depression - Homo sapiens (human),
path:hsa04740 → Olfactory transduction - Homo sapiens (human),
path:hsa04742 → Taste transduction - Homo sapiens (human),
path:hsa04744 → Phototransduction - Homo sapiens (human),
path:hsa04750 → Inflammatory mediator regulation of TRP channels - Homo sapiens (human),
path:hsa04810 → Regulation of actin cytoskeleton - Homo sapiens (human),
path:hsa04910 → Insulin signaling pathway - Homo sapiens (human),
path:hsa04911 → Insulin secretion - Homo sapiens (human),
path:hsa04912 → GnRH signaling pathway - Homo sapiens (human),
path:hsa04913 → Ovarian steroidogenesis - Homo sapiens (human),
path:hsa04914 → Progesterone-mediated oocyte maturation - Homo sapiens (human),
path:hsa04915 → Estrogen signaling pathway - Homo sapiens (human),
path:hsa04916 → Melanogenesis - Homo sapiens (human),
path:hsa04917 → Prolactin signaling pathway - Homo sapiens (human),
path:hsa04918 → Thyroid hormone synthesis - Homo sapiens (human),
path:hsa04919 → Thyroid hormone signaling pathway - Homo sapiens (human),
path:hsa04920 → Adipocytokine signaling pathway - Homo sapiens (human),
path:hsa04921 → Oxytocin signaling pathway - Homo sapiens (human),
path:hsa04922 → Glucagon signaling pathway - Homo sapiens (human),
path:hsa04923 → Regulation of lipolysis in adipocytes - Homo sapiens (human),
path:hsa04924 → Renin secretion - Homo sapiens (human),
path:hsa04925 → Aldosterone synthesis and secretion - Homo sapiens (human),
path:hsa04926 → Relaxin signaling pathway - Homo sapiens (human),
path:hsa04927 → Cortisol synthesis and secretion - Homo sapiens (human),
path:hsa04928 → Parathyroid hormone synthesis, secretion and action - Homo sapiens (human),
path:hsa04930 → Type II diabetes mellitus - Homo sapiens (human),
path:hsa04931 → Insulin resistance - Homo sapiens (human),
path:hsa04932 → Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
path:hsa04933 → AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human),
path:hsa04934 → Cushing syndrome - Homo sapiens (human),
path:hsa04940 → Type I diabetes mellitus - Homo sapiens (human),
path:hsa04950 → Maturity onset diabetes of the young - Homo sapiens (human),
path:hsa04960 → Aldosterone-regulated sodium reabsorption - Homo sapiens (human),
path:hsa04961 → Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
path:hsa04962 → Vasopressin-regulated water reabsorption - Homo sapiens (human),
path:hsa04964 → Proximal tubule bicarbonate reclamation - Homo sapiens (human),
path:hsa04966 → Collecting duct acid secretion - Homo sapiens (human),
path:hsa04970 → Salivary secretion - Homo sapiens (human),
path:hsa04971 → Gastric acid secretion - Homo sapiens (human),
path:hsa04972 → Pancreatic secretion - Homo sapiens (human),
path:hsa04973 → Carbohydrate digestion and absorption - Homo sapiens (human),
path:hsa04974 → Protein digestion and absorption - Homo sapiens (human),
path:hsa04975 → Fat digestion and absorption - Homo sapiens (human),
path:hsa04976 → Bile secretion - Homo sapiens (human),
path:hsa04977 → Vitamin digestion and absorption - Homo sapiens (human),
path:hsa04978 → Mineral absorption - Homo sapiens (human),
path:hsa04979 → Cholesterol metabolism - Homo sapiens (human),
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path:hsa05010 → Alzheimer disease - Homo sapiens (human),
path:hsa05012 → Parkinson disease - Homo sapiens (human),
path:hsa05014 → Amyotrophic lateral sclerosis (ALS) - Homo sapiens (human),
path:hsa05016 → Huntington disease - Homo sapiens (human),
path:hsa05020 → Prion diseases - Homo sapiens (human),
path:hsa05030 → Cocaine addiction - Homo sapiens (human),
path:hsa05031 → Amphetamine addiction - Homo sapiens (human),
path:hsa05032 → Morphine addiction - Homo sapiens (human),
path:hsa05033 → Nicotine addiction - Homo sapiens (human),
path:hsa05034 → Alcoholism - Homo sapiens (human),
path:hsa05100 → Bacterial invasion of epithelial cells - Homo sapiens (human),
path:hsa05110 → Vibrio cholerae infection - Homo sapiens (human),
path:hsa05120 → Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
path:hsa05130 → Pathogenic Escherichia coli infection - Homo sapiens (human),
path:hsa05131 → Shigellosis - Homo sapiens (human),
path:hsa05132 → Salmonella infection - Homo sapiens (human),
path:hsa05133 → Pertussis - Homo sapiens (human), path:hsa05134 → Legionellosis - Homo sapiens (human),
path:hsa05135 → Yersinia infection - Homo sapiens (human),
path:hsa05140 → Leishmaniasis - Homo sapiens (human),
path:hsa05142 → Chagas disease (American trypanosomiasis) - Homo sapiens (human),
path:hsa05143 → African trypanosomiasis - Homo sapiens (human),
path:hsa05144 → Malaria - Homo sapiens (human), path:hsa05145 → Toxoplasmosis - Homo sapiens (human),
path:hsa05146 → Amoebiasis - Homo sapiens (human),
path:hsa05150 → Staphylococcus aureus infection - Homo sapiens (human),
path:hsa05152 → Tuberculosis - Homo sapiens (human), path:hsa05160 → Hepatitis C - Homo sapiens (human),
path:hsa05161 → Hepatitis B - Homo sapiens (human), path:hsa05162 → Measles - Homo sapiens (human),
path:hsa05163 → Human cytomegalovirus infection - Homo sapiens (human),
path:hsa05164 → Influenza A - Homo sapiens (human),
path:hsa05165 → Human papillomavirus infection - Homo sapiens (human),
path:hsa05166 → Human T-cell leukemia virus 1 infection - Homo sapiens (human),
path:hsa05167 → Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human),
path:hsa05168 → Herpes simplex virus 1 infection - Homo sapiens (human),
path:hsa05169 → Epstein-Barr virus infection - Homo sapiens (human),
path:hsa05170 → Human immunodeficiency virus 1 infection - Homo sapiens (human),
path:hsa05200 → Pathways in cancer - Homo sapiens (human),
path:hsa05202 → Transcriptional misregulation in cancer - Homo sapiens (human),
path:hsa05203 → Viral carcinogenesis - Homo sapiens (human),
path:hsa05204 → Chemical carcinogenesis - Homo sapiens (human),
path:hsa05205 → Proteoglycans in cancer - Homo sapiens (human),
path:hsa05206 → MicroRNAs in cancer - Homo sapiens (human),
path:hsa05210 → Colorectal cancer - Homo sapiens (human),
path:hsa05211 → Renal cell carcinoma - Homo sapiens (human),
path:hsa05212 → Pancreatic cancer - Homo sapiens (human),
path:hsa05213 → Endometrial cancer - Homo sapiens (human),
path:hsa05214 → Glioma - Homo sapiens (human), path:hsa05215 → Prostate cancer - Homo sapiens (human),
path:hsa05216 → Thyroid cancer - Homo sapiens (human),
path:hsa05217 → Basal cell carcinoma - Homo sapiens (human),
path:hsa05218 → Melanoma - Homo sapiens (human), path:hsa05219 → Bladder cancer - Homo sapiens (human),
path:hsa05220 → Chronic myeloid leukemia - Homo sapiens (human),
path:hsa05221 → Acute myeloid leukemia - Homo sapiens (human),
path:hsa05222 → Small cell lung cancer - Homo sapiens (human),
path:hsa05223 → Non-small cell lung cancer - Homo sapiens (human),
path:hsa05224 → Breast cancer - Homo sapiens (human),
path:hsa05225 → Hepatocellular carcinoma - Homo sapiens (human),
path:hsa05226 → Gastric cancer - Homo sapiens (human),
path:hsa05230 → Central carbon metabolism in cancer - Homo sapiens (human),
path:hsa05231 → Choline metabolism in cancer - Homo sapiens (human),
path:hsa05235 → PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
path:hsa05310 → Asthma - Homo sapiens (human),
path:hsa05320 → Autoimmune thyroid disease - Homo sapiens (human),
path:hsa05321 → Inflammatory bowel disease (IBD) - Homo sapiens (human),
path:hsa05322 → Systemic lupus erythematosus - Homo sapiens (human),
path:hsa05323 → Rheumatoid arthritis - Homo sapiens (human),
path:hsa05330 → Allograft rejection - Homo sapiens (human),
path:hsa05332 → Graft-versus-host disease - Homo sapiens (human),
path:hsa05340 → Primary immunodeficiency - Homo sapiens (human),
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path:hsa05410 → Hypertrophic cardiomyopathy (HCM) - Homo sapiens (human),
path:hsa05412 → Arrhythmogenic right ventricular cardiomyopathy (ARVC) - Homo sapiens (human),
path:hsa05414 → Dilated cardiomyopathy (DCM) - Homo sapiens (human),
path:hsa05416 → Viral myocarditis - Homo sapiens (human),
path:hsa05418 → Fluid shear stress and atherosclerosis - Homo sapiens (human) |〉
```

In[3]:=
```
keggExampleDictionaryOpts1 =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
   "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1",
   "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, KEGGDictionaryVariable → keggDictionaryVar]
```

Out[3]=
```
〈|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
   {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
 path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
   {Epstein-Barr virus infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
   {Toll-like receptor signaling pathway - Homo sapiens (human),
    {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05168 → {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8},
   {Herpes simplex virus 1 infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
 path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
   {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
   {B cell receptor signaling pathway - Homo sapiens (human),
    {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
 path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
   {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
   {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
 path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
   {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
    {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
   {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
    {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
   {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
   {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
 path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
   {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
   {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
    {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
 path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
   {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
 path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
   {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
 path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
   {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
 path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
   {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
 path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
   {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
 path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
   {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
```

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```
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

KEGGMolecular (1)

```
In[1]:= Needs["MathIOmica`"]
```

KEGGMolecular specifies which database to use for molecular analysis. The default is the compound database ("cpd").

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```
In[2]:= compoundsExample =
  {{"cpd:C19691", 325.2075`, 10.677681`, "Meta"}, {"cpd:C17905", 594.2002`, 8.727458`, "Meta"},
   {"cpd:C09921", 204.0784`, 12.3909445`, "Meta"}, {"cpd:C18218", 272.2356`, 13.473582`, "Meta"},
   {"cpd:C14169", 235.1573`, 12.267084`, "Meta"}, {"cpd:C14245", 262.2296`, 13.545572`, "Meta"},
   {"cpd:C09137", 352.2615`, 14.0554285`, "Meta"}, {"cpd:C09674", 296.1624`, 12.147417`, "Meta"},
   {"cpd:C00449", 276.1334`, 11.004139`, "Meta"}, {"cpd:C02999", 364.1497`, 12.147243`, "Meta"},
   {"cpd:C07915", 309.194`, 7.3625283`, "Meta"}, {"cpd:C08760", 496.2309`, 8.7241125`, "Meta"},
   {"cpd:C14549", 276.0972`, 11.078914`, "Meta"}, {"cpd:C20533", 601.3378`, 12.75722`, "Meta"},
   {"cpd:C20790", 212.1051`, 7.127666`, "Meta"}, {"cpd:C09137", 352.2613`, 12.869867`, "Meta"},
   {"cpd:C17648", 400.2085`, 10.843841`, "Meta"}, {"cpd:C07807", 240.1471`, 0.48564285`, "Meta"},
   {"cpd:C08564", 324.0948`, 10.281`, "Meta"}, {"cpd:C19426", 338.2818`, 13.758765`, "Meta"},
   {"cpd:C02943", 468.3218`, 14.263261`, "Meta"}, {"cpd:C04882", 1193.342`, 14.707576`, "Meta"}};

In[3]:= KEGGAnalysis[compoundsExample, AnalysisType → "Molecular", KEGGMolecular → "cpd"]

Out[3]= <|path:map00300 → {{0.00020774, 0.00186966, True}, {4, 35, 5841, 2}, {Lysine biosynthesis,
    {{{cpd:C00449, 276.133, 11.0041, Meta}}, {{cpd:C04882, 1193.34, 14.7076, Meta}}}}}|>
```

KEGGOrganism (1)

```
In[1]:= Needs["MathIOmica`"]
```

KEGGOrganism indicates which organism (org) to use for "Genomic" type of analysis. The default is human analysis org="hsa".

```
In[2]:= keggExampleOrg = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1",
   "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
   "NFKBIA", "IRAK4", "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"}, KEGGOrganism → "hsa"]

Out[2]= <|path:hsa04064 → {{3.27957×10^-37, 2.62366×10^-35, True},
    {25, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05169 → {{2.69713×10^-11, 1.07885×10^-9, True}, {25, 204, 7086, 11},
    {Epstein-Barr virus infection - Homo sapiens (human), {{TAB1}, {CHUK}, {CSNK2A1},
      {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
  path:hsa05162 → {{1.23085×10^-8, 3.28226×10^-7, True}, {25, 136, 7086, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04620 → {{5.28996×10^-8, 1.05799×10^-6, True}, {25, 106, 7086, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05168 → {{1.43121×10^-7, 2.28994×10^-6, True}, {25, 186, 7086, 8},
    {Herpes simplex virus 1 infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa04623 → {{2.37065×10^-6, 0.0000308255, True}, {25, 64, 7086, 5},
    {Cytosolic DNA-sensing pathway - Homo sapiens (human),
     {{CHUK}, {NFKB1}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
  path:hsa05145 → {{2.69723×10^-6, 0.0000308255, True}, {25, 119, 7086, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04662 → {{4.57186×10^-6, 0.0000434807, True}, {25, 73, 7086, 5},
    {B cell receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05140 → {{4.89158×10^-6, 0.0000434807, True}, {25, 74, 7086, 5},
    {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{6.94486×10^-6, 0.0000555589, True}, {25, 140, 7086, 6},
    {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{0.0000219498, 0.000159635, True}, {25, 259, 7086, 7},
    {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
     {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000260113, 0.000173409, True}, {25, 104, 7086, 5},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
```

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```
 {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05134 → {{0.0000364135, 0.000224083, True}, {25, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{0.0000419741, 0.000239852, True}, {25, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000818726, 0.000421518, True}, {25, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000843036, 0.000421518, True}, {25, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05133 → {{0.000123744, 0.000582327, True},
  {25, 75, 7086, 4}, {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05161 → {{0.000132079, 0.000587018, True}, {25, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05152 → {{0.000342678, 0.00144285, True}, {25, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa00240 → {{0.000453162, 0.00172633, True}, {25, 105, 7086, 4},
  {Pyrimidine metabolism - Homo sapiens (human), {{POLR3B}, {NME1}, {CTPS1}, {POLR3A}}}},
path:hsa04660 → {{0.000453162, 0.00172633, True}, {25, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.000540824, 0.00196663, True}, {25, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.00063924, 0.00222344, True}, {25, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.000681647, 0.00227216, True}, {25, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa05131 → {{0.001467, 0.00469441, True},
  {25, 65, 7086, 3}, {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04010 → {{0.00170641, 0.00519202, True}, {25, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04622 → {{0.00181721, 0.00519202, True}, {25, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00181721, 0.00519202, True}, {25, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00205037, 0.00565621, True}, {25, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00213205, 0.00568546, True}, {25, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00309301, 0.00798195, True}, {25, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00327339, 0.00818346, True}, {25, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00360717, 0.00848745, True}, {25, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00360717, 0.00848745, True}, {25, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00384779, 0.00879494, True}, {25, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03020 → {{0.00555558, 0.0123457, True}, {25, 32, 7086, 2},
  {RNA polymerase - Homo sapiens (human), {{POLR3B}, {POLR3A}}}},
path:hsa04722 → {{0.00830127, 0.0179487, True}, {25, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0109938, 0.0230144, True}, {25, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.0112195, 0.0230144, True}, {25, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.0123888, 0.0247777, True}, {25, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.0133733, 0.0260942, True}, {25, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0169404, 0.0322673, True}, {25, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05212 → {{0.0223323, 0.0415485, True}, {25, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa00230 → {{0.0231928, 0.0421686, True}, {25, 176, 7086, 3},
```

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```
    {Purine metabolism - Homo sapiens (human), {{POLR3B}, {NME1}, {POLR3A}}}},
  path:hsa04115 → {{0.0242685, 0.0427679, True}, {25, 69, 7086, 2},
    {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa05202 → {{0.0245915, 0.0427679, True}, {25, 180, 7086, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}}|⟩
```

MathIOmicaDataDirectory (1)

```
In[1]:= Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value point to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

```
In[2]:= KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
    "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4",
    "PIAS4", "PLAU", "POLR3B", "NME1", "CTPS1", "POLR3A"}, MathIOmicaDataDirectory → FileNameJoin[
     Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]

Out[2]= ⟨|path:hsa04064 → {{3.27957×10^-37, 2.62366×10^-35, True},
    {25, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05169 → {{2.69713×10^-11, 1.07885×10^-9, True}, {25, 204, 7086, 11},
    {Epstein-Barr virus infection - Homo sapiens (human), {{TAB1}, {CHUK}, {CSNK2A1},
      {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
  path:hsa05162 → {{1.23085×10^-8, 3.28226×10^-7, True}, {25, 136, 7086, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04620 → {{5.28996×10^-8, 1.05799×10^-6, True}, {25, 106, 7086, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05168 → {{1.43121×10^-7, 2.28994×10^-6, True}, {25, 186, 7086, 8},
    {Herpes simplex virus 1 infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa04623 → {{2.37065×10^-6, 0.0000308255, True}, {25, 64, 7086, 5},
    {Cytosolic DNA-sensing pathway - Homo sapiens (human),
     {{CHUK}, {NFKB1}, {NFKBIA}, {POLR3B}, {POLR3A}}}},
  path:hsa05145 → {{2.69723×10^-6, 0.0000308255, True}, {25, 119, 7086, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04662 → {{4.57186×10^-6, 0.0000434807, True}, {25, 73, 7086, 5},
    {B cell receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05140 → {{4.89158×10^-6, 0.0000434807, True}, {25, 74, 7086, 5},
    {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{6.94486×10^-6, 0.0000555589, True}, {25, 140, 7086, 6},
    {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{0.0000219498, 0.000159635, True}, {25, 259, 7086, 7},
    {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
     {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000260113, 0.000173409, True}, {25, 104, 7086, 5},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
     {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05134 → {{0.0000364135, 0.000224083, True}, {25, 55, 7086, 4},
    {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04621 → {{0.0000419741, 0.000239852, True}, {25, 57, 7086, 4},
    {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04380 → {{0.0000818726, 0.000421518, True}, {25, 132, 7086, 5},
    {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05120 → {{0.0000843036, 0.000421518, True}, {25, 68, 7086, 4},
    {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
```

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```
  {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05133 → {{0.000123744, 0.000582327, True},
  {25, 75, 7086, 4}, {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05161 → {{0.000132079, 0.000587018, True}, {25, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05152 → {{0.000342678, 0.00144285, True}, {25, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa00240 → {{0.000453162, 0.00172633, True}, {25, 105, 7086, 4},
  {Pyrimidine metabolism - Homo sapiens (human), {{POLR3B}, {NME1}, {CTPS1}, {POLR3A}}}},
path:hsa04660 → {{0.000453162, 0.00172633, True}, {25, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.000540824, 0.00196663, True}, {25, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.00063924, 0.00222344, True}, {25, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.000681647, 0.00227216, True}, {25, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa05131 → {{0.001467, 0.00469441, True},
  {25, 65, 7086, 3}, {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04010 → {{0.00170641, 0.00519202, True}, {25, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04622 → {{0.00181721, 0.00519202, True}, {25, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00181721, 0.00519202, True}, {25, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00205037, 0.00565621, True}, {25, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00213205, 0.00568546, True}, {25, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00309301, 0.00798195, True}, {25, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00327339, 0.00818346, True}, {25, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00360717, 0.00848745, True}, {25, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00360717, 0.00848745, True}, {25, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00384779, 0.00879494, True}, {25, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03020 → {{0.00555558, 0.0123457, True}, {25, 32, 7086, 2},
  {RNA polymerase - Homo sapiens (human), {{POLR3B}, {POLR3A}}}},
path:hsa04722 → {{0.00830127, 0.0179487, True}, {25, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0109938, 0.0230144, True}, {25, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.0112195, 0.0230144, True}, {25, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.0123888, 0.0247777, True}, {25, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.0133733, 0.0260942, True}, {25, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0169404, 0.0322673, True}, {25, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05212 → {{0.0223323, 0.0415485, True}, {25, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa00230 → {{0.0231928, 0.0421686, True}, {25, 176, 7086, 3},
  {Purine metabolism - Homo sapiens (human), {{POLR3B}, {NME1}, {POLR3A}}}},
path:hsa04115 → {{0.0242685, 0.0427679, True}, {25, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05202 → {{0.0245915, 0.0427679, True}, {25, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}}|>
```

MolecularInputID (1)

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```
In[1]:= Needs["MathIOmica`"]
```

MolecularInputID is a string list to indicate the kind of ID to use for the input molecule entries. The default is {"cpd"}:

```
In[2]:= KEGGAnalysis[{{"cpd:C19691", 325.2075`, 10.677681`, "Meta"}, {"cpd:C17905", 594.2002`, 8.727458`, "Meta"},
   {"cpd:C09921", 204.0784`, 12.3909445`, "Meta"}, {"cpd:C18218", 272.2356`, 13.473582`, "Meta"},
   {"cpd:C14169", 235.1573`, 12.267084`, "Meta"}, {"cpd:C14245", 262.2296`, 13.545572`, "Meta"},
   {"cpd:C09137", 352.2615`, 14.0554285`, "Meta"}, {"cpd:C09674", 296.1624`, 12.147417`, "Meta"},
   {"cpd:C00449", 276.1334`, 11.004139`, "Meta"}, {"cpd:C02999", 364.1497`, 12.147243`, "Meta"},
   {"cpd:C07915", 309.194`, 7.3625283`, "Meta"}, {"cpd:C08760", 496.2309`, 8.7241125`, "Meta"},
   {"cpd:C14549", 276.0972`, 11.078914`, "Meta"}, {"cpd:C20533", 601.3378`, 12.75722`, "Meta"},
   {"cpd:C20790", 212.1051`, 7.127666`, "Meta"}, {"cpd:C09137", 352.2613`, 12.869867`, "Meta"},
   {"cpd:C17648", 400.2085`, 10.843841`, "Meta"}, {"cpd:C07807", 240.1471`, 0.48564285`, "Meta"},
   {"cpd:C08564", 324.0948`, 10.281`, "Meta"}, {"cpd:C19426", 338.2818`, 13.758765`, "Meta"},
   {"cpd:C02943", 468.3218`, 14.263261`, "Meta"}, {"cpd:C04882", 1193.342`, 14.707576`, "Meta"}},
  AnalysisType → "Molecular", MolecularInputID → {"cpd"}]

Out[2]= <|path:map00300 → {{0.00020774, 0.00186966, True}, {4, 35, 5841, 2}, {Lysine biosynthesis,
      {{{cpd:C00449, 276.133, 11.0041, Meta}}, {{cpd:C04882, 1193.34, 14.7076, Meta}}}}}|>
```

MolecularOutputID (1)

```
In[1]:= Needs["MathIOmica`"]
```

MolecularOutputID is a string to indicate the kind of ID to convert input molecule entries. The default is "cpd" consistently with use of the "cpd" database as the default molecular analysis.

```
In[2]:= KEGGAnalysis[{{"cpd:C19691", 325.2075`, 10.677681`, "Meta"}, {"cpd:C17905", 594.2002`, 8.727458`, "Meta"},
   {"cpd:C09921", 204.0784`, 12.3909445`, "Meta"}, {"cpd:C18218", 272.2356`, 13.473582`, "Meta"},
   {"cpd:C14169", 235.1573`, 12.267084`, "Meta"}, {"cpd:C14245", 262.2296`, 13.545572`, "Meta"},
   {"cpd:C09137", 352.2615`, 14.0554285`, "Meta"}, {"cpd:C09674", 296.1624`, 12.147417`, "Meta"},
   {"cpd:C00449", 276.1334`, 11.004139`, "Meta"}, {"cpd:C02999", 364.1497`, 12.147243`, "Meta"},
   {"cpd:C07915", 309.194`, 7.3625283`, "Meta"}, {"cpd:C08760", 496.2309`, 8.7241125`, "Meta"},
   {"cpd:C14549", 276.0972`, 11.078914`, "Meta"}, {"cpd:C20533", 601.3378`, 12.75722`, "Meta"},
   {"cpd:C20790", 212.1051`, 7.127666`, "Meta"}, {"cpd:C09137", 352.2613`, 12.869867`, "Meta"},
   {"cpd:C17648", 400.2085`, 10.843841`, "Meta"}, {"cpd:C07807", 240.1471`, 0.48564285`, "Meta"},
   {"cpd:C08564", 324.0948`, 10.281`, "Meta"}, {"cpd:C19426", 338.2818`, 13.758765`, "Meta"},
   {"cpd:C02943", 468.3218`, 14.263261`, "Meta"}, {"cpd:C04882", 1193.342`, 14.707576`, "Meta"}},
  AnalysisType → "Molecular", MolecularOutputID → "cpd"]

Out[2]= <|path:map00300 → {{0.00020774, 0.00186966, True}, {4, 35, 5841, 2}, {Lysine biosynthesis,
      {{{cpd:C00449, 276.133, 11.0041, Meta}}, {{cpd:C04882, 1193.34, 14.7076, Meta}}}}}|>
```

MolecularSpecies (1)

```
In[1]:= Needs["MathIOmica`"]
```

MolecularSpecies specifies the kind of molecular input. The default is "compound":

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```
In[2]:= KEGGAnalysis[{{"cpd:C19691", 325.2075`, 10.677681`, "Meta"}, {"cpd:C17905", 594.2002`, 8.727458`, "Meta"},
  {"cpd:C09921", 204.0784`, 12.3909445`, "Meta"}, {"cpd:C18218", 272.2356`, 13.473582`, "Meta"},
  {"cpd:C14169", 235.1573`, 12.267084`, "Meta"}, {"cpd:C14245", 262.2296`, 13.545572`, "Meta"},
  {"cpd:C09137", 352.2615`, 14.0554285`, "Meta"}, {"cpd:C09674", 296.1624`, 12.147417`, "Meta"},
  {"cpd:C00449", 276.1334`, 11.004139`, "Meta"}, {"cpd:C02999", 364.1497`, 12.147243`, "Meta"},
  {"cpd:C07915", 309.194`, 7.3625283`, "Meta"}, {"cpd:C08760", 496.2309`, 8.7241125`, "Meta"},
  {"cpd:C14549", 276.0972`, 11.078914`, "Meta"}, {"cpd:C20533", 601.3378`, 12.75722`, "Meta"},
  {"cpd:C20790", 212.1051`, 7.127666`, "Meta"}, {"cpd:C09137", 352.2613`, 12.869867`, "Meta"},
  {"cpd:C17648", 400.2085`, 10.843841`, "Meta"}, {"cpd:C07807", 240.1471`, 0.48564285`, "Meta"},
  {"cpd:C08564", 324.0948`, 10.281`, "Meta"}, {"cpd:C19426", 338.2818`, 13.758765`, "Meta"},
  {"cpd:C02943", 468.3218`, 14.263261`, "Meta"}, {"cpd:C04882", 1193.342`, 14.707576`, "Meta"}},
 AnalysisType → "Molecular", MolecularSpecies → "compound"]

Out[2]= <|path:map00300 → {{0.00020774, 0.00186966, True}, {4, 35, 5841, 2}, {Lysine biosynthesis,
    {{{cpd:C00449, 276.133, 11.0041, Meta}}, {{cpd:C04882, 1193.34, 14.7076, Meta}}}}}|>
```

MultipleList (1)

```
In[1]:= Needs["MathIOmica`"]
```

MultipleList option specifies whether the input accessions list constituted a multi-omics list input that is annotated so. Each ID j input must be a list form, i.e. enclosed as $\{ID_j\}$. If this is the case, MultipleList is set to True and each input list ID should have the form {ID,"Omics Type Label"}, e.g. {"NFKB1","Protein"}, and the different omics type are treated as different for each ID. If MultipleList is set to False, and labeled IDs are provided, labels corresponding to the same ID are treated as equivalent to avoid overcounting.

```
In[2]:= analysisKEGGMultipleListFalse =
 KEGGAnalysis[{{"TAB1", "Protein"}, {"TAB1", "RNA"}, {"TNFSF13B", "Protein"}, {"MALT1", "RNA"},
   {"TIRAP", "RNA"}, {"CHUK", "Protein"}, {"TNFRSF13C", "Protein"}, {"PARP1", "RNA"},
   {"CSNK2A1", "RNA"}, {"CSNK2A2", "RNA"}, {"CSNK2B", "RNA"}, {"LTBR", "Protein"}, {"LTBR", "RNA"},
   {"LYN", "RNA"}, {"MYD88", "Protein"}, {"GADD45B", "Protein"} {"ATM", "RNA"}, {"NFKB1", "Protein"},
   {"NFKB1", "RNA"}, {"NFKB2", "Protein"}, {"NFKBIA", "RNA"}, {"NFKBIA", "Protein"},
   {"IRAK4", "RNA"}, {"PIAS4", "RNA"}, {"PLAU", "Protein"}}, MultipleList → False]

Out[2]= <|path:hsa04064 → {{2.4921×10^-37, 1.81923×10^-35, True}, {19, 93, 7086, 19},
   {NF-kappa B signaling pathway - Homo sapiens (human), {{{TAB1, Protein}, {TAB1, RNA}},
     {{TNFSF13B, Protein}}, {{MALT1, RNA}}, {{TIRAP, RNA}}, {{CHUK, Protein}}, {{TNFRSF13C, Protein}},
     {{PARP1, RNA}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}, {{LTBR, Protein}, {LTBR, RNA}},
     {{LYN, RNA}}, {{MYD88, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKB2, Protein}},
     {{NFKBIA, Protein}, {NFKBIA, RNA}}, {{IRAK4, RNA}}, {{PIAS4, RNA}}, {{PLAU, Protein}}}}},
 path:hsa05169 → {{8.20575×10^-10, 2.30647×10^-8, True}, {19, 204, 7086, 9},
   {Epstein-Barr virus infection - Homo sapiens (human), {{{TAB1, Protein}, {TAB1, RNA}},
     {{CHUK, Protein}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}, {{LYN, RNA}},
     {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
 path:hsa05162 → {{9.47866×10^-10, 2.30647×10^-8, True}, {19, 136, 7086, 8}, {Measles - Homo sapiens (human),
    {{{CHUK, Protein}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}, {{MYD88, Protein}},
     {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}, {{IRAK4, RNA}}}}},
 path:hsa04620 → {{5.96971×10^-9, 1.08947×10^-7, True}, {19, 106, 7086, 7},
   {Toll-like receptor signaling pathway - Homo sapiens (human),
    {{{TAB1, Protein}, {TAB1, RNA}}, {{TIRAP, RNA}}, {{CHUK, Protein}}, {{MYD88, Protein}},
     {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}, {{IRAK4, RNA}}}}},
 path:hsa05168 → {{1.14509×10^-8, 1.67184×10^-7, True}, {19, 186, 7086, 8},
   {Herpes simplex virus 1 infection - Homo sapiens (human),
    {{{TAB1, Protein}, {TAB1, RNA}}, {{CHUK, Protein}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}},
     {{MYD88, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
 path:hsa05145 → {{4.48724×10^-7, 5.45947×10^-6, True}, {19, 119, 7086, 6},
   {Toxoplasmosis - Homo sapiens (human),
    {{{TAB1, Protein}, {TAB1, RNA}}, {{CHUK, Protein}}, {{MYD88, Protein}},
```

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```
    {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}, {{IRAK4, RNA}}}}},
path:hsa04662 → {{1.04992×10^-6, 0.0000102577, True}, {19, 73, 7086, 5},
  {B cell receptor signaling pathway - Homo sapiens (human), {{{MALT1, RNA}}, {{CHUK, Protein}},
    {{LYN, RNA}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}}},
path:hsa05140 → {{1.12414×10^-6, 0.0000102577, True}, {19, 74, 7086, 5},
  {Leishmaniasis - Homo sapiens (human), {{{TAB1, Protein}, {TAB1, RNA}}, {{MYD88, Protein}},
    {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}, {{IRAK4, RNA}}}}},
path:hsa05142 → {{6.10593×10^-6, 0.0000495259, True}, {19, 104, 7086, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{{CHUK, Protein}}, {{MYD88, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}},
    {{NFKBIA, Protein}, {NFKBIA, RNA}}, {{IRAK4, RNA}}}}},
path:hsa05134 → {{0.0000115499, 0.0000843141, True}, {19, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{{MYD88, Protein}},
    {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
path:hsa04621 → {{0.0000133317, 0.0000884738, True}, {19, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{{TAB1, Protein}, {TAB1, RNA}},
    {{CHUK, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
path:hsa04380 → {{0.0000196034, 0.000119254, True}, {19, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{{TAB1, Protein}, {TAB1, RNA}}, {{CHUK, Protein}},
    {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
path:hsa05120 → {{0.0000269763, 0.000151483, True}, {19, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human), {{{CHUK, Protein}},
    {{LYN, RNA}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
path:hsa05161 → {{0.0000319395, 0.000166542, True}, {19, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{{TIRAP, RNA}}, {{CHUK, Protein}},
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path:hsa05133 → {{0.000039785, 0.000186475, True}, {19, 75, 7086, 4}, {Pertussis - Homo sapiens (human),
   {{{TIRAP, RNA}}, {{MYD88, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{IRAK4, RNA}}}}},
path:hsa05166 → {{0.0000408713, 0.000186475, True}, {19, 259, 7086, 6},
  {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
   {{{CHUK, Protein}}, {{TNFRSF13C, Protein}}, {{LTBR, Protein}, {LTBR, RNA}},
    {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
path:hsa05152 → {{0.0000848234, 0.000364242, True}, {19, 179, 7086, 5},
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   {{{MALT1, RNA}}, {{TIRAP, RNA}}, {{MYD88, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{IRAK4, RNA}}}}},
path:hsa04660 → {{0.000148679, 0.000602977, True}, {19, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{{MALT1, RNA}},
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  {Viral carcinogenesis - Homo sapiens (human), {{{LTBR, Protein}, {LTBR, RNA}}, {{LYN, RNA}},
    {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
path:hsa04668 → {{0.00017804, 0.000649845, True}, {19, 110, 7086, 4},
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    {{CHUK, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
path:hsa04672 → {{0.000295871, 0.0010285, True}, {19, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
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path:hsa04210 → {{0.000449179, 0.00149046, True}, {19, 140, 7086, 4},
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  {Chronic myeloid leukemia - Homo sapiens (human),
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    {{{CHUK, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}, {{NFKBIA, Protein}, {NFKBIA, RNA}}}}},
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  {Tight junction - Homo sapiens (human), {{{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}}}},
path:hsa04310 → {{0.0061529, 0.01182, True}, {19, 143, 7086, 3},
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  {Acute myeloid leukemia - Homo sapiens (human), {{{CHUK, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}}}},
path:hsa05212 → {{0.0131931, 0.0240774, True}, {19, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{{CHUK, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}}}},
path:hsa05200 → {{0.0192286, 0.0342363, True}, {19, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{{CHUK, Protein}}},
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path:hsa05132 → {{0.0217771, 0.0378507, True}, {19, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{{MYD88, Protein}}, {{NFKB1, Protein}, {NFKB1, RNA}}}}}|⟩
```

We can instead treat the data as different by setting the `MultipleList` option to True. In this case IDs with different label e.g ({NFKB1,Protein},{NFKB1,RNA}) are treated as different and counted as such:

```
In[3]:= analysisKEGGMultipleListTrue =
  KEGGAnalysis[{{"TAB1", "Protein"}, {"TAB1", "RNA"}, {"TNFSF13B", "Protein"}, {"MALT1", "RNA"},
    {"TIRAP", "RNA"}, {"CHUK", "Protein"}, {"TNFRSF13C", "Protein"}, {"PARP1", "RNA"},
    {"CSNK2A1", "RNA"}, {"CSNK2A2", "RNA"}, {"CSNK2B", "RNA"}, {"LTBR", "Protein"}, {"LTBR", "RNA"},
    {"LYN", "RNA"}, {"MYD88", "Protein"}, {"GADD45B", "Protein"} {"ATM", "RNA"}, {"NFKB1", "Protein"},
    {"NFKB1", "RNA"}, {"NFKB2", "Protein"}, {"NFKBIA", "RNA"}, {"NFKBIA", "Protein"},
    {"IRAK4", "RNA"}, {"PIAS4", "RNA"}, {"PLAU", "Protein"}}, MultipleList → True]

Out[3]= ⟨|path:hsa04064 → {{2.76146×10^-45, 2.01587×10^-43, True}, {23, 93, 7086, 23},
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    {{TNFSF13B, Protein}}, {{MALT1, RNA}}, {{TIRAP, RNA}}, {{CHUK, Protein}}, {{TNFRSF13C, Protein}},
    {{PARP1, RNA}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}, {{LTBR, Protein}}, {{LTBR, RNA}},
    {{LYN, RNA}}, {{MYD88, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKB2, Protein}},
    {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}, {{PIAS4, RNA}}, {{PLAU, Protein}}}}}},
path:hsa05169 → {{2.40644×10^-13, 8.63463×10^-12, True}, {23, 204, 7086, 12},
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    {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
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  {Toll-like receptor signaling pathway - Homo sapiens (human),
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  {Herpes simplex virus 1 infection - Homo sapiens (human), {{{TAB1, Protein}}, {{TAB1, RNA}},
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     {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
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     {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}}}}},
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     {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
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  {Adipocytokine signaling pathway - Homo sapiens (human),
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  {Pancreatic cancer - Homo sapiens (human), {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}}}}},
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  {Pathways in cancer - Homo sapiens (human), {{{CHUK, Protein}}, {{NFKB1, Protein}},
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  {Cytokine-cytokine receptor interaction - Homo sapiens (human),
   {{{TNFSF13B, Protein}}, {{TNFRSF13C, Protein}}, {{LTBR, Protein}}, {{LTBR, RNA}}}}}},
path:hsa04530 → {{0.00981492, 0.015922, True}, {23, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}}}}},
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  path:hsa05202 → {{0.019647, 0.02927, True}, {23, 180, 7086, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human),
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  path:hsa04917 → {{0.0224458, 0.0327708, True}, {23, 72, 7086, 2},
    {Prolactin signaling pathway - Homo sapiens (human), {{{NFKB1, Protein}}, {{NFKB1, RNA}}}}}}|⟩
```

We using the `MultipleList` option as True we should consider also whether to add a `MultipleListCorrection` option.

MultipleListCorrection (1)

```
In[1]:= Needs["MathIOmica`"]
```

MultipleListCorrection is an option whether or not to correct for multi-omics analysis. The choices are None, Automatic, or a custom number. This essentially enlarges the population by this factor to account for additional IDs being considered as the result of a multi-omics cluster analysis. If the value is set to Automatic the number of unique ID labels is used to make the correction.

```
In[2]:= analysisKEGGMultipleListTrue =
  KEGGAnalysis[{{"TAB1", "Protein"}, {"TAB1", "RNA"}, {"TNFSF13B", "Protein"}, {"MALT1", "RNA"},
    {"TIRAP", "RNA"}, {"CHUK", "Protein"}, {"TNFRSF13C", "Protein"}, {"PARP1", "RNA"},
    {"CSNK2A1", "RNA"}, {"CSNK2A2", "RNA"}, {"CSNK2B", "RNA"}, {"LTBR", "Protein"}, {"LTBR", "RNA"},
    {"LYN", "RNA"}, {"MYD88", "Protein"}, {"GADD45B", "Protein"}, {"ATM", "RNA"}, {"NFKB1", "Protein"},
    {"NFKB1", "RNA"}, {"NFKB2", "Protein"}, {"NFKBIA", "RNA"}, {"NFKBIA", "Protein"}, {"IRAK4", "RNA"},
    {"PIAS4", "RNA"}, {"PLAU", "Protein"}}, MultipleList → True, MultipleListCorrection → Automatic]

Out[2]= ⟨|path:hsa04064 → {{1.68971×10^-48, 1.28418×10^-46, True},
    {25, 186, 14172, 25}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{{TAB1, Protein}}, {{TAB1, RNA}}, {{TNFSF13B, Protein}}, {{MALT1, RNA}}, {{TIRAP, RNA}},
      {{CHUK, Protein}}, {{TNFRSF13C, Protein}}, {{PARP1, RNA}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}},
      {{CSNK2B, RNA}}, {{LTBR, Protein}}, {{LTBR, RNA}}, {{LYN, RNA}}, {{MYD88, Protein}},
      {{GADD45B, Protein}}, {{ATM, RNA}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKB2, Protein}},
      {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}, {{PIAS4, RNA}}, {{PLAU, Protein}}}}}},
  path:hsa05169 → {{1.024×10^-12, 3.08967×10^-11, True}, {25, 408, 14172, 12},
    {Epstein-Barr virus infection - Homo sapiens (human), {{{TAB1, Protein}}, {{TAB1, RNA}},
      {{CHUK, Protein}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}, {{LYN, RNA}},
      {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
  path:hsa04620 → {{1.21961×10^-12, 3.08967×10^-11, True}, {25, 212, 14172, 10},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{{TAB1, Protein}}, {{TAB1, RNA}}, {{TIRAP, RNA}}, {{CHUK, Protein}}, {{MYD88, Protein}},
      {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}}}}},
  path:hsa05168 → {{1.12851×10^-11, 2.14417×10^-10, True}, {25, 372, 14172, 11},
    {Herpes simplex virus 1 infection - Homo sapiens (human), {{{TAB1, Protein}}, {{TAB1, RNA}},
      {{CHUK, Protein}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}, {{MYD88, Protein}},
      {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
  path:hsa05162 → {{1.45884×10^-11, 2.21743×10^-10, True}, {25, 272, 14172, 10},
    {Measles - Homo sapiens (human),
     {{{CHUK, Protein}}, {{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}, {{MYD88, Protein}},
      {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}}}}},
  path:hsa05140 → {{1.08854×10^-10, 1.37881×10^-9, True}, {25, 148, 14172, 8},
    {Leishmaniasis - Homo sapiens (human), {{{TAB1, Protein}}, {{TAB1, RNA}}, {{MYD88, Protein}},
      {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}}}}},
```

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```
path:hsa05145 → {{1.47706×10^-10, 1.60366×10^-9, True}, {25, 238, 14172, 9},
  {Toxoplasmosis - Homo sapiens (human),
   {{{TAB1, Protein}}, {{TAB1, RNA}}, {{CHUK, Protein}}, {{MYD88, Protein}},
    {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}}}},
path:hsa04621 → {{7.71695×10^-10, 7.3311×10^-9, True}, {25, 114, 14172, 7},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{{TAB1, Protein}}, {{TAB1, RNA}},
    {{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa04662 → {{4.38719×10^-9, 3.70474×10^-8, True}, {25, 146, 14172, 7},
  {B cell receptor signaling pathway - Homo sapiens (human), {{{MALT1, RNA}}, {{CHUK, Protein}},
    {{LYN, RNA}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05166 → {{7.78315×10^-9, 5.9152×10^-8, True}, {25, 518, 14172, 10},
  {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
   {{{CHUK, Protein}}, {{TNFRSF13C, Protein}}, {{LTBR, Protein}}, {{LTBR, RNA}}, {{ATM, RNA}},
    {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa04380 → {{1.0724×10^-8, 7.40928×10^-8, True}, {25, 264, 14172, 8},
  {Osteoclast differentiation - Homo sapiens (human),
   {{{TAB1, Protein}}, {{TAB1, RNA}}, {{CHUK, Protein}}, {{NFKB1, Protein}},
    {{NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa04210 → {{1.69806×10^-8, 1.07544×10^-7, True}, {25, 280, 14172, 8},
  {Apoptosis - Homo sapiens (human), {{{CHUK, Protein}}, {{PARP1, RNA}}, {{GADD45B, Protein}},
    {{ATM, RNA}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05134 → {{2.99335×10^-8, 1.74996×10^-7, True}, {25, 110, 14172, 6},
  {Legionellosis - Homo sapiens (human), {{{MYD88, Protein}}, {{NFKB1, Protein}},
    {{NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05142 → {{5.09425×10^-8, 2.76545×10^-7, True}, {25, 208, 14172, 7},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{{CHUK, Protein}}, {{MYD88, Protein}}, {{NFKB1, Protein}},
    {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}}}},
path:hsa04668 → {{7.48488×10^-8, 3.79234×10^-7, True}, {25, 220, 14172, 7},
  {TNF signaling pathway - Homo sapiens (human), {{{TAB1, Protein}}, {{TAB1, RNA}},
    {{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05120 → {{1.06577×10^-7, 5.06242×10^-7, True}, {25, 136, 14172, 6},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human), {{{CHUK, Protein}},
    {{LYN, RNA}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05203 → {{3.2185×10^-7, 1.43886×10^-6, True}, {25, 410, 14172, 8},
  {Viral carcinogenesis - Homo sapiens (human), {{{LTBR, Protein}}, {{LTBR, RNA}}, {{LYN, RNA}},
    {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05161 → {{5.13018×10^-7, 2.16608×10^-6, True}, {25, 292, 14172, 7},
  {Hepatitis B - Homo sapiens (human), {{{TIRAP, RNA}}, {{CHUK, Protein}}, {{MYD88, Protein}},
    {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa04660 → {{1.37979×10^-6, 5.51916×10^-6, True}, {25, 210, 14172, 6},
  {T cell receptor signaling pathway - Homo sapiens (human), {{{MALT1, RNA}}, {{CHUK, Protein}},
    {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa04623 → {{2.55402×10^-6, 9.70529×10^-6, True}, {25, 128, 14172, 5},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05131 → {{2.75677×10^-6, 9.97688×10^-6, True}, {25, 130, 14172, 5},
  {Shigellosis - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa04622 → {{3.96858×10^-6, 0.0000131136, True}, {25, 140, 14172, 5},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa04920 → {{3.96858×10^-6, 0.0000131136, True}, {25, 140, 14172, 5},
  {Adipocytokine signaling pathway - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05220 → {{4.87509×10^-6, 0.0000154378, True}, {25, 146, 14172, 5},
  {Chronic myeloid leukemia - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}},
path:hsa05133 → {{5.56458×10^-6, 0.0000169163, True}, {25, 150, 14172, 5},
  {Pertussis - Homo sapiens (human),
   {{{TIRAP, RNA}}, {{MYD88, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{IRAK4, RNA}}}}},
```

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```
path:hsa05222 → {{0.0000108418, 0.0000316913, True}, {25, 172, 14172, 5},
  {Small cell lung cancer - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
path:hsa05215 → {{0.0000128039, 0.0000360407, True}, {25, 178, 14172, 5},
  {Prostate cancer - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
path:hsa04010 → {{0.0000205008, 0.000055645, True}, {25, 510, 14172, 7},
  {MAPK signaling pathway - Homo sapiens (human), {{{TAB1, Protein}}, {{TAB1, RNA}}, {{CHUK, Protein}},
    {{GADD45B, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKB2, Protein}}}}}},
path:hsa04672 → {{0.0000263448, 0.0000676828, True}, {25, 100, 14172, 4},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{{TNFSF13B, Protein}}, {{TNFRSF13C, Protein}}, {{LTBR, Protein}}, {{LTBR, RNA}}}}}},
path:hsa05164 → {{0.0000267169, 0.0000676828, True}, {25, 352, 14172, 6},
  {Influenza A - Homo sapiens (human), {{{MYD88, Protein}}, {{NFKB1, Protein}},
    {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}}}}},
path:hsa05152 → {{0.0000293836, 0.0000720373, True}, {25, 358, 14172, 6},
  {Tuberculosis - Homo sapiens (human), {{{MALT1, RNA}}, {{TIRAP, RNA}},
    {{MYD88, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{IRAK4, RNA}}}}}},
path:hsa04062 → {{0.0000375599, 0.0000892048, True}, {25, 374, 14172, 6},
  {Chemokine signaling pathway - Homo sapiens (human), {{{CHUK, Protein}}, {{LYN, RNA}},
    {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
path:hsa04722 → {{0.0000538065, 0.000123918, True}, {25, 240, 14172, 5},
  {Neurotrophin signaling pathway - Homo sapiens (human),
   {{{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}, {{IRAK4, RNA}}}}}},
path:hsa05160 → {{0.0000876196, 0.000195856, True}, {25, 266, 14172, 5},
  {Hepatitis C - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
path:hsa04066 → {{0.000431646, 0.000937288, True}, {25, 206, 14172, 4},
  {HIF-1 signaling pathway - Homo sapiens (human),
   {{{LTBR, Protein}}, {{LTBR, RNA}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}}}}}, path:hsa04931 →
 {{0.00053456, 0.00112852, True}, {25, 218, 14172, 4}, {Insulin resistance - Homo sapiens (human),
   {{{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
path:hsa05221 → {{0.00102477, 0.00210494, True}, {25, 114, 14172, 3},
  {Acute myeloid leukemia - Homo sapiens (human),
   {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}}}}},
path:hsa05212 → {{0.00156362, 0.00312724, True}, {25, 132, 14172, 3},
  {Pancreatic cancer - Homo sapiens (human), {{{CHUK, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}}}}},
path:hsa05200 → {{0.00214553, 0.00412058, True}, {25, 794, 14172, 6},
  {Pathways in cancer - Homo sapiens (human), {{{CHUK, Protein}}, {{NFKB1, Protein}},
    {{NFKB1, RNA}}, {{NFKB2, Protein}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}},
path:hsa04520 → {{0.00216872, 0.00412058, True}, {25, 148, 14172, 3},
  {Adherens junction - Homo sapiens (human), {{{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}}}}},
path:hsa05132 → {{0.00332007, 0.00614329, True}, {25, 172, 14172, 3},
  {Salmonella infection - Homo sapiens (human),
   {{{MYD88, Protein}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}}}}},
path:hsa05202 → {{0.00339498, 0.00614329, True}, {25, 360, 14172, 4},
  {Transcriptional misregulation in cancer - Homo sapiens (human),
   {{{ATM, RNA}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{PLAU, Protein}}}}}},
path:hsa03008 → {{0.00365642, 0.00646251, True}, {25, 178, 14172, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human),
   {{{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}}}}}, path:hsa04024 →
 {{0.00485552, 0.0083868, True}, {25, 398, 14172, 4}, {cAMP signaling pathway - Homo sapiens (human),
   {{{NFKB1, Protein}}, {{NFKB1, RNA}}, {{NFKBIA, RNA}}, {{NFKBIA, Protein}}}}}}, path:hsa04068 →
 {{0.0113081, 0.019098, True}, {25, 268, 14172, 3}, {FoxO signaling pathway - Homo sapiens (human),
   {{{CHUK, Protein}}, {{GADD45B, Protein}}, {{ATM, RNA}}}}}},
path:hsa04530 → {{0.0124816, 0.0206217, True}, {25, 278, 14172, 3},
  {Tight junction - Homo sapiens (human), {{{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}}}}},
path:hsa05030 → {{0.0128035, 0.0207035, True}, {25, 98, 14172, 2},
  {Cocaine addiction - Homo sapiens (human), {{{NFKB1, Protein}}, {{NFKB1, RNA}}}}}},
path:hsa04060 → {{0.0131008, 0.0207429, True}, {25, 530, 14172, 4},
  {Cytokine-cytokine receptor interaction - Homo sapiens (human),
   {{{TNFSF13B, Protein}}, {{TNFRSF13C, Protein}}, {{LTBR, Protein}}, {{LTBR, RNA}}}}}},
path:hsa04310 → {{0.0134693, 0.0208912, True}, {25, 286, 14172, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{{CSNK2A1, RNA}}, {{CSNK2A2, RNA}}, {{CSNK2B, RNA}}}}}},
path:hsa05206 → {{0.0196093, 0.0298062, True}, {25, 598, 14172, 4},
```

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```
  {MicroRNAs in cancer - Homo sapiens (human),
   {{{ATM, RNA}}, {{NFKB1, Protein}}, {{NFKB1, RNA}}, {{PLAU, Protein}}}}}},
path:hsa05321 → {{0.0224566, 0.0334647, True}, {25, 132, 14172, 2},
  {Inflammatory bowel disease (IBD) - Homo sapiens (human), {{{NFKB1, Protein}}, {{NFKB1, RNA}}}}},
path:hsa04115 → {{0.0243955, 0.0356549, True}, {25, 138, 14172, 2},
  {p53 signaling pathway - Homo sapiens (human), {{{GADD45B, Protein}}, {{ATM, RNA}}}}},
path:hsa04917 → {{0.026401, 0.037858, True}, {25, 144, 14172, 2},
  {Prolactin signaling pathway - Homo sapiens (human), {{{NFKB1, Protein}}, {{NFKB1, RNA}}}}}|>
```

NonUCSC (1)

```
In[1]:= Needs["MathIOmica`"]
```

NonUCSC option set to False assumes UCSC browser was used in determining an internal GeneDictionary used in ID translations where the KEGG identifiers for genes are number strings (e.g. 4790).

The NonUCSC option can be set to True if standard KEGG accessions are used in a user provided GeneDictionary variable, in the form OptionValue[KEGGOrganism] <>":"<>"number string", e.g. "hsa:4790"

We consider the following limited non UCSC generated dictionary as a simple example:

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```
In[2]:= nonUCSCGeneDictionary =
  <|"human" → <|"UCSC ID" → {"uc002lwb.2", "uc002lwb.2", "uc002lwb.2", "uc002lwc.1", "uc002lwc.1",
      "uc002lwc.1", "uc001pkb.1", "uc001pkb.1", "uc001pkb.1", "uc009yxr.1", "uc009yxr.1", "uc009yxr.1",
      "uc001pke.2", "uc001pke.2", "uc001pke.2", "uc001pkg.1", "uc001pkg.1", "uc001pkg.1", "uc009yxt.1",
      "uc009yxt.1", "uc009yxt.1", "uc001pkf.3", "uc001pkf.3", "uc001pkf.3", "uc001pkc.1", "uc001pkc.1",
      "uc001pkc.1", "uc001pkd.4", "uc001pkd.4", "uc001pkd.4", "uc009yxs.1", "uc009yxs.1", "uc009yxs.1",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
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      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc001kvb.4", "uc001kvb.4", "uc001kvd.4", "uc001kvd.4",
      "uc001kva.4", "uc001kva.4", "uc009xxc.4", "uc009xxc.4", "uc010qqk.2", "uc010qqk.2", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001rnu.3", "uc001rnu.3", "uc001rnu.3", "uc001rnu.3",
      "uc001rnu.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnx.3",
      "uc001rnx.3", "uc001rnx.3", "uc001rnx.3", "uc001rnx.3", "uc001rny.3", "uc001rny.3", "uc001rny.3",
      "uc001rny.3", "uc001rny.3", "uc010sky.1", "uc010sky.1", "uc010sky.1", "uc010sky.1", "uc010sky.1",
      "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnw.3", "uc001rnw.3",
      "uc001rnw.3", "uc001rnw.3", "uc001rnw.3", "uc002lzg.3", "uc002lzg.3", "uc002lzg.3", "uc002lzg.3",
      "uc010qkw.2", "uc001jwa.3", "uc010qkx.2", "uc001jwb.3", "uc001jwc.3", "uc009xrq.1"},
    "Gene Symbol" → {"GADD45B", "GADD45B", "GADD45B", "GADD45B", "GADD45B", "GADD45B", "ATM",
      "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM",
      "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
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    "KEGG Gene ID" → {"hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:472",
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```

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We can use this in the analysis:

```
In[3]:= analysisKEGGNonUCSC =
  KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
    "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
   GeneDictionary → nonUCSCGeneDictionary, NonUCSC → True]

Out[3]= ⟨|path:hsa04064 → {{6.48564×10^-16, 3.89138×10^-14, True},
    {8, 93, 7086, 8}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa04210 → {{9.61015×10^-6, 0.000288305, True}, {8, 140, 7086, 4},
    {Apoptosis - Homo sapiens (human), {{GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05134 → {{0.0000241111, 0.000482223, True}, {8, 55, 7086, 3},
    {Legionellosis - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05140 → {{0.0000589769, 0.000884653, True}, {8, 74, 7086, 3},
    {Leishmaniasis - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05166 → {{0.000108709, 0.00130451, True}, {8, 259, 7086, 4},
    {Human T-cell leukemia virus 1 infection - Homo sapiens (human), {{ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.00016305, 0.001479, True}, {8, 104, 7086, 3},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04620 → {{0.00017255, 0.001479, True}, {8, 106, 7086, 3},
    {Toll-like receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05145 → {{0.000243212, 0.0016621, True}, {8, 119, 7086, 3},
    {Toxoplasmosis - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04722 → {{0.000249315, 0.0016621, True}, {8, 120, 7086, 3},
    {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04380 → {{0.000330476, 0.0019686, True}, {8, 132, 7086, 3},
    {Osteoclast differentiation - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05162 → {{0.000360911, 0.0019686, True}, {8, 136, 7086, 3},
    {Measles - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05164 → {{0.000769509, 0.00379258, True}, {8, 176, 7086, 3},
    {Influenza A - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05202 → {{0.000821725, 0.00379258, True}, {8, 180, 7086, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
  path:hsa05169 → {{0.0011832, 0.0048005, True}, {8, 204, 7086, 3},
    {Epstein-Barr virus infection - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05203 → {{0.00120013, 0.0048005, True}, {8, 205, 7086, 3},
    {Viral carcinogenesis - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04621 → {{0.00172574, 0.00647153, True}, {8, 57, 7086, 2},
    {NOD-like receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa04623 → {{0.00217127, 0.00675844, True}, {8, 64, 7086, 2},
    {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa05131 → {{0.00223893, 0.00675844, True}, {8, 65, 7086, 2},
    {Shigellosis - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa04010 → {{0.00225496, 0.00675844, True}, {8, 255, 7086, 3},
    {MAPK signaling pathway - Homo sapiens (human), {{GADD45B}, {NFKB1}, {NFKB2}}}},
  path:hsa05120 → {{0.0024479, 0.00675844, True}, {8, 68, 7086, 2},
    {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
     {{NFKB1}, {NFKBIA}}}}, path:hsa04115 → {{0.00251954, 0.00675844, True},
    {8, 69, 7086, 2}, {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa04622 → {{0.00259218, 0.00675844, True}, {8, 70, 7086, 2},
    {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa04920 → {{0.00259218, 0.00675844, True}, {8, 70, 7086, 2},
    {Adipocytokine signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa04662 → {{0.00281602, 0.00675844, True}, {8, 73, 7086, 2},
    {B cell receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa05220 → {{0.00281602, 0.00675844, True}, {8, 73, 7086, 2},
    {Chronic myeloid leukemia - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa05133 → {{0.00297017, 0.00685423, True}, {8, 75, 7086, 2},
    {Pertussis - Homo sapiens (human), {{NFKB1}, {IRAK4}}}},
  path:hsa05206 → {{0.00355593, 0.00790206, True}, {8, 299, 7086, 3},
    {MicroRNAs in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
  path:hsa05222 → {{0.00388776, 0.00833092, True}, {8, 86, 7086, 2},
```

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```
  {Small cell lung cancer - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa05215 → {{0.00415831, 0.00860341, True}, {8, 89, 7086, 2},
  {Prostate cancer - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04660 → {{0.00574553, 0.0114911, True}, {8, 105, 7086, 2},
  {T cell receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04931 → {{0.00617978, 0.011795, True}, {8, 109, 7086, 2},
  {Insulin resistance - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00629065, 0.011795, True}, {8, 110, 7086, 2},
  {TNF signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa05200 → {{0.00791129, 0.0140097, True}, {8, 397, 7086, 3},
  {Pathways in cancer - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04110 → {{0.00793881, 0.0140097, True}, {8, 124, 7086, 2},
  {Cell cycle - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05160 → {{0.00909153, 0.0153734, True}, {8, 133, 7086, 2},
  {Hepatitis C - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00922405, 0.0153734, True}, {8, 134, 7086, 2},
  {FoxO signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05161 → {{0.0108825, 0.0176473, True}, {8, 146, 7086, 2},
  {Hepatitis B - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa05152 → {{0.0160747, 0.0253811, True}, {8, 179, 7086, 2},
  {Tuberculosis - Homo sapiens (human), {{NFKB1}, {IRAK4}}}},
path:hsa05168 → {{0.0172913, 0.0262024, True}, {8, 186, 7086, 2},
  {Herpes simplex virus 1 infection - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.0174683, 0.0262024, True}, {8, 187, 7086, 2},
  {Chemokine signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04024 → {{0.019654, 0.028762, True}, {8, 199, 7086, 2},
  {cAMP signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}}|>
```

OutputID (1)

```
In[1]:= Needs["MathIOmica`"]
```

OutputID is a string to indicate the kind of ID to convert input genomic analysis entries. The default is "KEGG Gene ID" consistently with use of the "pathway" database as the default genomic analysis.

```
In[2]:= analysisKEGGOutputID = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, OutputID → "KEGG Gene ID"]

Out[2]= <|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
  {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
   {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
    {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
   {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
  {Epstein-Barr virus infection - Homo sapiens (human),
   {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
  {Toll-like receptor signaling pathway - Homo sapiens (human),
   {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05168 → {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8},
  {Herpes simplex virus 1 infection - Homo sapiens (human),
   {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
  {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
  {B cell receptor signaling pathway - Homo sapiens (human),
   {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
```

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```
  {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
  {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
  {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
   {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
```

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```
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

We could be using an input gene dictionary where the label for the output is named differently, e.g. "kgene" below:

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```
In[3]:= exampleGeneDictionary =
  <|"human" → <|"UCSC ID" → {"uc002lwb.2", "uc002lwb.2", "uc002lwb.2", "uc002lwc.1", "uc002lwc.1",
      "uc002lwc.1", "uc001pkb.1", "uc001pkb.1", "uc001pkb.1", "uc009yxr.1", "uc009yxr.1", "uc009yxr.1",
      "uc001pke.2", "uc001pke.2", "uc001pke.2", "uc001pkg.1", "uc001pkg.1", "uc001pkg.1", "uc009yxt.1",
      "uc009yxt.1", "uc009yxt.1", "uc001pkf.3", "uc001pkf.3", "uc001pkf.3", "uc001pkc.1", "uc001pkc.1",
      "uc001pkc.1", "uc001pkd.4", "uc001pkd.4", "uc001pkd.4", "uc009yxs.1", "uc009yxs.1", "uc009yxs.1",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc001kvb.4", "uc001kvb.4", "uc001kvd.4", "uc001kvd.4",
      "uc001kva.4", "uc001kva.4", "uc009xxc.4", "uc009xxc.4", "uc010qqk.2", "uc010qqk.2", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001rnu.3", "uc001rnu.3", "uc001rnu.3", "uc001rnu.3",
      "uc001rnu.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnx.3",
      "uc001rnx.3", "uc001rnx.3", "uc001rnx.3", "uc001rnx.3", "uc001rny.3", "uc001rny.3", "uc001rny.3",
      "uc001rny.3", "uc001rny.3", "uc010sky.1", "uc010sky.1", "uc010sky.1", "uc010sky.1", "uc010sky.1",
      "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnw.3", "uc001rnw.3",
      "uc001rnw.3", "uc001rnw.3", "uc001rnw.3", "uc002lzg.3", "uc002lzg.3", "uc002lzg.3", "uc002lzg.3",
      "uc010qkw.2", "uc001jwa.3", "uc010qkx.2", "uc001jwb.3", "uc001jwc.3", "uc009xrq.1"},
    "Gene Symbol" → {"GADD45B", "GADD45B", "GADD45B", "GADD45B", "GADD45B", "GADD45B", "ATM",
      "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM",
      "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
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      "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4",
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      "IRAK4", "PIAS4", "PIAS4", "PIAS4", "PIAS4", "PLAU", "PLAU", "PLAU", "PLAU", "PLAU", "PLAU"},
    "kgene" → {"hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:472",
      "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472",
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      "hsa:4790", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791",
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      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51588", "hsa:51588", "hsa:51588",
      "hsa:51588", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328"}|>|>;
```

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```
In[4]:= analysisKEGGOutputIDNonDefault =
  KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
    "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
   GeneDictionary → exampleGeneDictionary, NonUCSC → True, OutputID → "kgene"]

Out[4]= ⟨|path:hsa04064 → {{6.48564×10^-16, 3.89138×10^-14, True},
    {8, 93, 7086, 8}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa04210 → {{9.61015×10^-6, 0.000288305, True}, {8, 140, 7086, 4},
    {Apoptosis - Homo sapiens (human), {{GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05134 → {{0.0000241111, 0.000482223, True}, {8, 55, 7086, 3},
    {Legionellosis - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05140 → {{0.0000589769, 0.000884653, True}, {8, 74, 7086, 3},
    {Leishmaniasis - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05166 → {{0.000108709, 0.00130451, True}, {8, 259, 7086, 4},
    {Human T-cell leukemia virus 1 infection - Homo sapiens (human), {{ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.00016305, 0.001479, True}, {8, 104, 7086, 3},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04620 → {{0.00017255, 0.001479, True}, {8, 106, 7086, 3},
    {Toll-like receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05145 → {{0.000243212, 0.0016621, True}, {8, 119, 7086, 3},
    {Toxoplasmosis - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04722 → {{0.000249315, 0.0016621, True}, {8, 120, 7086, 3},
    {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04380 → {{0.000330476, 0.0019686, True}, {8, 132, 7086, 3},
    {Osteoclast differentiation - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05162 → {{0.000360911, 0.0019686, True}, {8, 136, 7086, 3},
    {Measles - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05164 → {{0.000769509, 0.00379258, True}, {8, 176, 7086, 3},
    {Influenza A - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05202 → {{0.000821725, 0.00379258, True}, {8, 180, 7086, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
  path:hsa05169 → {{0.0011832, 0.0048005, True}, {8, 204, 7086, 3},
    {Epstein-Barr virus infection - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05203 → {{0.00120013, 0.0048005, True}, {8, 205, 7086, 3},
    {Viral carcinogenesis - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04621 → {{0.00172574, 0.00647153, True}, {8, 57, 7086, 2},
    {NOD-like receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa04623 → {{0.00217127, 0.00675844, True}, {8, 64, 7086, 2},
    {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa05131 → {{0.00223893, 0.00675844, True}, {8, 65, 7086, 2},
    {Shigellosis - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa04010 → {{0.00225496, 0.00675844, True}, {8, 255, 7086, 3},
    {MAPK signaling pathway - Homo sapiens (human), {{GADD45B}, {NFKB1}, {NFKB2}}}},
  path:hsa05120 → {{0.0024479, 0.00675844, True}, {8, 68, 7086, 2},
    {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
     {{NFKB1}, {NFKBIA}}}}, path:hsa04115 → {{0.00251954, 0.00675844, True},
    {8, 69, 7086, 2}, {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa04622 → {{0.00259218, 0.00675844, True}, {8, 70, 7086, 2},
    {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa04920 → {{0.00259218, 0.00675844, True}, {8, 70, 7086, 2},
    {Adipocytokine signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa04662 → {{0.00281602, 0.00675844, True}, {8, 73, 7086, 2},
    {B cell receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa05220 → {{0.00281602, 0.00675844, True}, {8, 73, 7086, 2},
    {Chronic myeloid leukemia - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa05133 → {{0.00297017, 0.00685423, True}, {8, 75, 7086, 2},
    {Pertussis - Homo sapiens (human), {{NFKB1}, {IRAK4}}}},
  path:hsa05206 → {{0.00355593, 0.00790206, True}, {8, 299, 7086, 3},
    {MicroRNAs in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
  path:hsa05222 → {{0.00388776, 0.00833092, True}, {8, 86, 7086, 2},
    {Small cell lung cancer - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
  path:hsa05215 → {{0.00415831, 0.00860341, True}, {8, 89, 7086, 2},
    {Prostate cancer - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
```

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```
path:hsa04660 → {{0.00574553, 0.0114911, True}, {8, 105, 7086, 2},
  {T cell receptor signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04931 → {{0.00617978, 0.011795, True}, {8, 109, 7086, 2},
  {Insulin resistance - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00629065, 0.011795, True}, {8, 110, 7086, 2},
  {TNF signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa05200 → {{0.00791129, 0.0140097, True}, {8, 397, 7086, 3},
  {Pathways in cancer - Homo sapiens (human), {{NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04110 → {{0.00793881, 0.0140097, True}, {8, 124, 7086, 2},
  {Cell cycle - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05160 → {{0.00909153, 0.0153734, True}, {8, 133, 7086, 2},
  {Hepatitis C - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00922405, 0.0153734, True}, {8, 134, 7086, 2},
  {FoxO signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05161 → {{0.0108825, 0.0176473, True}, {8, 146, 7086, 2},
  {Hepatitis B - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa05152 → {{0.0160747, 0.0253811, True}, {8, 179, 7086, 2},
  {Tuberculosis - Homo sapiens (human), {{NFKB1}, {IRAK4}}}},
path:hsa05168 → {{0.0172913, 0.0262024, True}, {8, 186, 7086, 2},
  {Herpes simplex virus 1 infection - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.0174683, 0.0262024, True}, {8, 187, 7086, 2},
  {Chemokine signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}},
path:hsa04024 → {{0.019654, 0.028762, True}, {8, 199, 7086, 2},
  {cAMP signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}}}}|>
```

PathwayLengthFilter (1)

```
In[1]:= Needs["MathIOmica`"]
```

`PathwayLengthFilter` can be used to set the value for which terms to consider in the computation, by excluding KEGG pathways that have fewer items compared to the PathwayLengthFilter value. It is used by the internal KEGGAnalysisAssigner function.

In this example we set the `PathwayLengthFilter` to 130:

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In[2]:=
```
analysisKEGGOLengthFilter =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1",
   "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2",
   "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, PathwayLengthFilter → 130]
```

Out[2]=
```
⟨|path:hsa05162 → {{2.12122×10^-8, 3.82364×10^-7, True}, {21, 136, 5371, 8}, {Measles - Homo sapiens (human),
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05169 → {{2.73117×10^-8, 3.82364×10^-7, True}, {21, 204, 5371, 9},
   {Epstein-Barr virus infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa05168 → {{2.46235×10^-7, 2.2982×10^-6, True}, {21, 186, 5371, 8},
   {Herpes simplex virus 1 infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
 path:hsa04210 → {{0.0000110747, 0.000077523, True}, {21, 140, 5371, 6},
   {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
 path:hsa05166 → {{0.0000363159, 0.000203369, True}, {21, 259, 5371, 7},
   {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
    {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa04380 → {{0.000123224, 0.000575045, True}, {21, 132, 5371, 5},
   {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa05161 → {{0.000198388, 0.000793552, True}, {21, 146, 5371, 5},
   {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
 path:hsa05152 → {{0.000512241, 0.00179284, True}, {21, 179, 5371, 5},
   {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
 path:hsa05203 → {{0.000951858, 0.00296134, True}, {21, 205, 5371, 5},
   {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa04010 → {{0.00252164, 0.00706061, True}, {21, 255, 5371, 5},
   {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
 path:hsa05164 → {{0.00430763, 0.0109649, True}, {21, 176, 5371, 4},
   {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa04062 → {{0.00534846, 0.0124797, True}, {21, 187, 5371, 4},
   {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
 path:hsa05160 → {{0.0142464, 0.0290723, True}, {21, 133, 5371, 3},
   {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
 path:hsa04068 → {{0.0145362, 0.0290723, True}, {21, 134, 5371, 3},
   {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
 path:hsa04530 → {{0.0160357, 0.0299334, True}, {21, 139, 5371, 3},
   {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
 path:hsa04310 → {{0.0172967, 0.0302692, True}, {21, 143, 5371, 3},
   {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}}|⟩
```

pValueCutoff (1)

In[1]:=
```
Needs["MathIOmica`"]
```

pValueCutoff provides a cutoff p-value for adjusted p-values to assess statistical significance. The default is 0.05. In this example we manually set the cutoff to to 10^{-6}:

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In[2]:=
```
analysisKEGGpValue = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, pValueCutoff → 10^-6]
```

Out[2]=
```
⟨|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
   {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
 path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
   {Epstein-Barr virus infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
   {Toll-like receptor signaling pathway - Homo sapiens (human),
    {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05168 → {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8},
   {Herpes simplex virus 1 infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}}|⟩
```

ReportFilter (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ReportFilter provides a cutoff for membership in pathways in selecting which terms/categories to return. It is used in conjunction with ReportFilterFunction. The default is 1.

We first consider data

In[2]:=
```
keggExampleReportFilter1 = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP",
   "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88",
   "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, ReportFilter → 1]
```

Out[2]=
```
⟨|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
   {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
 path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
    {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
   {Epstein-Barr virus infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
 path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
   {Toll-like receptor signaling pathway - Homo sapiens (human),
    {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa05168 → {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8},
   {Herpes simplex virus 1 infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
 path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
   {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
   {B cell receptor signaling pathway - Homo sapiens (human),
    {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
 path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
   {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
 path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
   {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
 path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
```

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```
  {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
   {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
   {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
  {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
```

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```
  path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
    {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
  path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
    {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
  path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
    {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
  path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
    {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
  path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
    {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

We now set a report filter. We may be interested in categories with at least 10 members in each result reported:

```
In[3]:= keggExampleReportFilter10 = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP",
          "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88",
          "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, ReportFilter → 10]

Out[3]= <|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
    {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}}|>
```

ReportFilterFunction (1)

```
In[1]:= Needs["MathIOmica`"]
```

`ReportFilterFunction` specifies what function will be used to compare against `ReportFilter` option value in selecting which terms/categories to return. The default value is GreaterEqualThan.

We first consider data filtering results with more than or equal to 8 members:

```
In[2]:= keggExampleReportFilterFn1 =
         KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
           "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
          ReportFilter → 8, ReportFilterFunction → GreaterEqualThan]

Out[2]= <|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
    {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05168 → {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8},
    {Herpes simplex virus 1 infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}}|>
```

For an example we change this to look at groups strictly having more than 8 members

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In[3]:=
```
keggExampleReportFilterFn2 =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
   "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
  ReportFilter → 8, ReportFilterFunction → GreaterThan]
```

Out[3]=
```
⟨|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
    {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|⟩
```

Species (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The Species option specifies the species considered in the calculation. The default implementation is "human":

In[2]:=
```
keggExampleSpecies = KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK",
   "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B",
   "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, Species → "human"]
```

Out[2]=
```
⟨|path:hsa04064 → {{2.69595×10^-41, 2.04892×10^-39, True},
    {21, 93, 7086, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
     {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
      {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05162 → {{2.47064×10^-9, 6.2908×10^-8, True}, {21, 136, 7086, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05169 → {{2.48321×10^-9, 6.2908×10^-8, True}, {21, 204, 7086, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04620 → {{1.34415×10^-8, 2.55388×10^-7, True}, {21, 106, 7086, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05168 → {{2.94691×10^-8, 4.4793×10^-7, True}, {21, 186, 7086, 8},
    {Herpes simplex virus 1 infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05145 → {{8.73117×10^-7, 0.0000110595, True}, {21, 119, 7086, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04662 → {{1.80812×10^-6, 0.000018387, True}, {21, 73, 7086, 5},
    {B cell receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa05140 → {{1.93547×10^-6, 0.000018387, True}, {21, 74, 7086, 5},
    {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04210 → {{2.27123×10^-6, 0.0000191793, True}, {21, 140, 7086, 6},
    {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05166 → {{6.02113×10^-6, 0.0000457606, True}, {21, 259, 7086, 7},
    {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
     {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa05142 → {{0.0000104386, 0.0000721215, True}, {21, 104, 7086, 5},
    {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
     {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05134 → {{0.0000176299, 0.000111656, True}, {21, 55, 7086, 4},
    {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04621 → {{0.0000203404, 0.000118913, True}, {21, 57, 7086, 4},
    {NOD-like receptor signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
  path:hsa04380 → {{0.0000332929, 0.000180733, True}, {21, 132, 7086, 5},
    {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
```

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```
path:hsa05120 → {{0.0000410563, 0.000208019, True}, {21, 68, 7086, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
   {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05161 → {{0.0000540644, 0.000256806, True}, {21, 146, 7086, 5},
  {Hepatitis B - Homo sapiens (human), {{TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}}}},
path:hsa05133 → {{0.0000604546, 0.000270268, True}, {21, 75, 7086, 4},
  {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05152 → {{0.000142467, 0.000601526, True}, {21, 179, 7086, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa04660 → {{0.000224399, 0.000897598, True}, {21, 105, 7086, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04668 → {{0.00026841, 0.000973642, True}, {21, 110, 7086, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000269033, 0.000973642, True}, {21, 205, 7086, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04672 → {{0.00040208, 0.001389, True}, {21, 50, 7086, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
   {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04010 → {{0.000735243, 0.0024295, True}, {21, 255, 7086, 5},
  {MAPK signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {GADD45B}, {NFKB1}, {NFKB2}}}},
path:hsa04623 → {{0.000832201, 0.0026353, True}, {21, 64, 7086, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05131 → {{0.000870807, 0.00264725, True}, {21, 65, 7086, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.00108095, 0.00304268, True}, {21, 70, 7086, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05220 → {{0.00122118, 0.00331464, True}, {21, 73, 7086, 3},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.00127036, 0.00332922, True}, {21, 74, 7086, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05164 → {{0.00158112, 0.00400551, True}, {21, 176, 7086, 4},
  {Influenza A - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05222 → {{0.00196023, 0.00469452, True}, {21, 86, 7086, 3},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04062 → {{0.00197664, 0.00469452, True}, {21, 187, 7086, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa03008 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05215 → {{0.00216283, 0.00483455, True}, {21, 89, 7086, 3},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04722 → {{0.00504204, 0.0109484, True}, {21, 120, 7086, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05160 → {{0.0067135, 0.0140789, True}, {21, 133, 7086, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04068 → {{0.00685419, 0.0140789, True}, {21, 134, 7086, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa04530 → {{0.00758419, 0.0151684, True}, {21, 139, 7086, 3},
  {Tight junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04310 → {{0.00820038, 0.0159802, True}, {21, 143, 7086, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05221 → {{0.0121041, 0.0229978, True}, {21, 57, 7086, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa05202 → {{0.0153105, 0.0283804, True}, {21, 180, 7086, 3},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{ATM}, {NFKB1}, {PLAU}}}},
path:hsa05212 → {{0.0160097, 0.0289699, True}, {21, 66, 7086, 2},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0174169, 0.0307833, True}, {21, 69, 7086, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0263294, 0.045478, True}, {21, 86, 7086, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05200 → {{0.0271904, 0.0459216, True}, {21, 397, 7086, 4},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}|>
```

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TestFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The TestFunction option provides a function for calculating the raw p-values for the enrichment of each term. It must be a function of four inputs, f[#1,#2,#3,#4]. The default is using a hypergeometric distribution CDF, CDF[HypergeometricDistribution[#1,#2,#3],#4-1]] . The four inputs refer to:

#1 is number of draws (members in group being tested),

#2 is number of successes for category in population,

#3 is total number of members in population,

#4 is number of successes (or more) in current group being tested for specific category.

The output must be a p-value (real positive number ≤ 1).

In[2]:=
```
KEGGExampleTestFunction =
 KEGGAnalysis[{"TAB1", "TNFSF13B", "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2",
   "CSNK2B", "LTBR", "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"},
  TestFunction → ((1 - N[CDF[HypergeometricDistribution[#1, #2, #3], #4 - 1]] &))]
```

Out[2]=
```
⟨|path:hsa04064 → {{0., 0., True}, {21, 100, 7873, 21}, {NF-kappa B signaling pathway - Homo sapiens (human),
    {{TAB1}, {TNFSF13B}, {MALT1}, {TIRAP}, {CHUK}, {TNFRSF13C}, {PARP1}, {CSNK2A1}, {CSNK2A2}, {CSNK2B},
     {LTBR}, {LYN}, {MYD88}, {GADD45B}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}, {PIAS4}, {PLAU}}}},
  path:hsa05235 → {{3.49561×10^-11, 1.80024×10^-9, True}, {21, 89, 7873, 8},
    {PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
     {{TIRAP}, {CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}}}},
  path:hsa05169 → {{8.6918×10^-10, 2.98418×10^-8, True}, {21, 201, 7873, 9},
    {Epstein-Barr virus infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {LYN}, {MYD88}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}, {IRAK4}}}},
  path:hsa05162 → {{1.22099×10^-9, 3.14404×10^-8, True}, {21, 138, 7873, 8}, {Measles - Homo sapiens (human),
     {{CHUK}, {CSNK2A1}, {CSNK2A2}, {CSNK2B}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04620 → {{5.72006×10^-9, 1.17833×10^-7, True}, {21, 104, 7873, 7},
    {Toll-like receptor signaling pathway - Homo sapiens (human),
     {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05161 → {{1.30608×10^-7, 2.2421×10^-6, True}, {21, 163, 7873, 7},
    {Hepatitis B - Homo sapiens (human), {{TAB1}, {TIRAP}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05145 → {{3.48371×10^-7, 5.12604×10^-6, True}, {21, 113, 7873, 6},
    {Toxoplasmosis - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05135 → {{5.22984×10^-7, 6.73342×10^-6, True}, {21, 121, 7873, 6},
    {Yersinia infection - Homo sapiens (human), {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05170 → {{7.84432×10^-7, 8.97739×10^-6, True}, {21, 212, 7873, 7},
    {Human immunodeficiency virus 1 infection - Homo sapiens (human),
     {{TAB1}, {CHUK}, {MYD88}, {ATM}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa05166 → {{9.76992×10^-7, 9.76816×10^-6, True}, {21, 219, 7873, 7},
    {Human T-cell leukemia virus 1 infection - Homo sapiens (human),
     {{CHUK}, {TNFRSF13C}, {LTBR}, {ATM}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
  path:hsa04210 → {{1.0432×10^-6, 9.76816×10^-6, True}, {21, 136, 7873, 6},
    {Apoptosis - Homo sapiens (human), {{CHUK}, {PARP1}, {GADD45B}, {ATM}, {NFKB1}, {NFKBIA}}}},
  path:hsa05140 → {{1.158×10^-6, 9.9395×10^-6, True}, {21, 74, 7873, 5},
    {Leishmaniasis - Homo sapiens (human), {{TAB1}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
  path:hsa04662 → {{1.93489×10^-6, 0.0000153303, True}, {21, 82, 7873, 5},
    {B cell receptor signaling pathway - Homo sapiens (human),
     {{MALT1}, {CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
  path:hsa04621 → {{5.02405×10^-6, 0.0000369627, True}, {21, 178, 7873, 6},
    {NOD-like receptor signaling pathway - Homo sapiens (human),
```

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```
    {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05142 → {{5.98952×10^-6, 0.0000404359, True}, {21, 103, 7873, 5},
  {Chagas disease (American trypanosomiasis) - Homo sapiens (human),
    {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04625 → {{6.2813×10^-6, 0.0000404359, True}, {21, 104, 7873, 5},
  {C-type lectin receptor signaling pathway - Homo sapiens (human),
    {{MALT1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}}, path:hsa04010 →
 {{7.14287×10^-6, 0.0000432774, True}, {21, 295, 7873, 7}, {MAPK signaling pathway - Homo sapiens (human),
    {{TAB1}, {CHUK}, {MYD88}, {GADD45B}, {NFKB1}, {NFKB2}, {IRAK4}}}},
path:hsa05134 → {{0.0000125591, 0.0000718657, True}, {21, 56, 7873, 4},
  {Legionellosis - Homo sapiens (human), {{MYD88}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04380 → {{0.0000173452, 0.0000940292, True}, {21, 128, 7873, 5},
  {Osteoclast differentiation - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05120 → {{0.0000306006, 0.000157593, True}, {21, 70, 7873, 4},
  {Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
    {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}}, path:hsa05133 → {{0.0000423752, 0.000198393, True},
  {21, 76, 7873, 4}, {Pertussis - Homo sapiens (human), {{TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05220 → {{0.0000423752, 0.000198393, True}, {21, 76, 7873, 4},
  {Chronic myeloid leukemia - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
path:hsa05164 → {{0.0000624936, 0.000279863, True}, {21, 167, 7873, 5},
  {Influenza A - Homo sapiens (human), {{CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa05152 → {{0.0000869695, 0.000373244, True}, {21, 179, 7873, 5},
  {Tuberculosis - Homo sapiens (human), {{MALT1}, {TIRAP}, {MYD88}, {NFKB1}, {IRAK4}}}},
path:hsa05222 → {{0.0000936338, 0.000385771, True}, {21, 93, 7873, 4},
  {Small cell lung cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKBIA}}}},
path:hsa05215 → {{0.000110347, 0.000437142, True}, {21, 97, 7873, 4},
  {Prostate cancer - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}, {PLAU}}}},
path:hsa04660 → {{0.000139348, 0.000531589, True}, {21, 103, 7873, 4},
  {T cell receptor signaling pathway - Homo sapiens (human), {{MALT1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa05203 → {{0.000150453, 0.000553452, True}, {21, 201, 7873, 5},
  {Viral carcinogenesis - Homo sapiens (human), {{LTBR}, {LYN}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa04668 → {{0.000192717, 0.000684478, True}, {21, 112, 7873, 4},
  {TNF signaling pathway - Homo sapiens (human), {{TAB1}, {CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04672 → {{0.000278512, 0.000956225, True}, {21, 49, 7873, 3},
  {Intestinal immune network for IgA production - Homo sapiens (human),
    {{TNFSF13B}, {TNFRSF13C}, {LTBR}}}}, path:hsa04623 → {{0.000586058, 0.00194722, True}, {21, 63, 7873, 3},
  {Cytosolic DNA-sensing pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04137 → {{0.000642425, 0.00206781, True}, {21, 65, 7873, 3},
  {Mitophagy - animal - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05131 → {{0.0007333, 0.00228878, True}, {21, 68, 7873, 3},
  {Shigellosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04920 → {{0.000765318, 0.00231846, True}, {21, 69, 7873, 3},
  {Adipocytokine signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04622 → {{0.000798216, 0.00234904, True}, {21, 70, 7873, 3},
  {RIG-I-like receptor signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04520 → {{0.000866689, 0.00247969, True}, {21, 72, 7873, 3},
  {Adherens junction - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05212 → {{0.000976239, 0.00271764, True}, {21, 75, 7873, 3},
  {Pancreatic cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}}}},
path:hsa05167 → {{0.00131728, 0.00347897, True}, {21, 186, 7873, 4},
  {Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human),
    {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa05202 → {{0.00131728, 0.00347897, True}, {21, 186, 7873, 4},
  {Transcriptional misregulation in cancer - Homo sapiens (human), {{GADD45B}, {ATM}, {NFKB1}, {PLAU}}}},
path:hsa05168 → {{0.00139769, 0.00358073, True}, {21, 492, 7873, 6},
  {Herpes simplex virus 1 infection - Homo sapiens (human),
    {{TAB1}, {CHUK}, {MYD88}, {NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04062 → {{0.00142534, 0.00358073, True}, {21, 190, 7873, 4},
  {Chemokine signaling pathway - Homo sapiens (human), {{CHUK}, {LYN}, {NFKB1}, {NFKBIA}}}},
path:hsa04658 → {{0.00176341, 0.00432455, True}, {21, 92, 7873, 3},
  {Th1 and Th2 cell differentiation - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04657 → {{0.00181907, 0.0043573, True}, {21, 93, 7873, 3},
  {IL-17 signaling pathway - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
```

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```
path:hsa03008 → {{0.00257433, 0.00602626, True}, {21, 105, 7873, 3},
  {Ribosome biogenesis in eukaryotes - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa04659 → {{0.0027164, 0.00621754, True}, {21, 107, 7873, 3},
  {Th17 cell differentiation - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa01523 → {{0.00300762, 0.00673445, True}, {21, 31, 7873, 2},
  {Antifolate resistance - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04722 → {{0.00367113, 0.00804524, True}, {21, 119, 7873, 3},
  {Neurotrophin signaling pathway - Homo sapiens (human), {{NFKB1}, {NFKBIA}, {IRAK4}}}},
path:hsa04068 → {{0.00491249, 0.0105414, True}, {21, 132, 7873, 3},
  {FoxO signaling pathway - Homo sapiens (human), {{CHUK}, {GADD45B}, {ATM}}}},
path:hsa05418 → {{0.00567441, 0.0119278, True}, {21, 139, 7873, 3},
  {Fluid shear stress and atherosclerosis - Homo sapiens (human), {{CHUK}, {NFKB1}, {PIAS4}}}},
path:hsa05160 → {{0.00767278, 0.0158059, True}, {21, 155, 7873, 3},
  {Hepatitis C - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}},
path:hsa04218 → {{0.00837271, 0.0165844, True}, {21, 160, 7873, 3},
  {Cellular senescence - Homo sapiens (human), {{GADD45B}, {ATM}, {NFKB1}}}},
path:hsa04310 → {{0.00837271, 0.0165844, True}, {21, 160, 7873, 3},
  {Wnt signaling pathway - Homo sapiens (human), {{CSNK2A1}, {CSNK2A2}, {CSNK2B}}}},
path:hsa05200 → {{0.0111981, 0.0217624, True}, {21, 530, 7873, 5},
  {Pathways in cancer - Homo sapiens (human), {{CHUK}, {GADD45B}, {NFKB1}, {NFKB2}, {NFKBIA}}}},
path:hsa05221 → {{0.0131171, 0.0250197, True}, {21, 66, 7873, 2},
  {Acute myeloid leukemia - Homo sapiens (human), {{CHUK}, {NFKB1}}}},
path:hsa04115 → {{0.0154813, 0.0289922, True}, {21, 72, 7873, 2},
  {p53 signaling pathway - Homo sapiens (human), {{GADD45B}, {ATM}}}},
path:hsa05132 → {{0.0202525, 0.0372501, True}, {21, 83, 7873, 2},
  {Salmonella infection - Homo sapiens (human), {{MYD88}, {NFKB1}}}},
path:hsa05163 → {{0.0209486, 0.0378544, True}, {21, 225, 7873, 3},
  {Human cytomegalovirus infection - Homo sapiens (human), {{CHUK}, {NFKB1}, {NFKBIA}}}}|>
```

Possible Issues (1)

The inbuilt "Genomic" analysis is geared to "hsa" human applications - certain options presented above relating to "Genomic" analysis are geared towards development applications.

The inbuilt "Molecular" analysis is using "cpd" annotations - the options presented above relating to "Molecular" analysis are geared towards development applications.

See Also

BenjaminiHochbergFDR ▪ **EnrichmentReportExport** ▪ **GeneTranslation** ▪ **GetGeneDictionary** ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysisAssigner** ▪ **KEGGDictionary** ▪ **KEGGPathwayVisual** ▪ **MassDictionary** ▪ **MassMatcher** ▪ **OBOGODictionary** ▪ **TimeSeriesClusters** ▪ **UCSCBrowserSQL**

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Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾ URL ▾

KEGGAnalysisAssigner

`KEGGAnalysisAssigner[]`
creates KEGG: Kyoto Encyclopedia of Genes and Genomes pathway associations, restricted to required background set, downloading the data if necessary.

Details

- `KEGGAnalysisAssigner[]` creates identifier to pathway accession associations, restricted to required background set, downloading the data if necessary. It utilizes information from KEGG: Kyoto Encyclopedia of Genes and Genomes.
- The form of the output is for n member IDs and m KEGG pathways (categories), schematically:
- $$\begin{aligned}\text{output} = \langle\, &\text{Organism} \to \langle\, \text{"IDToPath"} \to \langle|\, \text{ID}_1 \to \{\text{KEGG pathways associated to ID}_1\}, \\ &\quad \text{ID}_2 \to \{\text{KEGG pathways associated to ID}_2\}, \ldots, \text{ID}_n \to \{\text{KEGG pathways associated to ID}_n\} \,|\rangle, \\ &\text{"PathToID"} \to \langle|\, \text{KEGG : Pathway}_1 \to \{\text{IDs associated to KEGG pathway}_1\}, \\ &\quad \text{KEGG : Pathway}_2 \to \{\text{IDs associated to KEGG pathway}_2\}, \ldots, \text{KEGG : Pathway}_m \to \{\text{IDs associated to KEGG pathway}_m\} \,|\rangle \,|\rangle\end{aligned}$$
- If multiple organisms are considered in user applications the form above can easily be extended to accomodate more species as keys of the outer association, and provide the "IDToPath" and "PathToID" associations for each species accordingly.
- The following options can be given:

BackgroundSet	All	The BackgroundSet option allows the selection of what members to use as a background (e.g. genes), or to use All members as background.
ImportDirectly	False	ImportDirectly gives the option to import a new version of KEGG annotation directly using the KEGG API to either replace the current version of the ID/term associations in the MathIOmica package data directory or add a new one (e.g. for a different species).

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KEGGQuery1	"pathway"	KEGGQuery1 is the text used internally by KEGG API calls, specifically as string query1 in "http://rest.kegg.jp/link/" <> query1 <> "/" <> query2. Typically this will be used as the target database to find related entries by using database cross–references. The default use is to query pathway data.
KEGGQuery2	"hsa"	KEGGQuery2 is the text used internally by KEGG API calls, specifically as string query2 in "http://rest.kegg.jp/link/" <> query1 <> "/" <> query2. Typically this will be used as the source database to find related entries by using database cross–references. The default use is to retrieve human data and corresponds to setting the organism database org="hsa".
Labels	{"IDToPath", "PathToID"}	Labels is a string list indicates what the keys in the association will be named as. The first corresponds to IDs to membership association, the second for member categories to associated IDs association. The values should only be modified for advanced applications.
LengthFilter	None	LengthFilter gives the option to select how many members each KEGG category/pathway/map can have, as restricted by the LengthFilterFunction.
LengthFilterFunction	GreaterEqualThan	LengthFilterFunction is an option regarding which function to use to filter the number of members a reported KEGG category/pathway/map has compared to the number provided by LengthFilter.

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MathIOmicaDataDirectory	If[! DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]	MathIOmicaDataDirectory option specifies the directory where the default MathIOmica package data are stored. By default the option is set to create the standard directory if it does not exist already.

Examples (12)

Basic Examples (1)

First we need to load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

- We can now run KEGGAnalysisAssigner to create a dictionary between KEGG Identifiers and KEGG Pathway identifiers, and similary KEGG pathway identifiers to KEGG member identifiers.

In[2]:=
```
assignmentsKEGG = KEGGAnalysisAssigner[]
```

Out[2]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 328 ···, ... → ··· 1 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

- The assignment has two Keys for the "hsa" i.e. human organism:

In[3]:=
```
Query[All, Keys]@assignmentsKEGG
```

Out[3]=
```
<|hsa → {IDToPath, PathToID}|>
```

- For example for accession "hsa:4790" corresponding to NFKB1 we have:

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In[4]:=
```
pathwaysKEGG = Query["hsa", "IDToPath", "hsa:4790"]@assignmentsKEGG
```

Out[4]=
```
{path:hsa01523, path:hsa04010, path:hsa04014, path:hsa04024, path:hsa04062, path:hsa04064, path:hsa04066,
 path:hsa04071, path:hsa04151, path:hsa04210, path:hsa04211, path:hsa04218, path:hsa04380, path:hsa04620,
 path:hsa04621, path:hsa04622, path:hsa04623, path:hsa04625, path:hsa04657, path:hsa04658, path:hsa04659,
 path:hsa04660, path:hsa04662, path:hsa04668, path:hsa04722, path:hsa04917, path:hsa04920, path:hsa04926,
 path:hsa04931, path:hsa04932, path:hsa04933, path:hsa05030, path:hsa05120, path:hsa05131,
 path:hsa05132, path:hsa05133, path:hsa05134, path:hsa05140, path:hsa05142, path:hsa05145,
 path:hsa05146, path:hsa05152, path:hsa05160, path:hsa05161, path:hsa05162, path:hsa05163,
 path:hsa05164, path:hsa05165, path:hsa05166, path:hsa05167, path:hsa05168, path:hsa05169,
 path:hsa05170, path:hsa05200, path:hsa05202, path:hsa05203, path:hsa05206, path:hsa05212,
 path:hsa05215, path:hsa05220, path:hsa05221, path:hsa05222, path:hsa05321, path:hsa05418}
```

We can see what all these terms' annotations are by using the KEGGDictionary function

In[5]:=
```
pathwayAnnotationExample = KEGGDictionary[];
```

The dictionary contains the annotations for the pathways:

In[6]:=
```
pathwayAnnotationExample[[1 ;; 5]]
```

Out[6]=
```
<|path:hsa00010 → Glycolysis / Gluconeogenesis - Homo sapiens (human),
 path:hsa00020 → Citrate cycle (TCA cycle) - Homo sapiens (human),
 path:hsa00030 → Pentose phosphate pathway - Homo sapiens (human),
 path:hsa00040 → Pentose and glucuronate interconversions - Homo sapiens (human),
 path:hsa00051 → Fructose and mannose metabolism - Homo sapiens (human)|>
```

Here are all the pathway annotations relating to the NFKB1 accession:

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```
In[7]:= Query[pathwaysKEGG]@pathwayAnnotationExample

Out[7]= <|path:hsa01523 → Missing[KeyAbsent, path:hsa01523],
 path:hsa04010 → MAPK signaling pathway - Homo sapiens (human),
 path:hsa04014 → Ras signaling pathway - Homo sapiens (human),
 path:hsa04024 → cAMP signaling pathway - Homo sapiens (human),
 path:hsa04062 → Chemokine signaling pathway - Homo sapiens (human),
 path:hsa04064 → NF-kappa B signaling pathway - Homo sapiens (human),
 path:hsa04066 → HIF-1 signaling pathway - Homo sapiens (human),
 path:hsa04071 → Sphingolipid signaling pathway - Homo sapiens (human),
 path:hsa04151 → PI3K-Akt signaling pathway - Homo sapiens (human),
 path:hsa04210 → Apoptosis - Homo sapiens (human),
 path:hsa04211 → Longevity regulating pathway - Homo sapiens (human),
 path:hsa04218 → Missing[KeyAbsent, path:hsa04218],
 path:hsa04380 → Osteoclast differentiation - Homo sapiens (human),
 path:hsa04620 → Toll-like receptor signaling pathway - Homo sapiens (human),
 path:hsa04621 → NOD-like receptor signaling pathway - Homo sapiens (human),
 path:hsa04622 → RIG-I-like receptor signaling pathway - Homo sapiens (human),
 path:hsa04623 → Cytosolic DNA-sensing pathway - Homo sapiens (human),
 path:hsa04625 → Missing[KeyAbsent, path:hsa04625], path:hsa04657 → Missing[KeyAbsent, path:hsa04657],
 path:hsa04658 → Missing[KeyAbsent, path:hsa04658], path:hsa04659 → Missing[KeyAbsent, path:hsa04659],
 path:hsa04660 → T cell receptor signaling pathway - Homo sapiens (human),
 path:hsa04662 → B cell receptor signaling pathway - Homo sapiens (human),
 path:hsa04668 → TNF signaling pathway - Homo sapiens (human),
 path:hsa04722 → Neurotrophin signaling pathway - Homo sapiens (human),
 path:hsa04917 → Prolactin signaling pathway - Homo sapiens (human),
 path:hsa04920 → Adipocytokine signaling pathway - Homo sapiens (human),
 path:hsa04926 → Missing[KeyAbsent, path:hsa04926],
 path:hsa04931 → Insulin resistance - Homo sapiens (human),
 path:hsa04932 → Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
 path:hsa04933 → AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human),
 path:hsa05030 → Cocaine addiction - Homo sapiens (human),
 path:hsa05120 → Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
 path:hsa05131 → Shigellosis - Homo sapiens (human),
 path:hsa05132 → Salmonella infection - Homo sapiens (human),
 path:hsa05133 → Pertussis - Homo sapiens (human), path:hsa05134 → Legionellosis - Homo sapiens (human),
 path:hsa05140 → Leishmaniasis - Homo sapiens (human),
 path:hsa05142 → Chagas disease (American trypanosomiasis) - Homo sapiens (human),
 path:hsa05145 → Toxoplasmosis - Homo sapiens (human),
 path:hsa05146 → Amoebiasis - Homo sapiens (human), path:hsa05152 → Tuberculosis - Homo sapiens (human),
 path:hsa05160 → Hepatitis C - Homo sapiens (human), path:hsa05161 → Hepatitis B - Homo sapiens (human),
 path:hsa05162 → Measles - Homo sapiens (human), path:hsa05163 → Missing[KeyAbsent, path:hsa05163],
 path:hsa05164 → Influenza A - Homo sapiens (human), path:hsa05165 → Missing[KeyAbsent, path:hsa05165],
 path:hsa05166 → HTLV-I infection - Homo sapiens (human), path:hsa05167 → Missing[KeyAbsent, path:hsa05167],
 path:hsa05168 → Herpes simplex infection - Homo sapiens (human),
 path:hsa05169 → Epstein-Barr virus infection - Homo sapiens (human),
 path:hsa05170 → Missing[KeyAbsent, path:hsa05170],
 path:hsa05200 → Pathways in cancer - Homo sapiens (human),
 path:hsa05202 → Transcriptional misregulation in cancer - Homo sapiens (human),
 path:hsa05203 → Viral carcinogenesis - Homo sapiens (human),
 path:hsa05206 → MicroRNAs in cancer - Homo sapiens (human),
 path:hsa05212 → Pancreatic cancer - Homo sapiens (human),
 path:hsa05215 → Prostate cancer - Homo sapiens (human),
 path:hsa05220 → Chronic myeloid leukemia - Homo sapiens (human),
 path:hsa05221 → Acute myeloid leukemia - Homo sapiens (human),
 path:hsa05222 → Small cell lung cancer - Homo sapiens (human),
 path:hsa05321 → Inflammatory bowel disease (IBD) - Homo sapiens (human),
 path:hsa05418 → Missing[KeyAbsent, path:hsa05418]|>
```

We can also query the members of a given KEGG pathway, e.g. "path:hsa04064" ("NF-kappa B signaling pathway - Homo sapiens (human)"):

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In[8]:=
```
identitiesKEGG = Query["hsa", "PathToID", "path:hsa04064"]@assignmentsKEGG
```

Out[8]=
```
{hsa:102723407, hsa:10454, hsa:10673, hsa:10892, hsa:114609, hsa:1147, hsa:115650, hsa:142, hsa:1457,
 hsa:1459, hsa:1460, hsa:148022, hsa:23085, hsa:23118, hsa:23586, hsa:23643, hsa:257397, hsa:27040,
 hsa:283106, hsa:2920, hsa:29760, hsa:29775, hsa:329, hsa:330, hsa:331, hsa:3383, hsa:353376,
 hsa:3551, hsa:3553, hsa:3554, hsa:3576, hsa:3654, hsa:388372, hsa:3929, hsa:3932, hsa:4049,
 hsa:4050, hsa:4055, hsa:4067, hsa:4615, hsa:4616, hsa:472, hsa:4790, hsa:4791, hsa:4792, hsa:51135,
 hsa:51588, hsa:5328, hsa:5335, hsa:5336, hsa:55367, hsa:5579, hsa:5588, hsa:5743, hsa:596, hsa:597,
 hsa:5970, hsa:5971, hsa:598, hsa:6351, hsa:6357, hsa:6363, hsa:6366, hsa:6387, hsa:6850, hsa:6885,
 hsa:695, hsa:7099, hsa:7124, hsa:7128, hsa:7132, hsa:7185, hsa:7186, hsa:7187, hsa:7188, hsa:7189,
 hsa:7329, hsa:7412, hsa:7535, hsa:7706, hsa:79092, hsa:84433, hsa:8517, hsa:8600, hsa:8717,
 hsa:8737, hsa:8740, hsa:8792, hsa:8837, hsa:8915, hsa:9020, hsa:929, hsa:9560, hsa:958, hsa:959}
```

Options (11)

BackgroundSet (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The `BackgroundSet` option allows the selection of what members (IDs) to use as a background (e.g. genes), or to use All genes as background. In effect this restricts the reported dictionary to only these members.

As an example, we limit the set to the following IDs {"hsa:4790","hsa:5328"}:

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In[2]:=
```
KEGGAnalysisAssigner[BackgroundSet → {"hsa:4790", "hsa:5328"}]
```

Out[2]=
```
<|hsa → <|IDToPath →
    <|hsa:4790 → {path:hsa01523, path:hsa04010, path:hsa04014, path:hsa04024, path:hsa04062, path:hsa04064,
       path:hsa04066, path:hsa04071, path:hsa04151, path:hsa04210, path:hsa04211, path:hsa04218,
       path:hsa04380, path:hsa04620, path:hsa04621, path:hsa04622, path:hsa04623,
       path:hsa04625, path:hsa04657, path:hsa04658, path:hsa04659, path:hsa04660, path:hsa04662,
       path:hsa04668, path:hsa04722, path:hsa04917, path:hsa04920, path:hsa04926, path:hsa04931,
       path:hsa04932, path:hsa04933, path:hsa05030, path:hsa05120, path:hsa05131, path:hsa05132,
       path:hsa05133, path:hsa05134, path:hsa05140, path:hsa05142, path:hsa05145, path:hsa05146,
       path:hsa05152, path:hsa05160, path:hsa05161, path:hsa05162, path:hsa05163, path:hsa05164,
       path:hsa05165, path:hsa05166, path:hsa05167, path:hsa05168, path:hsa05169, path:hsa05170,
       path:hsa05200, path:hsa05202, path:hsa05203, path:hsa05206, path:hsa05212, path:hsa05215,
       path:hsa05220, path:hsa05221, path:hsa05222, path:hsa05321, path:hsa05418}, hsa:5328 →
      {path:hsa04064, path:hsa04610, path:hsa05202, path:hsa05205, path:hsa05206, path:hsa05215}|>,
  PathToID → <|path:hsa01523 → {hsa:4790}, path:hsa04010 → {hsa:4790}, path:hsa04014 → {hsa:4790},
    path:hsa04024 → {hsa:4790}, path:hsa04062 → {hsa:4790}, path:hsa04064 → {hsa:4790, hsa:5328},
    path:hsa04066 → {hsa:4790}, path:hsa04071 → {hsa:4790}, path:hsa04151 → {hsa:4790},
    path:hsa04210 → {hsa:4790}, path:hsa04211 → {hsa:4790}, path:hsa04218 → {hsa:4790},
    path:hsa04380 → {hsa:4790}, path:hsa04620 → {hsa:4790}, path:hsa04621 → {hsa:4790},
    path:hsa04622 → {hsa:4790}, path:hsa04623 → {hsa:4790}, path:hsa04625 → {hsa:4790},
    path:hsa04657 → {hsa:4790}, path:hsa04658 → {hsa:4790}, path:hsa04659 → {hsa:4790},
    path:hsa04660 → {hsa:4790}, path:hsa04662 → {hsa:4790}, path:hsa04668 → {hsa:4790},
    path:hsa04722 → {hsa:4790}, path:hsa04917 → {hsa:4790}, path:hsa04920 → {hsa:4790},
    path:hsa04926 → {hsa:4790}, path:hsa04931 → {hsa:4790}, path:hsa04932 → {hsa:4790},
    path:hsa04933 → {hsa:4790}, path:hsa05030 → {hsa:4790}, path:hsa05120 → {hsa:4790},
    path:hsa05131 → {hsa:4790}, path:hsa05132 → {hsa:4790}, path:hsa05133 → {hsa:4790},
    path:hsa05134 → {hsa:4790}, path:hsa05140 → {hsa:4790}, path:hsa05142 → {hsa:4790},
    path:hsa05145 → {hsa:4790}, path:hsa05146 → {hsa:4790}, path:hsa05152 → {hsa:4790},
    path:hsa05160 → {hsa:4790}, path:hsa05161 → {hsa:4790}, path:hsa05162 → {hsa:4790},
    path:hsa05163 → {hsa:4790}, path:hsa05164 → {hsa:4790}, path:hsa05165 → {hsa:4790},
    path:hsa05166 → {hsa:4790}, path:hsa05167 → {hsa:4790}, path:hsa05168 → {hsa:4790},
    path:hsa05169 → {hsa:4790}, path:hsa05170 → {hsa:4790}, path:hsa05200 → {hsa:4790},
    path:hsa05202 → {hsa:4790, hsa:5328}, path:hsa05203 → {hsa:4790}, path:hsa05206 → {hsa:4790, hsa:5328},
    path:hsa05212 → {hsa:4790}, path:hsa05215 → {hsa:4790, hsa:5328}, path:hsa05220 → {hsa:4790},
    path:hsa05221 → {hsa:4790}, path:hsa05222 → {hsa:4790}, path:hsa05321 → {hsa:4790},
    path:hsa05418 → {hsa:4790}, path:hsa04610 → {hsa:5328}, path:hsa05205 → {hsa:5328}|>|>|>
```

Setting `BackgroundSet` to All retrieves all the ID/KEGG pathway associations:

In[3]:=
```
KEGGAnalysisAssigner[BackgroundSet → All]
```

Out[3]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 329 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

ImportDirectly (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`ImportDirectly` gives the option to import a new version of KEGG annotation directly using the KEGG API to either replace the current version of the ID/term associations in the MathIOmica package data directory or add a new one (e.g. for a different species).

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In[2]:=
```
KEGGAnalysisAssigner[ImportDirectly → True]
```

Out[2]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 329 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

KEGGQuery1 (2)

In[1]:=
```
Needs["MathIOmica`"]
```

KEGGQuery1 is the text used internally by KEGG API calls, specifically as string query1 in "http://rest.kegg.jp/link/" <> query1 <> "/" <> query2. Typically this will be used as the target database to find related entries by using database cross-references. The default use is to query pathway data.

For example, we can get pathway associations for human genes (default):

In[2]:=
```
pathwayQuery1 = KEGGAnalysisAssigner[KEGGQuery1 → "pathway"]
```

Out[2]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 329 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

In[1]:=
```
Needs["MathIOmica`"]
```

As another example, we can get disease associations for human genes:

In[2]:=
```
diseaseQuery1 = KEGGAnalysisAssigner[KEGGQuery1 → "disease"]
```

Out[2]=
```
<|hsa → <|IDToPath → <|hsa:7428 → {ds:H00021, ds:H00236, ds:H00559, ds:H01510},
      hsa:4233 → {ds:H00018, ds:H00021, ds:H00046}, ··· 2651 ···,
      hsa:9871 → {ds:H01572}, hsa:308 → {ds:H01639}|>, PathToID → <| ··· 1 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

KEGGQuery2 (3)

In[1]:=
```
Needs["MathIOmica`"]
```

KEGGQuery2 is the text used internally by KEGG API calls, specifically as string query2 in "http://rest.kegg.jp/link/" <> query1 <> "/" <> query2. Typically this will be used as the source database to find related entries by using database cross-references. The default use is to retrieve human data and corresponds to setting the organism database org="hsa".

For example, we can get pathway associations for human genes (default):

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In[2]:=
```
pathwayHumanQuery2 = KEGGAnalysisAssigner[KEGGQuery2 → "hsa"]
```

Out[2]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 329 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

In[1]:=
```
Needs["MathIOmica`"]
```

For example, we can get pathway associations for mouse genes:

In[2]:=
```
pathwayMouseQuery2 = KEGGAnalysisAssigner[KEGGQuery2 → "mmu"]
```

Out[2]=
```
<|mmu → <|IDToPath → <|mmu:100042025 →
      {path:mmu00010, path:mmu01100, path:mmu01200, path:mmu01230, path:mmu04066, path:mmu05010},
      ··· 7915 ···, mmu:13052 → {path:mmu05416}|>, PathToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

In[1]:=
```
Needs["MathIOmica`"]
```

As another example, we can get pathway associations for Arabidopsis thaliana genes:

In[2]:=
```
pathwayAthQuery2 = KEGGAnalysisAssigner[KEGGQuery2 → "ath"]
```

Out[2]=
```
<|ath → <|IDToPath → <|ath:AT1G01090 →
      {path:ath00010, path:ath00020, path:ath00620, path:ath01100, path:ath01110, path:ath01200},
      ··· 4779 ···, ath:AT3G59790 → {path:ath04933}|>, PathToID → <| ··· 1 ··· |>|>|>
```

large output | show less | show more | show all | set size limit...

Labels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

Labels is a string list indicates what the keys in the association will be named as. The first corresponds to IDs to membership association, the second for member categories to associated IDs association. The values should only be modified for advanced applications.

For example, we can get pathway associations:

In[2]:=
```
pathwayLabelsDefault = KEGGAnalysisAssigner[Labels → {"IDToPath", "PathToID"}]
```

Out[2]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 329 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

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We can choose to name the labels differently:

In[3]:=
```
pathwayLabelsCustom = KEGGAnalysisAssigner[Labels → {"IdentifierToMap", "MapToIdentifer"}]
```

Out[3]=
```
<|hsa → <|IdentifierToMap → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   MapToIdentifer → <|path:hsa00010 → {··· 1 ···}, ··· 328 ···, ... → ··· 1 ···|>|>|>
```
large output | show less | show more | show all | set size limit...

LengthFilter (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`LengthFilter` gives the option to select how many members each KEGG pathway can have, as restricted by the `LengthFilterFunction`, the default is number of members in each KEGG pathway
`number of members in each KEGG pathway ≥ OptionValue[LengthFilter]`.
By default LengthFilter is set to None, i.e. no filtering is performed:

For example, we can get pathway associations:

In[2]:=
```
pathwayLengthFilterNone = KEGGAnalysisAssigner[LengthFilter → None]
```

Out[2]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 328 ···, ··· 1 ···|>|>|>
```
large output | show less | show more | show all | set size limit...

The number of "PathToID" entries are:

In[3]:=
```
Query["hsa", "PathToID", Length[#] &]@pathwayLengthFilterNone
```

Out[3]= 330

We can calculate the minimum length of these pathway lists:

In[4]:=
```
Query["hsa", "PathToID", All /* Min, Length[#] &]@pathwayLengthFilterNone
```

Out[4]= 1

We now restrict the pathways to have membership greater than or equal to 10:

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In[5]:=
```
pathwayLengthFilter10 = KEGGAnalysisAssigner[LengthFilter → 10]
```

Out[5]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7460 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 315 ···, ··· 1 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

The number of "PathToID" entries are:

In[6]:=
```
Query["hsa", "PathToID", Length[#] &]@pathwayLengthFilter10
```

Out[6]= 317

As expected the smallest list of IDs for a given KEGG pathway is 10:

In[7]:=
```
Query["hsa", "PathToID", All /* Min, Length[#] &]@pathwayLengthFilter10
```

Out[7]= 10

LengthFilterFunction (1)

`LengthFilterFunction` is an option regarding which function to use to filter the number of members a reported KEGG pathaway has compared to the number provided by `LengthFilter`. If LengthFilter is set to None no filtering is implemented. The default comparison function is GreaterEqualThan

For example we can create the IDs/pathway associations listing only the IDs/pathway terms, for which for all pathways have at least 10 IDs associated to them.

In[1]:=
```
pathwaysFilterGreater = KEGGAnalysisAssigner[LengthFilterFunction → GreaterEqualThan, LengthFilter → 10]
```

Out[1]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7460 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 316 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

We can see that the maximum number of IDs associated to a KEGG patway is:

In[2]:=
```
Query["hsa", "PathToID", All /* Max, Length[#] &]@pathwaysFilterGreater
```

Out[2]= 1305

Instead, we can look at all KEGG pathways that have less than 10 IDs associated to them:

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```
In[3]:= pathwaysFilterLess = KEGGAnalysisAssigner[LengthFilterFunction → LessThan, LengthFilter → 10]
```

```
Out[3]= <|hsa →
  <|IDToPath → <|hsa:10 → {path:hsa00232}, hsa:1544 → {path:hsa00232}, hsa:1548 → {path:hsa00232}, hsa:7498 →
      {path:hsa00232}, hsa:9 → {path:hsa00232}, hsa:10993 → {path:hsa00290}, hsa:113675 → {path:hsa00290},
    hsa:586 → {path:hsa00290}, hsa:587 → {path:hsa00290}, hsa:259307 → {path:hsa00400},
    hsa:2805 → {path:hsa00400}, hsa:2806 → {path:hsa00400}, hsa:5053 → {path:hsa00400},
    hsa:6898 → {path:hsa00400}, hsa:10390 → {path:hsa00440}, hsa:5130 → {path:hsa00440},
    hsa:56994 → {path:hsa00440}, hsa:5833 → {path:hsa00440}, hsa:85465 → {path:hsa00440},
    hsa:9468 → {path:hsa00440}, hsa:27165 → {path:hsa00471}, hsa:2744 → {path:hsa00471},
    hsa:2746 → {path:hsa00471}, hsa:2747 → {path:hsa00471}, hsa:80017 → {path:hsa00471},
    hsa:1610 → {path:hsa00472}, hsa:2645 → {path:hsa00524}, hsa:3098 → {path:hsa00524},
    hsa:3099 → {path:hsa00524}, hsa:3101 → {path:hsa00524}, hsa:80201 → {path:hsa00524},
    hsa:5167 → {path:hsa00740}, hsa:5169 → {path:hsa00740}, hsa:52 → {path:hsa00740},
    hsa:53 → {path:hsa00740}, hsa:54 → {path:hsa00740}, hsa:55312 → {path:hsa00740},
    hsa:645 → {path:hsa00740}, hsa:80308 → {path:hsa00740}, hsa:29968 → {path:hsa00750},
    hsa:316 → {path:hsa00750}, hsa:493911 → {path:hsa00750}, hsa:55163 → {path:hsa00750},
    hsa:57026 → {path:hsa00750}, hsa:8566 → {path:hsa00750}, hsa:3141 → {path:hsa00780},
    hsa:54995 → {path:hsa00780}, hsa:686 → {path:hsa00780}, hsa:11019 → {path:hsa00785},
    hsa:387787 → {path:hsa00785}, hsa:51601 → {path:hsa00785}, hsa:10380 → {path:hsa00920},
    hsa:23474 → {path:hsa00920}, hsa:4357 → {path:hsa00920, path:hsa04122},
    hsa:54928 → {path:hsa00920}, hsa:58472 → {path:hsa00920}, hsa:6821 → {path:hsa00920},
    hsa:7263 → {path:hsa00920, path:hsa04122}, hsa:9060 → {path:hsa00920}, hsa:9061 → {path:hsa00920},
    hsa:27304 → {path:hsa04122}, hsa:348180 → {path:hsa04122}, hsa:4338 → {path:hsa04122},
    hsa:81605 → {path:hsa04122}, hsa:90353 → {path:hsa04122}, hsa:9054 → {path:hsa04122}|>,
  PathToID → <|path:hsa00232 → {hsa:10, hsa:1544, hsa:1548, hsa:7498, hsa:9},
    path:hsa00290 → {hsa:10993, hsa:113675, hsa:586, hsa:587},
    path:hsa00400 → {hsa:259307, hsa:2805, hsa:2806, hsa:5053, hsa:6898},
    path:hsa00440 → {hsa:10390, hsa:5130, hsa:56994, hsa:5833, hsa:85465, hsa:9468},
    path:hsa00471 → {hsa:27165, hsa:2744, hsa:2746, hsa:2747, hsa:80017},
    path:hsa00472 → {hsa:1610}, path:hsa00524 → {hsa:2645, hsa:3098, hsa:3099, hsa:3101, hsa:80201},
    path:hsa00740 → {hsa:5167, hsa:5169, hsa:52, hsa:53, hsa:54, hsa:55312, hsa:645, hsa:80308},
    path:hsa00750 → {hsa:29968, hsa:316, hsa:493911, hsa:55163, hsa:57026, hsa:8566},
    path:hsa00780 → {hsa:3141, hsa:54995, hsa:686}, path:hsa00785 → {hsa:11019, hsa:387787, hsa:51601},
    path:hsa00920 → {hsa:10380, hsa:23474, hsa:4357, hsa:54928,
      hsa:58472, hsa:6821, hsa:7263, hsa:9060, hsa:9061}, path:hsa04122 →
     {hsa:27304, hsa:348180, hsa:4338, hsa:4357, hsa:7263, hsa:81605, hsa:90353, hsa:9054}|>|>|>
```

We can now see that the maximum number of IDs associated to a KEGG pathway is less than 10, as we have restricted the possibilities:

```
In[4]:= Query["hsa", "PathToID", All /* Max, Length[#] &]@pathwaysFilterLess
```

```
Out[4]= 9
```

MathIOmicaDataDirectory (1)

```
In[1]:= Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value point to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

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In[2]:=
```
KEGGAnalysisAssigner[MathIOmicaDataDirectory → FileNameJoin[
   Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]
```

Out[2]=
```
<|hsa → <|IDToPath → <|hsa:10327 → {path:hsa00010, path:hsa00040, path:hsa00561, path:hsa01100},
      ··· 7467 ···, hsa:4880 → {path:hsa05418}|>,
   PathToID → <|path:hsa00010 → {hsa:10327, ··· 66 ···, hsa:9562}, ··· 329 ···|>|>|>
```

large output | show less | show more | show all | set size limit...

See Also

GeneTranslation ▪ **GetGeneDictionary** ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGDictionary** ▪ **KEGGPathwayVisual** ▪ **OBOGODictionary** ▪ **TimeSeriesClusters** ▪ **UCSCBrowserSQL**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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KEGGDictionary

`KEGGDictionary[]`
creates a dictionary from KEGG: Kyoto Encyclopedia of Genes and Genomes terms – typically association of pathways and members therein.

Details

- `KEGGDictionary[]` generates an annotation dictionary (association) of KEGG: Kyoto Encyclopedia of Genes and pathways entries to definition, based on KEGG databse information. The form of the output for n KEGG entries (e.g. pathway accessions) is:
- output = <|KEGG : $entry_1$ → description of KEGG : $entry_1$,
  KEGG : $entry_2$ → description of KEGG : $entry_2$, ...,
  KEGG : $entry_n$ → description of KEGG : $entry_n$
  |>
- The following options can be given:

ImportDirectly	False	ImportDirectly gives the option to import a new version of the KEGG dictionary information file directly from KEGG to either replace the current version in the MathIOmica package data directory or add a new one (e.g. for a different species).
KEGGQuery1	"pathway"	KEGGQuery1 is the text used internally by KEGG API calls, specifically as string query1 in "http://rest.kegg.jp/list/" <> query1 <> "/" <> query2. Typically this will be used as the target database to return a list of entry identifiers and associated definition for this database entries.

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KEGGQuery2	"hsa"	KEGGQuery2 is the text used internally by KEGG API calls, specifically as specifically as string query2 in "http://rest.kegg.jp/list/" <> query1 <> "/" <> query2. Typically this will be used as the organism code (org) to return a list of entry identifiers and associated definition for the database specified by KEGGQuery1. The default use is to list human pathway annotations and corresponds to setting the organism org="hsa".
MathIOmicaDataDirectory	If[! DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]	MathIOmicaDataDirectory option specifies the directory where the default MathIOmica package data are stored. By default the option is set to create the standard directory if it does not exist already.

Examples (10)

Basic Examples (1)

First we need to load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

In[2]:=
```
exampleKEGGDictionary = KEGGDictionary[]
```

Out[2]=
```
<|path:hsa00010 → Glycolysis / Gluconeogenesis - Homo sapiens (human),
 path:hsa00020 → Citrate cycle (TCA cycle) - Homo sapiens (human),
 path:hsa00030 → Pentose phosphate pathway - Homo sapiens (human),
 path:hsa00040 → Pentose and glucuronate interconversions - Homo sapiens (human),
 path:hsa00051 → Fructose and mannose metabolism - Homo sapiens (human),
 path:hsa00052 → Galactose metabolism - Homo sapiens (human),
 path:hsa00053 → Ascorbate and aldarate metabolism - Homo sapiens (human),
 path:hsa00061 → Fatty acid biosynthesis - Homo sapiens (human),
 path:hsa00062 → Fatty acid elongation - Homo sapiens (human),
 path:hsa00071 → Fatty acid degradation - Homo sapiens (human),
 path:hsa00072 → Synthesis and degradation of ketone bodies - Homo sapiens (human),
 path:hsa00100 → Steroid biosynthesis - Homo sapiens (human),
 path:hsa00120 → Primary bile acid biosynthesis - Homo sapiens (human),
```

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```
path:hsa00130 → Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human),
path:hsa00140 → Steroid hormone biosynthesis - Homo sapiens (human),
path:hsa00190 → Oxidative phosphorylation - Homo sapiens (human),
path:hsa00220 → Arginine biosynthesis - Homo sapiens (human),
path:hsa00230 → Purine metabolism - Homo sapiens (human),
path:hsa00232 → Caffeine metabolism - Homo sapiens (human),
path:hsa00240 → Pyrimidine metabolism - Homo sapiens (human),
path:hsa00250 → Alanine, aspartate and glutamate metabolism - Homo sapiens (human),
path:hsa00260 → Glycine, serine and threonine metabolism - Homo sapiens (human),
path:hsa00270 → Cysteine and methionine metabolism - Homo sapiens (human),
path:hsa00280 → Valine, leucine and isoleucine degradation - Homo sapiens (human),
path:hsa00290 → Valine, leucine and isoleucine biosynthesis - Homo sapiens (human),
path:hsa00300 → Lysine biosynthesis - Homo sapiens (human),
path:hsa00310 → Lysine degradation - Homo sapiens (human),
path:hsa00330 → Arginine and proline metabolism - Homo sapiens (human),
path:hsa00340 → Histidine metabolism - Homo sapiens (human),
path:hsa00350 → Tyrosine metabolism - Homo sapiens (human),
path:hsa00360 → Phenylalanine metabolism - Homo sapiens (human),
path:hsa00380 → Tryptophan metabolism - Homo sapiens (human),
path:hsa00400 → Phenylalanine, tyrosine and tryptophan biosynthesis - Homo sapiens (human),
path:hsa00410 → beta-Alanine metabolism - Homo sapiens (human),
path:hsa00430 → Taurine and hypotaurine metabolism - Homo sapiens (human),
path:hsa00450 → Selenocompound metabolism - Homo sapiens (human),
path:hsa00471 → D-Glutamine and D-glutamate metabolism - Homo sapiens (human),
path:hsa00472 → D-Arginine and D-ornithine metabolism - Homo sapiens (human),
path:hsa00480 → Glutathione metabolism - Homo sapiens (human),
path:hsa00500 → Starch and sucrose metabolism - Homo sapiens (human),
path:hsa00510 → N-Glycan biosynthesis - Homo sapiens (human),
path:hsa00511 → Other glycan degradation - Homo sapiens (human),
path:hsa00512 → Mucin type O-Glycan biosynthesis - Homo sapiens (human),
path:hsa00514 → Other types of O-glycan biosynthesis - Homo sapiens (human),
path:hsa00520 → Amino sugar and nucleotide sugar metabolism - Homo sapiens (human),
path:hsa00524 → Neomycin, kanamycin and gentamicin biosynthesis - Homo sapiens (human),
path:hsa00531 → Glycosaminoglycan degradation - Homo sapiens (human), path:hsa00532 →
 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Homo sapiens (human),
path:hsa00533 → Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human),
path:hsa00534 → Glycosaminoglycan biosynthesis - heparan sulfate / heparin - Homo sapiens (human),
path:hsa00561 → Glycerolipid metabolism - Homo sapiens (human),
path:hsa00562 → Inositol phosphate metabolism - Homo sapiens (human),
path:hsa00563 → Glycosylphosphatidylinositol(GPI)-anchor biosynthesis - Homo sapiens (human),
path:hsa00564 → Glycerophospholipid metabolism - Homo sapiens (human),
path:hsa00565 → Ether lipid metabolism - Homo sapiens (human),
path:hsa00590 → Arachidonic acid metabolism - Homo sapiens (human),
path:hsa00591 → Linoleic acid metabolism - Homo sapiens (human),
path:hsa00592 → alpha-Linolenic acid metabolism - Homo sapiens (human),
path:hsa00600 → Sphingolipid metabolism - Homo sapiens (human),
path:hsa00601 → Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human),
path:hsa00603 → Glycosphingolipid biosynthesis - globo series - Homo sapiens (human),
path:hsa00604 → Glycosphingolipid biosynthesis - ganglio series - Homo sapiens (human),
path:hsa00620 → Pyruvate metabolism - Homo sapiens (human),
path:hsa00630 → Glyoxylate and dicarboxylate metabolism - Homo sapiens (human),
path:hsa00640 → Propanoate metabolism - Homo sapiens (human),
path:hsa00650 → Butanoate metabolism - Homo sapiens (human),
path:hsa00670 → One carbon pool by folate - Homo sapiens (human),
path:hsa00730 → Thiamine metabolism - Homo sapiens (human),
path:hsa00740 → Riboflavin metabolism - Homo sapiens (human),
path:hsa00750 → Vitamin B6 metabolism - Homo sapiens (human),
path:hsa00760 → Nicotinate and nicotinamide metabolism - Homo sapiens (human),
path:hsa00770 → Pantothenate and CoA biosynthesis - Homo sapiens (human),
path:hsa00780 → Biotin metabolism - Homo sapiens (human),
path:hsa00785 → Lipoic acid metabolism - Homo sapiens (human),
path:hsa00790 → Folate biosynthesis - Homo sapiens (human),
path:hsa00830 → Retinol metabolism - Homo sapiens (human),
path:hsa00860 → Porphyrin and chlorophyll metabolism - Homo sapiens (human),
path:hsa00900 → Terpenoid backbone biosynthesis - Homo sapiens (human),
path:hsa00910 → Nitrogen metabolism - Homo sapiens (human),
```

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```
path:hsa00920 → Sulfur metabolism - Homo sapiens (human),
path:hsa00970 → Aminoacyl-tRNA biosynthesis - Homo sapiens (human),
path:hsa00980 → Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human),
path:hsa00982 → Drug metabolism - cytochrome P450 - Homo sapiens (human),
path:hsa00983 → Drug metabolism - other enzymes - Homo sapiens (human),
path:hsa01040 → Biosynthesis of unsaturated fatty acids - Homo sapiens (human),
path:hsa01100 → Metabolic pathways - Homo sapiens (human),
path:hsa01200 → Carbon metabolism - Homo sapiens (human),
path:hsa01210 → 2-Oxocarboxylic acid metabolism - Homo sapiens (human),
path:hsa01212 → Fatty acid metabolism - Homo sapiens (human),
path:hsa01230 → Biosynthesis of amino acids - Homo sapiens (human),
path:hsa01521 → EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human),
path:hsa01522 → Endocrine resistance - Homo sapiens (human),
path:hsa01524 → Platinum drug resistance - Homo sapiens (human),
path:hsa02010 → ABC transporters - Homo sapiens (human),
path:hsa03008 → Ribosome biogenesis in eukaryotes - Homo sapiens (human),
path:hsa03010 → Ribosome - Homo sapiens (human), path:hsa03013 → RNA transport - Homo sapiens (human),
path:hsa03015 → mRNA surveillance pathway - Homo sapiens (human),
path:hsa03018 → RNA degradation - Homo sapiens (human),
path:hsa03020 → RNA polymerase - Homo sapiens (human),
path:hsa03022 → Basal transcription factors - Homo sapiens (human),
path:hsa03030 → DNA replication - Homo sapiens (human), path:hsa03040 → Spliceosome - Homo sapiens (human),
path:hsa03050 → Proteasome - Homo sapiens (human), path:hsa03060 → Protein export - Homo sapiens (human),
path:hsa03320 → PPAR signaling pathway - Homo sapiens (human),
path:hsa03410 → Base excision repair - Homo sapiens (human),
path:hsa03420 → Nucleotide excision repair - Homo sapiens (human),
path:hsa03430 → Mismatch repair - Homo sapiens (human),
path:hsa03440 → Homologous recombination - Homo sapiens (human),
path:hsa03450 → Non-homologous end-joining - Homo sapiens (human),
path:hsa03460 → Fanconi anemia pathway - Homo sapiens (human),
path:hsa04010 → MAPK signaling pathway - Homo sapiens (human),
path:hsa04012 → ErbB signaling pathway - Homo sapiens (human),
path:hsa04014 → Ras signaling pathway - Homo sapiens (human),
path:hsa04015 → Rap1 signaling pathway - Homo sapiens (human),
path:hsa04020 → Calcium signaling pathway - Homo sapiens (human),
path:hsa04022 → cGMP-PKG signaling pathway - Homo sapiens (human),
path:hsa04024 → cAMP signaling pathway - Homo sapiens (human),
path:hsa04060 → Cytokine-cytokine receptor interaction - Homo sapiens (human),
path:hsa04062 → Chemokine signaling pathway - Homo sapiens (human),
path:hsa04064 → NF-kappa B signaling pathway - Homo sapiens (human),
path:hsa04066 → HIF-1 signaling pathway - Homo sapiens (human),
path:hsa04068 → FoxO signaling pathway - Homo sapiens (human),
path:hsa04070 → Phosphatidylinositol signaling system - Homo sapiens (human),
path:hsa04071 → Sphingolipid signaling pathway - Homo sapiens (human),
path:hsa04072 → Phospholipase D signaling pathway - Homo sapiens (human),
path:hsa04080 → Neuroactive ligand-receptor interaction - Homo sapiens (human),
path:hsa04110 → Cell cycle - Homo sapiens (human), path:hsa04114 → Oocyte meiosis - Homo sapiens (human),
path:hsa04115 → p53 signaling pathway - Homo sapiens (human),
path:hsa04120 → Ubiquitin mediated proteolysis - Homo sapiens (human),
path:hsa04122 → Sulfur relay system - Homo sapiens (human),
path:hsa04130 → SNARE interactions in vesicular transport - Homo sapiens (human),
path:hsa04140 → Regulation of autophagy - Homo sapiens (human),
path:hsa04141 → Protein processing in endoplasmic reticulum - Homo sapiens (human),
path:hsa04142 → Lysosome - Homo sapiens (human), path:hsa04144 → Endocytosis - Homo sapiens (human),
path:hsa04145 → Phagosome - Homo sapiens (human), path:hsa04146 → Peroxisome - Homo sapiens (human),
path:hsa04150 → mTOR signaling pathway - Homo sapiens (human),
path:hsa04151 → PI3K-Akt signaling pathway - Homo sapiens (human),
path:hsa04152 → AMPK signaling pathway - Homo sapiens (human),
path:hsa04210 → Apoptosis - Homo sapiens (human),
path:hsa04211 → Longevity regulating pathway - Homo sapiens (human),
path:hsa04213 → Longevity regulating pathway - multiple species - Homo sapiens (human),
path:hsa04215 → Apoptosis - multiple species - Homo sapiens (human),
path:hsa04260 → Cardiac muscle contraction - Homo sapiens (human),
path:hsa04261 → Adrenergic signaling in cardiomyocytes - Homo sapiens (human),
path:hsa04270 → Vascular smooth muscle contraction - Homo sapiens (human),
path:hsa04310 → Wnt signaling pathway - Homo sapiens (human),
```

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```
path:hsa04320 → Dorso-ventral axis formation - Homo sapiens (human),
path:hsa04330 → Notch signaling pathway - Homo sapiens (human),
path:hsa04340 → Hedgehog signaling pathway - Homo sapiens (human),
path:hsa04350 → TGF-beta signaling pathway - Homo sapiens (human),
path:hsa04360 → Axon guidance - Homo sapiens (human),
path:hsa04370 → VEGF signaling pathway - Homo sapiens (human),
path:hsa04380 → Osteoclast differentiation - Homo sapiens (human),
path:hsa04390 → Hippo signaling pathway - Homo sapiens (human),
path:hsa04392 → Hippo signaling pathway -multiple species - Homo sapiens (human),
path:hsa04510 → Focal adhesion - Homo sapiens (human),
path:hsa04512 → ECM-receptor interaction - Homo sapiens (human),
path:hsa04514 → Cell adhesion molecules (CAMs) - Homo sapiens (human),
path:hsa04520 → Adherens junction - Homo sapiens (human),
path:hsa04530 → Tight junction - Homo sapiens (human), path:hsa04540 → Gap junction - Homo sapiens (human),
path:hsa04550 → Signaling pathways regulating pluripotency of stem cells - Homo sapiens (human),
path:hsa04610 → Complement and coagulation cascades - Homo sapiens (human),
path:hsa04611 → Platelet activation - Homo sapiens (human),
path:hsa04612 → Antigen processing and presentation - Homo sapiens (human),
path:hsa04614 → Renin-angiotensin system - Homo sapiens (human),
path:hsa04620 → Toll-like receptor signaling pathway - Homo sapiens (human),
path:hsa04621 → NOD-like receptor signaling pathway - Homo sapiens (human),
path:hsa04622 → RIG-I-like receptor signaling pathway - Homo sapiens (human),
path:hsa04623 → Cytosolic DNA-sensing pathway - Homo sapiens (human),
path:hsa04630 → Jak-STAT signaling pathway - Homo sapiens (human),
path:hsa04640 → Hematopoietic cell lineage - Homo sapiens (human),
path:hsa04650 → Natural killer cell mediated cytotoxicity - Homo sapiens (human),
path:hsa04660 → T cell receptor signaling pathway - Homo sapiens (human),
path:hsa04662 → B cell receptor signaling pathway - Homo sapiens (human),
path:hsa04664 → Fc epsilon RI signaling pathway - Homo sapiens (human),
path:hsa04666 → Fc gamma R-mediated phagocytosis - Homo sapiens (human),
path:hsa04668 → TNF signaling pathway - Homo sapiens (human),
path:hsa04670 → Leukocyte transendothelial migration - Homo sapiens (human),
path:hsa04672 → Intestinal immune network for IgA production - Homo sapiens (human),
path:hsa04710 → Circadian rhythm - Homo sapiens (human),
path:hsa04713 → Circadian entrainment - Homo sapiens (human),
path:hsa04720 → Long-term potentiation - Homo sapiens (human),
path:hsa04721 → Synaptic vesicle cycle - Homo sapiens (human),
path:hsa04722 → Neurotrophin signaling pathway - Homo sapiens (human),
path:hsa04723 → Retrograde endocannabinoid signaling - Homo sapiens (human),
path:hsa04724 → Glutamatergic synapse - Homo sapiens (human),
path:hsa04725 → Cholinergic synapse - Homo sapiens (human),
path:hsa04726 → Serotonergic synapse - Homo sapiens (human),
path:hsa04727 → GABAergic synapse - Homo sapiens (human),
path:hsa04728 → Dopaminergic synapse - Homo sapiens (human),
path:hsa04730 → Long-term depression - Homo sapiens (human),
path:hsa04740 → Olfactory transduction - Homo sapiens (human),
path:hsa04742 → Taste transduction - Homo sapiens (human),
path:hsa04744 → Phototransduction - Homo sapiens (human),
path:hsa04750 → Inflammatory mediator regulation of TRP channels - Homo sapiens (human),
path:hsa04810 → Regulation of actin cytoskeleton - Homo sapiens (human),
path:hsa04910 → Insulin signaling pathway - Homo sapiens (human),
path:hsa04911 → Insulin secretion - Homo sapiens (human),
path:hsa04912 → GnRH signaling pathway - Homo sapiens (human),
path:hsa04913 → Ovarian steroidogenesis - Homo sapiens (human),
path:hsa04914 → Progesterone-mediated oocyte maturation - Homo sapiens (human),
path:hsa04915 → Estrogen signaling pathway - Homo sapiens (human),
path:hsa04916 → Melanogenesis - Homo sapiens (human),
path:hsa04917 → Prolactin signaling pathway - Homo sapiens (human),
path:hsa04918 → Thyroid hormone synthesis - Homo sapiens (human),
path:hsa04919 → Thyroid hormone signaling pathway - Homo sapiens (human),
path:hsa04920 → Adipocytokine signaling pathway - Homo sapiens (human),
path:hsa04921 → Oxytocin signaling pathway - Homo sapiens (human),
path:hsa04922 → Glucagon signaling pathway - Homo sapiens (human),
path:hsa04923 → Regulation of lipolysis in adipocytes - Homo sapiens (human),
path:hsa04924 → Renin secretion - Homo sapiens (human),
path:hsa04925 → Aldosterone synthesis and secretion - Homo sapiens (human),
```

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```
path:hsa04930 → Type II diabetes mellitus - Homo sapiens (human),
path:hsa04931 → Insulin resistance - Homo sapiens (human),
path:hsa04932 → Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
path:hsa04933 → AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human),
path:hsa04940 → Type I diabetes mellitus - Homo sapiens (human),
path:hsa04950 → Maturity onset diabetes of the young - Homo sapiens (human),
path:hsa04960 → Aldosterone-regulated sodium reabsorption - Homo sapiens (human),
path:hsa04961 → Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
path:hsa04962 → Vasopressin-regulated water reabsorption - Homo sapiens (human),
path:hsa04964 → Proximal tubule bicarbonate reclamation - Homo sapiens (human),
path:hsa04966 → Collecting duct acid secretion - Homo sapiens (human),
path:hsa04970 → Salivary secretion - Homo sapiens (human),
path:hsa04971 → Gastric acid secretion - Homo sapiens (human),
path:hsa04972 → Pancreatic secretion - Homo sapiens (human),
path:hsa04973 → Carbohydrate digestion and absorption - Homo sapiens (human),
path:hsa04974 → Protein digestion and absorption - Homo sapiens (human),
path:hsa04975 → Fat digestion and absorption - Homo sapiens (human),
path:hsa04976 → Bile secretion - Homo sapiens (human),
path:hsa04977 → Vitamin digestion and absorption - Homo sapiens (human),
path:hsa04978 → Mineral absorption - Homo sapiens (human),
path:hsa05010 → Alzheimer's disease - Homo sapiens (human),
path:hsa05012 → Parkinson's disease - Homo sapiens (human),
path:hsa05014 → Amyotrophic lateral sclerosis (ALS) - Homo sapiens (human),
path:hsa05016 → Huntington's disease - Homo sapiens (human),
path:hsa05020 → Prion diseases - Homo sapiens (human),
path:hsa05030 → Cocaine addiction - Homo sapiens (human),
path:hsa05031 → Amphetamine addiction - Homo sapiens (human),
path:hsa05032 → Morphine addiction - Homo sapiens (human),
path:hsa05033 → Nicotine addiction - Homo sapiens (human),
path:hsa05034 → Alcoholism - Homo sapiens (human),
path:hsa05100 → Bacterial invasion of epithelial cells - Homo sapiens (human),
path:hsa05110 → Vibrio cholerae infection - Homo sapiens (human),
path:hsa05120 → Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
path:hsa05130 → Pathogenic Escherichia coli infection - Homo sapiens (human),
path:hsa05131 → Shigellosis - Homo sapiens (human),
path:hsa05132 → Salmonella infection - Homo sapiens (human),
path:hsa05133 → Pertussis - Homo sapiens (human), path:hsa05134 → Legionellosis - Homo sapiens (human),
path:hsa05140 → Leishmaniasis - Homo sapiens (human),
path:hsa05142 → Chagas disease (American trypanosomiasis) - Homo sapiens (human),
path:hsa05143 → African trypanosomiasis - Homo sapiens (human),
path:hsa05144 → Malaria - Homo sapiens (human), path:hsa05145 → Toxoplasmosis - Homo sapiens (human),
path:hsa05146 → Amoebiasis - Homo sapiens (human),
path:hsa05150 → Staphylococcus aureus infection - Homo sapiens (human),
path:hsa05152 → Tuberculosis - Homo sapiens (human),
path:hsa05160 → Hepatitis C - Homo sapiens (human), path:hsa05161 → Hepatitis B - Homo sapiens (human),
path:hsa05162 → Measles - Homo sapiens (human), path:hsa05164 → Influenza A - Homo sapiens (human),
path:hsa05166 → HTLV-I infection - Homo sapiens (human),
path:hsa05168 → Herpes simplex infection - Homo sapiens (human),
path:hsa05169 → Epstein-Barr virus infection - Homo sapiens (human),
path:hsa05200 → Pathways in cancer - Homo sapiens (human),
path:hsa05202 → Transcriptional misregulation in cancer - Homo sapiens (human),
path:hsa05203 → Viral carcinogenesis - Homo sapiens (human),
path:hsa05204 → Chemical carcinogenesis - Homo sapiens (human),
path:hsa05205 → Proteoglycans in cancer - Homo sapiens (human),
path:hsa05206 → MicroRNAs in cancer - Homo sapiens (human),
path:hsa05210 → Colorectal cancer - Homo sapiens (human),
path:hsa05211 → Renal cell carcinoma - Homo sapiens (human),
path:hsa05212 → Pancreatic cancer - Homo sapiens (human),
path:hsa05213 → Endometrial cancer - Homo sapiens (human),
path:hsa05214 → Glioma - Homo sapiens (human), path:hsa05215 → Prostate cancer - Homo sapiens (human),
path:hsa05216 → Thyroid cancer - Homo sapiens (human),
path:hsa05217 → Basal cell carcinoma - Homo sapiens (human),
path:hsa05218 → Melanoma - Homo sapiens (human), path:hsa05219 → Bladder cancer - Homo sapiens (human),
path:hsa05220 → Chronic myeloid leukemia - Homo sapiens (human),
path:hsa05221 → Acute myeloid leukemia - Homo sapiens (human),
path:hsa05222 → Small cell lung cancer - Homo sapiens (human),
```

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```
path:hsa05223 → Non-small cell lung cancer - Homo sapiens (human),
path:hsa05230 → Central carbon metabolism in cancer - Homo sapiens (human),
path:hsa05231 → Choline metabolism in cancer - Homo sapiens (human),
path:hsa05310 → Asthma - Homo sapiens (human),
path:hsa05320 → Autoimmune thyroid disease - Homo sapiens (human),
path:hsa05321 → Inflammatory bowel disease (IBD) - Homo sapiens (human),
path:hsa05322 → Systemic lupus erythematosus - Homo sapiens (human),
path:hsa05323 → Rheumatoid arthritis - Homo sapiens (human),
path:hsa05330 → Allograft rejection - Homo sapiens (human),
path:hsa05332 → Graft-versus-host disease - Homo sapiens (human),
path:hsa05340 → Primary immunodeficiency - Homo sapiens (human),
path:hsa05410 → Hypertrophic cardiomyopathy (HCM) - Homo sapiens (human),
path:hsa05412 → Arrhythmogenic right ventricular cardiomyopathy (ARVC) - Homo sapiens (human),
path:hsa05414 → Dilated cardiomyopathy - Homo sapiens (human),
path:hsa05416 → Viral myocarditis - Homo sapiens (human)|>
```

For example, we query "path:hsa04064":

```
In[3]:= exampleKEGGDictionary["path:hsa04064"]
Out[3]= NF-kappa B signaling pathway - Homo sapiens (human)
```

Options (9)

ImportDirectly (1)

```
In[1]:= Needs["MathIOmica`"]
```

ImportDirectly gives the option to import a new version of the KEGG dictionary information file directly from KEGG to either replace the current version in the MathIOmica package data directory or add a new one (e.g. for a different species).

```
In[2]:= KEGGDictionary[ImportDirectly → True]
Out[2]= <|path:hsa00010 → Glycolysis / Gluconeogenesis - Homo sapiens (human),
 path:hsa00020 → Citrate cycle (TCA cycle) - Homo sapiens (human),
 path:hsa00030 → Pentose phosphate pathway - Homo sapiens (human),
 path:hsa00040 → Pentose and glucuronate interconversions - Homo sapiens (human),
 path:hsa00051 → Fructose and mannose metabolism - Homo sapiens (human),
 path:hsa00052 → Galactose metabolism - Homo sapiens (human),
 path:hsa00053 → Ascorbate and aldarate metabolism - Homo sapiens (human),
 path:hsa00061 → Fatty acid biosynthesis - Homo sapiens (human),
 path:hsa00062 → Fatty acid elongation - Homo sapiens (human),
 path:hsa00071 → Fatty acid degradation - Homo sapiens (human),
 path:hsa00072 → Synthesis and degradation of ketone bodies - Homo sapiens (human),
 path:hsa00100 → Steroid biosynthesis - Homo sapiens (human),
 path:hsa00120 → Primary bile acid biosynthesis - Homo sapiens (human),
 path:hsa00130 → Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human),
 path:hsa00140 → Steroid hormone biosynthesis - Homo sapiens (human),
 path:hsa00190 → Oxidative phosphorylation - Homo sapiens (human),
 path:hsa00220 → Arginine biosynthesis - Homo sapiens (human),
 path:hsa00230 → Purine metabolism - Homo sapiens (human),
 path:hsa00232 → Caffeine metabolism - Homo sapiens (human),
 path:hsa00240 → Pyrimidine metabolism - Homo sapiens (human),
 path:hsa00250 → Alanine, aspartate and glutamate metabolism - Homo sapiens (human),
 path:hsa00260 → Glycine, serine and threonine metabolism - Homo sapiens (human),
 path:hsa00270 → Cysteine and methionine metabolism - Homo sapiens (human),
 path:hsa00280 → Valine, leucine and isoleucine degradation - Homo sapiens (human),
 path:hsa00290 → Valine, leucine and isoleucine biosynthesis - Homo sapiens (human),
 path:hsa00310 → Lysine degradation - Homo sapiens (human),
 path:hsa00330 → Arginine and proline metabolism - Homo sapiens (human),
 path:hsa00340 → Histidine metabolism - Homo sapiens (human),
```

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```
path:hsa00350 → Tyrosine metabolism - Homo sapiens (human),
path:hsa00360 → Phenylalanine metabolism - Homo sapiens (human),
path:hsa00380 → Tryptophan metabolism - Homo sapiens (human),
path:hsa00400 → Phenylalanine, tyrosine and tryptophan biosynthesis - Homo sapiens (human),
path:hsa00410 → beta-Alanine metabolism - Homo sapiens (human),
path:hsa00430 → Taurine and hypotaurine metabolism - Homo sapiens (human),
path:hsa00440 → Phosphonate and phosphinate metabolism - Homo sapiens (human),
path:hsa00450 → Selenocompound metabolism - Homo sapiens (human),
path:hsa00471 → D-Glutamine and D-glutamate metabolism - Homo sapiens (human),
path:hsa00472 → D-Arginine and D-ornithine metabolism - Homo sapiens (human),
path:hsa00480 → Glutathione metabolism - Homo sapiens (human),
path:hsa00500 → Starch and sucrose metabolism - Homo sapiens (human),
path:hsa00510 → N-Glycan biosynthesis - Homo sapiens (human),
path:hsa00511 → Other glycan degradation - Homo sapiens (human),
path:hsa00512 → Mucin type O-glycan biosynthesis - Homo sapiens (human),
path:hsa00514 → Other types of O-glycan biosynthesis - Homo sapiens (human),
path:hsa00515 → Mannose type O-glycan biosynthesis - Homo sapiens (human),
path:hsa00520 → Amino sugar and nucleotide sugar metabolism - Homo sapiens (human),
path:hsa00524 → Neomycin, kanamycin and gentamicin biosynthesis - Homo sapiens (human),
path:hsa00531 → Glycosaminoglycan degradation - Homo sapiens (human), path:hsa00532 →
 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Homo sapiens (human),
path:hsa00533 → Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human),
path:hsa00534 → Glycosaminoglycan biosynthesis - heparan sulfate / heparin - Homo sapiens (human),
path:hsa00561 → Glycerolipid metabolism - Homo sapiens (human),
path:hsa00562 → Inositol phosphate metabolism - Homo sapiens (human),
path:hsa00563 → Glycosylphosphatidylinositol (GPI)-anchor biosynthesis - Homo sapiens (human),
path:hsa00564 → Glycerophospholipid metabolism - Homo sapiens (human),
path:hsa00565 → Ether lipid metabolism - Homo sapiens (human),
path:hsa00590 → Arachidonic acid metabolism - Homo sapiens (human),
path:hsa00591 → Linoleic acid metabolism - Homo sapiens (human),
path:hsa00592 → alpha-Linolenic acid metabolism - Homo sapiens (human),
path:hsa00600 → Sphingolipid metabolism - Homo sapiens (human),
path:hsa00601 → Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human),
path:hsa00603 → Glycosphingolipid biosynthesis - globo and isoglobo series - Homo sapiens (human),
path:hsa00604 → Glycosphingolipid biosynthesis - ganglio series - Homo sapiens (human),
path:hsa00620 → Pyruvate metabolism - Homo sapiens (human),
path:hsa00630 → Glyoxylate and dicarboxylate metabolism - Homo sapiens (human),
path:hsa00640 → Propanoate metabolism - Homo sapiens (human),
path:hsa00650 → Butanoate metabolism - Homo sapiens (human),
path:hsa00670 → One carbon pool by folate - Homo sapiens (human),
path:hsa00730 → Thiamine metabolism - Homo sapiens (human),
path:hsa00740 → Riboflavin metabolism - Homo sapiens (human),
path:hsa00750 → Vitamin B6 metabolism - Homo sapiens (human),
path:hsa00760 → Nicotinate and nicotinamide metabolism - Homo sapiens (human),
path:hsa00770 → Pantothenate and CoA biosynthesis - Homo sapiens (human),
path:hsa00780 → Biotin metabolism - Homo sapiens (human),
path:hsa00785 → Lipoic acid metabolism - Homo sapiens (human),
path:hsa00790 → Folate biosynthesis - Homo sapiens (human),
path:hsa00830 → Retinol metabolism - Homo sapiens (human),
path:hsa00860 → Porphyrin and chlorophyll metabolism - Homo sapiens (human),
path:hsa00900 → Terpenoid backbone biosynthesis - Homo sapiens (human),
path:hsa00910 → Nitrogen metabolism - Homo sapiens (human),
path:hsa00920 → Sulfur metabolism - Homo sapiens (human),
path:hsa00970 → Aminoacyl-tRNA biosynthesis - Homo sapiens (human),
path:hsa00980 → Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human),
path:hsa00982 → Drug metabolism - cytochrome P450 - Homo sapiens (human),
path:hsa00983 → Drug metabolism - other enzymes - Homo sapiens (human),
path:hsa01040 → Biosynthesis of unsaturated fatty acids - Homo sapiens (human),
path:hsa01100 → Metabolic pathways - Homo sapiens (human),
path:hsa01200 → Carbon metabolism - Homo sapiens (human),
path:hsa01210 → 2-Oxocarboxylic acid metabolism - Homo sapiens (human),
path:hsa01212 → Fatty acid metabolism - Homo sapiens (human),
path:hsa01230 → Biosynthesis of amino acids - Homo sapiens (human),
path:hsa01521 → EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human),
path:hsa01522 → Endocrine resistance - Homo sapiens (human),
path:hsa01523 → Antifolate resistance - Homo sapiens (human),
```

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```
path:hsa01524 → Platinum drug resistance - Homo sapiens (human),
path:hsa02010 → ABC transporters - Homo sapiens (human),
path:hsa03008 → Ribosome biogenesis in eukaryotes - Homo sapiens (human),
path:hsa03010 → Ribosome - Homo sapiens (human), path:hsa03013 → RNA transport - Homo sapiens (human),
path:hsa03015 → mRNA surveillance pathway - Homo sapiens (human),
path:hsa03018 → RNA degradation - Homo sapiens (human),
path:hsa03020 → RNA polymerase - Homo sapiens (human),
path:hsa03022 → Basal transcription factors - Homo sapiens (human),
path:hsa03030 → DNA replication - Homo sapiens (human), path:hsa03040 → Spliceosome - Homo sapiens (human),
path:hsa03050 → Proteasome - Homo sapiens (human), path:hsa03060 → Protein export - Homo sapiens (human),
path:hsa03320 → PPAR signaling pathway - Homo sapiens (human),
path:hsa03410 → Base excision repair - Homo sapiens (human),
path:hsa03420 → Nucleotide excision repair - Homo sapiens (human),
path:hsa03430 → Mismatch repair - Homo sapiens (human),
path:hsa03440 → Homologous recombination - Homo sapiens (human),
path:hsa03450 → Non-homologous end-joining - Homo sapiens (human),
path:hsa03460 → Fanconi anemia pathway - Homo sapiens (human),
path:hsa04010 → MAPK signaling pathway - Homo sapiens (human),
path:hsa04012 → ErbB signaling pathway - Homo sapiens (human),
path:hsa04014 → Ras signaling pathway - Homo sapiens (human),
path:hsa04015 → Rap1 signaling pathway - Homo sapiens (human),
path:hsa04020 → Calcium signaling pathway - Homo sapiens (human),
path:hsa04022 → cGMP-PKG signaling pathway - Homo sapiens (human),
path:hsa04024 → cAMP signaling pathway - Homo sapiens (human),
path:hsa04060 → Cytokine-cytokine receptor interaction - Homo sapiens (human),
path:hsa04061 → Viral protein interaction with cytokine and cytokine receptor - Homo sapiens (human),
path:hsa04062 → Chemokine signaling pathway - Homo sapiens (human),
path:hsa04064 → NF-kappa B signaling pathway - Homo sapiens (human),
path:hsa04066 → HIF-1 signaling pathway - Homo sapiens (human),
path:hsa04068 → FoxO signaling pathway - Homo sapiens (human),
path:hsa04070 → Phosphatidylinositol signaling system - Homo sapiens (human),
path:hsa04071 → Sphingolipid signaling pathway - Homo sapiens (human),
path:hsa04072 → Phospholipase D signaling pathway - Homo sapiens (human),
path:hsa04080 → Neuroactive ligand-receptor interaction - Homo sapiens (human),
path:hsa04110 → Cell cycle - Homo sapiens (human), path:hsa04114 → Oocyte meiosis - Homo sapiens (human),
path:hsa04115 → p53 signaling pathway - Homo sapiens (human),
path:hsa04120 → Ubiquitin mediated proteolysis - Homo sapiens (human),
path:hsa04122 → Sulfur relay system - Homo sapiens (human),
path:hsa04130 → SNARE interactions in vesicular transport - Homo sapiens (human),
path:hsa04136 → Autophagy - other - Homo sapiens (human),
path:hsa04137 → Mitophagy - animal - Homo sapiens (human),
path:hsa04140 → Autophagy - animal - Homo sapiens (human),
path:hsa04141 → Protein processing in endoplasmic reticulum - Homo sapiens (human),
path:hsa04142 → Lysosome - Homo sapiens (human), path:hsa04144 → Endocytosis - Homo sapiens (human),
path:hsa04145 → Phagosome - Homo sapiens (human), path:hsa04146 → Peroxisome - Homo sapiens (human),
path:hsa04150 → mTOR signaling pathway - Homo sapiens (human),
path:hsa04151 → PI3K-Akt signaling pathway - Homo sapiens (human),
path:hsa04152 → AMPK signaling pathway - Homo sapiens (human),
path:hsa04210 → Apoptosis - Homo sapiens (human),
path:hsa04211 → Longevity regulating pathway - Homo sapiens (human),
path:hsa04213 → Longevity regulating pathway - multiple species - Homo sapiens (human),
path:hsa04215 → Apoptosis - multiple species - Homo sapiens (human),
path:hsa04216 → Ferroptosis - Homo sapiens (human), path:hsa04217 → Necroptosis - Homo sapiens (human),
path:hsa04218 → Cellular senescence - Homo sapiens (human),
path:hsa04260 → Cardiac muscle contraction - Homo sapiens (human),
path:hsa04261 → Adrenergic signaling in cardiomyocytes - Homo sapiens (human),
path:hsa04270 → Vascular smooth muscle contraction - Homo sapiens (human),
path:hsa04310 → Wnt signaling pathway - Homo sapiens (human),
path:hsa04330 → Notch signaling pathway - Homo sapiens (human),
path:hsa04340 → Hedgehog signaling pathway - Homo sapiens (human),
path:hsa04350 → TGF-beta signaling pathway - Homo sapiens (human),
path:hsa04360 → Axon guidance - Homo sapiens (human),
path:hsa04370 → VEGF signaling pathway - Homo sapiens (human),
path:hsa04371 → Apelin signaling pathway - Homo sapiens (human),
path:hsa04380 → Osteoclast differentiation - Homo sapiens (human),
path:hsa04390 → Hippo signaling pathway - Homo sapiens (human),
```

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```
path:hsa04392 → Hippo signaling pathway - multiple species - Homo sapiens (human),
path:hsa04510 → Focal adhesion - Homo sapiens (human),
path:hsa04512 → ECM-receptor interaction - Homo sapiens (human),
path:hsa04514 → Cell adhesion molecules (CAMs) - Homo sapiens (human),
path:hsa04520 → Adherens junction - Homo sapiens (human),
path:hsa04530 → Tight junction - Homo sapiens (human), path:hsa04540 → Gap junction - Homo sapiens (human),
path:hsa04550 → Signaling pathways regulating pluripotency of stem cells - Homo sapiens (human),
path:hsa04610 → Complement and coagulation cascades - Homo sapiens (human),
path:hsa04611 → Platelet activation - Homo sapiens (human),
path:hsa04612 → Antigen processing and presentation - Homo sapiens (human),
path:hsa04614 → Renin-angiotensin system - Homo sapiens (human),
path:hsa04620 → Toll-like receptor signaling pathway - Homo sapiens (human),
path:hsa04621 → NOD-like receptor signaling pathway - Homo sapiens (human),
path:hsa04622 → RIG-I-like receptor signaling pathway - Homo sapiens (human),
path:hsa04623 → Cytosolic DNA-sensing pathway - Homo sapiens (human),
path:hsa04625 → C-type lectin receptor signaling pathway - Homo sapiens (human),
path:hsa04630 → JAK-STAT signaling pathway - Homo sapiens (human),
path:hsa04640 → Hematopoietic cell lineage - Homo sapiens (human),
path:hsa04650 → Natural killer cell mediated cytotoxicity - Homo sapiens (human),
path:hsa04657 → IL-17 signaling pathway - Homo sapiens (human),
path:hsa04658 → Th1 and Th2 cell differentiation - Homo sapiens (human),
path:hsa04659 → Th17 cell differentiation - Homo sapiens (human),
path:hsa04660 → T cell receptor signaling pathway - Homo sapiens (human),
path:hsa04662 → B cell receptor signaling pathway - Homo sapiens (human),
path:hsa04664 → Fc epsilon RI signaling pathway - Homo sapiens (human),
path:hsa04666 → Fc gamma R-mediated phagocytosis - Homo sapiens (human),
path:hsa04668 → TNF signaling pathway - Homo sapiens (human),
path:hsa04670 → Leukocyte transendothelial migration - Homo sapiens (human),
path:hsa04672 → Intestinal immune network for IgA production - Homo sapiens (human),
path:hsa04710 → Circadian rhythm - Homo sapiens (human),
path:hsa04713 → Circadian entrainment - Homo sapiens (human),
path:hsa04714 → Thermogenesis - Homo sapiens (human),
path:hsa04720 → Long-term potentiation - Homo sapiens (human),
path:hsa04721 → Synaptic vesicle cycle - Homo sapiens (human),
path:hsa04722 → Neurotrophin signaling pathway - Homo sapiens (human),
path:hsa04723 → Retrograde endocannabinoid signaling - Homo sapiens (human),
path:hsa04724 → Glutamatergic synapse - Homo sapiens (human),
path:hsa04725 → Cholinergic synapse - Homo sapiens (human),
path:hsa04726 → Serotonergic synapse - Homo sapiens (human),
path:hsa04727 → GABAergic synapse - Homo sapiens (human),
path:hsa04728 → Dopaminergic synapse - Homo sapiens (human),
path:hsa04730 → Long-term depression - Homo sapiens (human),
path:hsa04740 → Olfactory transduction - Homo sapiens (human),
path:hsa04742 → Taste transduction - Homo sapiens (human),
path:hsa04744 → Phototransduction - Homo sapiens (human),
path:hsa04750 → Inflammatory mediator regulation of TRP channels - Homo sapiens (human),
path:hsa04810 → Regulation of actin cytoskeleton - Homo sapiens (human),
path:hsa04910 → Insulin signaling pathway - Homo sapiens (human),
path:hsa04911 → Insulin secretion - Homo sapiens (human),
path:hsa04912 → GnRH signaling pathway - Homo sapiens (human),
path:hsa04913 → Ovarian steroidogenesis - Homo sapiens (human),
path:hsa04914 → Progesterone-mediated oocyte maturation - Homo sapiens (human),
path:hsa04915 → Estrogen signaling pathway - Homo sapiens (human),
path:hsa04916 → Melanogenesis - Homo sapiens (human),
path:hsa04917 → Prolactin signaling pathway - Homo sapiens (human),
path:hsa04918 → Thyroid hormone synthesis - Homo sapiens (human),
path:hsa04919 → Thyroid hormone signaling pathway - Homo sapiens (human),
path:hsa04920 → Adipocytokine signaling pathway - Homo sapiens (human),
path:hsa04921 → Oxytocin signaling pathway - Homo sapiens (human),
path:hsa04922 → Glucagon signaling pathway - Homo sapiens (human),
path:hsa04923 → Regulation of lipolysis in adipocytes - Homo sapiens (human),
path:hsa04924 → Renin secretion - Homo sapiens (human),
path:hsa04925 → Aldosterone synthesis and secretion - Homo sapiens (human),
path:hsa04926 → Relaxin signaling pathway - Homo sapiens (human),
path:hsa04927 → Cortisol synthesis and secretion - Homo sapiens (human),
path:hsa04928 → Parathyroid hormone synthesis, secretion and action - Homo sapiens (human),
```

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```
path:hsa04930 → Type II diabetes mellitus - Homo sapiens (human),
path:hsa04931 → Insulin resistance - Homo sapiens (human),
path:hsa04932 → Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
path:hsa04933 → AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human),
path:hsa04934 → Cushing syndrome - Homo sapiens (human),
path:hsa04940 → Type I diabetes mellitus - Homo sapiens (human),
path:hsa04950 → Maturity onset diabetes of the young - Homo sapiens (human),
path:hsa04960 → Aldosterone-regulated sodium reabsorption - Homo sapiens (human),
path:hsa04961 → Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
path:hsa04962 → Vasopressin-regulated water reabsorption - Homo sapiens (human),
path:hsa04964 → Proximal tubule bicarbonate reclamation - Homo sapiens (human),
path:hsa04966 → Collecting duct acid secretion - Homo sapiens (human),
path:hsa04970 → Salivary secretion - Homo sapiens (human),
path:hsa04971 → Gastric acid secretion - Homo sapiens (human),
path:hsa04972 → Pancreatic secretion - Homo sapiens (human),
path:hsa04973 → Carbohydrate digestion and absorption - Homo sapiens (human),
path:hsa04974 → Protein digestion and absorption - Homo sapiens (human),
path:hsa04975 → Fat digestion and absorption - Homo sapiens (human),
path:hsa04976 → Bile secretion - Homo sapiens (human),
path:hsa04977 → Vitamin digestion and absorption - Homo sapiens (human),
path:hsa04978 → Mineral absorption - Homo sapiens (human),
path:hsa04979 → Cholesterol metabolism - Homo sapiens (human),
path:hsa05010 → Alzheimer disease - Homo sapiens (human),
path:hsa05012 → Parkinson disease - Homo sapiens (human),
path:hsa05014 → Amyotrophic lateral sclerosis (ALS) - Homo sapiens (human),
path:hsa05016 → Huntington disease - Homo sapiens (human),
path:hsa05020 → Prion diseases - Homo sapiens (human),
path:hsa05030 → Cocaine addiction - Homo sapiens (human),
path:hsa05031 → Amphetamine addiction - Homo sapiens (human),
path:hsa05032 → Morphine addiction - Homo sapiens (human),
path:hsa05033 → Nicotine addiction - Homo sapiens (human),
path:hsa05034 → Alcoholism - Homo sapiens (human),
path:hsa05100 → Bacterial invasion of epithelial cells - Homo sapiens (human),
path:hsa05110 → Vibrio cholerae infection - Homo sapiens (human),
path:hsa05120 → Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
path:hsa05130 → Pathogenic Escherichia coli infection - Homo sapiens (human),
path:hsa05131 → Shigellosis - Homo sapiens (human),
path:hsa05132 → Salmonella infection - Homo sapiens (human),
path:hsa05133 → Pertussis - Homo sapiens (human), path:hsa05134 → Legionellosis - Homo sapiens (human),
path:hsa05135 → Yersinia infection - Homo sapiens (human),
path:hsa05140 → Leishmaniasis - Homo sapiens (human),
path:hsa05142 → Chagas disease (American trypanosomiasis) - Homo sapiens (human),
path:hsa05143 → African trypanosomiasis - Homo sapiens (human),
path:hsa05144 → Malaria - Homo sapiens (human), path:hsa05145 → Toxoplasmosis - Homo sapiens (human),
path:hsa05146 → Amoebiasis - Homo sapiens (human),
path:hsa05150 → Staphylococcus aureus infection - Homo sapiens (human),
path:hsa05152 → Tuberculosis - Homo sapiens (human), path:hsa05160 → Hepatitis C - Homo sapiens (human),
path:hsa05161 → Hepatitis B - Homo sapiens (human), path:hsa05162 → Measles - Homo sapiens (human),
path:hsa05163 → Human cytomegalovirus infection - Homo sapiens (human),
path:hsa05164 → Influenza A - Homo sapiens (human),
path:hsa05165 → Human papillomavirus infection - Homo sapiens (human),
path:hsa05166 → Human T-cell leukemia virus 1 infection - Homo sapiens (human),
path:hsa05167 → Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human),
path:hsa05168 → Herpes simplex virus 1 infection - Homo sapiens (human),
path:hsa05169 → Epstein-Barr virus infection - Homo sapiens (human),
path:hsa05170 → Human immunodeficiency virus 1 infection - Homo sapiens (human),
path:hsa05200 → Pathways in cancer - Homo sapiens (human),
path:hsa05202 → Transcriptional misregulation in cancer - Homo sapiens (human),
path:hsa05203 → Viral carcinogenesis - Homo sapiens (human),
path:hsa05204 → Chemical carcinogenesis - Homo sapiens (human),
path:hsa05205 → Proteoglycans in cancer - Homo sapiens (human),
path:hsa05206 → MicroRNAs in cancer - Homo sapiens (human),
path:hsa05210 → Colorectal cancer - Homo sapiens (human),
path:hsa05211 → Renal cell carcinoma - Homo sapiens (human),
path:hsa05212 → Pancreatic cancer - Homo sapiens (human),
path:hsa05213 → Endometrial cancer - Homo sapiens (human),
```

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```
path:hsa05214 → Glioma - Homo sapiens (human), path:hsa05215 → Prostate cancer - Homo sapiens (human),
path:hsa05216 → Thyroid cancer - Homo sapiens (human),
path:hsa05217 → Basal cell carcinoma - Homo sapiens (human),
path:hsa05218 → Melanoma - Homo sapiens (human), path:hsa05219 → Bladder cancer - Homo sapiens (human),
path:hsa05220 → Chronic myeloid leukemia - Homo sapiens (human),
path:hsa05221 → Acute myeloid leukemia - Homo sapiens (human),
path:hsa05222 → Small cell lung cancer - Homo sapiens (human),
path:hsa05223 → Non-small cell lung cancer - Homo sapiens (human),
path:hsa05224 → Breast cancer - Homo sapiens (human),
path:hsa05225 → Hepatocellular carcinoma - Homo sapiens (human),
path:hsa05226 → Gastric cancer - Homo sapiens (human),
path:hsa05230 → Central carbon metabolism in cancer - Homo sapiens (human),
path:hsa05231 → Choline metabolism in cancer - Homo sapiens (human),
path:hsa05235 → PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
path:hsa05310 → Asthma - Homo sapiens (human),
path:hsa05320 → Autoimmune thyroid disease - Homo sapiens (human),
path:hsa05321 → Inflammatory bowel disease (IBD) - Homo sapiens (human),
path:hsa05322 → Systemic lupus erythematosus - Homo sapiens (human),
path:hsa05323 → Rheumatoid arthritis - Homo sapiens (human),
path:hsa05330 → Allograft rejection - Homo sapiens (human),
path:hsa05332 → Graft-versus-host disease - Homo sapiens (human),
path:hsa05340 → Primary immunodeficiency - Homo sapiens (human),
path:hsa05410 → Hypertrophic cardiomyopathy (HCM) - Homo sapiens (human),
path:hsa05412 → Arrhythmogenic right ventricular cardiomyopathy (ARVC) - Homo sapiens (human),
path:hsa05414 → Dilated cardiomyopathy (DCM) - Homo sapiens (human),
path:hsa05416 → Viral myocarditis - Homo sapiens (human),
path:hsa05418 → Fluid shear stress and atherosclerosis - Homo sapiens (human)|⟩
```

KEGGQuery1 (3)

KEGGQuery1 is the text used internally by KEGG API calls, specifically as string query1 in "http://rest.kegg.jp/list/" <> query1 <> "/" <> query2. Typically this will be used as the target database to return a list of entry identifiers and associated definition for this database entries.

The default is to query pathways:

```
In[1]:= dictionaryPathwayQuery1 = KEGGDictionary[KEGGQuery1 → "pathway"]
```

```
Out[1]= ⟨|path:hsa00010 → Glycolysis / Gluconeogenesis - Homo sapiens (human),
path:hsa00020 → Citrate cycle (TCA cycle) - Homo sapiens (human),
path:hsa00030 → Pentose phosphate pathway - Homo sapiens (human),
path:hsa00040 → Pentose and glucuronate interconversions - Homo sapiens (human),
path:hsa00051 → Fructose and mannose metabolism - Homo sapiens (human),
path:hsa00052 → Galactose metabolism - Homo sapiens (human),
path:hsa00053 → Ascorbate and aldarate metabolism - Homo sapiens (human),
path:hsa00061 → Fatty acid biosynthesis - Homo sapiens (human),
path:hsa00062 → Fatty acid elongation - Homo sapiens (human),
path:hsa00071 → Fatty acid degradation - Homo sapiens (human),
path:hsa00072 → Synthesis and degradation of ketone bodies - Homo sapiens (human),
path:hsa00100 → Steroid biosynthesis - Homo sapiens (human),
path:hsa00120 → Primary bile acid biosynthesis - Homo sapiens (human),
path:hsa00130 → Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human),
path:hsa00140 → Steroid hormone biosynthesis - Homo sapiens (human),
path:hsa00190 → Oxidative phosphorylation - Homo sapiens (human),
path:hsa00220 → Arginine biosynthesis - Homo sapiens (human),
path:hsa00230 → Purine metabolism - Homo sapiens (human),
path:hsa00232 → Caffeine metabolism - Homo sapiens (human),
path:hsa00240 → Pyrimidine metabolism - Homo sapiens (human),
path:hsa00250 → Alanine, aspartate and glutamate metabolism - Homo sapiens (human),
path:hsa00260 → Glycine, serine and threonine metabolism - Homo sapiens (human),
path:hsa00270 → Cysteine and methionine metabolism - Homo sapiens (human),
```

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```
path:hsa00280 → Valine, leucine and isoleucine degradation - Homo sapiens (human),
path:hsa00290 → Valine, leucine and isoleucine biosynthesis - Homo sapiens (human),
path:hsa00310 → Lysine degradation - Homo sapiens (human),
path:hsa00330 → Arginine and proline metabolism - Homo sapiens (human),
path:hsa00340 → Histidine metabolism - Homo sapiens (human),
path:hsa00350 → Tyrosine metabolism - Homo sapiens (human),
path:hsa00360 → Phenylalanine metabolism - Homo sapiens (human),
path:hsa00380 → Tryptophan metabolism - Homo sapiens (human),
path:hsa00400 → Phenylalanine, tyrosine and tryptophan biosynthesis - Homo sapiens (human),
path:hsa00410 → beta-Alanine metabolism - Homo sapiens (human),
path:hsa00430 → Taurine and hypotaurine metabolism - Homo sapiens (human),
path:hsa00440 → Phosphonate and phosphinate metabolism - Homo sapiens (human),
path:hsa00450 → Selenocompound metabolism - Homo sapiens (human),
path:hsa00471 → D-Glutamine and D-glutamate metabolism - Homo sapiens (human),
path:hsa00472 → D-Arginine and D-ornithine metabolism - Homo sapiens (human),
path:hsa00480 → Glutathione metabolism - Homo sapiens (human),
path:hsa00500 → Starch and sucrose metabolism - Homo sapiens (human),
path:hsa00510 → N-Glycan biosynthesis - Homo sapiens (human),
path:hsa00511 → Other glycan degradation - Homo sapiens (human),
path:hsa00512 → Mucin type O-glycan biosynthesis - Homo sapiens (human),
path:hsa00514 → Other types of O-glycan biosynthesis - Homo sapiens (human),
path:hsa00515 → Mannose type O-glycan biosynthesis - Homo sapiens (human),
path:hsa00520 → Amino sugar and nucleotide sugar metabolism - Homo sapiens (human),
path:hsa00524 → Neomycin, kanamycin and gentamicin biosynthesis - Homo sapiens (human),
path:hsa00531 → Glycosaminoglycan degradation - Homo sapiens (human), path:hsa00532 →
 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Homo sapiens (human),
path:hsa00533 → Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human),
path:hsa00534 → Glycosaminoglycan biosynthesis - heparan sulfate / heparin - Homo sapiens (human),
path:hsa00561 → Glycerolipid metabolism - Homo sapiens (human),
path:hsa00562 → Inositol phosphate metabolism - Homo sapiens (human),
path:hsa00563 → Glycosylphosphatidylinositol (GPI)-anchor biosynthesis - Homo sapiens (human),
path:hsa00564 → Glycerophospholipid metabolism - Homo sapiens (human),
path:hsa00565 → Ether lipid metabolism - Homo sapiens (human),
path:hsa00590 → Arachidonic acid metabolism - Homo sapiens (human),
path:hsa00591 → Linoleic acid metabolism - Homo sapiens (human),
path:hsa00592 → alpha-Linolenic acid metabolism - Homo sapiens (human),
path:hsa00600 → Sphingolipid metabolism - Homo sapiens (human),
path:hsa00601 → Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human),
path:hsa00603 → Glycosphingolipid biosynthesis - globo and isoglobo series - Homo sapiens (human),
path:hsa00604 → Glycosphingolipid biosynthesis - ganglio series - Homo sapiens (human),
path:hsa00620 → Pyruvate metabolism - Homo sapiens (human),
path:hsa00630 → Glyoxylate and dicarboxylate metabolism - Homo sapiens (human),
path:hsa00640 → Propanoate metabolism - Homo sapiens (human),
path:hsa00650 → Butanoate metabolism - Homo sapiens (human),
path:hsa00670 → One carbon pool by folate - Homo sapiens (human),
path:hsa00730 → Thiamine metabolism - Homo sapiens (human),
path:hsa00740 → Riboflavin metabolism - Homo sapiens (human),
path:hsa00750 → Vitamin B6 metabolism - Homo sapiens (human),
path:hsa00760 → Nicotinate and nicotinamide metabolism - Homo sapiens (human),
path:hsa00770 → Pantothenate and CoA biosynthesis - Homo sapiens (human),
path:hsa00780 → Biotin metabolism - Homo sapiens (human),
path:hsa00785 → Lipoic acid metabolism - Homo sapiens (human),
path:hsa00790 → Folate biosynthesis - Homo sapiens (human),
path:hsa00830 → Retinol metabolism - Homo sapiens (human),
path:hsa00860 → Porphyrin and chlorophyll metabolism - Homo sapiens (human),
path:hsa00900 → Terpenoid backbone biosynthesis - Homo sapiens (human),
path:hsa00910 → Nitrogen metabolism - Homo sapiens (human),
path:hsa00920 → Sulfur metabolism - Homo sapiens (human),
path:hsa00970 → Aminoacyl-tRNA biosynthesis - Homo sapiens (human),
path:hsa00980 → Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human),
path:hsa00982 → Drug metabolism - cytochrome P450 - Homo sapiens (human),
path:hsa00983 → Drug metabolism - other enzymes - Homo sapiens (human),
path:hsa01040 → Biosynthesis of unsaturated fatty acids - Homo sapiens (human),
path:hsa01100 → Metabolic pathways - Homo sapiens (human),
path:hsa01200 → Carbon metabolism - Homo sapiens (human),
path:hsa01210 → 2-Oxocarboxylic acid metabolism - Homo sapiens (human),
```

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```
path:hsa01212 → Fatty acid metabolism - Homo sapiens (human),
path:hsa01230 → Biosynthesis of amino acids - Homo sapiens (human),
path:hsa01521 → EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human),
path:hsa01522 → Endocrine resistance - Homo sapiens (human),
path:hsa01523 → Antifolate resistance - Homo sapiens (human),
path:hsa01524 → Platinum drug resistance - Homo sapiens (human),
path:hsa02010 → ABC transporters - Homo sapiens (human),
path:hsa03008 → Ribosome biogenesis in eukaryotes - Homo sapiens (human),
path:hsa03010 → Ribosome - Homo sapiens (human), path:hsa03013 → RNA transport - Homo sapiens (human),
path:hsa03015 → mRNA surveillance pathway - Homo sapiens (human),
path:hsa03018 → RNA degradation - Homo sapiens (human),
path:hsa03020 → RNA polymerase - Homo sapiens (human),
path:hsa03022 → Basal transcription factors - Homo sapiens (human),
path:hsa03030 → DNA replication - Homo sapiens (human), path:hsa03040 → Spliceosome - Homo sapiens (human),
path:hsa03050 → Proteasome - Homo sapiens (human), path:hsa03060 → Protein export - Homo sapiens (human),
path:hsa03320 → PPAR signaling pathway - Homo sapiens (human),
path:hsa03410 → Base excision repair - Homo sapiens (human),
path:hsa03420 → Nucleotide excision repair - Homo sapiens (human),
path:hsa03430 → Mismatch repair - Homo sapiens (human),
path:hsa03440 → Homologous recombination - Homo sapiens (human),
path:hsa03450 → Non-homologous end-joining - Homo sapiens (human),
path:hsa03460 → Fanconi anemia pathway - Homo sapiens (human),
path:hsa04010 → MAPK signaling pathway - Homo sapiens (human),
path:hsa04012 → ErbB signaling pathway - Homo sapiens (human),
path:hsa04014 → Ras signaling pathway - Homo sapiens (human),
path:hsa04015 → Rap1 signaling pathway - Homo sapiens (human),
path:hsa04020 → Calcium signaling pathway - Homo sapiens (human),
path:hsa04022 → cGMP-PKG signaling pathway - Homo sapiens (human),
path:hsa04024 → cAMP signaling pathway - Homo sapiens (human),
path:hsa04060 → Cytokine-cytokine receptor interaction - Homo sapiens (human),
path:hsa04061 → Viral protein interaction with cytokine and cytokine receptor - Homo sapiens (human),
path:hsa04062 → Chemokine signaling pathway - Homo sapiens (human),
path:hsa04064 → NF-kappa B signaling pathway - Homo sapiens (human),
path:hsa04066 → HIF-1 signaling pathway - Homo sapiens (human),
path:hsa04068 → FoxO signaling pathway - Homo sapiens (human),
path:hsa04070 → Phosphatidylinositol signaling system - Homo sapiens (human),
path:hsa04071 → Sphingolipid signaling pathway - Homo sapiens (human),
path:hsa04072 → Phospholipase D signaling pathway - Homo sapiens (human),
path:hsa04080 → Neuroactive ligand-receptor interaction - Homo sapiens (human),
path:hsa04110 → Cell cycle - Homo sapiens (human), path:hsa04114 → Oocyte meiosis - Homo sapiens (human),
path:hsa04115 → p53 signaling pathway - Homo sapiens (human),
path:hsa04120 → Ubiquitin mediated proteolysis - Homo sapiens (human),
path:hsa04122 → Sulfur relay system - Homo sapiens (human),
path:hsa04130 → SNARE interactions in vesicular transport - Homo sapiens (human),
path:hsa04136 → Autophagy - other - Homo sapiens (human),
path:hsa04137 → Mitophagy - animal - Homo sapiens (human),
path:hsa04140 → Autophagy - animal - Homo sapiens (human),
path:hsa04141 → Protein processing in endoplasmic reticulum - Homo sapiens (human),
path:hsa04142 → Lysosome - Homo sapiens (human), path:hsa04144 → Endocytosis - Homo sapiens (human),
path:hsa04145 → Phagosome - Homo sapiens (human), path:hsa04146 → Peroxisome - Homo sapiens (human),
path:hsa04150 → mTOR signaling pathway - Homo sapiens (human),
path:hsa04151 → PI3K-Akt signaling pathway - Homo sapiens (human),
path:hsa04152 → AMPK signaling pathway - Homo sapiens (human),
path:hsa04210 → Apoptosis - Homo sapiens (human),
path:hsa04211 → Longevity regulating pathway - Homo sapiens (human),
path:hsa04213 → Longevity regulating pathway - multiple species - Homo sapiens (human),
path:hsa04215 → Apoptosis - multiple species - Homo sapiens (human),
path:hsa04216 → Ferroptosis - Homo sapiens (human), path:hsa04217 → Necroptosis - Homo sapiens (human),
path:hsa04218 → Cellular senescence - Homo sapiens (human),
path:hsa04260 → Cardiac muscle contraction - Homo sapiens (human),
path:hsa04261 → Adrenergic signaling in cardiomyocytes - Homo sapiens (human),
path:hsa04270 → Vascular smooth muscle contraction - Homo sapiens (human),
path:hsa04310 → Wnt signaling pathway - Homo sapiens (human),
path:hsa04330 → Notch signaling pathway - Homo sapiens (human),
path:hsa04340 → Hedgehog signaling pathway - Homo sapiens (human),
path:hsa04350 → TGF-beta signaling pathway - Homo sapiens (human),
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path:hsa04360 → Axon guidance - Homo sapiens (human),
path:hsa04370 → VEGF signaling pathway - Homo sapiens (human),
path:hsa04371 → Apelin signaling pathway - Homo sapiens (human),
path:hsa04380 → Osteoclast differentiation - Homo sapiens (human),
path:hsa04390 → Hippo signaling pathway - Homo sapiens (human),
path:hsa04392 → Hippo signaling pathway - multiple species - Homo sapiens (human),
path:hsa04510 → Focal adhesion - Homo sapiens (human),
path:hsa04512 → ECM-receptor interaction - Homo sapiens (human),
path:hsa04514 → Cell adhesion molecules (CAMs) - Homo sapiens (human),
path:hsa04520 → Adherens junction - Homo sapiens (human),
path:hsa04530 → Tight junction - Homo sapiens (human), path:hsa04540 → Gap junction - Homo sapiens (human),
path:hsa04550 → Signaling pathways regulating pluripotency of stem cells - Homo sapiens (human),
path:hsa04610 → Complement and coagulation cascades - Homo sapiens (human),
path:hsa04611 → Platelet activation - Homo sapiens (human),
path:hsa04612 → Antigen processing and presentation - Homo sapiens (human),
path:hsa04614 → Renin-angiotensin system - Homo sapiens (human),
path:hsa04620 → Toll-like receptor signaling pathway - Homo sapiens (human),
path:hsa04621 → NOD-like receptor signaling pathway - Homo sapiens (human),
path:hsa04622 → RIG-I-like receptor signaling pathway - Homo sapiens (human),
path:hsa04623 → Cytosolic DNA-sensing pathway - Homo sapiens (human),
path:hsa04625 → C-type lectin receptor signaling pathway - Homo sapiens (human),
path:hsa04630 → JAK-STAT signaling pathway - Homo sapiens (human),
path:hsa04640 → Hematopoietic cell lineage - Homo sapiens (human),
path:hsa04650 → Natural killer cell mediated cytotoxicity - Homo sapiens (human),
path:hsa04657 → IL-17 signaling pathway - Homo sapiens (human),
path:hsa04658 → Th1 and Th2 cell differentiation - Homo sapiens (human),
path:hsa04659 → Th17 cell differentiation - Homo sapiens (human),
path:hsa04660 → T cell receptor signaling pathway - Homo sapiens (human),
path:hsa04662 → B cell receptor signaling pathway - Homo sapiens (human),
path:hsa04664 → Fc epsilon RI signaling pathway - Homo sapiens (human),
path:hsa04666 → Fc gamma R-mediated phagocytosis - Homo sapiens (human),
path:hsa04668 → TNF signaling pathway - Homo sapiens (human),
path:hsa04670 → Leukocyte transendothelial migration - Homo sapiens (human),
path:hsa04672 → Intestinal immune network for IgA production - Homo sapiens (human),
path:hsa04710 → Circadian rhythm - Homo sapiens (human),
path:hsa04713 → Circadian entrainment - Homo sapiens (human),
path:hsa04714 → Thermogenesis - Homo sapiens (human),
path:hsa04720 → Long-term potentiation - Homo sapiens (human),
path:hsa04721 → Synaptic vesicle cycle - Homo sapiens (human),
path:hsa04722 → Neurotrophin signaling pathway - Homo sapiens (human),
path:hsa04723 → Retrograde endocannabinoid signaling - Homo sapiens (human),
path:hsa04724 → Glutamatergic synapse - Homo sapiens (human),
path:hsa04725 → Cholinergic synapse - Homo sapiens (human),
path:hsa04726 → Serotonergic synapse - Homo sapiens (human),
path:hsa04727 → GABAergic synapse - Homo sapiens (human),
path:hsa04728 → Dopaminergic synapse - Homo sapiens (human),
path:hsa04730 → Long-term depression - Homo sapiens (human),
path:hsa04740 → Olfactory transduction - Homo sapiens (human),
path:hsa04742 → Taste transduction - Homo sapiens (human),
path:hsa04744 → Phototransduction - Homo sapiens (human),
path:hsa04750 → Inflammatory mediator regulation of TRP channels - Homo sapiens (human),
path:hsa04810 → Regulation of actin cytoskeleton - Homo sapiens (human),
path:hsa04910 → Insulin signaling pathway - Homo sapiens (human),
path:hsa04911 → Insulin secretion - Homo sapiens (human),
path:hsa04912 → GnRH signaling pathway - Homo sapiens (human),
path:hsa04913 → Ovarian steroidogenesis - Homo sapiens (human),
path:hsa04914 → Progesterone-mediated oocyte maturation - Homo sapiens (human),
path:hsa04915 → Estrogen signaling pathway - Homo sapiens (human),
path:hsa04916 → Melanogenesis - Homo sapiens (human),
path:hsa04917 → Prolactin signaling pathway - Homo sapiens (human),
path:hsa04918 → Thyroid hormone synthesis - Homo sapiens (human),
path:hsa04919 → Thyroid hormone signaling pathway - Homo sapiens (human),
path:hsa04920 → Adipocytokine signaling pathway - Homo sapiens (human),
path:hsa04921 → Oxytocin signaling pathway - Homo sapiens (human),
path:hsa04922 → Glucagon signaling pathway - Homo sapiens (human),
path:hsa04923 → Regulation of lipolysis in adipocytes - Homo sapiens (human),
```

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```
path:hsa04924 → Renin secretion - Homo sapiens (human),
path:hsa04925 → Aldosterone synthesis and secretion - Homo sapiens (human),
path:hsa04926 → Relaxin signaling pathway - Homo sapiens (human),
path:hsa04927 → Cortisol synthesis and secretion - Homo sapiens (human),
path:hsa04928 → Parathyroid hormone synthesis, secretion and action - Homo sapiens (human),
path:hsa04930 → Type II diabetes mellitus - Homo sapiens (human),
path:hsa04931 → Insulin resistance - Homo sapiens (human),
path:hsa04932 → Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
path:hsa04933 → AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human),
path:hsa04934 → Cushing syndrome - Homo sapiens (human),
path:hsa04940 → Type I diabetes mellitus - Homo sapiens (human),
path:hsa04950 → Maturity onset diabetes of the young - Homo sapiens (human),
path:hsa04960 → Aldosterone-regulated sodium reabsorption - Homo sapiens (human),
path:hsa04961 → Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
path:hsa04962 → Vasopressin-regulated water reabsorption - Homo sapiens (human),
path:hsa04964 → Proximal tubule bicarbonate reclamation - Homo sapiens (human),
path:hsa04966 → Collecting duct acid secretion - Homo sapiens (human),
path:hsa04970 → Salivary secretion - Homo sapiens (human),
path:hsa04971 → Gastric acid secretion - Homo sapiens (human),
path:hsa04972 → Pancreatic secretion - Homo sapiens (human),
path:hsa04973 → Carbohydrate digestion and absorption - Homo sapiens (human),
path:hsa04974 → Protein digestion and absorption - Homo sapiens (human),
path:hsa04975 → Fat digestion and absorption - Homo sapiens (human),
path:hsa04976 → Bile secretion - Homo sapiens (human),
path:hsa04977 → Vitamin digestion and absorption - Homo sapiens (human),
path:hsa04978 → Mineral absorption - Homo sapiens (human),
path:hsa04979 → Cholesterol metabolism - Homo sapiens (human),
path:hsa05010 → Alzheimer disease - Homo sapiens (human),
path:hsa05012 → Parkinson disease - Homo sapiens (human),
path:hsa05014 → Amyotrophic lateral sclerosis (ALS) - Homo sapiens (human),
path:hsa05016 → Huntington disease - Homo sapiens (human),
path:hsa05020 → Prion diseases - Homo sapiens (human),
path:hsa05030 → Cocaine addiction - Homo sapiens (human),
path:hsa05031 → Amphetamine addiction - Homo sapiens (human),
path:hsa05032 → Morphine addiction - Homo sapiens (human),
path:hsa05033 → Nicotine addiction - Homo sapiens (human),
path:hsa05034 → Alcoholism - Homo sapiens (human),
path:hsa05100 → Bacterial invasion of epithelial cells - Homo sapiens (human),
path:hsa05110 → Vibrio cholerae infection - Homo sapiens (human),
path:hsa05120 → Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
path:hsa05130 → Pathogenic Escherichia coli infection - Homo sapiens (human),
path:hsa05131 → Shigellosis - Homo sapiens (human),
path:hsa05132 → Salmonella infection - Homo sapiens (human),
path:hsa05133 → Pertussis - Homo sapiens (human), path:hsa05134 → Legionellosis - Homo sapiens (human),
path:hsa05135 → Yersinia infection - Homo sapiens (human),
path:hsa05140 → Leishmaniasis - Homo sapiens (human),
path:hsa05142 → Chagas disease (American trypanosomiasis) - Homo sapiens (human),
path:hsa05143 → African trypanosomiasis - Homo sapiens (human),
path:hsa05144 → Malaria - Homo sapiens (human), path:hsa05145 → Toxoplasmosis - Homo sapiens (human),
path:hsa05146 → Amoebiasis - Homo sapiens (human),
path:hsa05150 → Staphylococcus aureus infection - Homo sapiens (human),
path:hsa05152 → Tuberculosis - Homo sapiens (human), path:hsa05160 → Hepatitis C - Homo sapiens (human),
path:hsa05161 → Hepatitis B - Homo sapiens (human), path:hsa05162 → Measles - Homo sapiens (human),
path:hsa05163 → Human cytomegalovirus infection - Homo sapiens (human),
path:hsa05164 → Influenza A - Homo sapiens (human),
path:hsa05165 → Human papillomavirus infection - Homo sapiens (human),
path:hsa05166 → Human T-cell leukemia virus 1 infection - Homo sapiens (human),
path:hsa05167 → Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human),
path:hsa05168 → Herpes simplex virus 1 infection - Homo sapiens (human),
path:hsa05169 → Epstein-Barr virus infection - Homo sapiens (human),
path:hsa05170 → Human immunodeficiency virus 1 infection - Homo sapiens (human),
path:hsa05200 → Pathways in cancer - Homo sapiens (human),
path:hsa05202 → Transcriptional misregulation in cancer - Homo sapiens (human),
path:hsa05203 → Viral carcinogenesis - Homo sapiens (human),
path:hsa05204 → Chemical carcinogenesis - Homo sapiens (human),
path:hsa05205 → Proteoglycans in cancer - Homo sapiens (human),
```

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```
path:hsa05206 → MicroRNAs in cancer - Homo sapiens (human),
path:hsa05210 → Colorectal cancer - Homo sapiens (human),
path:hsa05211 → Renal cell carcinoma - Homo sapiens (human),
path:hsa05212 → Pancreatic cancer - Homo sapiens (human),
path:hsa05213 → Endometrial cancer - Homo sapiens (human),
path:hsa05214 → Glioma - Homo sapiens (human), path:hsa05215 → Prostate cancer - Homo sapiens (human),
path:hsa05216 → Thyroid cancer - Homo sapiens (human),
path:hsa05217 → Basal cell carcinoma - Homo sapiens (human),
path:hsa05218 → Melanoma - Homo sapiens (human), path:hsa05219 → Bladder cancer - Homo sapiens (human),
path:hsa05220 → Chronic myeloid leukemia - Homo sapiens (human),
path:hsa05221 → Acute myeloid leukemia - Homo sapiens (human),
path:hsa05222 → Small cell lung cancer - Homo sapiens (human),
path:hsa05223 → Non-small cell lung cancer - Homo sapiens (human),
path:hsa05224 → Breast cancer - Homo sapiens (human),
path:hsa05225 → Hepatocellular carcinoma - Homo sapiens (human),
path:hsa05226 → Gastric cancer - Homo sapiens (human),
path:hsa05230 → Central carbon metabolism in cancer - Homo sapiens (human),
path:hsa05231 → Choline metabolism in cancer - Homo sapiens (human),
path:hsa05235 → PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
path:hsa05310 → Asthma - Homo sapiens (human),
path:hsa05320 → Autoimmune thyroid disease - Homo sapiens (human),
path:hsa05321 → Inflammatory bowel disease (IBD) - Homo sapiens (human),
path:hsa05322 → Systemic lupus erythematosus - Homo sapiens (human),
path:hsa05323 → Rheumatoid arthritis - Homo sapiens (human),
path:hsa05330 → Allograft rejection - Homo sapiens (human),
path:hsa05332 → Graft-versus-host disease - Homo sapiens (human),
path:hsa05340 → Primary immunodeficiency - Homo sapiens (human),
path:hsa05410 → Hypertrophic cardiomyopathy (HCM) - Homo sapiens (human),
path:hsa05412 → Arrhythmogenic right ventricular cardiomyopathy (ARVC) - Homo sapiens (human),
path:hsa05414 → Dilated cardiomyopathy (DCM) - Homo sapiens (human),
path:hsa05416 → Viral myocarditis - Homo sapiens (human),
path:hsa05418 → Fluid shear stress and atherosclerosis - Homo sapiens (human)|>
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can query for modules:

In[2]:=
```
dictionaryModuleQuery1 = KEGGDictionary[KEGGQuery1 → "module"]
```

Out[2]=
```
<|md:hsa_M00001 → Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate,
md:hsa_M00002 → Glycolysis, core module involving three-carbon compounds,
md:hsa_M00003 → Gluconeogenesis, oxaloacetate => fructose-6P,
md:hsa_M00004 → Pentose phosphate pathway (Pentose phosphate cycle),
md:hsa_M00005 → PRPP biosynthesis, ribose 5P => PRPP,
md:hsa_M00006 → Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P,
md:hsa_M00007 → Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P,
md:hsa_M00009 → Citrate cycle (TCA cycle, Krebs cycle),
md:hsa_M00010 → Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate,
md:hsa_M00011 → Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate,
md:hsa_M00013 → Malonate semialdehyde pathway, propanoyl-CoA => acetyl-CoA,
md:hsa_M00014 → Glucuronate pathway (uronate pathway),
md:hsa_M00015 → Proline biosynthesis, glutamate => proline,
md:hsa_M00020 → Serine biosynthesis, glycerate-3P => serine,
md:hsa_M00027 → GABA (gamma-Aminobutyrate) shunt, md:hsa_M00029 → Urea cycle,
md:hsa_M00032 → Lysine degradation, lysine => saccharopine => acetoacetyl-CoA,
md:hsa_M00034 → Methionine salvage pathway, md:hsa_M00035 → Methionine degradation,
md:hsa_M00036 → Leucine degradation, leucine => acetoacetate + acetyl-CoA,
md:hsa_M00037 → Melatonin biosynthesis, tryptophan => serotonin => melatonin,
md:hsa_M00042 → Catecholamine biosynthesis, tyrosine => dopamine => noradrenaline => adrenaline,
md:hsa_M00043 → Thyroid hormone biosynthesis, tyrosine => triiodothyronine/thyroxine,
md:hsa_M00044 → Tyrosine degradation, tyrosine => homogentisate,
md:hsa_M00046 → Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate,
md:hsa_M00047 → Creatine pathway,
md:hsa_M00048 → Inosine monophosphate biosynthesis, PRPP + glutamine => IMP,
```

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```
md:hsa_M00049 → Adenine ribonucleotide biosynthesis, IMP => ADP,ATP,
md:hsa_M00050 → Guanine ribonucleotide biosynthesis IMP => GDP,GTP,
md:hsa_M00051 → Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP,
md:hsa_M00052 → Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP,
md:hsa_M00055 → N-glycan precursor biosynthesis, md:hsa_M00056 → O-glycan biosynthesis, mucin type core,
md:hsa_M00057 → Glycosaminoglycan biosynthesis, linkage tetrasaccharide,
md:hsa_M00058 → Glycosaminoglycan biosynthesis, chondroitin sulfate backbone,
md:hsa_M00059 → Glycosaminoglycan biosynthesis, heparan sulfate backbone,
md:hsa_M00065 → GPI-anchor biosynthesis, core oligosaccharide,
md:hsa_M00066 → Lactosylceramide biosynthesis,
md:hsa_M00067 → Sulfoglycolipids biosynthesis, ceramide/1-alkyl-2-acylglycerol => sulfatide/seminolipid,
md:hsa_M00068 → Glycosphingolipid biosynthesis, globo-series, LacCer => Gb4Cer,
md:hsa_M00069 → Glycosphingolipid biosynthesis, ganglio series, LacCer => GT3,
md:hsa_M00070 → Glycosphingolipid biosynthesis, lacto-series, LacCer => Lc4Cer,
md:hsa_M00071 → Glycosphingolipid biosynthesis, neolacto-series, LacCer => nLc4Cer,
md:hsa_M00072 → N-glycosylation by oligosaccharyltransferase,
md:hsa_M00073 → N-glycan precursor trimming, md:hsa_M00075 → N-glycan biosynthesis, complex type,
md:hsa_M00076 → Dermatan sulfate degradation, md:hsa_M00077 → Chondroitin sulfate degradation,
md:hsa_M00078 → Heparan sulfate degradation, md:hsa_M00079 → Keratan sulfate degradation,
md:hsa_M00082 → Fatty acid biosynthesis, initiation, md:hsa_M00083 → Fatty acid biosynthesis, elongation,
md:hsa_M00085 → Fatty acid biosynthesis, elongation, mitochondria,
md:hsa_M00086 → beta-Oxidation, acyl-CoA synthesis,
md:hsa_M00087 → beta-Oxidation, md:hsa_M00089 → Triacylglycerol biosynthesis,
md:hsa_M00090 → Phosphatidylcholine (PC) biosynthesis, choline => PC,
md:hsa_M00091 → Phosphatidylcholine (PC) biosynthesis, PE => PC,
md:hsa_M00092 → Phosphatidylethanolamine (PE) biosynthesis, ethanolamine => PE,
md:hsa_M00094 → Ceramide biosynthesis, md:hsa_M00095 → C5 isoprenoid biosynthesis, mevalonate pathway,
md:hsa_M00098 → Acylglycerol degradation,
md:hsa_M00099 → Sphingosine biosynthesis, md:hsa_M00100 → Sphingosine degradation,
md:hsa_M00101 → Cholesterol biosynthesis, squalene 2,3-epoxide => cholesterol,
md:hsa_M00103 → Cholecalciferol biosynthesis,
md:hsa_M00104 → Bile acid biosynthesis, cholesterol => cholate/chenodeoxycholate,
md:hsa_M00106 → Conjugated bile acid biosynthesis, cholate => taurocholate/glycocholate,
md:hsa_M00107 → Steroid hormone biosynthesis, cholesterol => prognenolone => progesterone,
md:hsa_M00108 → C21-Steroid hormone biosynthesis, progesterone => corticosterone/aldosterone,
md:hsa_M00109 → C21-Steroid hormone biosynthesis, progesterone => cortisol/cortisone,
md:hsa_M00110 → C19/C18-Steroid hormone biosynthesis, pregnenolone => androstenedione => estrone,
md:hsa_M00118 → Glutathione biosynthesis, glutamate => glutathione,
md:hsa_M00120 → Coenzyme A biosynthesis, pantothenate => CoA,
md:hsa_M00128 → Ubiquinone biosynthesis, eukaryotes, 4-hydroxybenzoate => ubiquinone,
md:hsa_M00130 → Inositol phosphate metabolism, PI=> PIP2 => Ins(1,4,5)P3 => Ins(1,3,4,5)P4,
md:hsa_M00131 → Inositol phosphate metabolism, Ins(1,3,4,5)P4 => Ins(1,3,4)P3 => myo-inositol,
md:hsa_M00132 → Inositol phosphate metabolism, Ins(1,3,4)P3 => phytate,
md:hsa_M00133 → Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine,
md:hsa_M00134 → Polyamine biosynthesis, arginine => ornithine => putrescine,
md:hsa_M00135 → GABA biosynthesis, eukaryotes, putrescine => GABA,
md:hsa_M00141 → C1-unit interconversion, eukaryotes,
md:hsa_M00142 → NADH:ubiquinone oxidoreductase, mitochondria,
md:hsa_M00143 → NADH dehydrogenase (ubiquinone) Fe-S protein/flavoprotein complex, mitochondria,
md:hsa_M00146 → NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,
md:hsa_M00147 → NADH dehydrogenase (ubiquinone) 1 beta subcomplex,
md:hsa_M00148 → Succinate dehydrogenase (ubiquinone),
md:hsa_M00151 → Cytochrome bc1 complex respiratory unit, md:hsa_M00152 → Cytochrome bc1 complex,
md:hsa_M00154 → Cytochrome c oxidase, md:hsa_M00158 → F-type ATPase, eukaryotes,
md:hsa_M00160 → V-type ATPase, eukaryotes, md:hsa_M00177 → Ribosome, eukaryotes,
md:hsa_M00180 → RNA polymerase II, eukaryotes, md:hsa_M00181 → RNA polymerase III, eukaryotes,
md:hsa_M00182 → RNA polymerase I, eukaryotes, md:hsa_M00261 → DNA polymerase alpha / primase complex,
md:hsa_M00262 → DNA polymerase delta complex, md:hsa_M00263 → DNA polymerase epsilon complex,
md:hsa_M00284 → Origin recognition complex, md:hsa_M00285 → MCM complex,
md:hsa_M00286 → GINS complex, md:hsa_M00288 → RPA complex, md:hsa_M00289 → RF-C complex,
md:hsa_M00290 → Holo-TFIIH complex, md:hsa_M00291 → MRN complex,
md:hsa_M00293 → DNA polymerase zeta  complex, md:hsa_M00294 → DNA polymerase gamma complex,
md:hsa_M00295 → BRCA1-associated genome surveillance complex (BASC), md:hsa_M00296 → BER complex,
md:hsa_M00297 → DNA-PK complex, md:hsa_M00307 → Pyruvate oxidation, pyruvate => acetyl-CoA,
md:hsa_M00337 → Immunoproteasome, md:hsa_M00338 → Cysteine biosynthesis, homocysteine + serine => cysteine,
md:hsa_M00340 → Proteasome, 20S core particle, md:hsa_M00341 → Proteasome, 19S regulatory particle (PA700),
```

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```
md:hsa_M00351 → Spliceosome, U1-snRNP, md:hsa_M00352 → Spliceosome, U2-snRNP,
md:hsa_M00353 → Spliceosome, Prp19/CDC5L complex, md:hsa_M00354 → Spliceosome, U4/U6.U5 tri-snRNP,
md:hsa_M00355 → Spliceosome, 35S U5-snRNP, md:hsa_M00359 → Aminoacyl-tRNA biosynthesis, eukaryotes,
md:hsa_M00361 → Nucleotide sugar biosynthesis, eukaryotes,
md:hsa_M00367 → C10-C20 isoprenoid biosynthesis, non-plant eukaryotes, md:hsa_M00380 → SCF-BTRC complex,
md:hsa_M00381 → SCF-SKP2 complex, md:hsa_M00382 → SCF-FBS complex, md:hsa_M00383 → ECV complex,
md:hsa_M00384 → Cul3-SPOP complex, md:hsa_M00385 → Cul4-DDB1-DDB2 complex,
md:hsa_M00386 → Cul4-DDB1-CSA complex, md:hsa_M00387 → SCF-FBW7 complex, md:hsa_M00388 → ECS complex,
md:hsa_M00389 → APC/C complex, md:hsa_M00390 → Exosome, archaea, md:hsa_M00391 → Exosome, eukaryotes,
md:hsa_M00392 → Ski complex, md:hsa_M00393 → TRAMP complex, md:hsa_M00395 → Decapping complex,
md:hsa_M00396 → Lsm 2-8 complex, md:hsa_M00397 → Lsm 1-7 complex, md:hsa_M00398 → Sm core complex,
md:hsa_M00399 → Cap binding complex, md:hsa_M00400 → p97-Ufd1-Npl4 complex,
md:hsa_M00401 → Sec61 complex, md:hsa_M00402 → Translocon-associated protein (TRAP) complex,
md:hsa_M00403 → HRD1/SEL1 ERAD complex, md:hsa_M00404 → COPII complex,
md:hsa_M00405 → THC complex, md:hsa_M00406 → TREX complex, md:hsa_M00408 → ESCRT-0 complex,
md:hsa_M00409 → ESCRT-I complex, md:hsa_M00410 → ESCRT-II complex, md:hsa_M00412 → ESCRT-III complex,
md:hsa_M00413 → FA core complex, md:hsa_M00414 → Bloom's syndrome complex,
md:hsa_M00415 → Fatty acid biosynthesis, elongation, endoplasmic reticulum,
md:hsa_M00424 → Shelterin complex, md:hsa_M00425 → H/ACA ribonucleoprotein complex,
md:hsa_M00426 → Survival motor neuron (SMN) complex, md:hsa_M00427 → Nuclear pore complex,
md:hsa_M00428 → eIF4F complex, md:hsa_M00430 → Exon junction complex (EJC),
md:hsa_M00549 → Nucleotide sugar biosynthesis, glucose => UDP-glucose,
md:hsa_M00554 → Nucleotide sugar biosynthesis, galactose => UDP-galactose,
md:hsa_M00632 → Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P,
md:hsa_M00676 → PI3K-Akt signaling, md:hsa_M00677 → Wnt signaling, md:hsa_M00678 → Hedgehog signaling,
md:hsa_M00679 → BMP signaling, md:hsa_M00680 → TGF-beta signaling, md:hsa_M00681 → Activin signaling,
md:hsa_M00682 → Notch signaling, md:hsa_M00683 → Hippo signaling, md:hsa_M00684 → JAK-STAT signaling,
md:hsa_M00685 → Apoptotic machinery, md:hsa_M00686 → Toll-like receptor signaling,
md:hsa_M00687 → MAPK (ERK1/2) signaling, md:hsa_M00688 → MAPK (JNK) signaling,
md:hsa_M00689 → MAPK (p38) signaling, md:hsa_M00690 → MAPK (ERK5) signaling,
md:hsa_M00691 → DNA damage-induced cell cycle checkpoints, md:hsa_M00692 → Cell cycle - G1/S transition,
md:hsa_M00693 → Cell cycle - G2/M transition, md:hsa_M00694 → cGMP signaling,
md:hsa_M00695 → cAMP signaling, md:hsa_M00741 → Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA|〉
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can also query memberships by setting at the same time KEGGQuery2 to "":

In[2]:=
```
dictionaryPathwayQuery12 = KEGGDictionary[KEGGQuery1 → "disease", KEGGQuery2 → ""]
```

Out[2]=
```
〈|ds:H00001 → Acute lymphoblastic leukemia (ALL) (precursor B lymphoblastic leukemia/lymphoma),
 ds:H00002 → Acute lymphoblastic leukemia (ALL) (precursor T lymphoblastic leukemia/lymphoma),
 ds:H00003 → Acute myeloid leukemia (AML), ds:H00004 → Chronic myeloid leukemia (CML),
 ds:H00005 → Chronic lymphocytic leukemia (CLL), ds:H00006 → Hairy-cell leukemia,
 ds:H00007 → Hodgkin lymphoma, ds:H00008 → Burkitt lymphoma, ds:H00009 → Adult T-cell leukemia,
 ds:H00010 → Multiple myeloma, ds:H00011 → Lymphoplasmacytic lymphoma, ds:H00012 → Polycythemia vera,
 ds:H00013 → Small cell lung cancer, ds:H00014 → Non-small cell lung cancer,
 ds:H00015 → Malignant pleural mesothelioma, ds:H00016 → Oral cancer, ds:H00017 → Esophageal cancer,
 ds:H00018 → Gastric cancer, ds:H00019 → Pancreatic cancer, ds:H00020 → Colorectal cancer,
 ds:H00021 → Renal cell carcinoma, ds:H00022 → Bladder cancer, ds:H00023 → Testicular cancer,
 ds:H00024 → Prostate cancer, ds:H00025 → Penile cancer, ds:H00026 → Endometrial Cancer,
 ds:H00027 → Ovarian cancer, ds:H00028 → Choriocarcinoma, ds:H00029 → Vulvar cancer,
 ds:H00030 → Cervical cancer, ds:H00031 → Breast cancer, ds:H00032 → Thyroid cancer,
 ds:H00033 → Adrenal carcinoma, ds:H00034 → Carcinoid, ds:H00035 → Ewing's sarcoma,
 ds:H00036 → Osteosarcoma, ds:H00037 → Alveolar rhabdomyosarcoma, ds:H00038 → Malignant melanoma,
 ds:H00039 → Basal cell carcinoma, ds:H00040 → Squamous cell carcinoma, ds:H00041 → Kaposi's sarcoma,
 ds:H00042 → Glioma, ds:H00043 → Neuroblastoma, ds:H00044 → Cancer of the anal canal,
 ds:H00045 → Pancreatic neuroendocrine tumor, ds:H00046 → Cholangiocarcinoma, ds:H00047 → Gallbladder cancer,
 ds:H00048 → Hepatocellular carcinoma, ds:H00049 → Myxoid liposarcoma, ds:H00050 → Synovial sarcoma,
 ds:H00051 → Alveolar soft part sarcoma, ds:H00052 → Clear cell sarcoma of soft tissue,
 ds:H00053 → Extraskeletal myxoid chondrosarcoma, ds:H00054 → Nasopharyngeal cancer,
 ds:H00055 → Laryngeal cancer, ds:H00056 → Alzheimer's disease (AD), ds:H00057 → Parkinson's disease (PD),
 ds:H00058 → Amyotrophic lateral sclerosis (ALS); Lou Gehrig's disease,
 ds:H00059 → Huntington's disease (HD), ds:H00060 → Dentatorubropallidoluysian atrophy (DRPLA),
```

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ds:H00061 → Prion diseases; Creutzfeldt-Jacob disease (CJD); Gerstmann-Straussler disease (GSD); Gerstmann-Straussler-Scheinker disease (GSSD); Fatal familial insomnia (FFI),
ds:H00062 → Spinal and bulbar muscular atrophy (SBMA); Kennedy's disease,
ds:H00063 → Spinocerebellar ataxia (SCA),
ds:H00064 → Ataxia telangiectasia (AT); Louis-Bar syndrome; Boder-Sedgwick syndrome,
ds:H00065 → Alexander disease, ds:H00066 → Lewy body dementia (LBD); Dementia with Lewy bodies (DLB),
ds:H00067 → Friedreich ataxia, ds:H00068 → Leber optic atrophy; Leber hereditary optic atrophy (LHON),
ds:H00069 → Glycogen storage diseases (GSD), including: von Gierke disease (GSD type Ia); Pompe disease (GSD type II); Cori disease, Forbe disease (GSD type III); Andersen disease (GSD type IV); McArdle disease (GSD type V); Hers disease (GSD type VI); Tarui disease (GSD type VII); Phosphorylase kinase deficiency (GSD type IX); Fanconi-Bickel syndrome (GSD type XI); Glycogen synthase deficiency (GSD type 0),
ds:H00070 → Galactosemia, ds:H00071 → Hereditary fructose intolerance; Fructosemia,
ds:H00072 → Pyruvate dehydrogenase complex deficiency, including: Leigh syndrome [DS:H01354]; Pyruvate dehydrogenase phosphatase deficiency; Pyruvate dehydrogenase E3-binding protein deficiency (PDHXD),
ds:H00073 → Pyruvate carboxylase deficiency, ds:H00074 → Canavan disease (CD),
ds:H00075 → Refsum disease; Heredopathia atactica polyneuritiformis, ds:H00076 → Cockayne syndrome,
ds:H00077 → Progressive supranuclear palsy (PSP); Steele-Richardson-Olszewski syndrome,
ds:H00078 → Frontotemporal lobar degeneration (FTLD), including: Pick disease of brain; Frontotemporal dementia (FTD); Ubiquitin-positive frontotemporal dementia (UP-FTD); Progressive supranuclear palsy type 1 (PSNP1); Inclusion body myopathy with early-onset paget disease and frontotemporal dementia (IBMPFD); Frontotemporal dementia, chromosome 3-linked (FTD3),
ds:H00079 → Asthma, ds:H00080 → Systemic lupus erythematosus, ds:H00081 → Hashimoto's thyroiditis,
ds:H00082 → Graves' disease, ds:H00083 → Allograft rejection,
ds:H00084 → Graft-versus-host disease, ds:H00085 →
Agammaglobulinemias, including the following six diseases: X-linked agammaglobulinemia (Bruton's agammaglobulinemia, XLA); IgM heavy chain gene deletions; Ig-alpha defect; Autosomal recessive agammaglobulinaemia; B cell-linker protein (BLNK) deficiency; Leucine-rich repeat-containing 8,
ds:H00086 → Hyper IgM syndromes, autosomal recessive type, including the following three diseases: Activation-induced cytidine deaminase (AICD) defect; Uracil nucleotide glycoside glycosylase (UNG) defect; Immunodeficiency with hyper-IgM type 3,
ds:H00087 → Other humoral immunodeficiencies, including the following three diseases: Immunodeficiency, centromeric instability, facial anomalies (ICF)-syndrome; kappa light-chain deficiency; Ig heavy chain gene deletions,
ds:H00088 → Common variable immunodeficiency (CVID), including the following four diseases: Inducible T Cell costimulator (ICOS) defect; TACI defect; CD19 defect; BAFFR defect; CD20 defect; CD81 defect,
ds:H00089 → IFN-gamma/IL-12 axis, including the following five diseases: IL-12 p40 subunit deficiency; IL-12 receptor (IL-12R) beta1 chain deficiency; IFN-gamma receptor (IFN gamma R) alpha chain deficiency; IFN-gamma receptor (IFN gamma R) beta chain deficiency; STAT-1 deficiency,
ds:H00090 → NK cell defects, including the following disease: CD16 deficiency,
ds:H00091 → T-B+Severe combined immunodeficiencies (SCIDs), including the following eight diseases: X-linked SCID; Janus kinase-3 (Jak3) deficiency; IL-7 receptor alpha (IL7R alpha) deficiency; IL-2 receptor alpha (IL2R alpha) deficiency; CD45 deficiency; CD3 deficiency; Winged Helix Nude (WHN) deficiency; Immunodeficiency with thynoma,
ds:H00092 → T-B-Severe combined immunodeficiencies (SCIDs), including the following four diseases: Adenosine deaminase (ADA) deficiency; Recombinase activating gene (RAG) deficiencies; Artemis deficiency; Reticular dysgenesis,
ds:H00093 → Combined immunodeficiencies (CIDs), including the following nine diseases: X-linked hyper IgM syndrome; X-linked, moderate; CD40 deficiency hyper IgM syndrome; Purine nucleoside phosphorylase (PNP) deficiency; RAG deficiency with granulomas; Omenn syndrome; MHC deficiency (HLA-class I); MHC deficiency (HLA-class II); Zap-70 deficiency; Ca2+ channel deficiency; p56 Lck deficiency; CD8 deficiency,
ds:H00094 → Immunodeficiency associated with DNA repair defects, including the following six diseases: Ataxia telangiectasia (AT) [DS:H00064]; Ataxia-talangiectasia-like syndrome; Nijmegen syndrome [DS:H01344]; DNA ligase I deficiency; DNA ligase IV deficiency; Bloom syndrome [DS:H01346],
ds:H00095 → Ectodermal dysplasia associated immunodeficiency (EDA-ID), including the following two diseases: NF-kappa-B essential modulator (NEMO) defect; Inhibitor of kappa-B (I-kappa-B) defect,
ds:H00096 → Defects of toll-like receptor signaling, including the following disease: Il-1 receptor-associated kinase 4 (IRAK-4) deficiency,
ds:H00097 → Chemokine receptor defect, including the following disease: WHIM syndrome,
ds:H00098 → Chronic granulomatous disease, including the following four diseases: X-linked CGD (gp91 phox CGD); p22phox deficiency (p22phox CGD); p47phox deficiency (p47phox CGD); p67phox deficiency (p67phox CGD),
ds:H00099 → Leukocyte adhesion deficiency (LAD), including the following four diseases: Leukocyte adhesion deficiency (I); Leukocyte adhesion deficiency (II); Leukocyte adhesion deficiency (III); LAD with Rac2 deficiency,

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ds:H00100 → Neutropenic disorders, including the following three diseases: Kostmann syndrome; Cyclic neutropenia; X-linked neutropenia/myelodysplasia,
ds:H00101 → Other phagocyte defects, including the following eight diseases: Chediak-Higashi syndrome; Griscelli syndrome, type 1 (GS1); Griscelli syndrome, type 2 (GS2); Griscelli syndrome, type 3 (GS3); beta-actin deficiency; Neutrophil-specific granule deficiency; Myeloperoxidase deficiency; Glucose 6-phosphate dehydrogenase deficiency; Shwachman syndrome,
ds:H00102 → Classic complement pathway component defects, including the following eight diseases: C1q alpha-chain deficiency; C1q beta-chain deficiency; C1q gamma-chain deficiency; C1r deficiency; C1s deficiency; C2 deficiency; C3 deficiency; C4 deficiency,
ds:H00103 → Late complement pathway defects, including the following seven diseases: C5 deficiency; C6 deficiency; C7 deficiency; C8 alpha-chain deficiency; C8 beta-chain deficiency; C8 gamma-chain deficiency; C9 deficiency,
ds:H00104 → Alternative complement pathway component defects, including the following four diseases: Factor B deficiency; Factor D deficiency; Factor H deficiency; Properdin deficiency, ds:H00105 → Mannose-binding lectin pathway component defects, including the following two diseases: Mannose-binding lectin deficiency; Mannose-binding lectin-associated serine protease (MASP) 2 deficiency,
ds:H00106 → Complement regulatory protein defects, including the following six diseases: C1 inhibitor deficiency (hereditary angioedema); C4 binding protein alpha deficiency; C4 binding protein beta deficiency; Factor I deficiency; Decay-accelerating factor (CD55) deficiency; CD59 deficiency,
ds:H00107 → Other well-defined immunodeficiency syndromes, including the following eight diseases: Wiskott-Aldrich syndrome; DiGeorge syndrome; Hyper-IgE syndrome; X-linked lymphoproliferative syndrome; Lymphoproliferative syndrome, EBV-associated, autosomal, 1; Immunodeficiency, Polyendocrinopathy, Enteropathy, X-linked Syndrome (IPEX); Cartilage-Hair Hypoplasia; Autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED),
ds:H00108 → Autoimmune lymphoproliferative syndromes (ALPS), including the following five diseases: CD95 (Fas) defect, ALPS type 1a; CD95L (Fas ligand) defect, ALPS type 1b; Caspase 10 defect, ALPS type 2a; Caspase 8 defext, ALPS type 2b; Activaing N-Ras defect, N-Ras ALPS,
ds:H00109 → Familial hemophagocytic lymphohistiocytosis (FHPL), including the following three diseases: Perforin deficiency; Munc deficiency; STX11 deficiency,
ds:H00110 → Cholera, ds:H00111 → Typhoid fever, ds:H00112 → Paratyphoid fever,
ds:H00113 → Salmonellosis,
ds:H00114 → Fructose-1,6-bisphosphatase deficiency,
ds:H00115 → Congenital sucrase-isomaltase deficiency; Disaccharide intolerance I,
ds:H00116 → Congenital lactase deficiency; Disaccharide intolerance II,
ds:H00117 → Primary hyperoxaluria (HP),
ds:H00118 → Congenital disorders of glycosylation (CDG) type I,
ds:H00119 → Congenital disorders of glycosylation (CDG) type II,
ds:H00120 → Dystroglycanopathy; Walker-Warburg syndrome (WWS); Muscle-eye-brain disease (MEB); Fukuyama congenital muscular dystrophy (FCMD); Congenital muscular dystrophy with muscle hypertrophy (MDC1C); Congenital muscular dystrophy with severe intellectual impairment and abnormal glycosylation (MDC1D), ds:H00122 → Multiple exostoses, ds:H00123 → Mucopolysaccharidosis type IV (MPS4), including: Morquio syndrome A (MPS4A); Morquio syndrome B (MPS4B),
ds:H00124 → GM2 gangliosidoses, including: Tay-Sachs disease (type I); Sandhoff disease (type II); Tay-Sachs disease AB variant, ds:H00125 → Fabry disease,
ds:H00126 → Gaucher disease, ds:H00127 → Metachromatic leukodystrophy (MLD),
ds:H00128 → Mucopolysaccharidosis type I (MPS1); Hurler-Scheie syndrome (MPS1HS); Hurler syndrome (MPS1H); Scheie syndrome (MPS1S),
ds:H00129 → Mucopolysaccharidosis type II (MPS2); Hunter syndrome,
ds:H00130 → Mucopolysaccharidosis type III (MPS3), including: Sanfilippo A syndrome (MPS3A); Sanfilippo B syndrome (MPS3B); Sanfilippo C syndrome (MPS3C); Sanfilippo D syndrome (MPS3D),
ds:H00131 → Mucopolysaccharidosis type VI (MPS6); Maroteaux-Lamy syndrome,
ds:H00132 → Mucopolysaccharidosis type VII (MPS7); Sly syndrome,
ds:H00133 → Mucopolysaccharidosis type IX (MPS9); Hyaluronidase deficiency,
ds:H00134 → X-linked ichthyosis (XLI),
ds:H00135 → Krabbe disease; Globoid cell leukodystrophy,
ds:H00136 → Niemann-Pick disease type C (NPC), including: Niemann-Pick disease type C1; Niemann-Pick disease type C2,
ds:H00137 → Niemann-Pick disease (NPD) typeA and B, including: Niemann-Pick disease, type A; Niemann-Pick disease, type B,
ds:H00138 → Farber lipogranulomatosis; Farber disease, ds:H00139 → alpha-Mannosidosis,
ds:H00140 → beta-Mannosidosis,
ds:H00141 → Fucosidosis,
ds:H00142 → Sialidosis; Mucolipidosis I,
ds:H00143 → Mucolipidosis II and III, including: Mucolipidosis II / I-cell disease; Mucolipidosis III A / Pseudo-Hurler polydystrophy; Mucolipidosis III C,
ds:H00144 → Mucolipidosis IV, ds:H00145 → Aspartylglucosaminuria (AGU),

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ds:H00146 → Alpha-N-acetylgalactosaminidase deficiency, including: Schindler disease; Kanzaki disease,
ds:H00147 → Sialuria/ Sialic acid storage disease, including: Infantile sialic acid storage disease (ISSD); Sialuria, Finnish type / Salla disease (SD); Sialuria, French type, ds:H00148 → Lysosomal acid lipase deficiency, including: Wolman disease; Cholesterol ester storage disease (CESD),
ds:H00149 → Neuronal ceroid lipofuscinosis, including: Infantile Neuronal Ceroid Lipofuscinosis (INCL)/ Santavuori-Haltia Disease (CLN1); Late-Infantile Neuronal Ceroid Lipofuscinosis (LINCL)/ Jansky-Bielschowsky Disease (CLN2); Juvenile Neuronal Ceroid Lipofuscinosis (JNCL)/Batten Disease/ Spielmeyer-Vogt Disease (CLN3); Adult Neuronal Ceroid Lipofuscinosis (ANCL)/ Kufs Disease (CLN4); LINCL variant (CLN5, CLN6, CLN7, CLN8); Batten Disease variant (CLN9); Congenital NCL (CLN10),
ds:H00150 → Danon disease; X-linked vacuolar cardiomyopathy and myopathy,
ds:H00151 → Cerebrotendinous xanthomatosis; Van Bogaert-Scherer-Epstein Disease,
ds:H00152 → Sitosterolemia,
ds:H00153 → Familial combined hyperlipidemia (FCHL),
ds:H00154 → Hyperlipoproteinemia, type I,
ds:H00155 → Hypercholesterolemia, including: Hypercholesterolemia, autosomal dominant; Hyperlipoproteinemia, type IIa; Hypercholesterolemia, autosomal recessive (ARH),
ds:H00156 → Hyperlipoproteinemia, type III; Dysbetalipoproteinemia,
ds:H00157 → Hyperlipoproteinemia, type V,
ds:H00158 → Lecithin:cholesterol acyltransferase deficiency; Norum disease; Fish-eye disease,
ds:H00159 → Tangier disease,
ds:H00160 → Abetalipoproteinemia; Bassen-Kornzweig Disease,
ds:H00161 → Smith-Lemli-Opitz syndrome,
ds:H00162 → Sjogren-Larsson syndrome,
ds:H00163 → Alkaptonuria,
ds:H00164 → Carbamoyl phosphate synthetase I deficiency,
ds:H00165 → Tyrosinemia; Tyrosinemia, type I; Tyrosinemia, type II; Tyrosinemia, type III; Hawkinsinuria,
ds:H00166 → Hermansky-Pudlak syndrome (HPS),
ds:H00167 → Phenylketonuria (PKU); Hyperphenylalaninemia, BH4-deficient,
ds:H00168 → Oculocutaneous albinism (OCA),
ds:H00169 → Ocular albinism; Ocular albinism, type I (OA1); Waardenburg syndrome, type II (WS2-OA),
ds:H00170 → Piebaldism,
ds:H00171 → Histidinemia,
ds:H00172 → Maple syrup urine disease (MSUD),
ds:H00173 → Isovaleric acidemia (IVA),
ds:H00174 → Methylmalonic aciduria (MMA),
ds:H00175 → Propionic acidemia,
ds:H00176 → Adrenoleukodystrophy (ALD), including: Schilder-Addison Complex; Childhood cerebral adrenoleukodystrophy (CCER); adrenomyeloneuropathy (AMN),
ds:H00177 → Adrenoleukodystrophy, neonatal (NALD), ds:H00178 → Glutaric acidemia, including: Glutaric acidemia, type I (GA1); Glutaric acidemia, type II (GA2); Multiple acyl coenzyme A dehydrogenase deficiency,
ds:H00179 → 3-Hydroxy-3-methylglutaryl-CoA lyase deficiency,
ds:H00180 → Holocarboxylase synthetase deficiency,
ds:H00181 → 3-Methylcrotonylglycinuria; 3-Methylcrotonyl-CoA carboxylase deficiency,
ds:H00182 → Cystathioninuria,
ds:H00183 → Homocystinuria,
ds:H00184 → Hypermethioninemia; Methionine adenosyltransferase deficiency; S-adenosylhomocysteine hydrolase deficiency,
ds:H00185 → Citrullinemia (CTLN), ds:H00186 → Hyperargininemia,
ds:H00187 → Ornithine transcarbamylase deficiency,
ds:H00188 → Hyperlysinemia,
ds:H00189 → Ornithinaemia; Gyrate Atrophy,
ds:H00190 → Hyperprolinemia (HP),
ds:H00191 → Nonketotic hyperglycinemia; Glycine encephalopathy (GCE),
ds:H00192 → Xanthinuria,
ds:H00193 → Dihydropyrimidine dehydrogenase deficiency,
ds:H00194 → Lesch-Nyhan syndrome; Hypoxanthine-guanine phosophoribosyltransferase deficiency,
ds:H00195 → Adenine phosphoribosyltransferase deficiency; 2,8-Dihydroxyadenine urolithiasis,
ds:H00196 → Phosphoribosylpyrophosphate synthetase I superactivity,
ds:H00197 → Adenylosuccinate lyase deficiency,
ds:H00198 → Orotic aciduria,
ds:H00199 → Dihydropyrimidinase deficiency; Dihydropyrimidinuria,
ds:H00200 → Beta-ureidopropionase deficiency,
ds:H00201 → Erythropoietic porphyria (EP), including: Erythropoietic protoporphyria (EPP); Congenital erythropoietic porphyria (CEP); Gunther Disease; X-linked erythropoietic protoporphyria (XLEPP),
ds:H00202 → Hepatic porphyria, including: Porphyria Cutanea Tarda (PCT); VHepatoerythropoietic

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    porphyria; Acute Intermittent Porphyria (AIP); Variegate porphyria (VP);
    ALA-dehydratase deficiency porphyria (ALADP); Hereditary Coproporphyria (HCP),
ds:H00203 → Acatalasia, including: Acatalasemia; Takahara's disease; Hypocatalasemia,
ds:H00204 → Infantile Refsum disease (IRD); Infantile phytanic acid storage disease,
ds:H00205 → Peroxisome biogenesis disorder, including: Zellweger syndrome (ZS)
    [DS:H01342]; Adrenoleukodystrophy, neonatal (NALD) [DS:H00177]; Infantile Refsum
    disease (IRD) [DS:H00204]; Rhizomelic chondrodysplasia punctata (RCDP1) [DS:H00207],
ds:H00206 → Mevalonate kinase deficiency; Hyperimmunoglobulinemia D; Mevalonic aciduria,
ds:H00207 → Rhizomelic chondrodysplasia punctata, including: Rhizomelic
    chondrodysplasia punctata, type I (RCDP1); Rhizomelic chondrodysplasia punctata,
    type II (RCDP2); Rhizomelic chondrodysplasia punctata, type III (RCDP3),
ds:H00208 → Hyperbilirubinemia; Crigler-Najjar syndrome, type I (CN1); Crigler-Najjar
    syndrome, type II (CN2); Gilbert Syndrome; Dubin-Johnson syndrome (DJS),
ds:H00209 → Menkes disease (MD); Menkes kinky hair syndrome,
ds:H00210 → Wilson disease; Hepatolenticular degeneration,
ds:H00211 → Hemochromatosis (HFE); Juvenile hemochromatosis (JH),
ds:H00212 → Acrodermatitis enteropathica (AEZ),
ds:H00213 → Hypophosphatasia,
ds:H00214 →
 Hypophosphatemic rickets, including: X-Linked dominant hypophosphatemia (XLH); X-Linked recessive
    hypophosphatemia (XLRH); Autosomal dominant hypophosphatemic rickets (ADHR); Autosomal recessive
    hypophosphatemic rickets (ARHR); Hereditary hypophophatemic rickets with hypercalciuria (HHRH),
ds:H00215 → Periodic paralysis, including: ; Hyperkalemic periodic paralysis (HyperPP) [DS:H00745];
    Hypokalemic periodic paralysis (HypoPP) [DS:H00746]; Andersen-Tawil syndrome (ATS) [DS:H00748],
ds:H00216 → Congenital adrenal hyperplasia (CAH), ds:H00217 →
 Pulmonary surfactant metabolism dysfunction (SMDP), ds:H00218 → Cystic fibrosis (CF),
ds:H00219 → Hemophilia, including: Hemophilia A (HEMA); Hemophilia B (HEMB);
    von Willebrand disease (VWD); von Willebrand disease, platelet-type,
ds:H00220 → Factor V deficiency; Owren disease, ds:H00221 →
 Combined deficiency of factors V and VIII (F5F8D),
ds:H00222 → Afibrinogenemia; Dysfibrinogenemia,
ds:H00223 → Inherited thrombophilia,
ds:H00224 → Bernard-Soulier syndrome; Giant platelet syndrome,
ds:H00225 → Thrombotic thrombocytopenic purpura; Moschcowitz disease; Schulman-Upshaw syndrome,
ds:H00226 → Glanzmann thrombasthenia,
ds:H00227 → Congenital amegakaryocytic thrombocytopenia (CAMT),
ds:H00228 → Thalassemia; Alpha thalassemia; Beta thalassemia; Alpha thalassemia, X-linked (ATRX),
ds:H00229 → Sickle cell anemia (SCA),
ds:H00230 → Hereditary spherocytosis (SPH),
ds:H00231 → Hereditary elliptocytosis (HE),
ds:H00232 → Hereditary stomatocytosis (HSt); Dehydrated hereditary stomatocytosis (DHS);
    Overhydrated hereditary stomatocytosis (OHS); Familial pseudohyperkalemia (FP), ds:H00233 →
 Macrothrombocytopenia; May-Hegglin anomaly; Sebastian syndrome; Fechtner syndrome; Epstein syndrome,
ds:H00234 → Pelger-Huet anomaly, ds:H00235 → Methemoglobinemia,
ds:H00236 → Congenital polycythemia; Familial erythrocytosis (ECYT),
ds:H00237 → Diamond-Blackfan anemia (DBA),
ds:H00238 → Fanconi anemia,
ds:H00239 → Bartter syndrome,
ds:H00240 → Gitelman syndrome,
ds:H00241 → Combined proximal and distal renal tubular acidosis (RTA type 3),
ds:H00242 → Liddle syndrome, ds:H00243 →
 Hyperkalemic distal renal tubular acidosis (RTA type 4), including: Pseudohypoaldosteronism type I
    (PHA1); Pseudohypoaldosteronism type II (Gordon's syndrome), ds:H00244 → Pseudohypoparathyroidism,
ds:H00245 → Familial hypocalciuric hypercalcemia (FHH1); Neonatal severe hyperparathyroidism
    (NSHPT); Autosomal dominant hypocalcemia (ADH); Familial hypercalciuric hypocalcemia,
ds:H00246 → Primary hyperparathyroidism; Familial hyperparathyroidism (HRPT),
ds:H00247 → Multiple endocrine neoplasia syndrome (MEN); Wermer syndrome; Sipple's syndrome,
ds:H00249 → Thyroid hormone resistance syndrome, including: Generalized thyroid hormone
    resistance; Refetoff Syndrome; Selective pituitary thyroid hormone resistance,
ds:H00250 → Congenital nongoitrous hypothyroidism (CHNG),
ds:H00251 → Thyroid dyshormonogenesis; Dyshormogenetic goiter,
ds:H00252 → Congenital nephrogenic diabetes insipidus (NDI),
ds:H00253 → Neurohypophyseal diabetes insipidus (NPDI); Central Diabetes Insipidus,
ds:H00254 → Pituitary Dwarfism (PD); Laron Syndrome (PD2); Isolated growth hormone
    deficiency (IGHD); Short Stature and Pituitary Defects (SSPD); Insulin-like growth
    factor 1 deficiency (IGFD); Combined pituitary hormone deficiency (CPHD), ds:H00255 →
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 Hypogonadotropic hypogonadism, including: Kallmann syndrome (KAL); Fertile eunuch syndrome (FEUNS),
ds:H00256 → Familial glucocorticoid deficiency (FGD),
ds:H00257 → Achalasia-Addisonianism-Alacrima syndrome; Triple A syndrome; Allogrove syndrome,
ds:H00258 → Aldosterone synthase deficiency; Corticosterone methyloxidase
   type I deficiency; Corticosterone methyloxidase type II deficiency,
ds:H00259 → Apparent mineralocorticoid excess syndrome; 11-beta-ketoreductase deficiency,
ds:H00260 → Pigmented micronodular adrenocortical disease (PPNAD),
ds:H00261 → Meckel syndrome (MKS); Meckel-Gruber syndrome,
ds:H00262 → Spina bifida,
ds:H00263 → Acrocallosal syndrome; Greig cephalopolysyndactyly syndrome,
ds:H00264 →
 Charcot-Marie-Tooth disease (CMT); Hereditary motor and sensory neuropathy; Peroneal muscular atrophy,
ds:H00265 → Hereditary sensory and autonomic neuropathy (HSAN), including: Familial dysautonomia
   (FD/HSAN3); Riley-Day syndrome (HSAN3); Congenital pain insensitivity with anhidrosis (CIPA/HSAN4),
ds:H00266 → Hereditary spastic paraplegia (SPG), ds:H00267 → Holoprosencephaly (HPE),
ds:H00268 → Lissencephaly (LIS); Miller-Dieker syndrome (MDLS),
ds:H00269 → Primary microcephaly (MCPH),
ds:H00270 → Periventricular nodular heterotopia (PVNH),
ds:H00271 → Polymicrogyria, including: Bilateral frontal polymicrogyria (BFP); Bilateral
   frontoparietal polymicrogyria (BFPP); Bilateral perisylvian polymicrogyria (BPP); Bilateral
   parasagittal parieto-occipital polymicrogyria (BPOP); Bilateral generalised polymicrogyria
   (BGP); Unilateral Polymicrogyria (ULP); Polymicrogyria with optic nerve hypoplasia;
   Polymicrogyria, symmetric or asymmetric (PMGYSA); Polymicrogyria with seizures (PMGYS),
ds:H00272 → Multiple sulfatase deficiency (MSD), ds:H00273 → Pycnodysostosis,
ds:H00274 → Papillon-Lefevre syndrome,
ds:H00275 → Cystinosis,
ds:H00276 → Galactosialidosis,
ds:H00277 → Enterohemorrhagic Escherichia coli (EHEC) infection,
ds:H00278 → Enteropathogenic Escherichia coli (EPEC) infection,
ds:H00279 → Uropathogenic Escherichia coli (UPEC) infection,
ds:H00280 → Enterotoxigenic Escherichia coli (ETEC) infection,
ds:H00281 → GM1 gangliosidosis,
ds:H00282 → Cryopyrin associated periodic syndrome (CAPS), including:
   Muckle-Wells syndrome (MWS); Familial cold autoinflammatory syndrome
   (FCAS); Chronic infantile neurologic, cutaneous, articular (CINCA) syndrome,
ds:H00283 → Ebola haemorrhagic fever, ds:H00284 → Crimean-Congo hemorrhagic fever,
ds:H00285 → Blau syndrome,
ds:H00286 → Crohn's disease,
ds:H00287 → Pyogenic sterile arthritis, pyoderma gangrenosum, and acne (PAPA) syndrome,
ds:H00288 → Familial Mediterranean fever (FMF); Familial hereditary periodic fever syndromes,
ds:H00289 → Recurrent hydatidiform moles (RHM); Familial biparental hydatidiform,
ds:H00290 → Aicardi-Goutieres Syndrome (AGS),
ds:H00291 → Familial chilblain lupus (FCL); Chilblain lupus erythematosus (CHLE),
ds:H00292 → Hypertrophic cardiomyopathy (HCM),
ds:H00293 → Arrhythmogenic right ventricular cardiomyopathy (ARVC),
ds:H00294 → Dilated cardiomyopathy (DCM),
ds:H00295 → Viral myocarditis,
ds:H00296 → Defects in RecQ helicases, including: Bloom's syndrome [DS:H01346];
   Werner's syndrome; Rothmund-Thomson syndrome; RAPADILINO syndrome [DS:H00965],
ds:H00297 → Plague, ds:H00298 → Yersiniosis, ds:H00299 → Shigellosis; Bacillary dysentery,
ds:H00300 → Enterobacter infection,
ds:H00301 → Klebsiella infection,
ds:H00302 → Citrobacter infection,
ds:H00303 → Serratia infection,
ds:H00304 → Haemophilus influenzae infection,
ds:H00305 → Chancroid,
ds:H00306 → Pasteurellosis,
ds:H00307 → Vibrio parahaemolyticus infection,
ds:H00308 → Vibrio vulnificus infection,
ds:H00309 → Multidrug-resistant Acinetobacter infection,
ds:H00310 → Q fever,
ds:H00311 → Legionellosis; Legionnaires disease,
ds:H00312 → Tularemia,
ds:H00313 → Multidrug-resistant Pseudomonas aeruginosa infection,
ds:H00314 → Meningococcal infections,
ds:H00315 → Gonococcal infections; Gonorrhea,
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ds:H00316 → Glanders,
ds:H00317 → Melioidosis,
ds:H00319 → Pertussis; Whooping cough,
ds:H00320 → Helicobacter pylori infection,
ds:H00321 → Campylobacter infection; Campylobacteriosis,
ds:H00322 → Typhus fever,
ds:H00323 → Spotted fever; Tick-borne rickettsioses,
ds:H00324 → Scrub typhus,
ds:H00325 → Brucellosis,
ds:H00326 → Bartonellosis, including: Cat-scratch disease;
   Bacillary Angiomatosis; Oroya Fever; Carrion Disease; Trench Fever,
ds:H00327 → Trench fever, ds:H00328 → Anthrax, ds:H00329 → Foodborne Bacillus cereus intoxication,
ds:H00330 → Methicillin-resistant Staphylococcal aureus (MRSA) infection,
ds:H00331 → Vancomycin-resistant Staphylococcal aureus (VRSA) infection,
ds:H00332 → Listeriosis,
ds:H00333 → Streptococcal infection,
ds:H00334 → Bacterial endocarditis; Infective endocarditis,
ds:H00335 → Foodborne Clostridium perfringens intoxication,
ds:H00336 → Gas gangrene; Clostridial myonecrosis,
ds:H00337 → Tetanus,
ds:H00338 → Pseudomembranous colitis,
ds:H00339 → Botulism,
ds:H00340 → Vancomycin-resistant enterococci infection,
ds:H00341 → Mycoplasma pneumonia,
ds:H00342 → Tuberculosis, ds:H00343 → Diphtheria,
ds:H00344 → Leprosy; Hansen disease,
ds:H00345 → Nocardiosis,
ds:H00346 → Extrinsic allergic alveolitis (EAA); Hypersensitivity pneumonitis,
ds:H00347 → Chlamydia infection, including the following disease: Chlamydial urethritis,
ds:H00348 → Lymphogranuloma venereum,
ds:H00349 → Trachoma,
ds:H00350 → Psittacosis; Parrot fever,
ds:H00351 → Chlamydial pneumonia,
ds:H00352 → Whipple's disease,
ds:H00353 → Borreliosis, including: Lyme disease; Neuroborreliosis; Acrodermatitis chronica atrophicans,
ds:H00354 → Syphilis, ds:H00355 → Leptospirosis,
ds:H00356 → Cryptosporidiosis,
ds:H00357 → African trypanosomiasis; Sleeping sickness,
ds:H00358 → Chagas disease; American trypanosomiasis,
ds:H00359 → Leishmaniasis,
ds:H00360 → Amoebiasis, ds:H00361 → Malaria,
ds:H00362 → Giardiasis; Lambliasis,
ds:H00363 → Candidiasis, ds:H00364 → Cryptococcosis,
ds:H00365 → Herpes simplex infection; HSV infection,
ds:H00366 → Varicella; Chickenpox; Herpes zoster; Shingles,
ds:H00367 → Infectious mononucleosis; Epstein-Barr virus (EBV) infection,
ds:H00368 → Cytomegalovirus infection; CMV infection,
ds:H00369 → Exanthema subitum; Roseolovirus infection; Roseola; Pityriasis rosea,
ds:H00370 → Progressive multifocal leukoencephalopathy (PML),
ds:H00371 → Adenovirus infection, including: Viral conjunctivitis [DS:H01320],
ds:H00372 → Smallpox; Variola,
ds:H00373 → Monkeypox, ds:H00374 → Viral wart,
ds:H00376 → Acute poliomyelitis; Polio, ds:H00377 → Rabies,
ds:H00378 → Lyssavirus infection; Rabies-related virus infection,
ds:H00379 → Mosquito-borne viral encephalitis, including: Japanese encephalitis
   [DS:H01533]; Western equine encephalitis [DS:H01534]; Eastern equine encephalitis
   [DS:H01535]; Australian encephalitis [DS:H01536]; California encephalitis [DS:H01537],
ds:H00380 → Tick-borne viral encephalitis, ds:H00381 → Dengue,
ds:H00382 → Mosquito-borne viral fevers, including: Chikungunya fever;
   O'nyong-nyong fever; Venezuelan equine fever; West Nile fever; Rift Valley fever,
ds:H00383 → Arthropod-borne viral fevers, including: Oropouche fever; Sandfly fever; Colorado tick fever,
ds:H00384 → Yellow fever,
ds:H00385 → South American (new world arenaviral) hemorrhagic fevers, including: Argentine hemorrhagic
   fever; Bolivian haemorrhagic fever; Venezuelan hemorrhagic fever; Brazilian hemorrhagic fever,
ds:H00386 → Lassa fever, ds:H00387 → B virus infection,
ds:H00388 → Non-chlamydial non-gonococcal urethritis,
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ds:H00389 → Hemorrhagic fever with renal syndrome (HFRS),
ds:H00390 → Hantavirus pulmonary syndrome (HPS),
ds:H00391 → Henipavirus infection, including: Hendra virus infection; Nipah virus infection,
ds:H00393 → Enterovirus infection, ds:H00394 → Measles,
ds:H00395 → Rubella, including: Congenital rubella syndrome,
ds:H00396 → Mumps, ds:H00397 → Ross River fever,
ds:H00398 → Influenza,
ds:H00399 → Avian influenza; Bird flu; H5N1 flu,
ds:H00400 → Parainfluenza infections,
ds:H00401 → Respiratory syncytial virus infection; RSV infection,
ds:H00402 → Severe acute respiratory syndrome; SARS,
ds:H00403 → Disorders of nucleotide excision repair, including: Xeroderma pigmentosum
   (XP); Cockayne syndrome (CS); UV-sensitive syndrome (UVS); Trichothiodystrophy
   (TTD); Cerebro-oculo-facio-skeletal syndrome (COFS); XFE progeroid syndrome,
ds:H00404 → Erythema infectiosum; Fifth disease, ds:H00405 → Marburg disease,
ds:H00406 → Acquired immunodeficiency syndrome (AIDS),
ds:H00407 → Peroxisomal beta-oxidation enzyme deficiency, including: Acyl-CoA oxidase (ACOX)
   deficiency; D-bifunctional protein (DBP) deficiency; Perrault syndrome; Sterol carrier
   protein X (SCPx) deficiency; 2-Methylacyl-CoA racemase (AMCR) deficiency; Hypercholanemia,
ds:H00408 → Type I diabetes mellitus, ds:H00409 → Type II diabetes mellitus,
ds:H00410 → Maturity onset diabetes of the young (MODY),
ds:H00411 → Hepatitis A; Hepatitis A virus (HAV) infection,
ds:H00412 → Hepatitis B; Hepatitis B virus (HBV) infection,
ds:H00413 → Hepatitis C; Hepatitis C virus (HCV) infection,
ds:H00414 → Hepatitis D; Hepatitis delta virus (HDV) infection,
ds:H00415 → Hepatitis E; Hepatitis E virus (HEV) infection,
ds:H00416 → Omsk hemorrhagic fever,
ds:H00417 → Alstrom syndrome (AS),
ds:H00418 → Bardet-Biedl syndrome (BBS),
ds:H00419 → Congenital generalized lipodystrophy (CGL),
ds:H00420 → Familial partial lipodystrophy (FPL), including the following four
   diseases: Kobberling-type lipodystrophy (FPLD1); Dunnigan-type lipodystrophy
   (FPLD2); Dunnigan-like lipodystrophy (FPLD3); AKT2 associated lipodystrophy,
ds:H00421 → Mucopolysaccharidosis (MPS), including: Hurler-Scheie syndrome (type1) [DS:H00128];
   Hunter syndrome (type2) [DS:H00129]; Sanfilippo syndrome (type3) [DS:H00130];
   Morquio syndrome (type4) [DS:H00123]; Maroteaux-Lamy syndrome (type6) [DS:H00131];
   Sly syndrome (type7) [DS:H00132]; Hyaluronidase deficiency (type9) [DS:H00133],
ds:H00422 → Glycoproteinoses, including: Sialidosis/ Mucolipidosis I [DS:H00142]; Galactosialidosis
   [DS:H00276]; alpha-Mannosidosis [DS:H00139]; beta-Mannosidosis [DS:H00140]; Aspartylglucosaminuria
   (AGU) [DS:H00145]; Fucosidosis [DS:H00141]; Schindler/ Kanzaki disease [DS:H00146],
ds:H00423 → Defects in the degradation of sulfatide, including: Metachromatic leukodystrophy
   (MLD) [DS:H00127]; Krabbe disease/ Globoid cell leukodystrophy [DS:H00135],
ds:H00424 → Defects in the degradation of sphingomyelin, including: Niemann-Pick disease
   (NPD), type A/ B [DS:H00137]; Farber lipogranulomatosis [DS:H00138],
ds:H00425 → Lysosomal cysteine protease deficiencies, including: Papillon-Lefevre
   syndrome (PLS) [DS:H00274]; Pycnodysostosis [DS:H00273],
ds:H00426 → Defects in the degradation of ganglioside, including: GM1 gangliosidosis
   [DS:H00281]; Tay-Sachs disease (GM2 gangliosidoses type 1) [DS:H00124]; Sandhoff
   disease (GM2 gangliosidoses type 2) [DS:H00124]; Gaucher disease [DS:H00126],
ds:H00427 → Relapsing fever, ds:H00428 → Distal renal tubular acidosis (RTA type 1),
ds:H00429 → Proximal renal tubular acidosis (RTA type 2),
ds:H00430 → Fibrodysplasia ossificans progressiva (FOP),
ds:H00431 → Ossification of the posterior longitudinal ligament of spine (OPLL),
ds:H00432 → Hereditary dentine disorders, including the following three
   diseases: Dentine dysplasia, type II; Dentinogenesis imperfecta, types II and III,
ds:H00433 → Holt-Oram syndrome, ds:H00434 → Camurati-Engelmann disease; Progressive diaphyseal dysplasia,
ds:H00435 → Toxoplasmosis,
ds:H00436 → Osteopetrosis, including: Osteopetrosis, severe neonatal or infantile forms; Osteopetrosis,
   intermediate forms; Osteopetrosis with renal tubular acidosis; Osteopetrosis, late-onset
   form type 1; Osteopetrosis, late-onset form type 2; Osteopetrosis, osteoclast poor,
ds:H00437 → Paget's disease of bone and related disorders, including: ; Paget's disease of
   bone (PDB); Familial expansile osteolysis (FEO); Early-onset Paget's disease of bone
   (PDB2); Expansile skeletal hyperphosphatasia (ESH); Juvenile Paget's disease (JPD),
ds:H00438 → Polycystic lipomembranous osteodysplasia with sclerosing leukoencephalopathy
   (PLOSL); Nasu-Hakola disease, ds:H00439 → Shwachman-Diamond syndrome (SDS),
ds:H00440 → Rett syndrome, ds:H00441 → Progressive osseous heteroplasia (POH),
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ds:H00442 → Campomelic dysplasia (CD),
ds:H00443 → Osteoglophonic dysplasia (OD); Osteoglophonic dwarfism (OGD),
ds:H00444 → Osteopathia striata with cranial sclerosis,
ds:H00445 → Osteoarthritis with mild chondrodysplasia,
ds:H00446 → Craniofacial-deafness-hand syndrome,
ds:H00447 → HEM skeletal dysplasia; Greenberg dysplasia,
ds:H00448 → Familial osteochondritis dissecans; Osteochondritis dissecans, short
   stature, and early-onset osteoarthritis, ds:H00449 → Oculodentodigital dysplasia,
ds:H00450 → Sclerosing bone dysplasias, including: Endosteal hyperostosis; Van Buchem
   disease, type 2; Osteopetrosis, autosomal dominant 1 (OPTA1),
ds:H00451 → Osteoporosis-pseudoglioma syndrome (OPPG), ds:H00452 → Disorders caused by loss-of-function
   of LEMD3, including: Osteopoikilosis; Buschke-Ollendorff syndrome (BOS); Melorheostosis,
ds:H00453 → Contiguous gene deletion syndrome involving EYA1, including: Oto-facio-cervical
   syndrome (OFC); Branchiootic syndrome 1 (BOS1); Branchio-oto-renal syndrome (BOR),
ds:H00454 → Oral-facial-digital syndrome, ds:H00455 → Spinal muscular atrophy (SMA), including: SMA type
   I (SMA1) / Werdning-Hoffman disease; SMA type II (SMA2); SMA type III (SMA3) / Kugeleberg-Welander
   disease; SMA type IV (SMA4); X-linked SMA (SMAX); Distal SMA autosomal recessive (DSMA);
   Congenital distal spinal muscular atrophy (SMAL); SMA proximal adult autosomal dominant (SMAPAD),
ds:H00456 → Fronto-Otopalatodigital Osteodysplasia, including: Otopalatodigital syndrome, type
   I; Otopalatodigital syndrome, type II; Melnick-Needles syndrome; Frontometaphyseal dysplasia,
ds:H00457 → Primary hypertrophic osteoarthropathy (PHO), ds:H00458 →
 Craniosynostosis, including: Pfeiffer syndrome; Apert syndrome; Crouzon syndrome;
   Jackson-Weiss syndrome; Beare-Stevenson syndrome; Muenke craniosynostosis;
   Saethre-Chotzen syndrome; Craniosynostosis Boston type; Antley-Bixler syndrome;
   Carpenter syndrome; Craniofrontonasal dysplasia; Noonan syndrome; Baller-Gerold syndrome,
ds:H00459 → Synpolydactyly, ds:H00460 → Hand-foot-genital syndrome,
ds:H00461 → FLNB-related disorders, including: ; Atelostogenesis,
   type I; Boomerang dysplasia; Atelosteogenesis, type III; Larsen syndrome,
ds:H00462 → Stuve-Wiedemann syndrome, ds:H00463 → Currarino syndrome,
ds:H00464 → Patella dysplasias, including: Small patella syndrome
   (SPS); Nail-patella syndrome; Ear-patella-short statute syndrome, ds:H00465 →
 Fragile X Syndrome, including: Fragile X Syndrome (FXS); Fragile X tremor/ataxia syndrome (FXTAS),
ds:H00466 → Grebe dysplasia; Acromesomelic dysplasia Hunter-Thompson type,
ds:H00467 → Fibular hypoplasia and complex brachydactyly; Du Pan syndrome,
ds:H00468 → Acromesomelic dysplasia with genital anomalies,
ds:H00469 → Mitochondrial DNA depletion syndrome (MDS),
ds:H00470 → Acromesomelic dysplasia, Maroteaux type,
ds:H00471 → Split-hand/foot malformation (SHFM),
ds:H00472 → Torg-Winchester syndrome,
ds:H00473 → Mitochondrial respiratory chain deficiencies (MRCD), including: Mitochondrial
   complex I deficiency (MT-C1D); Complex II deficiency (MT-C2D); Complex III deficiency
   (MT-C3D); Leigh syndrome (LS) [DS:H01354]; Leber Hereditary Optic Neuropathy
   (LHON) [DS:H00068]; Leber Optic Atrophy and Dystonia (LDYT) [DS:H01365]; MELAS
   Syndrome [DS:H01347]; Kearns-Sayre Syndrome (KSS) [DS:H01355]; GRACILE Syndrome,
ds:H00474 → Schneckenbecken dysplasia, ds:H00475 → Enlarged parietal foramina/cranium bifidum,
ds:H00476 → Multiple epiphyseal dysplasia (MED),
ds:H00477 → Pseudoachondroplasia (PSACH), ds:H00478 →
 Prader-Willi and Angelman syndromes, including: Angelman syndrome (AS); Prader-Willi syndrome (PWS),
ds:H00479 → Metaphyseal dysplasias, including: Metaphyseal dysplasia, Schmid type;
   Metaphyseal dysplasia, McKusik type; Metaphyseal dysplasia, Jansen type;
   Shwachman-Bodian-Diamond syndrome (SBDS); Metaphyseal anadysplasia (MAD),
ds:H00480 → Non-syndromic X-linked mental retardation, ds:H00481 → Cone-rod dystrophy and cone dystrophy,
   including: Cone-rod dystrophy (CORD); Cone dystrophy (COD); Retinal cone dystrophy (RCD),
ds:H00482 → Brachydactyly, including: type A; type B; type D; type E, ds:H00483 →
 Brachydactyly, including: Brachydactyly type C; Angel shaped phalangoepiphyseal dysplasia (ASPED),
ds:H00484 → Other brachydactylies, including: Proximal symphalangism; Multiple synostosis syndrome,
ds:H00485 → Robinow syndrome,
ds:H00486 → SOST related disorders, including: Sclerosteosis ; Endosteal hyperostosis, van Buchem type,
ds:H00487 → Trichodentoosseous dysplasia,
ds:H00490 → Diaphyseal dysplasia with anemia (Ghosal),
ds:H00491 → Craniometaphyseal dysplasia,
ds:H00492 → SHOX-related haploinsufficiency disorders,
   including: Isolated short stature; Langer syndrome; Leri-Weill syndrome,
ds:H00493 → Heparan sulfate proteoglycan gene defects, including: Dyssegmental
   dysplasia, Silverman-Handmaker type; Schwartz-Jampel syndrome;
   Simpson-Golabi-Behmel syndrome, type 1; Omodysplasia 1; Multiple exostoses,
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ds:H00494 → Desbuquois syndrome; Desbuquois dysplasia (DBQD), ds:H00495 → Eiken dysplasia,
ds:H00496 → Congenital hemidysplasia with ichthyosiform nevus and limb defects (CHILD),
ds:H00497 → Cherubism,
ds:H00498 → Gnathodiaphyseal dysplasia,
ds:H00499 → Spondylocarpotarsal synostosis syndrome,
ds:H00500 → Keutel syndrome,
ds:H00501 → Fibrous dysplasia, polyostotic; Albright hereditary osteodystrophy,
ds:H00502 → Pallister-Hall syndrome,
ds:H00503 → EVC-related disorders, including: Ellis-van Creveld syndrome; Weyers acrodental dysostosis,
ds:H00504 → Rubinstein-Taybi syndrome,
ds:H00505 → FGFR3-related short limb skeletal dysplasias, including: Achondroplasia; Hypochondroplasia; Thanatophoric dysplasia, type 1; Thanatophoric dysplasia, type 2; Severe achondroplasia with developmental delay and acanthosis nigricans (SADDAN), ds:H00506 → Osteogenesis imperfecta,
ds:H00507 → Dyskeratosis congenita (DC), including: X-linked dyskeratosis congenita (DKCX); Autosomal dominant dyskeratosis congenita (DKCA1); Autosomal recessive dyskeratosis congenita (DKCB1),
ds:H00508 → Blomstrand syndrome; Blomstrand chondrodysplasia, ds:H00509 → 3M syndrome,
ds:H00510 → Feingold syndrome,
ds:H00511 → Short rib-polydactyly syndrome,
ds:H00512 → Permanent neonatal diabetes mellitus (PNDM),
ds:H00513 → Transient neonatal diabetes mellitus (TNDM),
ds:H00514 → Bruck syndrome,
ds:H00515 → The DTDST-related disorders, including: Achondrogenesis IB (ACG IB); Atelosteogenesis II (AO II); Diastrophic dysplasia (DTD),
ds:H00516 → Isolated orofacial clefts, including: Cleft lip with or without cleft palate; Cleft palate,
ds:H00517 → Spondylocostal dysostosis (SCD),
ds:H00518 → RMRP related disorders, including: Anauxetic dysplasia (AD); Cartilage-hair hypoplasia (CHH); Metaphyseal dysplasia without hypotrichosis (MDWH),
ds:H00519 → Type XI collagenopathies, including: Stickler syndrome type 2; Stickler syndrome type 3; Otospondylomegaepiphyseal dysplasia (OSMED); Marshall syndrome; Weissenbacher-Zweymuller syndrome,
ds:H00520 → Type II collagenopathies, including: Achondrogenesis II; Hypochondrogenesis; SED congenita; SMED Strudwick type; Kniest dysplasia; Spondyloperipheral dysplasia; Osteoarthritis with mild chondrodysplasia; Stickler syndrome 1; Platyspondylic skeletal dysplasia, Torrance type; Epiphyseal dysplasia, multiple, with myopia and deafness; Czech dysplasia,
ds:H00521 → Cleidocranial dysplasia, ds:H00522 → TRPV4-related skeletal dysplasias, including: Autosomal dominant brachyolmia; Spondylometaphyseal dysplasia, Kozlowski type (SMDK); Metatropic dysplasia; Spondyloepiphyseal dysplasia, Maroteaux type ; Parastremmatic dysplasia,
ds:H00523 → Noonan syndrome and related disorders, including: Noonan syndrome (NS); Leopard syndrome (LS); Noonan syndrome-like with loose anagen hair (NS/LAH); CBL-mutation associated syndrome (CBL); Neurofibromatosis type 1 (NF1); Neurofibromatosis type 2 (NF2); Neurofibromatosis-Noonan syndrome (NFNS); Legius syndrome; Cardiofaciocutaneous syndrome (CFCS); Costello syndrome (CS); Watson syndrome,
ds:H00524 → TRPV4-related peripheral neuropathies, including: Congenital distal spinal muscular atrophy (CDSMA); Scapuloperoneal spinal muscle atrophy (SPSMA); Hereditary motor and sensory neuropathy type IIC (HMSN IIC),
ds:H00525 → Disorders of fatty-acid oxidation, including: Medium-chain (MC) acyl-CoA dehydrogenase (AD) deficiency (MCADD); Short-chain AD deficiency (SCADD) ; Short-branched-chain AD deficiency (SBCADD) ; Very long-chain AD deficiency (VLCADD) ; Long-chain 3-hydroxyacyl CoA dehydrogenase deficiency (LCHADD) ; Trifunctional protein deficiency (TFP); Carnitine palmitoyltransferase deficiency (CPT); Carnitine-acylcarnitine translocase deficiency (CACT); Systemic primary carnitine deficiency (CDSP),
ds:H00526 → Camptodactyly-arthropathy-coxa vara-pericarditis syndrome; Jacobs syndrome,
ds:H00527 → Retinitis pigmentosa (RP),
ds:H00528 → Frontonasal dysplasia,
ds:H00529 → Cranioectodermal dysplasia,
ds:H00530 → Joubert syndrome,
ds:H00531 → Venous malformations, including: Sporadic venous malformation; Cutaneomucosal venous malformation; Glomuvenous malformation,
ds:H00532 → RASA1-related disorders, including: Parkes-Weber slndrome; Capillary malformation-arteriovenous malformation (CM-AVM); Arteriovenous fistula (AVF),
ds:H00533 → Hereditary hemorrhagic telangiectasia (HHT), ds:H00534 → Cerebral cavernous malformation,
ds:H00535 → Lymphedemas, including: Lymphedema, hereditary I; Lymphedema-distichiasis syndrome (LD); Hypotrichosis-lymphedema-telangiectasia syndrome (HLTS); Hennekam lymphangiectasia-lymphedema syndrome (HLLS), ds:H00536 → Cerebral autosomal dominant arteriopathy with subcortical infarcts and leucoencephalopathy (CADASIL),
ds:H00537 → Nephronophthisis-medullary cystic kidney disease, including: Nephronophthisis (NPH) ; Nephronophthisis-like nephropathy 1; Medullary cystic kidney disease

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    1; Medullary cystic kidney disease 2 (MSKD2), ds:H00538 → Senior-Loken syndrome,
ds:H00539 → PTEN hamartoma tumor syndrome (PHTS), including: Cowden syndrome;
    Bannayan-Riley-Ruvalcaba syndrome; Proteus syndrome; Proteus-like syndrome,
ds:H00540 → Osteoporosis, lymphedema, anhydrotic ectodermal dysplasia with immunodeficiency
    (OLEDAID); Ectodermal dysplasia, anhidrotic, with immunodeficiency, osteopetrosis, and lymphedema,
ds:H00541 → Uromodulin-associated kidney diseases, including: Medullary cystic kidney disease
    2; Familial juvenile hyperuremic nephropathy (HNFJ); Glomerulocystic kidney disease,
ds:H00542 → Polycystic kidney disease, ds:H00543 → Renal-hepatic-pancreatic dysplasia,
ds:H00544 → Septo-optic dysplasia,
ds:H00545 → Polycystic liver disease,
ds:H00546 → Atrial septal defect,
ds:H00547 → Atrioventricular septal defect; Atrioventricular canal defect,
ds:H00548 → Brunner syndrome; MAOA deficiency,
ds:H00549 → Tetralogy of Fallot,
ds:H00550 → Transposition of great arteries,
ds:H00551 → Alagille syndrome,
ds:H00552 → Glycerol kinase deficiency (GKD), including: Hyperglycerolemia; Chromosome Xp21
    deletion syndrome; X-linked Addison disease (AHX); Duchenne muscular dystrophy (DMD),
ds:H00553 → Congenital supravalvar aortic stenosis, ds:H00554 → Bicuspid aortic valve,
ds:H00555 → Char syndrome,
ds:H00556 → CHARGE syndrome,
ds:H00557 → Cutis laxa, including: Autosomal dominant cutis laxa (ADCL); Autosomal recessive
    cutis laxa I (ARCL1); Autosomal recessive cutis laxa II (ARCL2); Autosomal recessive
    cutis laxa III (ARCL3); X-linked recessive cutis laxa (XRCL); Wrinkly skin syndrome,
ds:H00558 → Geroderma osteodysplasticum, ds:H00559 → von Hippel-Lindau syndrome,
ds:H00560 → Pseudoxanthoma elasticum, including: Pseudoxanthoma elasticum (PXE);
    Pseudoxanthoma elasticum-like disorder with multiple coagulation factor deficiency,
ds:H00561 → Brachydacytly-mental retardation syndrome and Smith-Magenis syndrome,
ds:H00562 → Dystrophinopathies, including: Duchenne muscular dystrophy (DMD); Becker muscular dystrophy
    (BMD); X-linked dilated cardiomyopathy (XLCM), ds:H00563 → Emery-Dreifuss muscular dystrophy,
ds:H00564 → Primary ciliary dyskinesia, including: Primary ciliary dyskinesia; Kartagener syndrome,
ds:H00565 → Sarcoglycanopathies, including: Limb-girdle muscular
    dystrophy (LGMD) 2C; Limb-girdle muscular dystrophy (LGMD) 2D; Limb-girdle
    muscular dystrophy (LGMD) 2E; Limb-girdle muscular dystrophy (LGMD) 2F,
ds:H00566 → Dysferlinopathies, including: Miyoshi myopathy (MM); Limb-girdle muscular
    dystrophy (LGMD) 2B; Distal myopathy with anterior tibial onset (DMAT),
ds:H00567 → Caveolinopathies, including: Limb-girdle muscular dystrophy (LGMD) 1C;
    Rippling muscle disease (RMD); Idiopathic hyperCKemia; Distal
    myopathy with decreased caveolin 3; Hypertrophic cardiomyopathy (HCM),
ds:H00568 → Myotonic dystrophy (DM), ds:H00569 → Aarskog-Scott syndrome; Faciogenital dysplasia,
ds:H00570 → Kabuki syndrome,
ds:H00571 → Johanson-Blizzard syndrome,
ds:H00572 → ESCO2-related disorders, including: Roberts syndrome; SC phocomelia syndrome,
ds:H00573 → Townes-Brocks syndrome,
ds:H00574 → Coffin-Lowry syndrome (CLS),
ds:H00575 → Renal tubular dysgenesis,
ds:H00576 → Pierson syndrome,
ds:H00577 → Syndromic X-linked mental retardation with epilepsy or seizures, including: West
    syndrome (WS); Partington syndrome (PRTS); Proud syndrome (ACCAG); XMRE; MRXHF1; XMR
    OPHN1-related (MRXSO) ; XELBD; XMR, Christianson type (MRXSC); Creatine deficiency
    syndrome (XL-CDS); Renpenning syndrome (RENS1); Epilepsy and mental retardation limited
    to females (EFMR); Periventricular nodular heterotopia (PVNH); Hydrocephalus (XLH);
    XMR, JARID1C related (MRXSJ); BFLS; CK syndrome (CKS); MICPCH; Rolandic epilepsy,
ds:H00578 → MYH9-related kidney diseases, including: Epstein syndrome; Fechtner syndrome,
ds:H00579 → Hereditary angiopathy with nephropathy, aneurysms, and muscle cramps (HANAC),
ds:H00580 → Schimke immunoosseous dysplasia,
ds:H00581 → Alport syndrome,
ds:H00582 → Benign familial hematuria; Thin basement membrane nephropathy,
ds:H00583 → Opitz-GBBB syndrome,
ds:H00584 → Epidermolysis bullosa simplex, including: Epidermolysis bullosa simplex, Dowling-Meara
    type (EBS-DM); Epidermolysis bullosa simplex, Koebner type (EBS-K); Epidermolysis
    bullosa simplex, Weber-Cockayne type (EBS-WC); Epidermolysis bullosa simplex with mottled
    pigmentation (EBS-MP); Epidermolysis bullosa simplex with migratory circinate erythema;
    Epidermolysis bullosa simplex, recessive; Epidermolysis bullosa, lethal acantholytic,
ds:H00585 → Epidermolysis bullosa, hemidesmosomal, including: Epidermolysis bullosa, generalized atrophic
    benign (GABEB); Epidermolysis bullosa simplex with pyloric atresia (EBS-PA); Epidermolysis bullosa
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    simplex with muscular dystrophy (EBS-MD); Epidermolysis bullosa simplex, Ogna type (EBS-Ogna),
ds:H00586 → Epidermolysis bullosa, junctional, including: Epidermolysis bullosa, junctional,
    Herlitz type (JEB-H); Epidermolysis bullosa, junctional, non-Herlitz type (JEB-nH);
    Epidermolysis bullosa, junctional, with pyloric atresia (JEB-PA), ds:H00587 →
 Epidermolysis bullosa, dysprophica, including: ; Epidermolysis bullosa dystrophica, AD; Epidermolysis
    bullosa dystrophica, AR; Epidermolysis bullosa pruriginosa; Epidermolysis bullosa, pretibial,
ds:H00588 → Kindler syndrome, ds:H00589 → Familial exudative vitreoretinopathy (FEVR), including:
    Exudative vitreoretinopathy 1 (EVR1); Exudative vitreoretinopathy2, X-linked  (EVR2); Exudative
    vitreoretinopathy 4 (EVR4); Exudative vitreoretinopathy 5 (EVR5); Norrie disease (ND),
ds:H00590 → Congenital muscular dystrophies (CMD/MDC), including: Merosin-deficient CMD
    (MDC1A); Ullrich CMD (UCMD); Integrin alpha7-deficient CMD; CMD with joint hyperlaxity
    (CMDH); CMD with epidermolysis bullosa; Walker-Warburg syndrome (WWS); Muscle-eye-brain
    disease (MEB); Fukuyama CMD (FCMD); CMD with muscle hypertrophy (MDC1C); CMD with
    severe intellectual impairment and abnormal glycosylation (MDC1D); Rigid spine syndrome
    (RSS); LMNA-deficient CMD; CMD with respiratory failure and muscle hypertrophy (MDC1B),
ds:H00591 → Facioscapulohumeral muscular dystrophy (FSHD),
ds:H00592 → Calpainopathy; Limb-girdle muscular dystrophy 2A (LGMD2A),
ds:H00593 → Limb-girdle muscular dystrophy (LGMD),
ds:H00594 →
 Distal muscular dystrophies, including: Welander distal myopathy (WDM); Tibial muscular dystrophy
    (TMD); Nonaka distal myopathy with rimmed vacuoles (DMRV); Miyoshi myopathy (MM); Laing myopathy
    (MPD1); Distal nebulin myopathy (DNM); Distal desminopathy (MFM1); alpha-B Crystallinopathy
    (MFM2); Distal myotilinopathy (MFM3); Distal zaspopathy (MFM4); Distal myopathy 3 (MPD2, VCPDM),
ds:H00595 → Myofibrillar myopathies (MFM), including: Desminopathy (MFM1); alpha-B Crystallinopathy
    (MFM2); Myotilinopathy (MFM3); Zaspopathy (MFM4); Filaminopathy (MFM5); Bag3opathy,
ds:H00596 → Nonaka distal myopathy (NM); Distal myopathy with rimmed vacuoles (DMRV);
    Hereditary inclusion body myopathy (hIBM), ds:H00597 → Snyder-Robinson syndrome,
ds:H00598 → 46,XX disorders of sex development (Disorders of gonadal development),
    including: Ovotesticular DSD; Testicular DSD; Ovarian dysgenesis,
ds:H00599 → 46,XX disorders of sex development (Disorders related to androgen excess),
    including: Congenital adrenal hyperplasias; Glucocorticoid resistance; Aromatase deficiency,
ds:H00600 → 46,XX disorders of sex development (Other), including: Mullerian aplasia
    and hyperandrogenism; McKusick-Kaufman syndrome, ds:H00601 →
 Hutchinson-Gilford progeria syndrome, ds:H00602 → Glucocorticoid-remediable aldosteronism (GRA),
ds:H00603 → Hypertension exacerbated in pregnancy,
ds:H00604 → Deafness, autosomal dominant,
ds:H00605 → Deafness, autosomal recessive,
ds:H00606 → Early infantile epileptic encephalopathy; Ohtahara syndrome,
ds:H00607 → 46,XY disorders of sex development (Disorders of gonadal development), including: Gonadal
    agenesis; Complete and partial gonadal dysgenesis; Testis regression; Ovotesticular DSD,
ds:H00608 → 46,XY disorders of sex development (Disorders in androgen synthesis or action), including:
    Congenital adrenal hyperplasias; Leydig cell hypoplasia; Androgen insensitivity syndrome (AIS),
ds:H00609 → 46,XY disorders of sex development (Other), including: Persistent Mullerian duct
    syndrome; Hypospadias; Cryptorchidism, ds:H00610 → Treacher Collins syndrome, ds:H00611 →
 IRF6-related disorders, including: Popliteal pterygium syndrome (PPS); Van der Woude syndrome (VWS),
ds:H00612 → Primary open angle glaucoma,
ds:H00613 → Infantile cortical hyperostosis; Caffey disease,
ds:H00614 → Infantile systemic hyalinosis and juvenile hyaline fibromatosis,
ds:H00615 → Amelogenesis imperfecta,
ds:H00616 → Bowen-Conradi syndrome (BCS),
ds:H00617 → Desmosterolosis,
ds:H00618 → Amelogenesis imperfecta hypoplastic-hypomaturation with taurodontism (AIHHT),
ds:H00619 → Kenny-Caffey syndrome,
ds:H00620 → Axenfeld-Rieger syndrome (ARS),
ds:H00621 → Alopecia neurologic defects and endocrinopathy syndrome (ANE syndrome),
ds:H00622 → Hypoparathyroidism-retardation-dysmorphism syndrome; Sanjad-Sakati syndrome,
ds:H00623 → Hajdu-Cheney syndrome,
ds:H00624 → Familial cholestasis, including: Progressive familial intrahepatic cholestasis (PFIC); Benign
    recurrent intrahepatic cholestasis (BRIC); Intrahepatic cholestasis of pregnancy (ICP);
    North American Indian childhood cirrhosis (NAIC), ds:H00625 → Tooth agenesis; Hypodontia,
ds:H00626 → Nephrotic syndrome and focal segmental glomerulosclerosis,
ds:H00627 → Premature ovarian failure,
ds:H00628 → Congenital bile acid synthesis defect (CBAS), including: 3-beta-hydroxy-delta-5-C27-steroid
    oxidoreductase deficiency (CBAS1); Delta(4)-3-oxosteroid 5-beta-reductase deficiency (CBAS2);
    Oxysterol 7-alpha-hydroxylase deficiency (CBAS3); Alpha-methylacyl-CoA racemase deficiency (CBAS4),
ds:H00629 → Acheiropodia, ds:H00630 → Rheumatoid arthritis,
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ds:H00631 → Cornelia de Lange syndrome (CdLS),
ds:H00632 → Heterotaxy; Situs ambiguus,
ds:H00633 → Duane retraction syndrome,
ds:H00634 → Duane-radial ray syndrome and IVIC syndrome; Okihiro syndrome,
ds:H00635 → Aniridia,
ds:H00636 → Tetra-amelia,
ds:H00637 → Ulnar-mammary syndrome; Schinzel syndrome,
ds:H00638 → Ectrodactyly-ectodermal dysplasia cleft-palate syndrome (EEC syndrome),
ds:H00639 → Ectodermal dysplasia, ectrodactyly, and macular dystrophy (EEM syndrome),
ds:H00640 → Limb-mammary syndrome,
ds:H00641 → ADULT syndrome,
ds:H00642 → Lacrimo-auriculo-dento-digital syndrome (LADD); Levy-Hollister syndrome,
ds:H00643 → Tooth and nail syndrome; Witkop syndrome,
ds:H00644 → Ectodermal dysplasia/skin fragility syndrome,
ds:H00645 → Incontinentia pigmenti,
ds:H00646 → Odontoonychodermal dysplasia,
ds:H00647 → Ectodermal dysplasia-syndactyly syndrome (EDSS),
ds:H00648 → Ectodermal dysplasia, hidrotic; Clouston syndrome,
ds:H00649 → Ectodermal dysplasia, pure hair-nail type (HNED),
ds:H00650 → Allan-Herndon-Dudley syndrome; Monocarboxylate transporter 8 deficiency,
ds:H00651 →
 Ectodermal dysplasia, including: Ectodermal dysplasia, anhidrotic; Ectodermal dysplasia, hypohidrotic,
ds:H00652 → Solitary median maxillary central incisor syndrome,
ds:H00653 → Marfan syndrome, including: Marfan syndrome
   (MFS); Neonatal MFS; Atypically severe MFS; New variant of MFS,
ds:H00654 → Barth syndrome (BTHS), ds:H00655 → McLeod syndrome,
ds:H00656 → Scapuloperoneal myopathy (SPM),
ds:H00657 → Reducing body myopathy (RBM),
ds:H00658 → Syndromic X-linked mental retardation, including: Turner type (MRXST); Siderius type (MRXSSD)
   ; Cabezas type (MRXC); Raymond type (MRXSR); Type10 (MRXS10); Type14 (MRXS14); Mental retardation
   with isolated growth hormone deficiency (MRGH), ds:H00659 → Shprintzen-Goldberg syndrome,
ds:H00660 → Congenital contractural arachnodactyly (CCA); Beals syndrome,
ds:H00661 → MASS phenotype,
ds:H00662 → Ectopia lentis,
ds:H00663 → Restrictive dermopathy,
ds:H00664 → Anemia due to disorders of glycolytic enzymes, including: Hexokinase (HK) deficiency;
   Phosphoglycerate kinase 1 (PGK1) deficiency; Triose-phosphate isomerase (TPI) deficiency;
   Glucose phosphate isomerase (GPI) deficiency; Bisphosphoglycerate mutase (BPGM) deficiency,
ds:H00665 → Mandibuloacral dysplasia, ds:H00666 → Peutz-Jeghers syndrome,
ds:H00667 → Woolly hair, including: Autosomal-dominant woolly hair (ADWH); Autosomal-recessive
   woolly hair (ARWH); Autosomal-recessive woolly hair with or without hypotrichosis,
ds:H00668 → Anemia due to disorders of glutathione metabolism, including: Glucose-6-phosphate
   dehydrogenase deficiency [DS:H01375]; Glutathione peroxidase deficiency;
   Gamma-glutamylcysteine synthetase deficiency; Glutathione synthetase deficiency,
ds:H00669 → Naxos disease and Carvajal syndrome, ds:H00670 → Monilethrix,
ds:H00671 → Netherton syndrome,
ds:H00672 → Pseudofolliculitis barbae,
ds:H00673 →
 Weill-Marchesani syndrome, including: Weill-Marchesani syndrome; Weill-Marchesani-like syndrome,
ds:H00674 → Anemia due to disorders of nucleotide metabolism, including: Adenylate
   kinase (AK) deficiency; Uridine 5-prime monophosphate hydrolase (UMPH1) deficiency,
ds:H00675 → Acrocapitofemoral dysplasia, ds:H00676 → Congenital primary aphakia,
ds:H00677 → Aplasia of lacrimal and salivary glands,
ds:H00678 → Achondrogenesis type IA,
ds:H00679 → Hypomyelinating leukodystrophy (HLD); Pelizaeus-Merzbacher disease (PMD),
ds:H00680 → Primary failure of tooth eruption,
ds:H00681 → Acne inversa; Hidradenitis suppurativa,
ds:H00682 → Woodhouse-Sakati syndrome; Hypogonadism, alopecia,
   diabetes mellitus, mental retardation, and extrapyramidal syndrome,
ds:H00683 → Anonychia congenita, ds:H00684 → Pachyonychia congenita, including:
   Jadassohn-Lewandowsky syndrome; Jackson-Lawler syndrome ; Steatocystoma multiplex,
ds:H00685 → Bifid nose with or without anorectal and renal anomalies; BNAR syndrome,
ds:H00686 → Manitoba oculotrichoanal syndrome,
ds:H00687 → Fraser syndrome,
ds:H00688 → Familial advanced sleep phase syndrome,
ds:H00689 → Delayed sleep phase syndrome,
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ds:H00690 → Aland Island eye disease; Forsius-Eriksson syndrome,
ds:H00691 → Bullous congenital ichthyosiform erythroderma (BCIE); Epidermolytic hyperkeratosis (EHK),
ds:H00692 → Lowe syndrome; Oculocerebrorenal Dystrophy (OCRL),
ds:H00693 → Ichthyosis bullosa of Siemens,
ds:H00694 → Dent disease, including: Dent disease 1; Dent
disease 2; X-linked recessive nephrolithiasis ; Hypophosphatemic rickets;
Low-molecular-weight proteinuria with hypercalciuria and nephrocalcinosis,
ds:H00695 → Mal de Meleda; Meleda disease, ds:H00696 → Haim-Munk syndrome; Prepubertal periodontitis (PPP),
ds:H00697 → X-linked myopathy with postural muscle atrophy (XMPMA),
ds:H00698 → Nemaline myopathy,
ds:H00699 → Central core disease,
ds:H00700 → Centronuclear myopathy,
ds:H00701 → Congenital fiber type disproportion (CFTD),
ds:H00702 → Cap myopathy,
ds:H00703 → Myosin storage myopathy (MSM); Hyaline body myopathy,
ds:H00704 → Oculopharyngeal muscular dystrophy (OPMD),
ds:H00705 →
Myotonia congenita, including: Autosomal dominant myotonia congenita (Thomsen disease); Autosomal
recessive myotonia congenita (Becker disease); Fluctuating myotonia congenita; Myotonia levoir,
ds:H00706 → Bart-Pumphrey syndrome, ds:H00707 → Ichthyosis hystrix, Curth-Macklin type,
ds:H00708 → Naegeli-Franceschetti-Jadassohn syndrome,
ds:H00709 → Birk Barel mental retardation syndrome (BBMRS); Birk-Barel syndrome (BIBAS),
ds:H00710 → Erythrokeratodermia variabilis,
ds:H00711 → Russell-Silver syndrome; Silver-Russell syndrome,
ds:H00712 → Keratitis-ichthyosis-deafness syndrome; KID/HID syndrome,
ds:H00713 → Beckwith-Wiedemann syndrome,
ds:H00714 → Vohwinkel syndrome, including: Vohwinkel syndrome (VS); Vohwinkel syndrome with ichthyosis,
ds:H00715 → Darier disease; Dyskeratosis follicularis,
ds:H00716 → Palmoplantar keratoderma with deafness,
ds:H00717 → Striate palmoplantar keratoderma,
ds:H00718 → Sotos syndrome and Weaver syndrome,
ds:H00719 → Leprechaunism; Donohue syndrome,
ds:H00720 → Long QT syndrome, including: Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome (JLNS),
ds:H00721 → Pyogenic bacterial infections, recurrent, due to MYD88 deficiency,
ds:H00722 → Epidermolytic palmoplantar keratoderma (EPPK),
ds:H00723 → Non-epidermolytic palmoplantar keratoderma (NEPPK),
ds:H00724 → White sponge nevus,
ds:H00725 → Short QT syndrome,
ds:H00726 → Meesmann corneal dystrophy,
ds:H00727 → Bosley-Salih-Alorainy syndrome and Athabascan brainstem dysgenesis syndrome,
ds:H00728 → Brugada syndrome (BRS),
ds:H00729 → Sick sinus syndrome (SSS); Sinus node dysfunction,
ds:H00730 → Familial idiopathic ventricular fibrillation,
ds:H00731 → Atrial fibrillation,
ds:H00732 → Sorsby fundus dystrophy,
ds:H00733 → Harlequin ichthyosis,
ds:H00734 → Lamellar ichthyosis (LI) and Non-bullous congenital ichthyosiform erythroderma (NBCIE),
ds:H00735 → Ichthyosis vulgaris,
ds:H00736 → Dorfman-Chanarin syndrome; Chanarin-Dorfman syndrome,
ds:H00737 → Acral peeling skin syndrome,
ds:H00738 →
Ichthyosis with confetti; Congenital reticular ichthyosiform erythroderma; Ichthyosis variegata,
ds:H00739 → Ichthyosis with hypotrichosis,
ds:H00740 → Ichthyosis follicularis, alopecia, and photophobia syndrome,
ds:H00741 → Ichthyosis prematurity syndrome,
ds:H00742 → Neonatal ichthyosis-sclerosing cholangitis (NISCH) syndrome;
Ichthyosis, leukocyte vacuoles, alopecia, and sclerosing cholangitis (ILVASC),
ds:H00743 → Paramyotonia congenita (PMC), ds:H00744 → Potassium-aggravated myotonias (PAMs),
including: Myotonia fluctuans; Myotonia permanens; Acetazolamide responsive myotonia,
ds:H00745 → Hyperkalemic periodic paralysis (HyperPP), ds:H00746 → Hypokalemic periodic paralysis (HypoPP),
ds:H00747 → Thyrotoxic hypokalemic periodic paralysis (TPP),
ds:H00748 → Andersen-Tawil syndrome (ATS),
ds:H00749 → Episodic ataxias,
ds:H00750 → Keratosis follicularis spinulosa decalvans,
ds:H00751 → Asphyxiating thoracic dystrophy; Jeune syndrome,
ds:H00752 → Ankyloblepharon-ctodermal defects-cleft lip/palate (AEC) syndrome and Rapp-Hodgkin syndrome,

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ds:H00753 → Urofacial syndrome,
ds:H00754 → 3-Methylglutaconic aciduria (MGCA),
ds:H00755 → Acrokeratosis verruciformis,
ds:H00756 → Pitt-Hopkins syndrome, including: Pitt-Hopkins syndrome; Pitt-Hopkins-like syndrome,
ds:H00757 → Dyggve-Melchior-Clausen disease and Smith-McCort dysplasia,
ds:H00758 → Progressive pseudorheumatoid dysplasia (PPRD);
   Spondyloepiphyseal dysplasia tarda with progressive arthropathy (SEDT-PA),
ds:H00759 → Waardenburg syndrome (WS), ds:H00760 → Spondyloepiphyseal dysplasia tarda,
ds:H00761 → SEMD, Pakistani type,
ds:H00762 → SEMD, Omani type; Spondyloepiphyseal dysplasia with congenital joint dislocations,
ds:H00763 → Transient bullous dermolysis of the newborn,
ds:H00764 → Cri du chat syndrome; Cat cry syndrome; Chromosme 5p deletion syndrome,
ds:H00765 → Spondyloepiphyseal dysplasia, Kimberley type; Spondyloepimetaphyseal dysplasia, aggrecan type,
ds:H00766 → Wolcott-Rallison syndrome; SED, Wolcott-Rallison type,
ds:H00767 → SEMD, Matrilin type; Spondyloepimetaphyseal dysplasia,
ds:H00768 → Nonsyndromic autosomal recessive mental retardation (NS-ARMR),
ds:H00769 → Hyperekplexia,
ds:H00770 → Congenital myasthenic syndrome,
ds:H00771 → Inherited erythromelalgia (IEM); Primary erythromelalgia,
ds:H00772 → Paroxysmal extreme pain disorder (PEPD),
ds:H00773 → Autosomal dominant mental retardation,
ds:H00774 → Nav1.7-associated congenital insensitivity to pain (CIP),
ds:H00775 → Familial or sporadic hemiplegic migraine,
ds:H00776 → Congenital motor nystagmus (CMN); Idiopathic congenital nystagmus (ICN),
ds:H00777 → Spondylometaepiphyseal dysplasia, short limb-hand type;
   Spondylometaepiphyseal dysplasia, short limb-abnormal calcification type,
ds:H00778 → Tarsal-carpal coalition syndrome, ds:H00779 → Usher syndrome (US),
ds:H00780 → Atrichia with papular lesions, ds:H00781 →
 Schopf-Schulz-Passarge syndrome; Keratosis palmoplantaris-cystic eyelids-hypodontia-hypotrichosis,
ds:H00782 → Hypotrichosis and recurrent skin vesicles,
ds:H00783 → Febrile seizures, including: Febrile convulsions; Generalized epilepsy with febrile
   seizure plus (GEFS+); Dravet syndrome/ Severe myoclonic epilepsy in infancy (SMEI),
ds:H00784 → Localized autosomal recessive hypotrichosis,
ds:H00785 → Congenital hypotrichosis with juvenile macular dystrophy,
ds:H00786 → Hypotrichosis simplex of scalp,
ds:H00787 → Congenital stationary night blindness (CSNB), including: CSNB type 1 (CSNB1); CSNB type
   2 (CSNB2); CSNB autosomal dominant (CSNBAD); Oguchi disease/ CSNB Oguchi type (CSNBO),
ds:H00788 → Hoyeraal-Hreidarsson syndrome, ds:H00789 → Keratoconus,
ds:H00790 → Keratosis linearis with ichthyosis congenita and sclerosing keratoderma; KLICK syndrome,
ds:H00791 → Disseminated superficial actinic porokeratosis (DSAP),
ds:H00792 → Warburg micro syndrome,
ds:H00793 → Poikiloderma with neutropenia,
ds:H00794 → Aromatase excess syndrome,
ds:H00795 → Seborrhea-like dermatitis with psoriasiform element,
ds:H00796 → Dermatopathia pigmentosa reticularis,
ds:H00797 → Martsolf syndrome,
ds:H00798 → Familial carpal tunnel syndrome, ds:H00799 →
 Cerebral dysgenesis, neuropathy, ichthyosis, and palmoplantar keratoderma syndrome; CEDNIK syndrome,
ds:H00800 → Loeys-Dietz syndrome (LDS), ds:H00801 →
 Familial thoracic aortic aneurysm and dissection (TAAD); Aortic aneurysm familial thoracic type (AAT),
ds:H00802 → Ehlers-Danlos syndrome (EDS), including: EDS classical type (EDS1/2); EDS hypermobility
   type (EDS3); EDS vascular type (EDS4); EDS kyphoscoliosis type (EDS6); EDS arthrochalasia
   type (EDS7A/7B); EDS dermatospraxis type (EDS7C); EDS autosomal recessive cardiac valvular
   form (EDSCV); EDS musculocontractural type (EDSMC); EDS progeroid form (EDSP); Tenascin-X
   deficiency (TNXD); Brittle cornea syndrome (EDS6B); EDS-like spondylocheiro dysplasia (SCD-EDS),
ds:H00803 → Seizures-sensorineural deafness-ataxia-mental retardation-electrolyte
   imbalance (SESAME) ; SeSAME/EAST syndrome,
ds:H00804 → Multiple cutaneous and uterine leiomyomata, ds:H00805 →
 Vitreoretinal degeneration, including: Stickler syndrome type I (STL1); Stickler syndrome type II
   (STL2); Snowflake vitreoretinal degeneration (SVD); Wagner syndrome 1 (WGN1); Knobloch syndrome
   (KNO); Enhanced S-cone syndrome (ESCS); Autosomal dominant vitreoretinochoroidopathy (ADVIRC),
ds:H00806 → Benign familial neonatal and infantile epilepsies, including: Benign
   familial neonatal epilepsy (BFNE); Benign familial neonatal infantile
   epilepsy (BFNIE); Benign familial infantile epilepsy (BFIE), ds:H00807 →
 Autosomal dominant nocturnal frontal lobe epilepsy (ADNFLE); Nocturnal frontal lobe epilepsy (NFLE),
ds:H00808 → Idiopathic generalized epilepsies (IGEs), including: Childhood absence epilepsy
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    (CAE); Juvenile absence epilepsy (JAE); Juvenile myoclonic epilepsy (JME); Epilepsy with
    generalized tonic-clonic seizures alone; Familial infantile myoclonic epilepsy (FIME),
ds:H00809 → Autosomal dominant temporal lobe epilepsy (ADTLE); Autosomal dominant
    partial epilepsy with auditory features (ADPEAF),
ds:H00810 → Progressive myoclonic epilepsy (PME/ EPM), including: Lafora disease (LBD);
    Unverricht-Lundborg disease (ULD); Neuronal ceroid lipofuscinoses (NCL); Type I
    sialidosis; Action myoclonus-renal failure syndrome (DRPLA); Type III Gaucher disease (GD),
ds:H00811 → Distal arthrogryposis (DA), ds:H00812 → Trichomoniasis,
ds:H00813 → Laryngo onycho cutaneous syndrome,
ds:H00814 →
 Vitelliform macular dystrophy, including: Best disease / Juvenile vitelliform macular dystrophy (VMD2)
    ; Adult-onset vitelliform macular dystrophy (AVMD); Autosomal recessive bestrophinopathy (ARB),
ds:H00815 → Hyperpigmentation, cutaneous, with hypertrichosis, hepatosplenomegaly,
    heart anomalies, hearing loss, and hypogonadism; H syndrome,
ds:H00816 → Agenesis of the corpus callosum with peripheral neuropathy (ACCPN),
ds:H00817 → Branchiooculofacial syndrome (BOFS),
ds:H00818 → Birt-Hogg-Dube syndrome,
ds:H00819 → Stargardt disease (STGD); Fundus flavimaculatus,
ds:H00820 → Bjornstad syndrome,
ds:H00821 → Macular degeneration, including: Age-related macular
    degeneration; Patterned dystrophy of retinal pigment epithelium; Retinal
    macular dystrophy 2 (MCDR2); X-linked atrophic macular degeneration (MDXLA),
ds:H00822 → Renal agenesis and Renal adysplasia, ds:H00823 → ABCD syndrome,
ds:H00824 → Calcification of joints and arteries,
ds:H00825 → Familial flecked retina syndrome, including: Doyne honeycomb degeneration
    of retina (DHRD); Basal laminar drusen (BLD); Fundus albipunctatus (FA); Retinitis
    punctata albescens (RPA); Bietti crystalline corneoretinal dystrophy  (BCD),
ds:H00826 → Blepharophimosis-ptosis-epicanthus inversus syndrome (BPES),
ds:H00827 → Brooke-Spiegler syndrome,
ds:H00828 → Familial cylindromatosis,
ds:H00829 → Multiple familial trichoepithelioma,
ds:H00830 → Alveolar capillary dysplasia with misalignment of pulmonary veins (ACD/MPV),
ds:H00831 → Primary dystonia,
ds:H00832 → Core neuroacanthocytosis syndromes, including: Chorea-acanthocytosis (ChAc); McLeod syndrome
    (MLS); Huntington's disease-like 2 (HDL2); Pantothenate kinase associated neurodegeneration (PKAN),
ds:H00833 → Neurodegeneration with brain iron accumulation (NBIA); Hallervorden-Spatz syndrome;
    Pantothenate kinase-associated neurodegeneration (PKAN); Neuroferritinopathy; Aceruloplasminemia,
ds:H00834 → Guanidinoacetate methyltransferase (GAMT) deficiency,
ds:H00835 → Succinic semialdehyde dehydrogenase (SSADH) deficiency; 4-Hydroxybutyric aciduria (4-HBA),
ds:H00836 → GLUT1 deficiency syndrome (GLUT1DS); Glucose transport defect of the blood-brain barrier,
ds:H00837 → Leber congenital amaurosis (LCR),
ds:H00838 → Congenital fibrosis of the extraocular muscles (CFEOM),
ds:H00839 → Porencephaly, ds:H00840 →
 Band-like calcification with simplified gyration and polymicrogyria (BLC-PMG); Pseudo-TORCH syndrome,
ds:H00841 → Infantile progressive bulbar palsy, including:
    Brown-Vialetto-Van Laere syndrome (BVVLS) ; Fazio-Londe disease,
ds:H00842 → Epidermodysplasia verruciformis, ds:H00843 → Hartnup disorder,
ds:H00844 → Benign familial pemphigus; Hailey-Hailey disease,
ds:H00845 → Familial amyloidosis, ds:H00846 →
 Fuhrmann syndrome; Fibular aplasia or hypoplasia, femoral bowing and poly-, syn-, and oligodactyly,
ds:H00847 → Al-Awadi/Raas-Rothschild syndrome; Ulna and fibula, absence of, with sever limb deficiency,
ds:H00848 →
 Ataxia with ocular apraxia (AOA), including: Ataxia telangiectasia (AT); Ataxia telangiectasia like
    disorder (ATLD); Ataxia oculomotor apraxia type 1 (AOA1); Ataxia oculomotor apraxia type 2 (AOA2),
ds:H00849 → Creatine deficiency syndrome, including: Arginine:glycine amidinotransferase
    deficiency (AGAT deficiency); Guanidinoacetate methyltransferase deficiency (GAMT
    deficiency); X-linked creatine deficiency syndrome (XL-CDS), ds:H00850 → Frontorhiny,
ds:H00851 → Synpolydactyly 2; Synpolydactyly, 3/3'4, associated with metacarpal and metatarsal synostoses,
ds:H00852 → Klippel-Feil syndrome(KFS),
ds:H00853 → Cenani-Lenz syndactyly syndrome,
ds:H00854 → Wolfram syndrome (WFS); DIDMOAD syndrome,
ds:H00855 →
 Triphalangeal thumb, including: Triphalangeal thumb; Triphalangeal thumb-polysyndactyly syndrome,
ds:H00856 → Distal hereditary motor neuropathies (dHMN),
ds:H00857 → Oligodontia-colorectal cancer syndrome,
ds:H00858 → Marie-Unna hereditary hypotrichosis (MUHH),
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ds:H00859 → Guttmacher syndrome,
ds:H00860 → Benign hereditary chorea,
ds:H00861 → Pancreatic agenesis,
ds:H00862 → Tourette syndrome,
ds:H00863 → Spondylo-megaepiphyseal-metaphyseal dysplasia,
ds:H00864 → Trichotillomania,
ds:H00865 → Lethal congenital contractural syndrome (LCCS),
ds:H00866 → Trichothiodystrophy non-photosensitive type 1
   (TTDN1); Amish brittle hair syndrome; BIDS syndrome; Hair-brain syndrome,
ds:H00867 → Radioulnar synostosis with amegakaryocytic thrombocytopenia,
ds:H00868 → Stapes ankylosis with broad thumb and toes,
ds:H00869 → Leukoencephalopathy with vanishing white matter; Vanishing white matter disease; Childhood
   ataxia with diffuse central nervous system hypomyelination (CACH); Cree leukoencephalopathy (CLE),
ds:H00870 → Brachydactyly-syndactyly syndrome, ds:H00871 →
 Leukoencephalopathy with brain stem and spinal cord involvement and lactate elevation (LBSL),
ds:H00872 → Trismus-pseudocamptodactyly syndrome; Hecht-Beals Syndrome; Dutch-Kentucky syndrome,
ds:H00873 → Cousin syndrome,
ds:H00874 → Leukoencephalopathy with dystonia and motor neuropathy,
ds:H00875 → Megalencephalic leukoencephalopathy with subcortical cysts (MLC),
ds:H00876 → Mismatch repair deficiency, including: Hereditary non-polyposis
   colorectal cancer (HNPCC); Lynch syndrome; Muir-Torre syndrome; Turcot syndrome,
ds:H00877 → Brain small vessel disease with Axenfeld-Rieger anomaly,
ds:H00878 → Cystic leukoencephalopathy without megalencephaly,
ds:H00879 → Perry syndrome,
ds:H00880 → Dyschromatosis symmetrica hereditaria,
ds:H00881 → Li-Fraumeni syndrome, including: Classic Li-Fraumeni syndrome (LFS); LFS-like syndrome (LFSL),
ds:H00882 → Cocoon syndrome,
ds:H00883 → Lipoid proteinosis; Urbach-Wiethe disease,
ds:H00884 → Familial progressive hyperpigmentation,
ds:H00885 → Hypomelanosis of Ito; Pigmentary mosaicism,
ds:H00886 → Donnai-Barrow syndrome; Faciooculoacousticorenal syndrome,
ds:H00887 → Lipoprotein glomerulopathy,
ds:H00888 → Nephrolithiasis/osteoporosis, hypophosphatemic,
ds:H00889 → MED12-related disorders, including: Lujan-Fryns syndrome (LFS); Lujan syndrome; X-linked
   mental retardation with Marfanoid habitus; FG syndrome type 1 (FGS1); Opitz-Kaveggia syndrome,
ds:H00890 → Azoospermia, including: Azoospermia; Azoospermia due to perturbations of meiosis,
ds:H00891 → Combined oxidative phosphorylation deficiency (COXPD),
ds:H00892 → Bronchiectasis with or without elevated sweat chloride,
ds:H00893 → Skin fragility-woolly hair syndrome,
ds:H00894 → FG syndrome (FGS); Opitz-Kaveggia syndrome,
ds:H00895 → Basal cell nevus syndrome; Nevoid basal cell carcinoma syndrome; Gorlin syndrome,
ds:H00896 → Lymphangioleiomyomatosis (LAM),
ds:H00897 → Pontocerebellar hypoplasia,
ds:H00898 → Myopathy with lactic acidosis and sideroblastic anaemia (MLASA); Mitochondrial
   myopathy and sideroblastic anemia; Hereditary myopathy with lactic acidosis (HML),
ds:H00899 → Lysinuric protein intolerance (LPI), ds:H00900 → Geleophysic dysplasia,
ds:H00901 → Cystinuria,
ds:H00902 → Speech-language disorder 1 (SPCH1),
ds:H00903 → Congenital clubfoot; Congenital talipes equinovarus,
ds:H00904 → Cutis laxa with severe pulmonary, gastrointestinal, and
   urinary abnormalities; Urban-Rifkin-Davis syndrome, ds:H00905 → Iminoglycinuria,
ds:H00906 → Macrocephaly, alopecia, cutis laxa, and scoliosis; MACS syndrome,
ds:H00907 → Kleefstra syndrome; 9q Subtelomeric deletion syndrome,
ds:H00908 → Mowat-Wilson syndrome,
ds:H00909 → Cleft palate with ankyloglossia,
ds:H00910 → Hirschsprung disease (HD),
ds:H00911 → Dicarboxylic aminoaciduria,
ds:H00912 → Tumor necrosis factor receptor-associated periodic syndrome (TRAPS); Familial periodic fever,
ds:H00913 → Choreoathetosis, hypothyroidism, and neonatal respiratory distress,
ds:H00914 → Warsaw breakage syndrome,
ds:H00915 → Tuberous sclerosis complex (TSC); Bourneville-Pringle disease,
ds:H00916 → Congenital central hypoventilation syndrome (CCHS),
ds:H00917 → Congenital dyserythropoietic anemias (CDAs),
ds:H00918 → Conotruncal heart malformations, including: Double-outlet right ventricle; Persistent truncus
   arteriosus; Conotruncal anomaly face syndrome, ds:H00919 → Arterial tortuosity syndrome,
ds:H00920 → Exocrine pancreatic insufficiency, dyserythropoietic anemia, and calvarial hyperostosis,
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ds:H00921 → Revesz syndrome; Exudative retinopathy with bone marrow failure,
ds:H00922 → Schinzel-Giedion midface retraction syndrome,
ds:H00923 → Congenital systemic glutamine deficiency (CSGD); Glutamine synthetase deficiency,
ds:H00924 → Severe combined immunodeficiency with microcephaly,
   growth retardation, and sensitivity to ionizing radiation; NHEJ1 syndrome,
ds:H00925 → 2-Methyl-3-hydroxybutyryl-CoA dehydrogenase (MHBD) deficiency; HSD10 deficiency,
ds:H00926 → Growth retardation, developmental delay, coarse facies, and early death,
ds:H00927 → Chylomicron retention disease (CRD); Anderson disease,
ds:H00928 → Nephropathy with pretibial epidermolysis bullosa and deafness,
ds:H00929 → Congenital vertical talus,
ds:H00930 → Hypoalphalipoproteinemia,
ds:H00931 → Growth hormone insensitivity with immunodeficiency,
ds:H00932 → Tropical calcific pancreatitis,
ds:H00933 → Hereditary pancreatitis; Hereditary chronic pancreatitis,
ds:H00934 → Caudal duplication anomaly,
ds:H00935 → Cold-induced sweating syndrome (CISS) and Crisponi syndrome (CRISPS),
ds:H00936 → Goldberg-Shprintzen megacolon syndrome; Goldberg-Shprintzen syndrome (GOSHS),
ds:H00937 → Precocious puberty, including: Central
   precocious puberty (CEPREPU); Familial male precocious puberty (FMPP),
ds:H00938 → Factor XI deficiency; Plasma thromboplastin antecedent deficiency; Rosenthal syndrome,
ds:H00939 → Neutropenia, severe congenital 4, autosomal recessive; G6PC3 deficiency; Darsun syndrome,
ds:H00940 → Cohen syndrome,
ds:H00941 → Factor XII deficiency; Hageman factor deficiency,
ds:H00942 → Rabson-Mendenhall syndrome,
ds:H00943 → TARP syndrome,
ds:H00944 → Dowling-Degos disease,
ds:H00945 → Factor XIII deficiency,
ds:H00946 → Arts syndrome,
ds:H00947 → Pilomatricoma; Epithelioma calcificans of Malherbe,
ds:H00948 → Renal hypouricemia (RHUC),
ds:H00949 → Focal dermal hypoplasia; Goltz-Gorlin syndrome,
ds:H00950 → Arthrogryposis, renal dysfunction, and cholestasis; ARC syndrome,
ds:H00951 → Reis-Bucklers corneal dystrophy (RBCD); Corneal
   dystrophy of Bowman's type I; Granular corneal dystrophy type III,
ds:H00952 → Thiel-Behnke dystrophies (TBCD); Corneal dystrophy of Bowman layer type II;
   Honeycomb corneal dystrophy; Anterior limiting membrane dystrophy type II;
   Curly fibers corneal dystrophy; Waardenburg-Jonker corneal dystrophy, ds:H00953 →
 Gelatinous drop-like corneal dystrophy (GDCD); Subepithelial amyloidosis; Primary familial amyloidosis,
ds:H00954 → Macular corneal dystrophy (MCD); Corneal dystrophy Groenouw type II; Fehr corneal dystrophy,
ds:H00955 → Granular corneal dystrophies (GCD), including: Corneal dystrophy
   Groenouw type I; Avellino corneal dystrophy; Granular-lattice dystrophy,
ds:H00956 → Lattice corneal dystrophies (LCD), including: Biber-Haab-Dimmer dystrophy;
   Familial amyloid polyneuropathy type IV; Meretoja syndrome,
ds:H00957 → Fleck corneal dystrophy (FCD); Francois-Neetens speckled corneal dystrophy,
ds:H00958 → Congenital stromal corneal dystrophy
   (CSCD); Congenital hereditary stromal dystrophy; Witschel dystrophy,
ds:H00959 → Schnyder corneal dystrophy (SCD); Schnyder crystalline corneal dystrophy
   (SCCD); Crystalline stromal dystrophy; Schnyder crystalline dystrophy sine crystals,
ds:H00960 → Fuchs corneal dystrophy (FECD); Fuchs endothelial corneal dystrophy,
ds:H00961 → Posterior polymorphous corneal dystrophy (PPCD),
ds:H00962 → RIDDLE syndrome,
ds:H00963 → Congenital hereditary endothelial dystrophy (CHED); Congenital
   hereditary endothelial dystrophy type 1; Congenital hereditary endothelial dystrophy
   type 2; Corneal dystrophy and perceptive deafness (CDPD); Harboyan syndrome,
ds:H00964 → Thiopurine S-methyltransferase deficiency (TPMT deficiency),
ds:H00965 → RAPADILINO syndrome,
ds:H00966 → AICA-ribosiduria; ATIC deficiency,
ds:H00967 → Adiponectin deficiency,
ds:H00968 → Raine syndrome; Lethal osteosclerotic bone dysplasia,
ds:H00969 → Skeletal defects, genital hypoplasia, and mental retardation,
ds:H00970 → Juvenile primary lateral sclerosis,
ds:H00971 → Achromatopsia; Rod monochromacy,
ds:H00972 → Endocrine-cerebro-osteodysplasia syndrome,
ds:H00973 → Bradyopsia,
ds:H00974 → Blue cone monochromacy,
ds:H00975 → Rotaviral enteritis; Rotaviral gastroenteritis,
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ds:H00976 → Colorblindness, including: Dichromacy; Anomalous trichromacy,
ds:H00977 → Trichorhinophalangeal dysplasia, including: Trichorhinophalangeal syndrome, type I (TRPS1); Langer-Giedion Syndrome (TRPS2); Sugio-Kajii Syndrome (TRPS3),
ds:H00978 → Thrombocytopenia (THC); Familial platelet disorder with associated myeloid malignancy (FPDMM),
ds:H00979 → Caudal regression syndrome and Sirenomelia,
ds:H00980 → Nevo syndrome,
ds:H00981 → Ataxia with isolated vitamin E deficiency (AVED); Friedreich-like ataxia,
ds:H00982 →
Sideroblastic anemia, including: Pyridoxine-refractory autosomal recessive sideroblastic anemia (PRARSA); X-linked sideroblastic anemia (XLSA); X-linked sideroblastic anemia with ataxia (ASAT),
ds:H00983 → Alpha-2-plasmin inhibitor (a2-PI) deficiency, ds:H00984 → Bare lymphocyte syndrome (BLS) type1,
ds:H00985 → Bare lymphocyte syndrome (BLS) type2,
ds:H00986 → Multiple pterygium syndrome, including: Multiple pterygium syndrome, lethal type (LMPS); Multiple pterygium syndrome, Escobar variant (EVMPS),
ds:H00987 → Fetal akinesia deformation sequence (FADS); Pena-Shokeir syndrome, type 1,
ds:H00988 → Enterokinase deficiency,
ds:H00989 → Mohr-Tranebjaerg syndrome,
ds:H00990 → Microcephaly, Amish type,
ds:H00991 → Microcephalic osteodysplastic primordial dwarfism, type II (MOPD II),
ds:H00992 → Seckel syndrome,
ds:H00993 → Microcephalic osteodysplastic primordial dwarfism, type I (MOPD I); Taybi-Linder syndrome,
ds:H00994 → Familial skewed X-chromosome inactivation,
ds:H00995 → Combined deficiency of vitamin K-dependent clotting factors (VKCFD),
ds:H00996 → Amish infantile epilepsy syndrome,
ds:H00997 → CATSHL syndrome,
ds:H00998 → Alternating hemiplegia of childhood,
ds:H00999 → Coenzyme Q10 deficiency,
ds:H01000 → Retinal vasculopathy with cerebral leukodystrophy (RVCL),
ds:H01001 → COACH syndrome,
ds:H01002 → Generalized arterial calcification of infancy,
ds:H01003 → Dimethylglycine dehydrogenase deficiency (DMGDHD),
ds:H01004 → Velocardiofacial syndrome,
ds:H01005 → Dopamine beta-hydroxylase deficiency; Norepinephrine deficiency; Noradrenaline deficiency,
ds:H01006 → Hereditary angioedema,
ds:H01007 → Choroid plexus papilloma,
ds:H01008 → C syndrome, including: Opitz trigonocephaly syndrome; Bohring-Opitz syndrome (BOPS),
ds:H01009 → Newfoundland rod-cone dystrophy (NFRCD),
ds:H01010 → Occult macular dystrophy (OMD),
ds:H01011 → Adrenocorticotropic hormone deficiency; Isolated ACDH deficiency (IAD),
ds:H01012 → Oculo-auricular syndrome,
ds:H01013 → Adult i phenotype,
ds:H01014 → Sparganosis,
ds:H01015 → Jalili syndrome,
ds:H01016 → Primary bile acid malabsorption,
ds:H01017 → Choanal atresia and lymphedema,
ds:H01018 → Metachondromatosis,
ds:H01019 → Catecholaminergic polymorphic ventricular tachycardia,
ds:H01020 → Optic atrophy (OPA),
ds:H01021 → Rhodococcus equi infection,
ds:H01022 → Diseases of the tricarboxylic acid cycle, including: Fumarase (FH) deficiency; Succinate dehydrogenase (SDH) deficiency; Alpha-ketoglutarate dehydrogenase (AKGDH) deficiency,
ds:H01023 → Juvenile polyposis syndrome, ds:H01024 → Hereditary mixed polyposis syndrome,
ds:H01025 → Familial adenomatous polyposis,
ds:H01026 → Renal coloboma syndrome (RCS); Papillorenal syndrome,
ds:H01027 → Anophthalmia and microphthalmia (A/M),
ds:H01028 → Argininosuccinic aciduria (ARGINSA); Argininosuccinate lyase deficiency,
ds:H01029 → Cornea plana congenita,
ds:H01030 → Lethal arthrogryposis with anterior horn cell disease,
ds:H01031 → Orthostatic intolerance (OI); Postural tachycardia syndrome (POTS),
ds:H01032 → N-acetylglutamate synthase (NAGS) deficiency,
ds:H01033 → Congenital bilateral absence of vas deferens,
ds:H01034 → L1 syndrome, including: ; X-linked hydrocephalus; MASA syndrome; X-linked complicated spastic paraplegia type I ; X-linked partial agenesis of corpus callosum,
ds:H01035 → Corpus callosum, agenesis of, with mental retardation, ocular coloboma and micrognathia,
ds:H01036 → Posterior column ataxia with retinitis pigmentosa (PCARP),
ds:H01037 → Vesicoureteral reflux,

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ds:H01038 → Cerebellar ataxia cayman type (ATCAY); Cayman ataxia,
ds:H01039 → Ovarian hyperstimulation syndrome (OHSS),
ds:H01040 → Bamforth-Lazarus syndrome,
ds:H01041 → Aerococcus urinae infection,
ds:H01042 → Buruli ulcer,
ds:H01043 → Onchocerciasis; River blindness; Robles' Disease,
ds:H01044 → Dracunculiasis; Guinea worm disease,
ds:H01045 → Schistosomiasis,
ds:H01046 → Trichuriasis, ds:H01047 → Cysticercosis,
ds:H01048 → Liver fluke disease; Fascioliasis,
ds:H01049 → Gordonia bronchialis infection,
ds:H01050 → Tsukamurella infections,
ds:H01051 → Corynebacterium ulcerans infection,
ds:H01052 → Molluscum contagiosum,
ds:H01053 → Paroxysmal nocturnal hemoglobinuria (PNH),
ds:H01054 → Pediculosis, including: Head lice infestation; Body lice infestation,
ds:H01055 → Giant kidney worm infection; Dioctophymosis,
ds:H01056 → Toxocariasis, including: Visceral larva
   migrans; Ocular larva migrans; Covert toxocariasis; Common toxocariasis,
ds:H01057 → Gnathostomiasis, ds:H01058 → Anisakiasis, ds:H01059 → Capnocytophaga canimorsus infection,
ds:H01060 → Babesiosis, ds:H01061 → Mansonelliasis,
ds:H01062 → Histoplasmosis,
ds:H01063 → Human metapneumovirus infection,
ds:H01064 → Simkania negevensis infection,
ds:H01065 → Pentosuria,
ds:H01066 → Bordetella petrii infection,
ds:H01067 → Proteus mirabilis infection,
ds:H01068 → Aggregatibacter aphrophilus infection,
ds:H01069 → Stenotrophomonas maltophilia infection,
ds:H01070 → Vibrio furnissii infection,
ds:H01071 → Acute alcohol sensitivity,
ds:H01072 → Moraxella catarrhalis infection,
ds:H01073 → Shewanella infection,
ds:H01074 → Aeromonas infection,
ds:H01075 → Peters anomaly, including: Peters plus syndrome; Peters anomaly plus systemic features,
ds:H01076 → Alpha-methylacetoacetic aciduria; 3-Ketothiolase deficiency,
ds:H01077 → Bordetella hinzii infection,
ds:H01078 → Fletcher factor deficiency; Prekallikrein deficiency,
ds:H01079 → 3-Phosphoglycerate dehydrogenase (3-PGDH) deficiency; PHGDH Deficiency,
ds:H01080 → Ralstonia pickettii infection,
ds:H01081 → Achromobacter xylosoxidans keratitis,
ds:H01082 → Phosphoserine aminotransferase (PSAT) deficiency,
ds:H01083 → Bordetella bronchiseptica infection,
ds:H01084 → Bordetella holmesii infection,
ds:H01085 → Diphyllobothriasis,
ds:H01086 → Lymphatic filariasis,
ds:H01087 → Balantidiasis; Balantidial dysentery,
ds:H01088 → Pigmented paravenous chorioretinal atrophy (PPCA),
ds:H01089 → Dientamoebiasis, ds:H01090 → Ascariasis,
ds:H01091 → Enterobiasis; Oxyuriasis,
ds:H01092 → Human hookworm infections, including: Ancylostomiasis; Necatoriasis,
ds:H01093 → Paragonimiasis; Pulmonary distomatosis; Lung fluke disease; Benign endemic hemoptysis,
ds:H01094 → Eosinophil peroxidase deficiency,
ds:H01095 → Syndactyly,
ds:H01096 → Pyruvate kinase (PK) deficiency, including: Red
   cell pyruvate kinase (PK) deficiency; Pyruvate kinase hyperactivity,
ds:H01097 → Cerebral palsy, ds:H01098 → Pentastomiasis, ds:H01099 → Trichinosis; Trichinellosis,
ds:H01100 → Strongyloidiasis,
ds:H01101 → Combined lipase deficiency (CLD),
ds:H01102 → Pituitary adenomas, including: Multiple endocrine neoplasia type 1 (MEN1); MEN1-like
   syndrome (MEN4); Carney complex (CNC); Familial isolated pituitary adenomas (FIPA),
ds:H01103 → Alpha-1-antitrypsin (A1AT) deficiency, ds:H01104 → Loiasis,
ds:H01105 → Cranio-lenticulo-sutural dysplasia (CLSD); Boyadjiev-Jabs syndrome,
ds:H01106 → Plasminogen activator inhibitor type 1 (PAI-1) deficiency,
ds:H01107 → Intestinal fluke infections, including:
   Fasciolopsiasis; Echinostomiasis; Heterophyiasis; Metagonimiasis,
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ds:H01108 → CD36 deficiency; Platelet glycoprotein IV deficiency,
ds:H01109 → Chronic mucocutaneous candidiasis (CMC); Familial candidiasis (CANDF),
ds:H01110 → Pneumothorax,
ds:H01111 → Cortisone reductase deficiency (CRD),
ds:H01112 → Polyhydramnios, megalencephaly, and symptomatic epilepsy; PMSE syndrome,
ds:H01113 → Acid phosphatase deficiency,
ds:H01114 → Ocular coloboma, including: Coloboma of iris choroid
   and retina (COI); Coloboma of optic nerve (COLON); Optic nerve hypoplasia,
ds:H01115 → Polyneuropathy, hearing loss, ataxia, retinitis pigmentosa, and cataract (PHARC),
ds:H01116 → Choroideremia (CHM); Tapetochoroidal dystrophy,
ds:H01117 → Majeed syndrome; Chronic recurrent multifocal osteomyelitis (CRMO),
ds:H01118 → Progressive external ophthalmoplegia (PEO),
ds:H01119 → Prolidase deficiency (PD),
ds:H01120 → Proliferative vasculopathy and hydranencephaly-hydrocephaly syndrome
   (PVHH); Cerebral proliferative glomeruloid vasculopathy (PGV); Fowler syndrome,
ds:H01121 → Succinyl CoA:3-oxoacid CoA transferase (SCOT) deficiency,
ds:H01122 → Pulmonary alveolar proteinosis (PAP),
ds:H01123 → HMG-CoA synthase (HMGCS) deficiency,
ds:H01124 → Pyridox(am)ine-5'-phosphate oxidase (PNPO) deficiency,
ds:H01125 → Hereditary pyropoikilocytosis (HPP),
ds:H01126 → Familial renal glucosuria (FRG),
ds:H01127 → PIGM-congenital disorder of glycosylation (PIGM-CDG),
ds:H01128 → Reticular dysgenesis,
ds:H01129 → Brody myopathy,
ds:H01130 → Late-onset retinal degeneration (L-ORD),
ds:H01131 → Hereditary neuralgic amyotrophy (HNA); Hereditary brachial plexus neuropathy,
ds:H01132 → Aplastic anemia (AA),
ds:H01133 → Reynolds syndrome,
ds:H01134 → Rhabdoid predisposition syndrome (RPS),
ds:H01135 → Ribose 5-phosphate isomerase (RPI) deficiency,
ds:H01136 → Carboxypeptidase N deficiency,
ds:H01137 → Baylisascariasis,
ds:H01138 → Hymenolepiasis,
ds:H01139 → Human granulocytic anaplasmosis,
ds:H01140 → Sennetsu neorickettsiosis; Sennetsu ehrlichiosis,
ds:H01141 → Human monocytic ehrlichiosis,
ds:H01142 → Ehrlichia ewingii infection,
ds:H01143 → Vitamin D-dependent rickets,
ds:H01144 → Ochrobactrum anthropi infection,
ds:H01145 → Atransferrinemia; Congenital hypotransferrinemia,
ds:H01146 → Aminoacylase 1 deficiency,
ds:H01147 → Methylobacterium infection,
ds:H01148 → Caulobacter infection,
ds:H01149 → Ring dermoid of cornea,
ds:H01150 → Phenylobacterium infection,
ds:H01151 → Brevundimonas infection,
ds:H01152 → Taenia saginata infection,
ds:H01153 → Human echinococcosis,
ds:H01154 → Wolff-Parkinson-White (WPW) syndrome; Preexcitation syndrome,
ds:H01155 → Roussy-Levy syndrome,
ds:H01156 → STAR syndrome,
ds:H01157 → Agrobacterium radiobacter infection,
ds:H01158 → Alopecia universalis,
ds:H01159 → Anterior segment dysgenesis (ASD), including: Anterior segment mesenchymal dysgenesis;
   Aniridia; Axenfeld-Rieger syndrome (ARS); Peters anomaly; Iridogoniodysgenesis (IRID),
ds:H01160 → Schizencephaly, ds:H01161 → Aromatic L-amino acid decarboxylase (AADC) deficiency,
ds:H01162 → Scott syndrome,
ds:H01163 → Corticosteroid-binding globulin (CBG) deficiency,
ds:H01164 → Paracoccus yeei infection,
ds:H01165 → Novosphingobium aromaticivorans infection,
ds:H01166 → Sphingomonas paucimobilis infection,
ds:H01167 → Gluconobacter infection,
ds:H01168 → Sea-blue histiocyte disease,
ds:H01169 → Acetobacter infection,
ds:H01170 → Autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS),
ds:H01171 → Poor drug metabolism (PM),
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ds:H01172 → Infantile ascending hereditary spastic paralysis (IAHSP),
ds:H01173 → Stiff skin syndrome (SSS),
ds:H01174 → Congenital diarrhea, including: Congenital chloride diarrhea (DIAR1);
   Microvillus inclusion disease (DIAR2); Congenital sodium diarrhea (DIAR3);
   Congenital malabsorptive diarrhea (DIAR4); Congenital tufting enteropathy (DIAR5),
ds:H01175 → Staphylococcal infection, ds:H01176 → Uncomplicated urinary tract infection,
ds:H01177 → Infantile bilateral striatal necrosis (IBSN),
ds:H01178 → Myiasis,
ds:H01179 → Tungiasis; Chigoe flea, ds:H01180 →
 Sveinsson chorioretinal atrophy (SCRA); Helicoid peripapillary chorioretinal degeneration (HPCD),
ds:H01181 → T-cell immunodeficiency congenital alopecia and nail dystrophy (TIDAND),
ds:H01182 → Biotinidase deficiency; BTD deficiency; Late-onset multiple carboxylase deficiency,
ds:H01183 → Thiamine-responsive megaloblastic anemia (TRMA),
ds:H01184 → Familial dementia, including: Familial British dementia (FBD); Familial Danish dementia (FDD),
ds:H01185 → Cerebral amyloid angiopathy (CAA); Hereditary cerebral hemorrhage with amyloidosis,
ds:H01186 → Abnormal thyroid hormone metabolism,
ds:H01187 → Tietz syndrome; Albinism-deafness syndrome,
ds:H01188 → Tn syndrome,
ds:H01189 → Transaldolase (TALDO) deficiency,
ds:H01190 → Transcobalamin II deficiency,
ds:H01191 → Asthma with nasal polyps and aspirin intolerance, ds:H01192 →
 Lysyl hydroxylase 3 (LH3) deficiency; Bone fragility with contractures arterial rupture and deafness,
ds:H01193 → Familial tumoral calcinosis (FTC),
ds:H01194 → X-linked chondrodysplasia punctata, including: X-linked recessive
   chondrodysplasia punctata (CDPX1); X-linked dominant chondrodysplasia punctata (CDPX2),
ds:H01195 → VACTERL/VATER association, ds:H01196 → Hypochromic microcytic anemia,
ds:H01197 → Dihydrofolate reductase (DHFR) deficiency,
ds:H01198 → Fanconi renotubular syndrome (FTS),
ds:H01199 → Hyperalphalipoproteinemia,
ds:H01200 → Fatal infantile cardioencephalomyopathy,
ds:H01201 → Jensen syndrome; Opticoacoustic nerve atrophy,
ds:H01202 → Cataract,
ds:H01203 → Primary congenital glaucoma (PCG),
ds:H01204 → Cerebellar ataxia, mental retardation (MR), and dysequilibrium syndrome (CAMRQ),
ds:H01205 → Coumarin resistance; Warfarin resistance,
ds:H01206 → Plasminogen deficiency, including: Ligneous conjunctivitis; Dysplasminogenemia,
ds:H01207 → Trigonocephaly,
ds:H01208 → Globozoospermia; Round-headed spermatozoa,
ds:H01209 → Deafness, X-linked,
ds:H01210 → Hypomagnesemia,
ds:H01211 → MECP2-related severe neonatal encephalopathy,
ds:H01212 → Familial encephalopathy with neuroserpin inclusion bodies (FENIB),
ds:H01213 → Gallbladder disease; Cholecystitis; Cholelithiasis,
ds:H01214 → Rh-null hemolytic anemia (RHN); Rh-deficiency syndrome,
ds:H01215 → Simpson-Golabi-Behmel syndrome (SGBS),
ds:H01216 → Left ventricular noncompaction (LVNC),
ds:H01217 → Primary localized cutaneous amyloidosis (PLCA),
ds:H01218 → P14 deficiency,
ds:H01219 → Restrictive cardiomyopathy (RCM),
ds:H01220 → Congenital cataracts, facial dysmorphism, and neuropathy (CCFDN),
ds:H01221 → Epithelial basement membrane corneal dystrophy (EBMD);
   Cogan microcystic epithelial dystrophy; Map-dot-fingerprint dystrophy,
ds:H01222 → Cowden-like syndrome, ds:H01223 → Mental retardation-stereotypic movements-epilepsy
   and/or cerebral malformations (MRSME); Chromosome 5q14.3 deletion syndrome,
ds:H01224 → Ketosis-prone diabetes mellitus (KPD), ds:H01225 → D-2-hydroxyglutaric aciduria (D-2-HGA),
ds:H01226 → GLI3 morphopathies, including: Greig cephalopolysyndactyly syndrome; Pallister-Hall
   syndrome; Preaxial polydactyly type-IV; Postaxial polydactyly types A1 and B,
ds:H01227 → Inflammatory bowel disease (IBD), ds:H01228 →
 Insulin-resistant diabetes mellitus with acanthosis nigricans (IRAN); Type A insulin resistance,
ds:H01229 → Inclusion body myopathy 3 (IBM3),
ds:H01230 → Adult-onset autosomal dominant leukodystrophy (ADLD),
ds:H01231 → Biotin-responsive basal ganglia disease (BBGD),
ds:H01232 → Syndromic multisystem autoimmune disease,
ds:H01233 → Urocanase deficiency; Urocanic aciduria,
ds:H01234 → Trimethylaminuria (TMAU); Fish-odor syndrome,
ds:H01235 → Bleeding disorder platelet-type,
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ds:H01236 → Familial articular chondrocalcinosis,
ds:H01237 → Sulfite oxidase deficiency,
ds:H01238 → Phelan-McDermid syndrome; Chromosome 22q13.3 deletion syndrome,
ds:H01239 → Combined SAP deficiency; Prosaposin deficiency,
ds:H01240 → Immune thrombocytopenia (ITP); Autoimmune thrombocytopenic purpura,
ds:H01241 → Congenital diaphragmatic hernia (CDH),
ds:H01242 → Saccharopinuria,
ds:H01243 → Huntington's disease-like syndrome,
ds:H01244 → T+B+Severe combined immunodeficiencies (SCIDs),
ds:H01245 → Immunodeficiency without anhidrotic ectodermal  dysplasia,
ds:H01246 → Isolated congenital nail clubbing (ICNC); Isolated congenital digital clubbing,
ds:H01247 → Pyridoxine-dependent epilepsy (PDE),
ds:H01248 → Erythrocyte lactate transporter defect,
ds:H01249 → Ethylmalonic encephalopathy (EE),
ds:H01250 → Hereditary gingival fibromatosis (HGF),
ds:H01251 → Focal cortical dysplasia of Taylor; Focal cortical dysplasia  type II,
ds:H01252 → Hereditary folate malabsorption (HFM),
ds:H01253 → Isolated follicle-stimulating hormone deficiency (IFSHD),
ds:H01254 → Congenital prothrombin deficiency,
ds:H01255 → Juvenile-onset dystonia,
ds:H01256 → Foveal hypoplasia,
ds:H01257 → GABA-transaminase deficiency; 4-Aminobutyrate aminotransferase deficiency,
ds:H01258 → Generalized epilepsy and paroxysmal dyskinesia (GEPD),
ds:H01259 → Giant axonal neuropathy,
ds:H01260 → Glomerulopathy with fibronectin deposits (GFND),
ds:H01261 → Congenital glucose-galactose malabsorption (GGM),
ds:H01262 → Formiminotransferase deficiency,
ds:H01263 → Progressive cardiac conduction defect
   (PCCD); Progressive familial heart block (PFHB); Lenegre-Lev disease,
ds:H01264 → Hepatic venoocclusive disease with immunodeficiency (VODI),
ds:H01265 → Hydrolethalus syndrome,
ds:H01266 → Hypercarotenemia and vitamin A deficiency,
ds:H01267 → Familial hyperinsulinemic hypoglycemia (HHF),
ds:H01268 → Hyperornithinemia-hyperammonemia-homocitrullinuria syndrome; HHH syndrome,
ds:H01269 → Congenital hyperthyroidism, including: Familial
   gestational hyperthyroidism (HTFG); Hyperthyroidism non-autoimmune (HTNA),
ds:H01270 → Familial hypobetalipoproteinemia (FHBL), ds:H01271 →
 Hypoparathyroidism with sensorineural deafness and renal dysplasia; HDR syndrome; Barakat syndrome,
ds:H01272 → Hypoplastic left heart syndrome (HLHS),
ds:H01273 → Autosomal dominant keratitis (ADK); Hereditary keratitis,
ds:H01274 → Growth delay due to insulin-like growth factor I resistance; IGF-I resistance,
ds:H01275 → Interleukin 1 receptor antagonist deficiency
   (DIRA); Multifocal osteomyelitis with periostitis and pustulosis (OMPP),
ds:H01276 → X-linked chronic idiopathic intestinal pseudo-obstruction; CIIPX,
ds:H01277 → Vitamin B12 deficiency anaemia, including: Hereditary intrinsic factor
   deficiency (IFD); Imerslund-Grasbeck syndrome (IGS)/ Megaloblastic anemia 1,
ds:H01278 → Iron-refractory iron deficiency anemia (IRIDA),
ds:H01279 → Isobutyryl-CoA dehydrogenase (IBD) deficiency,
ds:H01280 → L-2-hydroxyglutaric aciduria (L2HGA),
ds:H01281 → Lathosterolosis,
ds:H01282 → Spermatogenic failure,
ds:H01283 → Malonyl-CoA decarboxylase deficiency,
ds:H01284 → Marinesco-Sjogren syndrome,
ds:H01285 → Methylcobalamin deficiency type G (cblG),
ds:H01286 → Microtia hearing impairment and cleft palate (MHICP),
ds:H01287 → Congenital mirror movements (CMM),
ds:H01288 → Mosaic variegated aneuploidy (MVA) syndrome,
ds:H01289 → Mulibrey nanism,
ds:H01290 → Acute recurrent myoglobinuria,
ds:H01291 → Spheroid body myopathy (SBM),
ds:H01292 → Nance-Horan syndrome, ds:H01293 → Narcolepsy,
ds:H01294 → Nephrogenic syndrome of inappropriate antidiuresis (NSIAD),
ds:H01295 → Neurodegeneration due to cerebral folate transport deficiency,
ds:H01296 → Hereditary neuropathy with liability to pressure palsies (HNPP),
ds:H01297 → Neutral lipid storage disease with myopathy,
ds:H01298 → Pulmonary alveolar microlithiasis (PALM),
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ds:H01299 → Idiopathic pulmonary fibrosis,
ds:H01301 → Hemorrhagic destruction of the brain, subependymal calcification, and cataracts,
ds:H01302 → Hyperchlorhidrosis isolated (HCHLH),
ds:H01303 → Hypercatabolic hypoproteinemia,
ds:H01304 → Hyperglycinuria,
ds:H01305 → Global cerebral hypomyelination,
ds:H01306 → FRA12A mental retardation,
ds:H01307 → Nonsyndromic congenital nail disorder (NDNC),
ds:H01308 → Macrocephaly macrosomia facial dysmorphism syndrome,
ds:H01309 → Sarcoidosis, early-onset,
ds:H01310 → Multi-minicore disease (MmD); Multicore myopathy with external ophthalmoplegia,
ds:H01311 → Enteroinvasive Escherichia coli (EIEC) infection,
ds:H01312 → Enteroaggregative Escherichia coli (EAEC)
   infection; Enteroaggregative Escherichia coli (EAggEC) infection,
ds:H01313 → Escherichia coli meningitis; Neonatal meningitis-associated Escherichia coli (NMEC) infection,
ds:H01314 → Rat-bite fever; Haverhill fever,
ds:H01315 → Erysipeloid; Swine erysipelas,
ds:H01316 → Dermatophytosis,
ds:H01317 → Periodontosis, ds:H01318 → Yaws,
ds:H01319 → Coccidioidomycosis; Valley fever,
ds:H01320 → Epidemic keratoconjunctivitis (EKC),
ds:H01321 → Pneumococcal disease, including: Invasive pneumoniae disease;
   Non-invasive pneumoniae disease; Pneumonia due to Streptococcus pneumoniae,
ds:H01322 → Kyasanur Forest disease, ds:H01323 → Acute gastroenteropathy due to Norwalk agent,
ds:H01324 → Lymphocytic choriomeningitis,
ds:H01325 → Actinomycosis,
ds:H01326 → Hand, foot and mouth disease,
ds:H01327 → Herpangina, ds:H01328 → Aspergillosis,
ds:H01329 → Paracoccidioidomycosis,
ds:H01330 → Brazilian purpuric fever (BPF),
ds:H01331 → Dental caries,
ds:H01332 → Helicobacter heilmannii infection,
ds:H01333 → Nonalcoholic fatty liver disease (NAFLD),
ds:H01334 → Tinea versicolor; Pityriasis versicolor,
ds:H01335 → Photorhabdus asymbiotica infection,
ds:H01336 → Encephalitozoon infection,
ds:H01337 → Laribacter hongkongensis infection,
ds:H01338 → Myosclerosis, ds:H01339 → Asymptomatic bacteriuria,
ds:H01340 → Bethlem myopathy,
ds:H01341 → Collagen VI myopathy, including: Ullrich congenital muscular dystrophy
   (UCMD) [DS:H00590]; Bethlem myopathy [DS:H01340]; Myosclerosis [DS:H01338],
ds:H01342 → Zellweger syndrome (ZS), ds:H01343 → Pantoea ananatis infection,
ds:H01344 → Nijmegen Breakage Syndrome, including: Nijmegen
   Breakage Syndrome (NBS); Nijmegen Breakage Syndrome-Like Disorder (NBSLD),
ds:H01345 → Providencia stuartii infection, ds:H01346 → Bloom syndrome,
ds:H01347 → MELAS Syndrome; Mitochondrial myopathy, Encephalopathy, Lactic Acidosis, Stroke-like episodes,
ds:H01348 → Mitochondrial phosphate carrier deficiency (MPCD),
ds:H01349 → Methacrylic aciduria; 3-Hydroxy-isobutyryl-CoA hydrolase (HIBCH) deficiency,
ds:H01350 → Morganella morganii infection,
ds:H01351 → Spastic ataxia (SPAX),
ds:H01352 → Mitochondrial trifunctional protein (TFP) deficiency, including: Long chain 3-hydroxyacyl-CoA
   dehydrogenase (LCHAD) deficiency, ds:H01353 → Chromobacterium violaceum infection, ds:H01354 →
 Leigh syndrome, including: Leigh syndrome, French-Canadian type (LSFC); X-linked Leigh syndrome,
ds:H01355 → Kearns-Sayre Syndrome,
ds:H01356 → Myoclonic Epilepsy and Ragged-Red Fiber Disease; MERRF syndrome; Fukuhara syndrome,
ds:H01357 → Allergic contact dermatitis,
ds:H01358 → Atopic dermatitis,
ds:H01359 → Anaphylaxis, ds:H01360 → Allergic rhinitis,
ds:H01361 → Eosinophilic esophagitis,
ds:H01362 → Dermatitis herpetiformis,
ds:H01363 → NARP syndrome; Neuropathy ataxia and retinis pigmentosa,
ds:H01364 → 3-Hydroxyacyl-CoA dehydrogenase deficiency; HADH deficiency; SCHAD deficiency,
ds:H01365 → Leber hereditary optic neuropathy and dystonia (LDYT),
ds:H01366 → Bacterial conjunctivitis,
ds:H01367 → Infantile liver failure, including: Infantile liver
   failure syndrome (IFLS); Transient infantile liver failure (LFIT), ds:H01368 →
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 Cytochrome c oxidase (COX) deficiency, including: Mitochondrial complex IV deficiency (MT-C4D);
    Fatal infantile cardioencephalomyopathy (CEMCOX) [DS:H01200]; Leigh syndrome (LS) [DS:H01354];
    Kearns-Sayre Syndrome (KSS) [DS:H01355]; Leber Hereditary Optic Neuropathy (LHON) [DS:H00068],
ds:H01369 → ATP synthase deficiency, including: Mitochondrial respiratory chain complex V deficiency
    nuclear type (MC5DN); Mitochondrial respiratory chain complex V deficiency mitochondrial type
    (MC5DM); Mitochondrial encephalo-cardio-myopathy due to mitochondrial respiratory chain complex V
    deficiency; NARP syndrome [DS:H01363]; Mitochondrial infantile bilateral striatal necrosis (MIBSN),
ds:H01370 → SHORT syndrome, ds:H01371 → Hypercalcemia infantile; Idiopathic infantile hypercalcemia,
ds:H01372 → Vitiligo,
ds:H01373 → Achromobacter xylosoxidans infection, including: Achromobacter xylosoxidans keratitis,
ds:H01374 → Helicobacter cinaedi infection,
ds:H01375 → Glucose 6-phosphate dehydrogenase deficiency,
ds:H01376 → Acrofacial dysostosis, including: Nager syndrome; Genee-Wiedemann syndrome; Miller syndrome,
ds:H01377 → Mitchell-Riley syndrome,
ds:H01378 → Bosch-Boonstra optic atrophy syndrome,
ds:H01379 → Arcobacter butzleri infection,
ds:H01380 → Bacterial vaginosis,
ds:H01381 → Antithrombin III deficiency; Inherited Antithrombin deficiency,
ds:H01382 → Polyarteritis nodosa; ADA2 deficiency,
ds:H01383 → LDL Receptor Disorder; Hyperlipoproteinemia type IIa,
ds:H01384 → The ataxia neuropathy spectrum (ANS), including: Mitochondrial recessive ataxia
    syndrome (MIRAS); Sensory ataxic neuropathy, dysarthria, and ophthalmoparesis (SANDO),
ds:H01385 → Rienhoff syndrome, ds:H01386 → Asparagine synthetase deficiency,
ds:H01387 → Activated PI3K-delta syndrome (APDS),
ds:H01388 → Hyperprolactinemia,
ds:H01389 → Alpers syndrome; Alpers-Huttenlocher syndrome; Diffuse cerebral sclerosis of Schilder;
    Hepatocerebral degeneration of childhood; Mitochondrial DNA depletion syndrome 4A,
ds:H01390 → Mitochondrial neurogastrointestinal encephalomyopathy; MNGIE Syndrome,
ds:H01391 → Familial episodic pain syndrome (FEPS),
ds:H01392 → Arthrogryposis, mental retardation, and seizures (AMRS),
ds:H01393 → Van Maldergem syndrome (VMLDS/VMS); Cerebro-facio-articular syndrome,
ds:H01394 → Cole disease, ds:H01395 →
 POLG related disorders, including: Alpers syndrome [DS:H01389]; Childhood myocerebrohepatopathy
    spectrum (MCHS); The ataxia neuropathy spectrum (ANS)  [DS:H01384]; Myoclonic epilepsy
    myopathy sensory ataxia (MEMSA); Progressive external ophthalmoplegia [DS:H01118],
ds:H01396 → Moyamoya Disease, ds:H01397 → Tick-borne lymphadenopathy; Tick-borne lymphadenitis,
ds:H01398 →
 Primary hyperammonemic disorders (Urea cycle disorders), including: N-acetylglutamate synthase (NAGS)
    deficiency [DS:H01032]; Carbamoylphosphate synthetase 1 (CPS1) deficiency [DS:H00164];
    Ornithine carbamoyltransferase (OTC) deficiency [DS:H00187]; Argininosuccinate synthetase
    (ASS) deficiency [DS:H00185]; Argininosuccinate lyase (ASL) deficiency [DS:H01028]; Arginase
    1 (AR1) deficiency [DS:H00186]; Hyperammonemia-Hyperornithinemia-Homocitrullinuria syndrome
    [DS:H01268]; Citrullinemia type II  [DS:H00185], ds:H01399 → Bacillus thuringiensis infection,
ds:H01400 → Secondary hyperammonemia, including: Methylmalonic aciduria [DS:H00174]; Propionic
    aciduria [DS:H00175]; Isovaleric aciduria [DS:H00173]; Fatty acid oxidation and carnitine
    cycle defects [DS:H00525]; Glutaric acidemia [DS:H00178]; Lysinuric protein intolerance
    [DS:H00899]; Pyruvate carboxylase deficiency [DS:H00073]; Ornithinaemia [DS:H00189];
    Hyperinsulinism-hyperammonemia syndrome; Glutamine synthetase deficiency [DS:H00923],
ds:H01401 → Methicillin-resistant Staphylococcus epidermidis (MRSE) infection,
ds:H01402 → Nicolaides-Baraitser syndrome,
ds:H01403 → Coffin-Siris syndrome,
ds:H01404 → Punctate palmoplantar keratoderma (PPKP), including: Brauer-Buschke-Fischer
    disease; Porokeratosis punctata palmaris et plantaris; Acrokeratoelastoidosis,
ds:H01405 → Lactococcus garvieae infection, ds:H01406 → Streptococcus suis infection,
ds:H01407 → Capnocytophaga ochracea infection,
ds:H01408 → Periodontal diseases,
ds:H01409 → Methicillin-sensitive Staphylococcus aureus (MSSA) infection,
ds:H01410 → Anaerobic infection,
ds:H01411 → Saccharomonospora viridis infection,
ds:H01412 → Perlman syndrome,
ds:H01413 → Adams-Oliver syndrome (AOS),
ds:H01414 → Hafnia alvei infection,
ds:H01415 → Donovanosis; Granuloma inguinale,
ds:H01416 → Severe fever with thrombocytopenia syndrome,
ds:H01417 → Acute encephalitis,
ds:H01418 → Condyloma acuminatum; Genital warts,
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ds:H01419 → Middle East respiratory syndrome (MERS),
ds:H01420 → Pharyngoconjunctival fever (PCF),
ds:H01421 → Acute hemorrhagic conjunctivitis,
ds:H01422 → Carbapenem-resistant Enterobacteriaceae (CRE) infection,
ds:H01423 → Penicillin-resistant Streptococcus pneumoniae infection,
ds:H01424 → Group A streptococcal pharyngitis; Group A
   streptococcal tonsillitis; Group A streptococcal pharyngotonsillitis,
ds:H01425 → Lysosomal storage diseases, ds:H01426 → Invasive streptococcal disease,
ds:H01427 → Mitochondrial diseases,
ds:H01428 → Xeroderma pigmentosum (XP),
ds:H01429 → Aseptic meningitis,
ds:H01430 → Viral gastroenteritis, including: Rotaviral enteritis
   [DS:H00975]; Acute gastroenteropathy due to Norwalk agent [DS:H01323],
ds:H01431 → Cushing's syndrome, ds:H01432 → Choreoacanthocytosis, ds:H01433 → Budd-Chiari syndrome,
ds:H01434 → Atypical hemolytic uremic syndrome (aHUS), ds:H01435 →
 Congenital asplenia, including: Isolated congenital asplenia; Asplenia syndrome; Ivemark syndrome,
ds:H01436 → Guillain-Barre syndrome, ds:H01437 → Neurofibromatosis type 1; Von Recklinghausen disease,
ds:H01438 → Neurofibromatosis type 2,
ds:H01439 → Williams-Beuren syndrome,
ds:H01440 → Acute necrotizing ulcerative gingivitis; Vincent's gingivitis; Vincent angina; Trench mouth,
ds:H01441 → Pseudomonas aeruginosa infection,
ds:H01442 → Septic arthritis; Pyogenic arthritis,
ds:H01443 → Viridans group streptococcal infection,
ds:H01444 → Enterococcal infection, ds:H01445 → Acne vulgaris,
ds:H01446 → Propionibacterium acnes infection,
ds:H01447 → Body Dysmorphic Disorder,
ds:H01448 → Hoarding disorder,
ds:H01449 → Excoriation disorder; Skin picking disorder,
ds:H01450 → Obsessive-compulsive disorder (OCD),
ds:H01451 → Actinomycetoma, ds:H01452 →
 Pediatric autoimmune neuropsychiatric disorders associated with streptococcal infection (PANDAS),
ds:H01453 → Obsessive-Compulsive and Related Disorder (OCRD),
ds:H01454 → Colonic spirochetosis,
ds:H01455 → Necrotizing fasciitis,
ds:H01456 → Diabetic nephropathy,
ds:H01457 → Diabetic retinopathy,
ds:H01458 → Nontuberculous mycobacterial infection,
ds:H01459 → Diabetic neuropathy,
ds:H01460 → West syndrome; Infantile spasms (IS),
ds:H01461 → POEMS syndrome; Crow-Fukase syndrome,
ds:H01462 → Rapidly growing mycobacteria infection,
ds:H01463 → Mycosis fungoides,
ds:H01464 → Mantle cell lymphoma, ds:H01465 →
 Large-vessel vasculitis (LVV), including: Giant cell arteritis (GCA); Takayasu arteritis (TAK),
ds:H01466 → Ulcerative colitis (UC), ds:H01467 → Primary biliary cirrhosis (PBC),
ds:H01468 → Eosinophilic granulomatosis with polyangiitis; Churg-Strauss syndrome,
ds:H01469 → Short bowel syndrome (SBS),
ds:H01470 → Giant cell tumor of bone, ds:H01471 → Lymphangioma,
ds:H01472 → Multi-drug-resistant tuberculosis,
ds:H01473 → Erythema nodosum leprosum (ENL),
ds:H01474 → Acquired generalized lipodystrophy (AGL) ; Lawrence syndrome,
ds:H01475 → Lipodystrophy ; Lipoatrophy,
ds:H01476 → Behcet Disease; Behcet Syndrome,
ds:H01477 → Congenital short bowel syndrome (CSBS),
ds:H01478 → Machado-Joseph disease; Spinocerebellar ataxia 3,
ds:H01479 → Castleman disease,
ds:H01480 → Idiopathic macular hole; Retinal Perforations,
ds:H01481 → Myelodysplastic syndrome,
ds:H01482 → Infantile hemangioma,
ds:H01483 → Acromegaly, ds:H01484 → 5q- syndrome,
ds:H01485 → Autosomal recessive mental retardation-42 (MRT42),
ds:H01486 → Multiple congenital anomalies-hypotonia-seizures syndrome (MCAHS),
ds:H01487 → CHIME syndrome; Coloboma, congenital heart disease, ichthyosiform dermatosis,
   mental retardation, and ear anomalies syndrome; Zunich neuroectodermal syndrome,
ds:H01488 → Hyperphosphatasia with mental retardation syndrome (HPMPS); Mabry syndrome,
ds:H01489 → Inherited glycosylphosphatidylinositol (GPI) deficiencies, including: PIGM-congenital
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    disorder of glycosylation (PIGM-CDG) [DS:H01127] ; Autosomal recessive mental retardation-42
    (MRT42) [DS:H01485]; Multiple congential anomalies-hypotonia-seizures (MCAHS) syndrom [DS:H01486];
    CHIME syndrome [DS:H01487]; Hyperphosphatasia with mental retardation syndrome (HPMRS) [DS:H01488],
ds:H01490 → Multiple sclerosis, ds:H01491 → Neuromyelitis optica; Devic disease,
ds:H01492 → Systemic sclerosis; Systemic scleroderma,
ds:H01493 → Localized Scleroderma; Morphea,
ds:H01494 → Spondyloepimetaphyseal dysplasia with joint laxity
    type (SEMD-JL) ; SEMDJL-Beighton type ; SEMDJL-Leptodactylic or Hall type,
ds:H01495 → Meniere disease, ds:H01496 → Spondyloocular syndrome (SOS),
ds:H01497 → Temtamy preaxial brachydactyly syndrome (TPBS),
ds:H01498 → Multiple joint dislocations, short stature, craniofacial
    dysmorphism, and congenital heart defects (JDSSDHD); Larsen-like syndrome,
ds:H01499 → Sporotrichosis, ds:H01500 → Lupus nephritis, ds:H01501 → Blastomycosis,
ds:H01502 → Sjogren's Syndrome,
ds:H01503 → Zygomycosis, including: Mucormycosis; Entomophthoramycosis,
ds:H01504 → Vogt-Koyanagi-Harada syndrome; Vogt-Koyanagi-Harada disease; Uveomeningoencephalitic syndrome,
ds:H01505 → Inclusion body myositis,
ds:H01506 → Hepatic encephalopathy; Hepatic coma,
ds:H01507 → Seronegative arthritis (SpA), including: Ankylosing spondylosis; Undifferentiated
    spondylarthritis; Reactive arthritis; Psoriatic arthritis; Enteropathic arthritis,
ds:H01508 → Salivary gland cancer, ds:H01509 → Tonsillar cancer, ds:H01510 → Malignant paraganglioma,
ds:H01511 → Mast-cell leukemia,
ds:H01512 → Langerhans cell histiocytosis,
ds:H01513 → Retinoblastoma,
ds:H01514 → Landau-Kleffner syndrome; Acquired epileptic aphasia,
ds:H01515 → Scarlet fever; Scarlatina,
ds:H01516 → Adult onset Still's disease; Adult Still's disease,
ds:H01517 → Erysipelas,
ds:H01518 → Lobomycosis; Lobo's disease; Lacaziosis,
ds:H01519 → Scabies, ds:H01520 → Chromomycosis; Chromoblastomycosis,
ds:H01521 → Pneumocystis pneumonia,
ds:H01522 → Zollinger-Ellison Syndrome (ZES),
ds:H01523 → Wiskott-Aldrich syndrome,
ds:H01524 → DiGeorge syndrome,
ds:H01525 → 22q11.2 deletion syndrome; DiGeorge/ Velo-Cardio-Facial syndrome; CATCH22,
ds:H01526 → Legg-Calve-Perthes Disease,
ds:H01529 → Avascular necrosis of femoral head; Osteonecrosis of the femoral head,
ds:H01530 → Pinta; Mal del pinto; Carate,
ds:H01531 → Bejel; Endemic syphilis,
ds:H01532 → Gout, ds:H01533 → Japanese encephalitis,
ds:H01534 → Western equine encephalitis,
ds:H01535 → Eastern equine encephalitis,
ds:H01536 → Murray Valley encephalitis; Australian encephalitis,
ds:H01537 → California encephalitis; La Crosse encephalitis,
ds:H01538 → Hendra virus infection,
ds:H01539 → Nipah virus infection,
ds:H01540 → Chikungunya fever,
ds:H01541 → Argentine hemorrhagic fever,
ds:H01542 → Bolivian hemorrhagic fever,
ds:H01543 → Venezuelan hemorrhagic fever,
ds:H01544 → Brazilian hemorrhagic fever,
ds:H01545 → O'nyong-nyong fever, ds:H01546 → Mayaro fever,
ds:H01547 → Venezuelan equine fever,
ds:H01548 → West Nile fever; West Nile virus infection,
ds:H01549 → Rift Valley fever, ds:H01550 → Bunyamwera fever,
ds:H01551 → Interstitial cystitis (IC); Bladder pain syndrome (BPS),
ds:H01552 → Down syndrome; Trisomy 21,
ds:H01553 → Zika fever; Zika virus disease,
ds:H01554 → Fallopian tube cancer,
ds:H01555 → Merkel cell carcinoma,
ds:H01556 → Meningioma, ds:H01557 → Hepatic angiosarcoma,
ds:H01558 → Parathyroid carcinoma,
ds:H01559 → Oropharyngeal cancer,
ds:H01560 → Alkhumra hemorrhagic fever (AHF),
ds:H01561 → Chiari malformation; Arnold-Chiari syndrome,
ds:H01562 → Patau syndrome; Trisomy 13,
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ds:H01563 → HIV infection,
ds:H01564 → Edwards syndrome; Trisomy 18,
ds:H01565 → Wernicke encephalopathy; Wernicke-Korsakoff syndrome,
ds:H01566 → Beriberi,
ds:H01567 → Thiamine pyrophosphokinase deficiency; Thiamine metabolism dysfunction syndrome 5,
ds:H01568 → 3C syndrome; Ritscher-Schinzel syndrome; Craniocerebellocardiac dysplasia,
ds:H01569 → CHOPS syndrome,
ds:H01570 → Autosomal dominant striatal degeneration (ADSD),
ds:H01571 → Singleton-Merten syndrome (SMS),
ds:H01572 → Cole-Carpenter syndrome,
ds:H01573 → Zimmermann-Laband syndrome (ZLS),
ds:H01574 → Familial idiopathic basal ganglia calcification;
   Bilateral striopallidodentate calcinosis (BSPDC); Fahr's disease,
ds:H01575 → Roifman syndrome; Spondyloepiphseal dysplasia, retinal dystrophy, and antibody deficiency,
ds:H01576 →
 Spondyloenchondrodysplasia with immune dysregulation (SPENCDI); Spondyloenchondrodysplasia (SPENCD),
ds:H01577 → Essential tremor, ds:H01578 → Subacute myelo-optico-neuropathy (SMON), ds:H01579 →
 Congenital symmetric circumferential skin creases; Kunze-Riehm syndrome; Michelin tire baby syndrome,
ds:H01580 → Vitamin C deficiency; Scurvy, ds:H01581 → IgA nephropathy; Berger disease,
ds:H01582 → Pellagra,
ds:H01583 → Hydroxykynureninuria; Xanthurenic aciduria; Kynureninase deficiency,
ds:H01584 → Allergic purpura; Henoch-Schonlein purpura,
ds:H01585 → Autoimmune hemolytic anemia (AIHA),
ds:H01586 → Acquired pure red cell aplasia,
ds:H01587 → Disseminated intravascular coagulation (DIC),
ds:H01588 → Cluster headache,
ds:H01589 → Systemic primary carnitine deficiency,
ds:H01590 → Chronic eosinophilic leukemia,
ds:H01591 → Gastrotintestinal stromal tumor,
ds:H01592 → Medullary thyroid cancer,
ds:H01593 → Osteoporosis, ds:H01594 → Myasthenia gravis,
ds:H01595 → Cutaneous lupus erythematosus,
ds:H01596 → Lambert-Eaton myasthenic syndrome (LEMS),
ds:H01597 → Restless legs syndrome; Willis Ekbom disease,
ds:H01598 → Primary adrenal insufficiency; Hypoadrenocorticism; Addison's disease,
ds:H01599 → Hypereosinophilic syndrome,
ds:H01600 → Parkinsonian syndrome,
ds:H01601 → Anaplastic large-cell lymphoma,
ds:H01602 → Gastroesophageal reflux disease (GERD), including:
   Non-erosive reflux disease (NERD); Erosive reflux disease (ERD),
ds:H01603 → Primary aldosteronism, ds:H01604 → Polymyositis and dermatomyositis (PM/DM),
ds:H01605 → Myelofibrosis, ds:H01606 → Polymyalgia rheumatica,
ds:H01607 → Galactorrhea; Lactation suppression,
ds:H01608 → Cervical dystonia; Spasmodic torticollis,
ds:H01609 → Insomnia, ds:H01610 → Clonorchiasis,
ds:H01611 → Alcohol dependence,
ds:H01612 → Essential thrombocytosis,
ds:H01613 → Follicular lymphoma,
ds:H01614 → Multiple system atrophy, including: Striatonigral
   degeneration; Olivopontocerebellar atrophy; Shy-Drager syndrome,
ds:H01615 → Irritable bowel syndrome, ds:H01616 → Spinocerebellar Degeneration, including:
   Spinocerebellar ataxia (SCA) [DS:H00063]; Dentatorubropallidoluysian atrophy (DRPLA)
   [DS:H00060]; Friedreich ataxia [DS:H00067]; Multiple system atrophy [DS:H01614],
ds:H01617 → Foodborne trematodiasis; Food-borne trematode infections,
ds:H01618 → Pituitary gigantism,
ds:H01619 → Primary pulmonary hypertension (PPH),
ds:H01620 → Raynaud syndrome, including: Raynaud disease; Raynaud phenomenon,
ds:H01621 → Pulmonary arterial hypertension (PAH),
ds:H01622 → Chronic thromboembolic pulmonary hypertension,
ds:H01624 → Postherpetic neuralgia,
ds:H01625 → Buerger's disease; Thromboangiitis obliterans,
ds:H01626 → Arteriosclerosis obliterans,
ds:H01628 → Opisthorchiasis,
ds:H01629 → Chronic arterial occlusive disease,
ds:H01630 → Patent ductus arteriosus,
ds:H01631 → Acute heart failure, ds:H01632 → Angina pectoris,
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ds:H01633 → High blood pressure; Hypertension,
ds:H01634 → Peptic ulcer,
ds:H01635 → Hyperlipidemia, including: Hyperlipoproteinemia;
   Hypercholesterolemia; Hypertriglyceridemia; Mixed dyslipidemia,
ds:H01636 → Fibromyalgia; Fibromyalgia syndrome, ds:H01637 → Hypertriglyceridemia,
ds:H01638 → Neuropathic pain; Neuralgia, ds:H01639 → Endometriosis,
ds:H01640 → Uterine leiomyoma; Fibroid|〉
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KEGGQuery2 (4)

```
In[1]:= Needs["MathIOmica`"]
```

KEGGQuery2 is the text used internally by KEGG API calls, specifically as specifically as string query2 in "http://rest.kegg.jp/list/" <> query1 <> "/" <> query2. Typically this will be used as the organism code (org) to return a list of entry identifiers and associated definition for the database specified by KEGGQuery1. The default use is to list human pathway annotations and corresponds to setting the organism org="hsa".

```
In[2]:= dictionaryPathwayHumanQuery2 = KEGGDictionary[KEGGQuery2 → "hsa"]

Out[2]= 〈|path:hsa00010 → Glycolysis / Gluconeogenesis - Homo sapiens (human),
 path:hsa00020 → Citrate cycle (TCA cycle) - Homo sapiens (human),
 path:hsa00030 → Pentose phosphate pathway - Homo sapiens (human),
 path:hsa00040 → Pentose and glucuronate interconversions - Homo sapiens (human),
 path:hsa00051 → Fructose and mannose metabolism - Homo sapiens (human),
 path:hsa00052 → Galactose metabolism - Homo sapiens (human),
 path:hsa00053 → Ascorbate and aldarate metabolism - Homo sapiens (human),
 path:hsa00061 → Fatty acid biosynthesis - Homo sapiens (human),
 path:hsa00062 → Fatty acid elongation - Homo sapiens (human),
 path:hsa00071 → Fatty acid degradation - Homo sapiens (human),
 path:hsa00072 → Synthesis and degradation of ketone bodies - Homo sapiens (human),
 path:hsa00100 → Steroid biosynthesis - Homo sapiens (human),
 path:hsa00120 → Primary bile acid biosynthesis - Homo sapiens (human),
 path:hsa00130 → Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human),
 path:hsa00140 → Steroid hormone biosynthesis - Homo sapiens (human),
 path:hsa00190 → Oxidative phosphorylation - Homo sapiens (human),
 path:hsa00220 → Arginine biosynthesis - Homo sapiens (human),
 path:hsa00230 → Purine metabolism - Homo sapiens (human),
 path:hsa00232 → Caffeine metabolism - Homo sapiens (human),
 path:hsa00240 → Pyrimidine metabolism - Homo sapiens (human),
 path:hsa00250 → Alanine, aspartate and glutamate metabolism - Homo sapiens (human),
 path:hsa00260 → Glycine, serine and threonine metabolism - Homo sapiens (human),
 path:hsa00270 → Cysteine and methionine metabolism - Homo sapiens (human),
 path:hsa00280 → Valine, leucine and isoleucine degradation - Homo sapiens (human),
 path:hsa00290 → Valine, leucine and isoleucine biosynthesis - Homo sapiens (human),
 path:hsa00310 → Lysine degradation - Homo sapiens (human),
 path:hsa00330 → Arginine and proline metabolism - Homo sapiens (human),
 path:hsa00340 → Histidine metabolism - Homo sapiens (human),
 path:hsa00350 → Tyrosine metabolism - Homo sapiens (human),
 path:hsa00360 → Phenylalanine metabolism - Homo sapiens (human),
 path:hsa00380 → Tryptophan metabolism - Homo sapiens (human),
 path:hsa00400 → Phenylalanine, tyrosine and tryptophan biosynthesis - Homo sapiens (human),
 path:hsa00410 → beta-Alanine metabolism - Homo sapiens (human),
 path:hsa00430 → Taurine and hypotaurine metabolism - Homo sapiens (human),
 path:hsa00440 → Phosphonate and phosphinate metabolism - Homo sapiens (human),
 path:hsa00450 → Selenocompound metabolism - Homo sapiens (human),
 path:hsa00471 → D-Glutamine and D-glutamate metabolism - Homo sapiens (human),
 path:hsa00472 → D-Arginine and D-ornithine metabolism - Homo sapiens (human),
 path:hsa00480 → Glutathione metabolism - Homo sapiens (human),
 path:hsa00500 → Starch and sucrose metabolism - Homo sapiens (human),
 path:hsa00510 → N-Glycan biosynthesis - Homo sapiens (human),
 path:hsa00511 → Other glycan degradation - Homo sapiens (human),
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path:hsa00512 → Mucin type O-glycan biosynthesis - Homo sapiens (human),
path:hsa00514 → Other types of O-glycan biosynthesis - Homo sapiens (human),
path:hsa00515 → Mannose type O-glycan biosynthesis - Homo sapiens (human),
path:hsa00520 → Amino sugar and nucleotide sugar metabolism - Homo sapiens (human),
path:hsa00524 → Neomycin, kanamycin and gentamicin biosynthesis - Homo sapiens (human),
path:hsa00531 → Glycosaminoglycan degradation - Homo sapiens (human), path:hsa00532 →
 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Homo sapiens (human),
path:hsa00533 → Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human),
path:hsa00534 → Glycosaminoglycan biosynthesis - heparan sulfate / heparin - Homo sapiens (human),
path:hsa00561 → Glycerolipid metabolism - Homo sapiens (human),
path:hsa00562 → Inositol phosphate metabolism - Homo sapiens (human),
path:hsa00563 → Glycosylphosphatidylinositol (GPI)-anchor biosynthesis - Homo sapiens (human),
path:hsa00564 → Glycerophospholipid metabolism - Homo sapiens (human),
path:hsa00565 → Ether lipid metabolism - Homo sapiens (human),
path:hsa00590 → Arachidonic acid metabolism - Homo sapiens (human),
path:hsa00591 → Linoleic acid metabolism - Homo sapiens (human),
path:hsa00592 → alpha-Linolenic acid metabolism - Homo sapiens (human),
path:hsa00600 → Sphingolipid metabolism - Homo sapiens (human),
path:hsa00601 → Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human),
path:hsa00603 → Glycosphingolipid biosynthesis - globo and isoglobo series - Homo sapiens (human),
path:hsa00604 → Glycosphingolipid biosynthesis - ganglio series - Homo sapiens (human),
path:hsa00620 → Pyruvate metabolism - Homo sapiens (human),
path:hsa00630 → Glyoxylate and dicarboxylate metabolism - Homo sapiens (human),
path:hsa00640 → Propanoate metabolism - Homo sapiens (human),
path:hsa00650 → Butanoate metabolism - Homo sapiens (human),
path:hsa00670 → One carbon pool by folate - Homo sapiens (human),
path:hsa00730 → Thiamine metabolism - Homo sapiens (human),
path:hsa00740 → Riboflavin metabolism - Homo sapiens (human),
path:hsa00750 → Vitamin B6 metabolism - Homo sapiens (human),
path:hsa00760 → Nicotinate and nicotinamide metabolism - Homo sapiens (human),
path:hsa00770 → Pantothenate and CoA biosynthesis - Homo sapiens (human),
path:hsa00780 → Biotin metabolism - Homo sapiens (human),
path:hsa00785 → Lipoic acid metabolism - Homo sapiens (human),
path:hsa00790 → Folate biosynthesis - Homo sapiens (human),
path:hsa00830 → Retinol metabolism - Homo sapiens (human),
path:hsa00860 → Porphyrin and chlorophyll metabolism - Homo sapiens (human),
path:hsa00900 → Terpenoid backbone biosynthesis - Homo sapiens (human),
path:hsa00910 → Nitrogen metabolism - Homo sapiens (human),
path:hsa00920 → Sulfur metabolism - Homo sapiens (human),
path:hsa00970 → Aminoacyl-tRNA biosynthesis - Homo sapiens (human),
path:hsa00980 → Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human),
path:hsa00982 → Drug metabolism - cytochrome P450 - Homo sapiens (human),
path:hsa00983 → Drug metabolism - other enzymes - Homo sapiens (human),
path:hsa01040 → Biosynthesis of unsaturated fatty acids - Homo sapiens (human),
path:hsa01100 → Metabolic pathways - Homo sapiens (human),
path:hsa01200 → Carbon metabolism - Homo sapiens (human),
path:hsa01210 → 2-Oxocarboxylic acid metabolism - Homo sapiens (human),
path:hsa01212 → Fatty acid metabolism - Homo sapiens (human),
path:hsa01230 → Biosynthesis of amino acids - Homo sapiens (human),
path:hsa01521 → EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human),
path:hsa01522 → Endocrine resistance - Homo sapiens (human),
path:hsa01523 → Antifolate resistance - Homo sapiens (human),
path:hsa01524 → Platinum drug resistance - Homo sapiens (human),
path:hsa02010 → ABC transporters - Homo sapiens (human),
path:hsa03008 → Ribosome biogenesis in eukaryotes - Homo sapiens (human),
path:hsa03010 → Ribosome - Homo sapiens (human), path:hsa03013 → RNA transport - Homo sapiens (human),
path:hsa03015 → mRNA surveillance pathway - Homo sapiens (human),
path:hsa03018 → RNA degradation - Homo sapiens (human),
path:hsa03020 → RNA polymerase - Homo sapiens (human),
path:hsa03022 → Basal transcription factors - Homo sapiens (human),
path:hsa03030 → DNA replication - Homo sapiens (human), path:hsa03040 → Spliceosome - Homo sapiens (human),
path:hsa03050 → Proteasome - Homo sapiens (human), path:hsa03060 → Protein export - Homo sapiens (human),
path:hsa03320 → PPAR signaling pathway - Homo sapiens (human),
path:hsa03410 → Base excision repair - Homo sapiens (human),
path:hsa03420 → Nucleotide excision repair - Homo sapiens (human),
path:hsa03430 → Mismatch repair - Homo sapiens (human),
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path:hsa03440 → Homologous recombination - Homo sapiens (human),
path:hsa03450 → Non-homologous end-joining - Homo sapiens (human),
path:hsa03460 → Fanconi anemia pathway - Homo sapiens (human),
path:hsa04010 → MAPK signaling pathway - Homo sapiens (human),
path:hsa04012 → ErbB signaling pathway - Homo sapiens (human),
path:hsa04014 → Ras signaling pathway - Homo sapiens (human),
path:hsa04015 → Rap1 signaling pathway - Homo sapiens (human),
path:hsa04020 → Calcium signaling pathway - Homo sapiens (human),
path:hsa04022 → cGMP-PKG signaling pathway - Homo sapiens (human),
path:hsa04024 → cAMP signaling pathway - Homo sapiens (human),
path:hsa04060 → Cytokine-cytokine receptor interaction - Homo sapiens (human),
path:hsa04061 → Viral protein interaction with cytokine and cytokine receptor - Homo sapiens (human),
path:hsa04062 → Chemokine signaling pathway - Homo sapiens (human),
path:hsa04064 → NF-kappa B signaling pathway - Homo sapiens (human),
path:hsa04066 → HIF-1 signaling pathway - Homo sapiens (human),
path:hsa04068 → FoxO signaling pathway - Homo sapiens (human),
path:hsa04070 → Phosphatidylinositol signaling system - Homo sapiens (human),
path:hsa04071 → Sphingolipid signaling pathway - Homo sapiens (human),
path:hsa04072 → Phospholipase D signaling pathway - Homo sapiens (human),
path:hsa04080 → Neuroactive ligand-receptor interaction - Homo sapiens (human),
path:hsa04110 → Cell cycle - Homo sapiens (human), path:hsa04114 → Oocyte meiosis - Homo sapiens (human),
path:hsa04115 → p53 signaling pathway - Homo sapiens (human),
path:hsa04120 → Ubiquitin mediated proteolysis - Homo sapiens (human),
path:hsa04122 → Sulfur relay system - Homo sapiens (human),
path:hsa04130 → SNARE interactions in vesicular transport - Homo sapiens (human),
path:hsa04136 → Autophagy - other - Homo sapiens (human),
path:hsa04137 → Mitophagy - animal - Homo sapiens (human),
path:hsa04140 → Autophagy - animal - Homo sapiens (human),
path:hsa04141 → Protein processing in endoplasmic reticulum - Homo sapiens (human),
path:hsa04142 → Lysosome - Homo sapiens (human), path:hsa04144 → Endocytosis - Homo sapiens (human),
path:hsa04145 → Phagosome - Homo sapiens (human), path:hsa04146 → Peroxisome - Homo sapiens (human),
path:hsa04150 → mTOR signaling pathway - Homo sapiens (human),
path:hsa04151 → PI3K-Akt signaling pathway - Homo sapiens (human),
path:hsa04152 → AMPK signaling pathway - Homo sapiens (human),
path:hsa04210 → Apoptosis - Homo sapiens (human),
path:hsa04211 → Longevity regulating pathway - Homo sapiens (human),
path:hsa04213 → Longevity regulating pathway - multiple species - Homo sapiens (human),
path:hsa04215 → Apoptosis - multiple species - Homo sapiens (human),
path:hsa04216 → Ferroptosis - Homo sapiens (human), path:hsa04217 → Necroptosis - Homo sapiens (human),
path:hsa04218 → Cellular senescence - Homo sapiens (human),
path:hsa04260 → Cardiac muscle contraction - Homo sapiens (human),
path:hsa04261 → Adrenergic signaling in cardiomyocytes - Homo sapiens (human),
path:hsa04270 → Vascular smooth muscle contraction - Homo sapiens (human),
path:hsa04310 → Wnt signaling pathway - Homo sapiens (human),
path:hsa04330 → Notch signaling pathway - Homo sapiens (human),
path:hsa04340 → Hedgehog signaling pathway - Homo sapiens (human),
path:hsa04350 → TGF-beta signaling pathway - Homo sapiens (human),
path:hsa04360 → Axon guidance - Homo sapiens (human),
path:hsa04370 → VEGF signaling pathway - Homo sapiens (human),
path:hsa04371 → Apelin signaling pathway - Homo sapiens (human),
path:hsa04380 → Osteoclast differentiation - Homo sapiens (human),
path:hsa04390 → Hippo signaling pathway - Homo sapiens (human),
path:hsa04392 → Hippo signaling pathway - multiple species - Homo sapiens (human),
path:hsa04510 → Focal adhesion - Homo sapiens (human),
path:hsa04512 → ECM-receptor interaction - Homo sapiens (human),
path:hsa04514 → Cell adhesion molecules (CAMs) - Homo sapiens (human),
path:hsa04520 → Adherens junction - Homo sapiens (human),
path:hsa04530 → Tight junction - Homo sapiens (human), path:hsa04540 → Gap junction - Homo sapiens (human),
path:hsa04550 → Signaling pathways regulating pluripotency of stem cells - Homo sapiens (human),
path:hsa04610 → Complement and coagulation cascades - Homo sapiens (human),
path:hsa04611 → Platelet activation - Homo sapiens (human),
path:hsa04612 → Antigen processing and presentation - Homo sapiens (human),
path:hsa04614 → Renin-angiotensin system - Homo sapiens (human),
path:hsa04620 → Toll-like receptor signaling pathway - Homo sapiens (human),
path:hsa04621 → NOD-like receptor signaling pathway - Homo sapiens (human),
path:hsa04622 → RIG-I-like receptor signaling pathway - Homo sapiens (human),
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path:hsa04623 → Cytosolic DNA-sensing pathway - Homo sapiens (human),
path:hsa04625 → C-type lectin receptor signaling pathway - Homo sapiens (human),
path:hsa04630 → JAK-STAT signaling pathway - Homo sapiens (human),
path:hsa04640 → Hematopoietic cell lineage - Homo sapiens (human),
path:hsa04650 → Natural killer cell mediated cytotoxicity - Homo sapiens (human),
path:hsa04657 → IL-17 signaling pathway - Homo sapiens (human),
path:hsa04658 → Th1 and Th2 cell differentiation - Homo sapiens (human),
path:hsa04659 → Th17 cell differentiation - Homo sapiens (human),
path:hsa04660 → T cell receptor signaling pathway - Homo sapiens (human),
path:hsa04662 → B cell receptor signaling pathway - Homo sapiens (human),
path:hsa04664 → Fc epsilon RI signaling pathway - Homo sapiens (human),
path:hsa04666 → Fc gamma R-mediated phagocytosis - Homo sapiens (human),
path:hsa04668 → TNF signaling pathway - Homo sapiens (human),
path:hsa04670 → Leukocyte transendothelial migration - Homo sapiens (human),
path:hsa04672 → Intestinal immune network for IgA production - Homo sapiens (human),
path:hsa04710 → Circadian rhythm - Homo sapiens (human),
path:hsa04713 → Circadian entrainment - Homo sapiens (human),
path:hsa04714 → Thermogenesis - Homo sapiens (human),
path:hsa04720 → Long-term potentiation - Homo sapiens (human),
path:hsa04721 → Synaptic vesicle cycle - Homo sapiens (human),
path:hsa04722 → Neurotrophin signaling pathway - Homo sapiens (human),
path:hsa04723 → Retrograde endocannabinoid signaling - Homo sapiens (human),
path:hsa04724 → Glutamatergic synapse - Homo sapiens (human),
path:hsa04725 → Cholinergic synapse - Homo sapiens (human),
path:hsa04726 → Serotonergic synapse - Homo sapiens (human),
path:hsa04727 → GABAergic synapse - Homo sapiens (human),
path:hsa04728 → Dopaminergic synapse - Homo sapiens (human),
path:hsa04730 → Long-term depression - Homo sapiens (human),
path:hsa04740 → Olfactory transduction - Homo sapiens (human),
path:hsa04742 → Taste transduction - Homo sapiens (human),
path:hsa04744 → Phototransduction - Homo sapiens (human),
path:hsa04750 → Inflammatory mediator regulation of TRP channels - Homo sapiens (human),
path:hsa04810 → Regulation of actin cytoskeleton - Homo sapiens (human),
path:hsa04910 → Insulin signaling pathway - Homo sapiens (human),
path:hsa04911 → Insulin secretion - Homo sapiens (human),
path:hsa04912 → GnRH signaling pathway - Homo sapiens (human),
path:hsa04913 → Ovarian steroidogenesis - Homo sapiens (human),
path:hsa04914 → Progesterone-mediated oocyte maturation - Homo sapiens (human),
path:hsa04915 → Estrogen signaling pathway - Homo sapiens (human),
path:hsa04916 → Melanogenesis - Homo sapiens (human),
path:hsa04917 → Prolactin signaling pathway - Homo sapiens (human),
path:hsa04918 → Thyroid hormone synthesis - Homo sapiens (human),
path:hsa04919 → Thyroid hormone signaling pathway - Homo sapiens (human),
path:hsa04920 → Adipocytokine signaling pathway - Homo sapiens (human),
path:hsa04921 → Oxytocin signaling pathway - Homo sapiens (human),
path:hsa04922 → Glucagon signaling pathway - Homo sapiens (human),
path:hsa04923 → Regulation of lipolysis in adipocytes - Homo sapiens (human),
path:hsa04924 → Renin secretion - Homo sapiens (human),
path:hsa04925 → Aldosterone synthesis and secretion - Homo sapiens (human),
path:hsa04926 → Relaxin signaling pathway - Homo sapiens (human),
path:hsa04927 → Cortisol synthesis and secretion - Homo sapiens (human),
path:hsa04928 → Parathyroid hormone synthesis, secretion and action - Homo sapiens (human),
path:hsa04930 → Type II diabetes mellitus - Homo sapiens (human),
path:hsa04931 → Insulin resistance - Homo sapiens (human),
path:hsa04932 → Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
path:hsa04933 → AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human),
path:hsa04934 → Cushing syndrome - Homo sapiens (human),
path:hsa04940 → Type I diabetes mellitus - Homo sapiens (human),
path:hsa04950 → Maturity onset diabetes of the young - Homo sapiens (human),
path:hsa04960 → Aldosterone-regulated sodium reabsorption - Homo sapiens (human),
path:hsa04961 → Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
path:hsa04962 → Vasopressin-regulated water reabsorption - Homo sapiens (human),
path:hsa04964 → Proximal tubule bicarbonate reclamation - Homo sapiens (human),
path:hsa04966 → Collecting duct acid secretion - Homo sapiens (human),
path:hsa04970 → Salivary secretion - Homo sapiens (human),
path:hsa04971 → Gastric acid secretion - Homo sapiens (human),
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path:hsa04972 → Pancreatic secretion - Homo sapiens (human),
path:hsa04973 → Carbohydrate digestion and absorption - Homo sapiens (human),
path:hsa04974 → Protein digestion and absorption - Homo sapiens (human),
path:hsa04975 → Fat digestion and absorption - Homo sapiens (human),
path:hsa04976 → Bile secretion - Homo sapiens (human),
path:hsa04977 → Vitamin digestion and absorption - Homo sapiens (human),
path:hsa04978 → Mineral absorption - Homo sapiens (human),
path:hsa04979 → Cholesterol metabolism - Homo sapiens (human),
path:hsa05010 → Alzheimer disease - Homo sapiens (human),
path:hsa05012 → Parkinson disease - Homo sapiens (human),
path:hsa05014 → Amyotrophic lateral sclerosis (ALS) - Homo sapiens (human),
path:hsa05016 → Huntington disease - Homo sapiens (human),
path:hsa05020 → Prion diseases - Homo sapiens (human),
path:hsa05030 → Cocaine addiction - Homo sapiens (human),
path:hsa05031 → Amphetamine addiction - Homo sapiens (human),
path:hsa05032 → Morphine addiction - Homo sapiens (human),
path:hsa05033 → Nicotine addiction - Homo sapiens (human),
path:hsa05034 → Alcoholism - Homo sapiens (human),
path:hsa05100 → Bacterial invasion of epithelial cells - Homo sapiens (human),
path:hsa05110 → Vibrio cholerae infection - Homo sapiens (human),
path:hsa05120 → Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
path:hsa05130 → Pathogenic Escherichia coli infection - Homo sapiens (human),
path:hsa05131 → Shigellosis - Homo sapiens (human),
path:hsa05132 → Salmonella infection - Homo sapiens (human),
path:hsa05133 → Pertussis - Homo sapiens (human), path:hsa05134 → Legionellosis - Homo sapiens (human),
path:hsa05135 → Yersinia infection - Homo sapiens (human),
path:hsa05140 → Leishmaniasis - Homo sapiens (human),
path:hsa05142 → Chagas disease (American trypanosomiasis) - Homo sapiens (human),
path:hsa05143 → African trypanosomiasis - Homo sapiens (human),
path:hsa05144 → Malaria - Homo sapiens (human), path:hsa05145 → Toxoplasmosis - Homo sapiens (human),
path:hsa05146 → Amoebiasis - Homo sapiens (human),
path:hsa05150 → Staphylococcus aureus infection - Homo sapiens (human),
path:hsa05152 → Tuberculosis - Homo sapiens (human), path:hsa05160 → Hepatitis C - Homo sapiens (human),
path:hsa05161 → Hepatitis B - Homo sapiens (human), path:hsa05162 → Measles - Homo sapiens (human),
path:hsa05163 → Human cytomegalovirus infection - Homo sapiens (human),
path:hsa05164 → Influenza A - Homo sapiens (human),
path:hsa05165 → Human papillomavirus infection - Homo sapiens (human),
path:hsa05166 → Human T-cell leukemia virus 1 infection - Homo sapiens (human),
path:hsa05167 → Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human),
path:hsa05168 → Herpes simplex virus 1 infection - Homo sapiens (human),
path:hsa05169 → Epstein-Barr virus infection - Homo sapiens (human),
path:hsa05170 → Human immunodeficiency virus 1 infection - Homo sapiens (human),
path:hsa05200 → Pathways in cancer - Homo sapiens (human),
path:hsa05202 → Transcriptional misregulation in cancer - Homo sapiens (human),
path:hsa05203 → Viral carcinogenesis - Homo sapiens (human),
path:hsa05204 → Chemical carcinogenesis - Homo sapiens (human),
path:hsa05205 → Proteoglycans in cancer - Homo sapiens (human),
path:hsa05206 → MicroRNAs in cancer - Homo sapiens (human),
path:hsa05210 → Colorectal cancer - Homo sapiens (human),
path:hsa05211 → Renal cell carcinoma - Homo sapiens (human),
path:hsa05212 → Pancreatic cancer - Homo sapiens (human),
path:hsa05213 → Endometrial cancer - Homo sapiens (human),
path:hsa05214 → Glioma - Homo sapiens (human), path:hsa05215 → Prostate cancer - Homo sapiens (human),
path:hsa05216 → Thyroid cancer - Homo sapiens (human),
path:hsa05217 → Basal cell carcinoma - Homo sapiens (human),
path:hsa05218 → Melanoma - Homo sapiens (human), path:hsa05219 → Bladder cancer - Homo sapiens (human),
path:hsa05220 → Chronic myeloid leukemia - Homo sapiens (human),
path:hsa05221 → Acute myeloid leukemia - Homo sapiens (human),
path:hsa05222 → Small cell lung cancer - Homo sapiens (human),
path:hsa05223 → Non-small cell lung cancer - Homo sapiens (human),
path:hsa05224 → Breast cancer - Homo sapiens (human),
path:hsa05225 → Hepatocellular carcinoma - Homo sapiens (human),
path:hsa05226 → Gastric cancer - Homo sapiens (human),
path:hsa05230 → Central carbon metabolism in cancer - Homo sapiens (human),
path:hsa05231 → Choline metabolism in cancer - Homo sapiens (human),
path:hsa05235 → PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
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path:hsa05310 → Asthma - Homo sapiens (human),
path:hsa05320 → Autoimmune thyroid disease - Homo sapiens (human),
path:hsa05321 → Inflammatory bowel disease (IBD) - Homo sapiens (human),
path:hsa05322 → Systemic lupus erythematosus - Homo sapiens (human),
path:hsa05323 → Rheumatoid arthritis - Homo sapiens (human),
path:hsa05330 → Allograft rejection - Homo sapiens (human),
path:hsa05332 → Graft-versus-host disease - Homo sapiens (human),
path:hsa05340 → Primary immunodeficiency - Homo sapiens (human),
path:hsa05410 → Hypertrophic cardiomyopathy (HCM) - Homo sapiens (human),
path:hsa05412 → Arrhythmogenic right ventricular cardiomyopathy (ARVC) - Homo sapiens (human),
path:hsa05414 → Dilated cardiomyopathy (DCM) - Homo sapiens (human),
path:hsa05416 → Viral myocarditis - Homo sapiens (human),
path:hsa05418 → Fluid shear stress and atherosclerosis - Homo sapiens (human)|⟩
```

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In[1]:= Needs["MathIOmica`"]
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We can query for example mouse information

```
In[2]:= dictionaryPathwayMmuQuery2 = KEGGDictionary[KEGGQuery2 → "mmu"]
```

```
Out[2]= ⟨|path:mmu00010 → Glycolysis / Gluconeogenesis - Mus musculus (mouse),
path:mmu00020 → Citrate cycle (TCA cycle) - Mus musculus (mouse),
path:mmu00030 → Pentose phosphate pathway - Mus musculus (mouse),
path:mmu00040 → Pentose and glucuronate interconversions - Mus musculus (mouse),
path:mmu00051 → Fructose and mannose metabolism - Mus musculus (mouse),
path:mmu00052 → Galactose metabolism - Mus musculus (mouse),
path:mmu00053 → Ascorbate and aldarate metabolism - Mus musculus (mouse),
path:mmu00061 → Fatty acid biosynthesis - Mus musculus (mouse),
path:mmu00062 → Fatty acid elongation - Mus musculus (mouse),
path:mmu00071 → Fatty acid degradation - Mus musculus (mouse),
path:mmu00072 → Synthesis and degradation of ketone bodies - Mus musculus (mouse),
path:mmu00100 → Steroid biosynthesis - Mus musculus (mouse),
path:mmu00120 → Primary bile acid biosynthesis - Mus musculus (mouse),
path:mmu00130 → Ubiquinone and other terpenoid-quinone biosynthesis - Mus musculus (mouse),
path:mmu00140 → Steroid hormone biosynthesis - Mus musculus (mouse),
path:mmu00190 → Oxidative phosphorylation - Mus musculus (mouse),
path:mmu00220 → Arginine biosynthesis - Mus musculus (mouse),
path:mmu00230 → Purine metabolism - Mus musculus (mouse),
path:mmu00232 → Caffeine metabolism - Mus musculus (mouse),
path:mmu00240 → Pyrimidine metabolism - Mus musculus (mouse),
path:mmu00250 → Alanine, aspartate and glutamate metabolism - Mus musculus (mouse),
path:mmu00260 → Glycine, serine and threonine metabolism - Mus musculus (mouse),
path:mmu00270 → Cysteine and methionine metabolism - Mus musculus (mouse),
path:mmu00280 → Valine, leucine and isoleucine degradation - Mus musculus (mouse),
path:mmu00290 → Valine, leucine and isoleucine biosynthesis - Mus musculus (mouse),
path:mmu00300 → Lysine biosynthesis - Mus musculus (mouse),
path:mmu00310 → Lysine degradation - Mus musculus (mouse),
path:mmu00330 → Arginine and proline metabolism - Mus musculus (mouse),
path:mmu00340 → Histidine metabolism - Mus musculus (mouse),
path:mmu00350 → Tyrosine metabolism - Mus musculus (mouse),
path:mmu00360 → Phenylalanine metabolism - Mus musculus (mouse),
path:mmu00380 → Tryptophan metabolism - Mus musculus (mouse),
path:mmu00400 → Phenylalanine, tyrosine and tryptophan biosynthesis - Mus musculus (mouse),
path:mmu00410 → beta-Alanine metabolism - Mus musculus (mouse),
path:mmu00430 → Taurine and hypotaurine metabolism - Mus musculus (mouse),
path:mmu00450 → Selenocompound metabolism - Mus musculus (mouse),
path:mmu00471 → D-Glutamine and D-glutamate metabolism - Mus musculus (mouse),
path:mmu00472 → D-Arginine and D-ornithine metabolism - Mus musculus (mouse),
path:mmu00480 → Glutathione metabolism - Mus musculus (mouse),
path:mmu00500 → Starch and sucrose metabolism - Mus musculus (mouse),
path:mmu00510 → N-Glycan biosynthesis - Mus musculus (mouse),
path:mmu00511 → Other glycan degradation - Mus musculus (mouse),
path:mmu00512 → Mucin type O-Glycan biosynthesis - Mus musculus (mouse),
path:mmu00514 → Other types of O-glycan biosynthesis - Mus musculus (mouse),
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path:mmu00520 → Amino sugar and nucleotide sugar metabolism - Mus musculus (mouse),
path:mmu00524 → Neomycin, kanamycin and gentamicin biosynthesis - Mus musculus (mouse),
path:mmu00531 → Glycosaminoglycan degradation - Mus musculus (mouse), path:mmu00532 →
 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Mus musculus (mouse),
path:mmu00533 → Glycosaminoglycan biosynthesis - keratan sulfate - Mus musculus (mouse),
path:mmu00534 → Glycosaminoglycan biosynthesis - heparan sulfate / heparin - Mus musculus (mouse),
path:mmu00561 → Glycerolipid metabolism - Mus musculus (mouse),
path:mmu00562 → Inositol phosphate metabolism - Mus musculus (mouse),
path:mmu00563 → Glycosylphosphatidylinositol(GPI)-anchor biosynthesis - Mus musculus (mouse),
path:mmu00564 → Glycerophospholipid metabolism - Mus musculus (mouse),
path:mmu00565 → Ether lipid metabolism - Mus musculus (mouse),
path:mmu00590 → Arachidonic acid metabolism - Mus musculus (mouse),
path:mmu00591 → Linoleic acid metabolism - Mus musculus (mouse),
path:mmu00592 → alpha-Linolenic acid metabolism - Mus musculus (mouse),
path:mmu00600 → Sphingolipid metabolism - Mus musculus (mouse),
path:mmu00601 → Glycosphingolipid biosynthesis - lacto and neolacto series - Mus musculus (mouse),
path:mmu00603 → Glycosphingolipid biosynthesis - globo series - Mus musculus (mouse),
path:mmu00604 → Glycosphingolipid biosynthesis - ganglio series - Mus musculus (mouse),
path:mmu00620 → Pyruvate metabolism - Mus musculus (mouse),
path:mmu00630 → Glyoxylate and dicarboxylate metabolism - Mus musculus (mouse),
path:mmu00640 → Propanoate metabolism - Mus musculus (mouse),
path:mmu00650 → Butanoate metabolism - Mus musculus (mouse),
path:mmu00670 → One carbon pool by folate - Mus musculus (mouse),
path:mmu00730 → Thiamine metabolism - Mus musculus (mouse),
path:mmu00740 → Riboflavin metabolism - Mus musculus (mouse),
path:mmu00750 → Vitamin B6 metabolism - Mus musculus (mouse),
path:mmu00760 → Nicotinate and nicotinamide metabolism - Mus musculus (mouse),
path:mmu00770 → Pantothenate and CoA biosynthesis - Mus musculus (mouse),
path:mmu00780 → Biotin metabolism - Mus musculus (mouse),
path:mmu00785 → Lipoic acid metabolism - Mus musculus (mouse),
path:mmu00790 → Folate biosynthesis - Mus musculus (mouse),
path:mmu00830 → Retinol metabolism - Mus musculus (mouse),
path:mmu00860 → Porphyrin and chlorophyll metabolism - Mus musculus (mouse),
path:mmu00900 → Terpenoid backbone biosynthesis - Mus musculus (mouse),
path:mmu00910 → Nitrogen metabolism - Mus musculus (mouse),
path:mmu00920 → Sulfur metabolism - Mus musculus (mouse),
path:mmu00970 → Aminoacyl-tRNA biosynthesis - Mus musculus (mouse),
path:mmu00980 → Metabolism of xenobiotics by cytochrome P450 - Mus musculus (mouse),
path:mmu00982 → Drug metabolism - cytochrome P450 - Mus musculus (mouse),
path:mmu00983 → Drug metabolism - other enzymes - Mus musculus (mouse),
path:mmu01040 → Biosynthesis of unsaturated fatty acids - Mus musculus (mouse),
path:mmu01100 → Metabolic pathways - Mus musculus (mouse),
path:mmu01200 → Carbon metabolism - Mus musculus (mouse),
path:mmu01210 → 2-Oxocarboxylic acid metabolism - Mus musculus (mouse),
path:mmu01212 → Fatty acid metabolism - Mus musculus (mouse),
path:mmu01230 → Biosynthesis of amino acids - Mus musculus (mouse),
path:mmu01521 → EGFR tyrosine kinase inhibitor resistance - Mus musculus (mouse),
path:mmu01522 → Endocrine resistance - Mus musculus (mouse),
path:mmu01524 → Platinum drug resistance - Mus musculus (mouse),
path:mmu02010 → ABC transporters - Mus musculus (mouse),
path:mmu03008 → Ribosome biogenesis in eukaryotes - Mus musculus (mouse),
path:mmu03010 → Ribosome - Mus musculus (mouse), path:mmu03013 → RNA transport - Mus musculus (mouse),
path:mmu03015 → mRNA surveillance pathway - Mus musculus (mouse),
path:mmu03018 → RNA degradation - Mus musculus (mouse),
path:mmu03020 → RNA polymerase - Mus musculus (mouse),
path:mmu03022 → Basal transcription factors - Mus musculus (mouse),
path:mmu03030 → DNA replication - Mus musculus (mouse), path:mmu03040 → Spliceosome - Mus musculus (mouse),
path:mmu03050 → Proteasome - Mus musculus (mouse), path:mmu03060 → Protein export - Mus musculus (mouse),
path:mmu03320 → PPAR signaling pathway - Mus musculus (mouse),
path:mmu03410 → Base excision repair - Mus musculus (mouse),
path:mmu03420 → Nucleotide excision repair - Mus musculus (mouse),
path:mmu03430 → Mismatch repair - Mus musculus (mouse),
path:mmu03440 → Homologous recombination - Mus musculus (mouse),
path:mmu03450 → Non-homologous end-joining - Mus musculus (mouse),
path:mmu03460 → Fanconi anemia pathway - Mus musculus (mouse),
path:mmu04010 → MAPK signaling pathway - Mus musculus (mouse),
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path:mmu04012 → ErbB signaling pathway - Mus musculus (mouse),
path:mmu04014 → Ras signaling pathway - Mus musculus (mouse),
path:mmu04015 → Rap1 signaling pathway - Mus musculus (mouse),
path:mmu04020 → Calcium signaling pathway - Mus musculus (mouse),
path:mmu04022 → cGMP-PKG signaling pathway - Mus musculus (mouse),
path:mmu04024 → cAMP signaling pathway - Mus musculus (mouse),
path:mmu04060 → Cytokine-cytokine receptor interaction - Mus musculus (mouse),
path:mmu04062 → Chemokine signaling pathway - Mus musculus (mouse),
path:mmu04064 → NF-kappa B signaling pathway - Mus musculus (mouse),
path:mmu04066 → HIF-1 signaling pathway - Mus musculus (mouse),
path:mmu04068 → FoxO signaling pathway - Mus musculus (mouse),
path:mmu04070 → Phosphatidylinositol signaling system - Mus musculus (mouse),
path:mmu04071 → Sphingolipid signaling pathway - Mus musculus (mouse),
path:mmu04072 → Phospholipase D signaling pathway - Mus musculus (mouse),
path:mmu04080 → Neuroactive ligand-receptor interaction - Mus musculus (mouse),
path:mmu04110 → Cell cycle - Mus musculus (mouse), path:mmu04114 → Oocyte meiosis - Mus musculus (mouse),
path:mmu04115 → p53 signaling pathway - Mus musculus (mouse),
path:mmu04120 → Ubiquitin mediated proteolysis - Mus musculus (mouse),
path:mmu04122 → Sulfur relay system - Mus musculus (mouse),
path:mmu04130 → SNARE interactions in vesicular transport - Mus musculus (mouse),
path:mmu04140 → Regulation of autophagy - Mus musculus (mouse),
path:mmu04141 → Protein processing in endoplasmic reticulum - Mus musculus (mouse),
path:mmu04142 → Lysosome - Mus musculus (mouse), path:mmu04144 → Endocytosis - Mus musculus (mouse),
path:mmu04145 → Phagosome - Mus musculus (mouse), path:mmu04146 → Peroxisome - Mus musculus (mouse),
path:mmu04150 → mTOR signaling pathway - Mus musculus (mouse),
path:mmu04151 → PI3K-Akt signaling pathway - Mus musculus (mouse),
path:mmu04152 → AMPK signaling pathway - Mus musculus (mouse),
path:mmu04210 → Apoptosis - Mus musculus (mouse),
path:mmu04211 → Longevity regulating pathway - Mus musculus (mouse),
path:mmu04213 → Longevity regulating pathway - multiple species - Mus musculus (mouse),
path:mmu04215 → Apoptosis - multiple species - Mus musculus (mouse),
path:mmu04260 → Cardiac muscle contraction - Mus musculus (mouse),
path:mmu04261 → Adrenergic signaling in cardiomyocytes - Mus musculus (mouse),
path:mmu04270 → Vascular smooth muscle contraction - Mus musculus (mouse),
path:mmu04310 → Wnt signaling pathway - Mus musculus (mouse),
path:mmu04320 → Dorso-ventral axis formation - Mus musculus (mouse),
path:mmu04330 → Notch signaling pathway - Mus musculus (mouse),
path:mmu04340 → Hedgehog signaling pathway - Mus musculus (mouse),
path:mmu04350 → TGF-beta signaling pathway - Mus musculus (mouse),
path:mmu04360 → Axon guidance - Mus musculus (mouse),
path:mmu04370 → VEGF signaling pathway - Mus musculus (mouse),
path:mmu04380 → Osteoclast differentiation - Mus musculus (mouse),
path:mmu04390 → Hippo signaling pathway - Mus musculus (mouse),
path:mmu04392 → Hippo signaling pathway -multiple species - Mus musculus (mouse),
path:mmu04510 → Focal adhesion - Mus musculus (mouse),
path:mmu04512 → ECM-receptor interaction - Mus musculus (mouse),
path:mmu04514 → Cell adhesion molecules (CAMs) - Mus musculus (mouse),
path:mmu04520 → Adherens junction - Mus musculus (mouse),
path:mmu04530 → Tight junction - Mus musculus (mouse), path:mmu04540 → Gap junction - Mus musculus (mouse),
path:mmu04550 → Signaling pathways regulating pluripotency of stem cells - Mus musculus (mouse),
path:mmu04610 → Complement and coagulation cascades - Mus musculus (mouse),
path:mmu04611 → Platelet activation - Mus musculus (mouse),
path:mmu04612 → Antigen processing and presentation - Mus musculus (mouse),
path:mmu04614 → Renin-angiotensin system - Mus musculus (mouse),
path:mmu04620 → Toll-like receptor signaling pathway - Mus musculus (mouse),
path:mmu04621 → NOD-like receptor signaling pathway - Mus musculus (mouse),
path:mmu04622 → RIG-I-like receptor signaling pathway - Mus musculus (mouse),
path:mmu04623 → Cytosolic DNA-sensing pathway - Mus musculus (mouse),
path:mmu04630 → Jak-STAT signaling pathway - Mus musculus (mouse),
path:mmu04640 → Hematopoietic cell lineage - Mus musculus (mouse),
path:mmu04650 → Natural killer cell mediated cytotoxicity - Mus musculus (mouse),
path:mmu04660 → T cell receptor signaling pathway - Mus musculus (mouse),
path:mmu04662 → B cell receptor signaling pathway - Mus musculus (mouse),
path:mmu04664 → Fc epsilon RI signaling pathway - Mus musculus (mouse),
path:mmu04666 → Fc gamma R-mediated phagocytosis - Mus musculus (mouse),
path:mmu04668 → TNF signaling pathway - Mus musculus (mouse),
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path:mmu04670 → Leukocyte transendothelial migration - Mus musculus (mouse),
path:mmu04672 → Intestinal immune network for IgA production - Mus musculus (mouse),
path:mmu04710 → Circadian rhythm - Mus musculus (mouse),
path:mmu04713 → Circadian entrainment - Mus musculus (mouse),
path:mmu04720 → Long-term potentiation - Mus musculus (mouse),
path:mmu04721 → Synaptic vesicle cycle - Mus musculus (mouse),
path:mmu04722 → Neurotrophin signaling pathway - Mus musculus (mouse),
path:mmu04723 → Retrograde endocannabinoid signaling - Mus musculus (mouse),
path:mmu04724 → Glutamatergic synapse - Mus musculus (mouse),
path:mmu04725 → Cholinergic synapse - Mus musculus (mouse),
path:mmu04726 → Serotonergic synapse - Mus musculus (mouse),
path:mmu04727 → GABAergic synapse - Mus musculus (mouse),
path:mmu04728 → Dopaminergic synapse - Mus musculus (mouse),
path:mmu04730 → Long-term depression - Mus musculus (mouse),
path:mmu04740 → Olfactory transduction - Mus musculus (mouse),
path:mmu04742 → Taste transduction - Mus musculus (mouse),
path:mmu04744 → Phototransduction - Mus musculus (mouse),
path:mmu04750 → Inflammatory mediator regulation of TRP channels - Mus musculus (mouse),
path:mmu04810 → Regulation of actin cytoskeleton - Mus musculus (mouse),
path:mmu04910 → Insulin signaling pathway - Mus musculus (mouse),
path:mmu04911 → Insulin secretion - Mus musculus (mouse),
path:mmu04912 → GnRH signaling pathway - Mus musculus (mouse),
path:mmu04913 → Ovarian steroidogenesis - Mus musculus (mouse),
path:mmu04914 → Progesterone-mediated oocyte maturation - Mus musculus (mouse),
path:mmu04915 → Estrogen signaling pathway - Mus musculus (mouse),
path:mmu04916 → Melanogenesis - Mus musculus (mouse),
path:mmu04917 → Prolactin signaling pathway - Mus musculus (mouse),
path:mmu04918 → Thyroid hormone synthesis - Mus musculus (mouse),
path:mmu04919 → Thyroid hormone signaling pathway - Mus musculus (mouse),
path:mmu04920 → Adipocytokine signaling pathway - Mus musculus (mouse),
path:mmu04921 → Oxytocin signaling pathway - Mus musculus (mouse),
path:mmu04922 → Glucagon signaling pathway - Mus musculus (mouse),
path:mmu04923 → Regulation of lipolysis in adipocytes - Mus musculus (mouse),
path:mmu04924 → Renin secretion - Mus musculus (mouse),
path:mmu04925 → Aldosterone synthesis and secretion - Mus musculus (mouse),
path:mmu04930 → Type II diabetes mellitus - Mus musculus (mouse),
path:mmu04931 → Insulin resistance - Mus musculus (mouse),
path:mmu04932 → Non-alcoholic fatty liver disease (NAFLD) - Mus musculus (mouse),
path:mmu04933 → AGE-RAGE signaling pathway in diabetic complications - Mus musculus (mouse),
path:mmu04940 → Type I diabetes mellitus - Mus musculus (mouse),
path:mmu04950 → Maturity onset diabetes of the young - Mus musculus (mouse),
path:mmu04960 → Aldosterone-regulated sodium reabsorption - Mus musculus (mouse),
path:mmu04961 → Endocrine and other factor-regulated calcium reabsorption - Mus musculus (mouse),
path:mmu04962 → Vasopressin-regulated water reabsorption - Mus musculus (mouse),
path:mmu04964 → Proximal tubule bicarbonate reclamation - Mus musculus (mouse),
path:mmu04966 → Collecting duct acid secretion - Mus musculus (mouse),
path:mmu04970 → Salivary secretion - Mus musculus (mouse),
path:mmu04971 → Gastric acid secretion - Mus musculus (mouse),
path:mmu04972 → Pancreatic secretion - Mus musculus (mouse),
path:mmu04973 → Carbohydrate digestion and absorption - Mus musculus (mouse),
path:mmu04974 → Protein digestion and absorption - Mus musculus (mouse),
path:mmu04975 → Fat digestion and absorption - Mus musculus (mouse),
path:mmu04976 → Bile secretion - Mus musculus (mouse),
path:mmu04977 → Vitamin digestion and absorption - Mus musculus (mouse),
path:mmu04978 → Mineral absorption - Mus musculus (mouse),
path:mmu05010 → Alzheimer's disease - Mus musculus (mouse),
path:mmu05012 → Parkinson's disease - Mus musculus (mouse),
path:mmu05014 → Amyotrophic lateral sclerosis (ALS) - Mus musculus (mouse),
path:mmu05016 → Huntington's disease - Mus musculus (mouse),
path:mmu05020 → Prion diseases - Mus musculus (mouse),
path:mmu05030 → Cocaine addiction - Mus musculus (mouse),
path:mmu05031 → Amphetamine addiction - Mus musculus (mouse),
path:mmu05032 → Morphine addiction - Mus musculus (mouse),
path:mmu05033 → Nicotine addiction - Mus musculus (mouse),
path:mmu05034 → Alcoholism - Mus musculus (mouse),
path:mmu05100 → Bacterial invasion of epithelial cells - Mus musculus (mouse),
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path:mmu05132 → Salmonella infection - Mus musculus (mouse),
path:mmu05133 → Pertussis - Mus musculus (mouse), path:mmu05134 → Legionellosis - Mus musculus (mouse),
path:mmu05140 → Leishmaniasis - Mus musculus (mouse),
path:mmu05142 → Chagas disease (American trypanosomiasis) - Mus musculus (mouse),
path:mmu05143 → African trypanosomiasis - Mus musculus (mouse),
path:mmu05144 → Malaria - Mus musculus (mouse), path:mmu05145 → Toxoplasmosis - Mus musculus (mouse),
path:mmu05146 → Amoebiasis - Mus musculus (mouse),
path:mmu05150 → Staphylococcus aureus infection - Mus musculus (mouse),
path:mmu05152 → Tuberculosis - Mus musculus (mouse),
path:mmu05160 → Hepatitis C - Mus musculus (mouse), path:mmu05161 → Hepatitis B - Mus musculus (mouse),
path:mmu05162 → Measles - Mus musculus (mouse), path:mmu05164 → Influenza A - Mus musculus (mouse),
path:mmu05166 → HTLV-I infection - Mus musculus (mouse),
path:mmu05168 → Herpes simplex infection - Mus musculus (mouse),
path:mmu05169 → Epstein-Barr virus infection - Mus musculus (mouse),
path:mmu05200 → Pathways in cancer - Mus musculus (mouse),
path:mmu05202 → Transcriptional misregulation in cancer - Mus musculus (mouse),
path:mmu05203 → Viral carcinogenesis - Mus musculus (mouse),
path:mmu05204 → Chemical carcinogenesis - Mus musculus (mouse),
path:mmu05205 → Proteoglycans in cancer - Mus musculus (mouse),
path:mmu05206 → MicroRNAs in cancer - Mus musculus (mouse),
path:mmu05210 → Colorectal cancer - Mus musculus (mouse),
path:mmu05211 → Renal cell carcinoma - Mus musculus (mouse),
path:mmu05212 → Pancreatic cancer - Mus musculus (mouse),
path:mmu05213 → Endometrial cancer - Mus musculus (mouse),
path:mmu05214 → Glioma - Mus musculus (mouse), path:mmu05215 → Prostate cancer - Mus musculus (mouse),
path:mmu05216 → Thyroid cancer - Mus musculus (mouse),
path:mmu05217 → Basal cell carcinoma - Mus musculus (mouse),
path:mmu05218 → Melanoma - Mus musculus (mouse), path:mmu05219 → Bladder cancer - Mus musculus (mouse),
path:mmu05220 → Chronic myeloid leukemia - Mus musculus (mouse),
path:mmu05221 → Acute myeloid leukemia - Mus musculus (mouse),
path:mmu05222 → Small cell lung cancer - Mus musculus (mouse),
path:mmu05223 → Non-small cell lung cancer - Mus musculus (mouse),
path:mmu05230 → Central carbon metabolism in cancer - Mus musculus (mouse),
path:mmu05231 → Choline metabolism in cancer - Mus musculus (mouse),
path:mmu05310 → Asthma - Mus musculus (mouse),
path:mmu05320 → Autoimmune thyroid disease - Mus musculus (mouse),
path:mmu05321 → Inflammatory bowel disease (IBD) - Mus musculus (mouse),
path:mmu05322 → Systemic lupus erythematosus - Mus musculus (mouse),
path:mmu05323 → Rheumatoid arthritis - Mus musculus (mouse),
path:mmu05330 → Allograft rejection - Mus musculus (mouse),
path:mmu05332 → Graft-versus-host disease - Mus musculus (mouse),
path:mmu05340 → Primary immunodeficiency - Mus musculus (mouse),
path:mmu05410 → Hypertrophic cardiomyopathy (HCM) - Mus musculus (mouse),
path:mmu05412 → Arrhythmogenic right ventricular cardiomyopathy (ARVC) - Mus musculus (mouse),
path:mmu05414 → Dilated cardiomyopathy - Mus musculus (mouse),
path:mmu05416 → Viral myocarditis - Mus musculus (mouse) |>
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can query for example Arabidopsis information

In[2]:=
```
dictionaryPathwayAthQuery2 = KEGGDictionary[KEGGQuery2 → "ath"]
```

Out[2]=
```
<| path:ath00010 → Glycolysis / Gluconeogenesis - Arabidopsis thaliana (thale cress),
path:ath00020 → Citrate cycle (TCA cycle) - Arabidopsis thaliana (thale cress),
path:ath00030 → Pentose phosphate pathway - Arabidopsis thaliana (thale cress),
path:ath00040 → Pentose and glucuronate interconversions - Arabidopsis thaliana (thale cress),
path:ath00051 → Fructose and mannose metabolism - Arabidopsis thaliana (thale cress),
path:ath00052 → Galactose metabolism - Arabidopsis thaliana (thale cress),
path:ath00053 → Ascorbate and aldarate metabolism - Arabidopsis thaliana (thale cress),
path:ath00061 → Fatty acid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00062 → Fatty acid elongation - Arabidopsis thaliana (thale cress),
path:ath00071 → Fatty acid degradation - Arabidopsis thaliana (thale cress),
path:ath00072 → Synthesis and degradation of ketone bodies - Arabidopsis thaliana (thale cress),
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path:ath00073 → Cutin, suberine and wax biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00100 → Steroid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00130 → Ubiquinone and other terpenoid-quinone biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00190 → Oxidative phosphorylation - Arabidopsis thaliana (thale cress),
path:ath00195 → Photosynthesis - Arabidopsis thaliana (thale cress),
path:ath00196 → Photosynthesis - antenna proteins - Arabidopsis thaliana (thale cress),
path:ath00220 → Arginine biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00230 → Purine metabolism - Arabidopsis thaliana (thale cress),
path:ath00232 → Caffeine metabolism - Arabidopsis thaliana (thale cress),
path:ath00240 → Pyrimidine metabolism - Arabidopsis thaliana (thale cress),
path:ath00250 → Alanine, aspartate and glutamate metabolism - Arabidopsis thaliana (thale cress),
path:ath00260 → Glycine, serine and threonine metabolism - Arabidopsis thaliana (thale cress),
path:ath00261 → Monobactam biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00270 → Cysteine and methionine metabolism - Arabidopsis thaliana (thale cress),
path:ath00280 → Valine, leucine and isoleucine degradation - Arabidopsis thaliana (thale cress),
path:ath00290 → Valine, leucine and isoleucine biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00300 → Lysine biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00310 → Lysine degradation - Arabidopsis thaliana (thale cress),
path:ath00330 → Arginine and proline metabolism - Arabidopsis thaliana (thale cress),
path:ath00340 → Histidine metabolism - Arabidopsis thaliana (thale cress),
path:ath00350 → Tyrosine metabolism - Arabidopsis thaliana (thale cress),
path:ath00360 → Phenylalanine metabolism - Arabidopsis thaliana (thale cress),
path:ath00380 → Tryptophan metabolism - Arabidopsis thaliana (thale cress),
path:ath00400 → Phenylalanine, tyrosine and tryptophan biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00410 → beta-Alanine metabolism - Arabidopsis thaliana (thale cress),
path:ath00430 → Taurine and hypotaurine metabolism - Arabidopsis thaliana (thale cress),
path:ath00450 → Selenocompound metabolism - Arabidopsis thaliana (thale cress),
path:ath00460 → Cyanoamino acid metabolism - Arabidopsis thaliana (thale cress),
path:ath00480 → Glutathione metabolism - Arabidopsis thaliana (thale cress),
path:ath00500 → Starch and sucrose metabolism - Arabidopsis thaliana (thale cress),
path:ath00510 → N-Glycan biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00511 → Other glycan degradation - Arabidopsis thaliana (thale cress),
path:ath00514 → Other types of O-glycan biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00520 → Amino sugar and nucleotide sugar metabolism - Arabidopsis thaliana (thale cress),
path:ath00531 → Glycosaminoglycan degradation - Arabidopsis thaliana (thale cress),
path:ath00561 → Glycerolipid metabolism - Arabidopsis thaliana (thale cress),
path:ath00562 → Inositol phosphate metabolism - Arabidopsis thaliana (thale cress), path:ath00563 →
 Glycosylphosphatidylinositol(GPI)-anchor biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00564 → Glycerophospholipid metabolism - Arabidopsis thaliana (thale cress),
path:ath00565 → Ether lipid metabolism - Arabidopsis thaliana (thale cress),
path:ath00590 → Arachidonic acid metabolism - Arabidopsis thaliana (thale cress),
path:ath00591 → Linoleic acid metabolism - Arabidopsis thaliana (thale cress),
path:ath00592 → alpha-Linolenic acid metabolism - Arabidopsis thaliana (thale cress),
path:ath00600 → Sphingolipid metabolism - Arabidopsis thaliana (thale cress),
path:ath00603 → Glycosphingolipid biosynthesis - globo series - Arabidopsis thaliana (thale cress),
path:ath00604 → Glycosphingolipid biosynthesis - ganglio series - Arabidopsis thaliana (thale cress),
path:ath00620 → Pyruvate metabolism - Arabidopsis thaliana (thale cress),
path:ath00630 → Glyoxylate and dicarboxylate metabolism - Arabidopsis thaliana (thale cress),
path:ath00640 → Propanoate metabolism - Arabidopsis thaliana (thale cress),
path:ath00650 → Butanoate metabolism - Arabidopsis thaliana (thale cress),
path:ath00660 → C5-Branched dibasic acid metabolism - Arabidopsis thaliana (thale cress),
path:ath00670 → One carbon pool by folate - Arabidopsis thaliana (thale cress),
path:ath00710 → Carbon fixation in photosynthetic organisms - Arabidopsis thaliana (thale cress),
path:ath00730 → Thiamine metabolism - Arabidopsis thaliana (thale cress),
path:ath00740 → Riboflavin metabolism - Arabidopsis thaliana (thale cress),
path:ath00750 → Vitamin B6 metabolism - Arabidopsis thaliana (thale cress),
path:ath00760 → Nicotinate and nicotinamide metabolism - Arabidopsis thaliana (thale cress),
path:ath00770 → Pantothenate and CoA biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00780 → Biotin metabolism - Arabidopsis thaliana (thale cress),
path:ath00785 → Lipoic acid metabolism - Arabidopsis thaliana (thale cress),
path:ath00790 → Folate biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00860 → Porphyrin and chlorophyll metabolism - Arabidopsis thaliana (thale cress),
path:ath00900 → Terpenoid backbone biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00901 → Indole alkaloid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00902 → Monoterpenoid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00903 → Limonene and pinene degradation - Arabidopsis thaliana (thale cress),
```

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```
path:ath00904 → Diterpenoid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00905 → Brassinosteroid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00906 → Carotenoid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00908 → Zeatin biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00909 → Sesquiterpenoid and triterpenoid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00910 → Nitrogen metabolism - Arabidopsis thaliana (thale cress),
path:ath00920 → Sulfur metabolism - Arabidopsis thaliana (thale cress),
path:ath00940 → Phenylpropanoid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00941 → Flavonoid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00942 → Anthocyanin biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00944 → Flavone and flavonol biosynthesis - Arabidopsis thaliana (thale cress), path:ath00945 →
 Stilbenoid, diarylheptanoid and gingerol biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00950 → Isoquinoline alkaloid biosynthesis - Arabidopsis thaliana (thale cress), path:ath00960 →
 Tropane, piperidine and pyridine alkaloid biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00966 → Glucosinolate biosynthesis - Arabidopsis thaliana (thale cress),
path:ath00970 → Aminoacyl-tRNA biosynthesis - Arabidopsis thaliana (thale cress),
path:ath01040 → Biosynthesis of unsaturated fatty acids - Arabidopsis thaliana (thale cress),
path:ath01100 → Metabolic pathways - Arabidopsis thaliana (thale cress),
path:ath01110 → Biosynthesis of secondary metabolites - Arabidopsis thaliana (thale cress),
path:ath01200 → Carbon metabolism - Arabidopsis thaliana (thale cress),
path:ath01210 → 2-Oxocarboxylic acid metabolism - Arabidopsis thaliana (thale cress),
path:ath01212 → Fatty acid metabolism - Arabidopsis thaliana (thale cress),
path:ath01230 → Biosynthesis of amino acids - Arabidopsis thaliana (thale cress),
path:ath01502 → Vancomycin resistance - Arabidopsis thaliana (thale cress),
path:ath02010 → ABC transporters - Arabidopsis thaliana (thale cress),
path:ath03008 → Ribosome biogenesis in eukaryotes - Arabidopsis thaliana (thale cress),
path:ath03010 → Ribosome - Arabidopsis thaliana (thale cress),
path:ath03013 → RNA transport - Arabidopsis thaliana (thale cress),
path:ath03015 → mRNA surveillance pathway - Arabidopsis thaliana (thale cress),
path:ath03018 → RNA degradation - Arabidopsis thaliana (thale cress),
path:ath03020 → RNA polymerase - Arabidopsis thaliana (thale cress),
path:ath03022 → Basal transcription factors - Arabidopsis thaliana (thale cress),
path:ath03030 → DNA replication - Arabidopsis thaliana (thale cress),
path:ath03040 → Spliceosome - Arabidopsis thaliana (thale cress),
path:ath03050 → Proteasome - Arabidopsis thaliana (thale cress),
path:ath03060 → Protein export - Arabidopsis thaliana (thale cress),
path:ath03410 → Base excision repair - Arabidopsis thaliana (thale cress),
path:ath03420 → Nucleotide excision repair - Arabidopsis thaliana (thale cress),
path:ath03430 → Mismatch repair - Arabidopsis thaliana (thale cress),
path:ath03440 → Homologous recombination - Arabidopsis thaliana (thale cress),
path:ath03450 → Non-homologous end-joining - Arabidopsis thaliana (thale cress),
path:ath04070 → Phosphatidylinositol signaling system - Arabidopsis thaliana (thale cress),
path:ath04075 → Plant hormone signal transduction - Arabidopsis thaliana (thale cress),
path:ath04120 → Ubiquitin mediated proteolysis - Arabidopsis thaliana (thale cress),
path:ath04122 → Sulfur relay system - Arabidopsis thaliana (thale cress),
path:ath04130 → SNARE interactions in vesicular transport - Arabidopsis thaliana (thale cress),
path:ath04140 → Regulation of autophagy - Arabidopsis thaliana (thale cress),
path:ath04141 → Protein processing in endoplasmic reticulum - Arabidopsis thaliana (thale cress),
path:ath04144 → Endocytosis - Arabidopsis thaliana (thale cress),
path:ath04145 → Phagosome - Arabidopsis thaliana (thale cress),
path:ath04146 → Peroxisome - Arabidopsis thaliana (thale cress),
path:ath04626 → Plant-pathogen interaction - Arabidopsis thaliana (thale cress),
path:ath04712 → Circadian rhythm - plant - Arabidopsis thaliana (thale cress), path:ath04933 →
 AGE-RAGE signaling pathway in diabetic complications - Arabidopsis thaliana (thale cress)|>
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can also query memberships set by KEGGQuery1 by setting at the same time KEGGQuery2 to "". For example, we can look at compounds (cpd):

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In[2]:=
```
dictionaryCpdQuery12 = KEGGDictionary[KEGGQuery1 → "cpd", KEGGQuery2 → ""]
```

Out[2]=
```
<|cpd:C00001 → H2O; Water, cpd:C00002 → ATP; Adenosine 5'-triphosphate,
 ··· 17 741 ···, cpd:C21270 → Gentamicin C2a, cpd:C21273 → Benfluralin|>
```

large output | show less | show more | show all | set size limit...

MathIOmicaDataDirectory (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value points to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

In[2]:=
```
KEGGDictionary[MathIOmicaDataDirectory → FileNameJoin[
   Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]
```

Out[2]=
```
<|path:hsa00010 → Glycolysis / Gluconeogenesis - Homo sapiens (human),
 path:hsa00020 → Citrate cycle (TCA cycle) - Homo sapiens (human),
 path:hsa00030 → Pentose phosphate pathway - Homo sapiens (human),
 path:hsa00040 → Pentose and glucuronate interconversions - Homo sapiens (human),
 path:hsa00051 → Fructose and mannose metabolism - Homo sapiens (human),
 path:hsa00052 → Galactose metabolism - Homo sapiens (human),
 path:hsa00053 → Ascorbate and aldarate metabolism - Homo sapiens (human),
 path:hsa00061 → Fatty acid biosynthesis - Homo sapiens (human),
 path:hsa00062 → Fatty acid elongation - Homo sapiens (human),
 path:hsa00071 → Fatty acid degradation - Homo sapiens (human),
 path:hsa00072 → Synthesis and degradation of ketone bodies - Homo sapiens (human),
 path:hsa00100 → Steroid biosynthesis - Homo sapiens (human),
 path:hsa00120 → Primary bile acid biosynthesis - Homo sapiens (human),
 path:hsa00130 → Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human),
 path:hsa00140 → Steroid hormone biosynthesis - Homo sapiens (human),
 path:hsa00190 → Oxidative phosphorylation - Homo sapiens (human),
 path:hsa00220 → Arginine biosynthesis - Homo sapiens (human),
 path:hsa00230 → Purine metabolism - Homo sapiens (human),
 path:hsa00232 → Caffeine metabolism - Homo sapiens (human),
 path:hsa00240 → Pyrimidine metabolism - Homo sapiens (human),
 path:hsa00250 → Alanine, aspartate and glutamate metabolism - Homo sapiens (human),
 path:hsa00260 → Glycine, serine and threonine metabolism - Homo sapiens (human),
 path:hsa00270 → Cysteine and methionine metabolism - Homo sapiens (human),
 path:hsa00280 → Valine, leucine and isoleucine degradation - Homo sapiens (human),
 path:hsa00290 → Valine, leucine and isoleucine biosynthesis - Homo sapiens (human),
 path:hsa00310 → Lysine degradation - Homo sapiens (human),
 path:hsa00330 → Arginine and proline metabolism - Homo sapiens (human),
 path:hsa00340 → Histidine metabolism - Homo sapiens (human),
 path:hsa00350 → Tyrosine metabolism - Homo sapiens (human),
 path:hsa00360 → Phenylalanine metabolism - Homo sapiens (human),
 path:hsa00380 → Tryptophan metabolism - Homo sapiens (human),
 path:hsa00400 → Phenylalanine, tyrosine and tryptophan biosynthesis - Homo sapiens (human),
 path:hsa00410 → beta-Alanine metabolism - Homo sapiens (human),
 path:hsa00430 → Taurine and hypotaurine metabolism - Homo sapiens (human),
 path:hsa00440 → Phosphonate and phosphinate metabolism - Homo sapiens (human),
 path:hsa00450 → Selenocompound metabolism - Homo sapiens (human),
 path:hsa00471 → D-Glutamine and D-glutamate metabolism - Homo sapiens (human),
 path:hsa00472 → D-Arginine and D-ornithine metabolism - Homo sapiens (human),
 path:hsa00480 → Glutathione metabolism - Homo sapiens (human),
 path:hsa00500 → Starch and sucrose metabolism - Homo sapiens (human),
 path:hsa00510 → N-Glycan biosynthesis - Homo sapiens (human),
 path:hsa00511 → Other glycan degradation - Homo sapiens (human),
 path:hsa00512 → Mucin type O-glycan biosynthesis - Homo sapiens (human),
```

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```
path:hsa00514 → Other types of O-glycan biosynthesis - Homo sapiens (human),
path:hsa00515 → Mannose type O-glycan biosynthesis - Homo sapiens (human),
path:hsa00520 → Amino sugar and nucleotide sugar metabolism - Homo sapiens (human),
path:hsa00524 → Neomycin, kanamycin and gentamicin biosynthesis - Homo sapiens (human),
path:hsa00531 → Glycosaminoglycan degradation - Homo sapiens (human), path:hsa00532 →
 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Homo sapiens (human),
path:hsa00533 → Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human),
path:hsa00534 → Glycosaminoglycan biosynthesis - heparan sulfate / heparin - Homo sapiens (human),
path:hsa00561 → Glycerolipid metabolism - Homo sapiens (human),
path:hsa00562 → Inositol phosphate metabolism - Homo sapiens (human),
path:hsa00563 → Glycosylphosphatidylinositol (GPI)-anchor biosynthesis - Homo sapiens (human),
path:hsa00564 → Glycerophospholipid metabolism - Homo sapiens (human),
path:hsa00565 → Ether lipid metabolism - Homo sapiens (human),
path:hsa00590 → Arachidonic acid metabolism - Homo sapiens (human),
path:hsa00591 → Linoleic acid metabolism - Homo sapiens (human),
path:hsa00592 → alpha-Linolenic acid metabolism - Homo sapiens (human),
path:hsa00600 → Sphingolipid metabolism - Homo sapiens (human),
path:hsa00601 → Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human),
path:hsa00603 → Glycosphingolipid biosynthesis - globo and isoglobo series - Homo sapiens (human),
path:hsa00604 → Glycosphingolipid biosynthesis - ganglio series - Homo sapiens (human),
path:hsa00620 → Pyruvate metabolism - Homo sapiens (human),
path:hsa00630 → Glyoxylate and dicarboxylate metabolism - Homo sapiens (human),
path:hsa00640 → Propanoate metabolism - Homo sapiens (human),
path:hsa00650 → Butanoate metabolism - Homo sapiens (human),
path:hsa00670 → One carbon pool by folate - Homo sapiens (human),
path:hsa00730 → Thiamine metabolism - Homo sapiens (human),
path:hsa00740 → Riboflavin metabolism - Homo sapiens (human),
path:hsa00750 → Vitamin B6 metabolism - Homo sapiens (human),
path:hsa00760 → Nicotinate and nicotinamide metabolism - Homo sapiens (human),
path:hsa00770 → Pantothenate and CoA biosynthesis - Homo sapiens (human),
path:hsa00780 → Biotin metabolism - Homo sapiens (human),
path:hsa00785 → Lipoic acid metabolism - Homo sapiens (human),
path:hsa00790 → Folate biosynthesis - Homo sapiens (human),
path:hsa00830 → Retinol metabolism - Homo sapiens (human),
path:hsa00860 → Porphyrin and chlorophyll metabolism - Homo sapiens (human),
path:hsa00900 → Terpenoid backbone biosynthesis - Homo sapiens (human),
path:hsa00910 → Nitrogen metabolism - Homo sapiens (human),
path:hsa00920 → Sulfur metabolism - Homo sapiens (human),
path:hsa00970 → Aminoacyl-tRNA biosynthesis - Homo sapiens (human),
path:hsa00980 → Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human),
path:hsa00982 → Drug metabolism - cytochrome P450 - Homo sapiens (human),
path:hsa00983 → Drug metabolism - other enzymes - Homo sapiens (human),
path:hsa01040 → Biosynthesis of unsaturated fatty acids - Homo sapiens (human),
path:hsa01100 → Metabolic pathways - Homo sapiens (human),
path:hsa01200 → Carbon metabolism - Homo sapiens (human),
path:hsa01210 → 2-Oxocarboxylic acid metabolism - Homo sapiens (human),
path:hsa01212 → Fatty acid metabolism - Homo sapiens (human),
path:hsa01230 → Biosynthesis of amino acids - Homo sapiens (human),
path:hsa01521 → EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human),
path:hsa01522 → Endocrine resistance - Homo sapiens (human),
path:hsa01523 → Antifolate resistance - Homo sapiens (human),
path:hsa01524 → Platinum drug resistance - Homo sapiens (human),
path:hsa02010 → ABC transporters - Homo sapiens (human),
path:hsa03008 → Ribosome biogenesis in eukaryotes - Homo sapiens (human),
path:hsa03010 → Ribosome - Homo sapiens (human), path:hsa03013 → RNA transport - Homo sapiens (human),
path:hsa03015 → mRNA surveillance pathway - Homo sapiens (human),
path:hsa03018 → RNA degradation - Homo sapiens (human),
path:hsa03020 → RNA polymerase - Homo sapiens (human),
path:hsa03022 → Basal transcription factors - Homo sapiens (human),
path:hsa03030 → DNA replication - Homo sapiens (human), path:hsa03040 → Spliceosome - Homo sapiens (human),
path:hsa03050 → Proteasome - Homo sapiens (human), path:hsa03060 → Protein export - Homo sapiens (human),
path:hsa03320 → PPAR signaling pathway - Homo sapiens (human),
path:hsa03410 → Base excision repair - Homo sapiens (human),
path:hsa03420 → Nucleotide excision repair - Homo sapiens (human),
path:hsa03430 → Mismatch repair - Homo sapiens (human),
path:hsa03440 → Homologous recombination - Homo sapiens (human),
```

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```
path:hsa03450 → Non-homologous end-joining - Homo sapiens (human),
path:hsa03460 → Fanconi anemia pathway - Homo sapiens (human),
path:hsa04010 → MAPK signaling pathway - Homo sapiens (human),
path:hsa04012 → ErbB signaling pathway - Homo sapiens (human),
path:hsa04014 → Ras signaling pathway - Homo sapiens (human),
path:hsa04015 → Rap1 signaling pathway - Homo sapiens (human),
path:hsa04020 → Calcium signaling pathway - Homo sapiens (human),
path:hsa04022 → cGMP-PKG signaling pathway - Homo sapiens (human),
path:hsa04024 → cAMP signaling pathway - Homo sapiens (human),
path:hsa04060 → Cytokine-cytokine receptor interaction - Homo sapiens (human),
path:hsa04061 → Viral protein interaction with cytokine and cytokine receptor - Homo sapiens (human),
path:hsa04062 → Chemokine signaling pathway - Homo sapiens (human),
path:hsa04064 → NF-kappa B signaling pathway - Homo sapiens (human),
path:hsa04066 → HIF-1 signaling pathway - Homo sapiens (human),
path:hsa04068 → FoxO signaling pathway - Homo sapiens (human),
path:hsa04070 → Phosphatidylinositol signaling system - Homo sapiens (human),
path:hsa04071 → Sphingolipid signaling pathway - Homo sapiens (human),
path:hsa04072 → Phospholipase D signaling pathway - Homo sapiens (human),
path:hsa04080 → Neuroactive ligand-receptor interaction - Homo sapiens (human),
path:hsa04110 → Cell cycle - Homo sapiens (human), path:hsa04114 → Oocyte meiosis - Homo sapiens (human),
path:hsa04115 → p53 signaling pathway - Homo sapiens (human),
path:hsa04120 → Ubiquitin mediated proteolysis - Homo sapiens (human),
path:hsa04122 → Sulfur relay system - Homo sapiens (human),
path:hsa04130 → SNARE interactions in vesicular transport - Homo sapiens (human),
path:hsa04136 → Autophagy - other - Homo sapiens (human),
path:hsa04137 → Mitophagy - animal - Homo sapiens (human),
path:hsa04140 → Autophagy - animal - Homo sapiens (human),
path:hsa04141 → Protein processing in endoplasmic reticulum - Homo sapiens (human),
path:hsa04142 → Lysosome - Homo sapiens (human), path:hsa04144 → Endocytosis - Homo sapiens (human),
path:hsa04145 → Phagosome - Homo sapiens (human), path:hsa04146 → Peroxisome - Homo sapiens (human),
path:hsa04150 → mTOR signaling pathway - Homo sapiens (human),
path:hsa04151 → PI3K-Akt signaling pathway - Homo sapiens (human),
path:hsa04152 → AMPK signaling pathway - Homo sapiens (human),
path:hsa04210 → Apoptosis - Homo sapiens (human),
path:hsa04211 → Longevity regulating pathway - Homo sapiens (human),
path:hsa04213 → Longevity regulating pathway - multiple species - Homo sapiens (human),
path:hsa04215 → Apoptosis - multiple species - Homo sapiens (human),
path:hsa04216 → Ferroptosis - Homo sapiens (human), path:hsa04217 → Necroptosis - Homo sapiens (human),
path:hsa04218 → Cellular senescence - Homo sapiens (human),
path:hsa04260 → Cardiac muscle contraction - Homo sapiens (human),
path:hsa04261 → Adrenergic signaling in cardiomyocytes - Homo sapiens (human),
path:hsa04270 → Vascular smooth muscle contraction - Homo sapiens (human),
path:hsa04310 → Wnt signaling pathway - Homo sapiens (human),
path:hsa04330 → Notch signaling pathway - Homo sapiens (human),
path:hsa04340 → Hedgehog signaling pathway - Homo sapiens (human),
path:hsa04350 → TGF-beta signaling pathway - Homo sapiens (human),
path:hsa04360 → Axon guidance - Homo sapiens (human),
path:hsa04370 → VEGF signaling pathway - Homo sapiens (human),
path:hsa04371 → Apelin signaling pathway - Homo sapiens (human),
path:hsa04380 → Osteoclast differentiation - Homo sapiens (human),
path:hsa04390 → Hippo signaling pathway - Homo sapiens (human),
path:hsa04392 → Hippo signaling pathway - multiple species - Homo sapiens (human),
path:hsa04510 → Focal adhesion - Homo sapiens (human),
path:hsa04512 → ECM-receptor interaction - Homo sapiens (human),
path:hsa04514 → Cell adhesion molecules (CAMs) - Homo sapiens (human),
path:hsa04520 → Adherens junction - Homo sapiens (human),
path:hsa04530 → Tight junction - Homo sapiens (human), path:hsa04540 → Gap junction - Homo sapiens (human),
path:hsa04550 → Signaling pathways regulating pluripotency of stem cells - Homo sapiens (human),
path:hsa04610 → Complement and coagulation cascades - Homo sapiens (human),
path:hsa04611 → Platelet activation - Homo sapiens (human),
path:hsa04612 → Antigen processing and presentation - Homo sapiens (human),
path:hsa04614 → Renin-angiotensin system - Homo sapiens (human),
path:hsa04620 → Toll-like receptor signaling pathway - Homo sapiens (human),
path:hsa04621 → NOD-like receptor signaling pathway - Homo sapiens (human),
path:hsa04622 → RIG-I-like receptor signaling pathway - Homo sapiens (human),
path:hsa04623 → Cytosolic DNA-sensing pathway - Homo sapiens (human),
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path:hsa04625 → C-type lectin receptor signaling pathway - Homo sapiens (human),
path:hsa04630 → JAK-STAT signaling pathway - Homo sapiens (human),
path:hsa04640 → Hematopoietic cell lineage - Homo sapiens (human),
path:hsa04650 → Natural killer cell mediated cytotoxicity - Homo sapiens (human),
path:hsa04657 → IL-17 signaling pathway - Homo sapiens (human),
path:hsa04658 → Th1 and Th2 cell differentiation - Homo sapiens (human),
path:hsa04659 → Th17 cell differentiation - Homo sapiens (human),
path:hsa04660 → T cell receptor signaling pathway - Homo sapiens (human),
path:hsa04662 → B cell receptor signaling pathway - Homo sapiens (human),
path:hsa04664 → Fc epsilon RI signaling pathway - Homo sapiens (human),
path:hsa04666 → Fc gamma R-mediated phagocytosis - Homo sapiens (human),
path:hsa04668 → TNF signaling pathway - Homo sapiens (human),
path:hsa04670 → Leukocyte transendothelial migration - Homo sapiens (human),
path:hsa04672 → Intestinal immune network for IgA production - Homo sapiens (human),
path:hsa04710 → Circadian rhythm - Homo sapiens (human),
path:hsa04713 → Circadian entrainment - Homo sapiens (human),
path:hsa04714 → Thermogenesis - Homo sapiens (human),
path:hsa04720 → Long-term potentiation - Homo sapiens (human),
path:hsa04721 → Synaptic vesicle cycle - Homo sapiens (human),
path:hsa04722 → Neurotrophin signaling pathway - Homo sapiens (human),
path:hsa04723 → Retrograde endocannabinoid signaling - Homo sapiens (human),
path:hsa04724 → Glutamatergic synapse - Homo sapiens (human),
path:hsa04725 → Cholinergic synapse - Homo sapiens (human),
path:hsa04726 → Serotonergic synapse - Homo sapiens (human),
path:hsa04727 → GABAergic synapse - Homo sapiens (human),
path:hsa04728 → Dopaminergic synapse - Homo sapiens (human),
path:hsa04730 → Long-term depression - Homo sapiens (human),
path:hsa04740 → Olfactory transduction - Homo sapiens (human),
path:hsa04742 → Taste transduction - Homo sapiens (human),
path:hsa04744 → Phototransduction - Homo sapiens (human),
path:hsa04750 → Inflammatory mediator regulation of TRP channels - Homo sapiens (human),
path:hsa04810 → Regulation of actin cytoskeleton - Homo sapiens (human),
path:hsa04910 → Insulin signaling pathway - Homo sapiens (human),
path:hsa04911 → Insulin secretion - Homo sapiens (human),
path:hsa04912 → GnRH signaling pathway - Homo sapiens (human),
path:hsa04913 → Ovarian steroidogenesis - Homo sapiens (human),
path:hsa04914 → Progesterone-mediated oocyte maturation - Homo sapiens (human),
path:hsa04915 → Estrogen signaling pathway - Homo sapiens (human),
path:hsa04916 → Melanogenesis - Homo sapiens (human),
path:hsa04917 → Prolactin signaling pathway - Homo sapiens (human),
path:hsa04918 → Thyroid hormone synthesis - Homo sapiens (human),
path:hsa04919 → Thyroid hormone signaling pathway - Homo sapiens (human),
path:hsa04920 → Adipocytokine signaling pathway - Homo sapiens (human),
path:hsa04921 → Oxytocin signaling pathway - Homo sapiens (human),
path:hsa04922 → Glucagon signaling pathway - Homo sapiens (human),
path:hsa04923 → Regulation of lipolysis in adipocytes - Homo sapiens (human),
path:hsa04924 → Renin secretion - Homo sapiens (human),
path:hsa04925 → Aldosterone synthesis and secretion - Homo sapiens (human),
path:hsa04926 → Relaxin signaling pathway - Homo sapiens (human),
path:hsa04927 → Cortisol synthesis and secretion - Homo sapiens (human),
path:hsa04928 → Parathyroid hormone synthesis, secretion and action - Homo sapiens (human),
path:hsa04930 → Type II diabetes mellitus - Homo sapiens (human),
path:hsa04931 → Insulin resistance - Homo sapiens (human),
path:hsa04932 → Non-alcoholic fatty liver disease (NAFLD) - Homo sapiens (human),
path:hsa04933 → AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human),
path:hsa04934 → Cushing syndrome - Homo sapiens (human),
path:hsa04940 → Type I diabetes mellitus - Homo sapiens (human),
path:hsa04950 → Maturity onset diabetes of the young - Homo sapiens (human),
path:hsa04960 → Aldosterone-regulated sodium reabsorption - Homo sapiens (human),
path:hsa04961 → Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human),
path:hsa04962 → Vasopressin-regulated water reabsorption - Homo sapiens (human),
path:hsa04964 → Proximal tubule bicarbonate reclamation - Homo sapiens (human),
path:hsa04966 → Collecting duct acid secretion - Homo sapiens (human),
path:hsa04970 → Salivary secretion - Homo sapiens (human),
path:hsa04971 → Gastric acid secretion - Homo sapiens (human),
path:hsa04972 → Pancreatic secretion - Homo sapiens (human),
```

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```
path:hsa04973 → Carbohydrate digestion and absorption - Homo sapiens (human),
path:hsa04974 → Protein digestion and absorption - Homo sapiens (human),
path:hsa04975 → Fat digestion and absorption - Homo sapiens (human),
path:hsa04976 → Bile secretion - Homo sapiens (human),
path:hsa04977 → Vitamin digestion and absorption - Homo sapiens (human),
path:hsa04978 → Mineral absorption - Homo sapiens (human),
path:hsa04979 → Cholesterol metabolism - Homo sapiens (human),
path:hsa05010 → Alzheimer disease - Homo sapiens (human),
path:hsa05012 → Parkinson disease - Homo sapiens (human),
path:hsa05014 → Amyotrophic lateral sclerosis (ALS) - Homo sapiens (human),
path:hsa05016 → Huntington disease - Homo sapiens (human),
path:hsa05020 → Prion diseases - Homo sapiens (human),
path:hsa05030 → Cocaine addiction - Homo sapiens (human),
path:hsa05031 → Amphetamine addiction - Homo sapiens (human),
path:hsa05032 → Morphine addiction - Homo sapiens (human),
path:hsa05033 → Nicotine addiction - Homo sapiens (human),
path:hsa05034 → Alcoholism - Homo sapiens (human),
path:hsa05100 → Bacterial invasion of epithelial cells - Homo sapiens (human),
path:hsa05110 → Vibrio cholerae infection - Homo sapiens (human),
path:hsa05120 → Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human),
path:hsa05130 → Pathogenic Escherichia coli infection - Homo sapiens (human),
path:hsa05131 → Shigellosis - Homo sapiens (human),
path:hsa05132 → Salmonella infection - Homo sapiens (human),
path:hsa05133 → Pertussis - Homo sapiens (human), path:hsa05134 → Legionellosis - Homo sapiens (human),
path:hsa05135 → Yersinia infection - Homo sapiens (human),
path:hsa05140 → Leishmaniasis - Homo sapiens (human),
path:hsa05142 → Chagas disease (American trypanosomiasis) - Homo sapiens (human),
path:hsa05143 → African trypanosomiasis - Homo sapiens (human),
path:hsa05144 → Malaria - Homo sapiens (human), path:hsa05145 → Toxoplasmosis - Homo sapiens (human),
path:hsa05146 → Amoebiasis - Homo sapiens (human),
path:hsa05150 → Staphylococcus aureus infection - Homo sapiens (human),
path:hsa05152 → Tuberculosis - Homo sapiens (human), path:hsa05160 → Hepatitis C - Homo sapiens (human),
path:hsa05161 → Hepatitis B - Homo sapiens (human), path:hsa05162 → Measles - Homo sapiens (human),
path:hsa05163 → Human cytomegalovirus infection - Homo sapiens (human),
path:hsa05164 → Influenza A - Homo sapiens (human),
path:hsa05165 → Human papillomavirus infection - Homo sapiens (human),
path:hsa05166 → Human T-cell leukemia virus 1 infection - Homo sapiens (human),
path:hsa05167 → Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human),
path:hsa05168 → Herpes simplex virus 1 infection - Homo sapiens (human),
path:hsa05169 → Epstein-Barr virus infection - Homo sapiens (human),
path:hsa05170 → Human immunodeficiency virus 1 infection - Homo sapiens (human),
path:hsa05200 → Pathways in cancer - Homo sapiens (human),
path:hsa05202 → Transcriptional misregulation in cancer - Homo sapiens (human),
path:hsa05203 → Viral carcinogenesis - Homo sapiens (human),
path:hsa05204 → Chemical carcinogenesis - Homo sapiens (human),
path:hsa05205 → Proteoglycans in cancer - Homo sapiens (human),
path:hsa05206 → MicroRNAs in cancer - Homo sapiens (human),
path:hsa05210 → Colorectal cancer - Homo sapiens (human),
path:hsa05211 → Renal cell carcinoma - Homo sapiens (human),
path:hsa05212 → Pancreatic cancer - Homo sapiens (human),
path:hsa05213 → Endometrial cancer - Homo sapiens (human),
path:hsa05214 → Glioma - Homo sapiens (human), path:hsa05215 → Prostate cancer - Homo sapiens (human),
path:hsa05216 → Thyroid cancer - Homo sapiens (human),
path:hsa05217 → Basal cell carcinoma - Homo sapiens (human),
path:hsa05218 → Melanoma - Homo sapiens (human), path:hsa05219 → Bladder cancer - Homo sapiens (human),
path:hsa05220 → Chronic myeloid leukemia - Homo sapiens (human),
path:hsa05221 → Acute myeloid leukemia - Homo sapiens (human),
path:hsa05222 → Small cell lung cancer - Homo sapiens (human),
path:hsa05223 → Non-small cell lung cancer - Homo sapiens (human),
path:hsa05224 → Breast cancer - Homo sapiens (human),
path:hsa05225 → Hepatocellular carcinoma - Homo sapiens (human),
path:hsa05226 → Gastric cancer - Homo sapiens (human),
path:hsa05230 → Central carbon metabolism in cancer - Homo sapiens (human),
path:hsa05231 → Choline metabolism in cancer - Homo sapiens (human),
path:hsa05235 → PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human),
path:hsa05310 → Asthma - Homo sapiens (human),
```

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```
path:hsa05320 → Autoimmune thyroid disease - Homo sapiens (human),
path:hsa05321 → Inflammatory bowel disease (IBD) - Homo sapiens (human),
path:hsa05322 → Systemic lupus erythematosus - Homo sapiens (human),
path:hsa05323 → Rheumatoid arthritis - Homo sapiens (human),
path:hsa05330 → Allograft rejection - Homo sapiens (human),
path:hsa05332 → Graft-versus-host disease - Homo sapiens (human),
path:hsa05340 → Primary immunodeficiency - Homo sapiens (human),
path:hsa05410 → Hypertrophic cardiomyopathy (HCM) - Homo sapiens (human),
path:hsa05412 → Arrhythmogenic right ventricular cardiomyopathy (ARVC) - Homo sapiens (human),
path:hsa05414 → Dilated cardiomyopathy (DCM) - Homo sapiens (human),
path:hsa05416 → Viral myocarditis - Homo sapiens (human),
path:hsa05418 → Fluid shear stress and atherosclerosis - Homo sapiens (human)|>
```

See Also

GeneTranslation ▪ **GetGeneDictionary** ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGAnalysisAssigner** ▪ **KEGGPathwayVisual** ▪ **OBOGODictionary** ▪ **UCSCBrowserSQL**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾ URL ▾

KEGGPathwayVisual

KEGGPathwayVisual[*pathway*]
generates a visual representation for a KEGG: Kyoto Encyclopedia of Genes and Genomes pathway.

Details

- KEGGPathwayVisual[*pathway*] generates a visual representation for a KEGG: Kyoto Encyclopedia of Genes and Genomes pathway. The input has to be a KEGG pathway accession string (e.g. "path:hsa04910").
- The output has the form of an association:
- output = <|"Pathway" → input pathway string, "Results" → returned data|>,
- The returned data format depend on the ResultsFormat option. By default a URL is returned for the pathway that may be used in a browser.

ResultsFormat option setting	"Results" value for returned data
"URL"	Browser URL pointing to pathway on KEGG database, or if a list of Intensities was provided a series of URLs corresponding to each time point or sequential data in the series.
"Figure"	Pathway figure downloaded from the KEGG database, or if a list of Intensities was provided a series of figures corresponding to each time point or sequential data in the series.
"Movie"	Name of the output file that contains the generated movie/animation that is based on the list of Intensities provided.

- The pathway can be colored to either highlight a set of IDs, or to represent multi-omics data that has been labeled if intensity values are provided through the Intensities option.
- An active internet connection is necessary for the KEGGPathwayVisual to function properly.
- If the ResultsFormat is set to "Figure" or "Movie" the computation can be intensive depending on internet connectivity, and number of IDs and correspoind number of data points in each ID's series considered.
- The following options can be given:

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AnalysisType	"Genomic"	AnalysisType provides a selection for the type of analysis to perform. "Genomic" analysis (default) uses gene identifier based pathway visualization. "Molecular" analysis uses molecular analysis map visualization.
AugmentDictionary	True	AugmentDictionary provides a choice whether or not to augment the current ConstantGeneDictionary variable or create a new one.
BlendColors	{RGBColor[0, 0, 1], RGBColor[0, 0, 1], RGBColor[0.5, 0.5, 0.5], RGBColor[1, 0, 0], RGBColor[1, 0, 0]}	BlendColors provides a list of colors to be used in coloring intensities provided and is used by the IntensityFunction as its first argument. The colors must be provided as RGBColor[] specification.
ColorSelection	<|"RNA" → "bg", "Protein" → "fg"|>	ColorSelection assigns foreground and background colors in the KEGG pathway through an association. The Keys point to labels for multi–omics data, and the values "bg" and "fg" can point to background and foreground representations respectively for each key.
DefaultColors	{"fg" –> RGBColor[0, 0, 0], "bg" –> RGBColor[0, 1, 0]}	DefaultColors provides a list of rules for setting the colors to be used as default values for the foreground "fg" and background "bg" respectively in the generated pathways. The colors must be provided as RGBColor[] specification.
ExportMovieOptions	{"VideoEncoding" → "MPEG–4 Video", "FrameRate" → 1}	ExportMovieOptions provides options for the Export function used internally to export the pathway list when Intensities have been provided for a time series representation of data.
FileExtend	".mov"	FileExtend provides a string to be appended to the file name if the ResultsFormat is set to "Movie".

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GeneDictionary	None	GeneDictionary points to an existing variable to use as a gene dictionary in annotations. The gene dictionary is used to convert MemberSet identities provided to corresponding KEGG identifiers. If GeneDictionary is set to None the default ConstantGeneDictionary will be created or augmented through the use of GetGeneDictionary.
GetGeneDicitonaryOptions	{}	The GetGeneDictionaryOptions option specifies a list of options that will be passed to the internal GetGeneDictionary function.
InputID	{"UniProt ID", "Gene Symbol"}	The InputID option specifies the kind of identifiers/accessions used as input when identifiers are provided through setting the MemberSet values.
Intensities	None	Intensities may be used to provide a set of intensities that will be used for coloring components of the pathway. The intensities are provided as an association for each ID as single values, or as a list of values in the case of series data: $<\|\mathrm{ID}_1 \to \{\text{intensity list for } \mathrm{ID}_1\}, \mathrm{ID}_2 \to \{\text{intensity list for } \mathrm{ID}_2\}, \ldots, \mathrm{ID}_N \to \{\text{intensity list for } \mathrm{ID}_N\}\|>$. Intensities must be scaled from –1 to 1, or selected such that the IntensityFunction can convert them to a number between 0 to 1.

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IntensityFunction	(Blend[#1, (#2 + 1) / 2] &)	IntensityFunction is a function of two arguments that allows customization of the coloring for the intensities. The IntensityFunction value can be any function which outputs a color, I(#1,#2), (*where#1 is the BlendColors option value, and #2 is an intensity vector, that has values typically ranging from [–1,1].
KEGGAnalysisAssignerOptions	{}	The KEGGAnalysisAssignerOptions option specifies a list of options that will be passed to the internal KEGGAnalysisAssigner function.
KEGGDatabase	"pathway"	KEGGDatabase value indicates which KEGG database to use as the target database.
KEGGMolecular	"cpd"	KEGGMolecular specifies which database to use for molecular analysis. The default is the compound database ("cpd").
KEGGOrganism	"hsa"	KEGGOrganism indicates which organism (org) to use for "Genomic" type of analysis. The default is human analysis org="hsa".
MathIOmicaDataDirectory	If[! DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]	MathIOmicaDataDirectory option specifies the directory where the default MathIOmica package data are stored. By default the option is set to create the standard directory if it does not exist already.

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MemberSet	All	MemberSet selects which members of the pathway are to be considered. The choices are: All: return the pathway only. {list of identifiers}: a list of identifiers that will be highlighted. If ORA is set to True the list must be the output from an over representation analysis, and the identifiers will be selected from the last list, second sublist. Only IDs that are found to match in the pathway are colored. An internal gene dictionary (see GetGeneDictionary) is used to convert IDs to KEGG IDs.
MissingValueColor	RGBColor[0.4, 0.4, 0.4]	MissingValueColor provides a color to be used when Intensities are provided to represent values that are tagged as Missing[]. The color must be provided as RGBColor[] specification.
MolecularInputID	{"cpd"}	MolecularInputID is a string list to indicate the kind of ID to use for the input molecule entries.
MolecularOutputID	"cpd"	MolecularOutputID is a string to indicate the kind of ID to convert input molecule entries. The default is "cpd" consistently with use of the "cpd" database as the default molecular analysis.
MolecularSpecies	"compound"	MolecularSpecies specifies the kind of molecular input.
MovieFilePath	None	MovieFilePath indicates the path (including file name) where if ResultsFormat is set to "Movie" the movie generated will be saved. The default value None will generate a file named after the pathway with extension set by the FileExtend option in the current directory.

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NonUCSC	False	NonUCSC option set to False assumes UCSC browser was used in determining an internal GeneDictionary used in ID translations where the KEGG identifiers for genes are number strings (e.g. 4790). The NonUCSC option can be set to True if standard KEGG accessions are used in a user provided GeneDictionary variable, in the form OptionValue[KEGGOrganism] <>":"<>"number string", e.g. "hsa:4790"
ORA	False	ORA can be set to True or False depending on whether the input is from an over representation analysis (e.g. output from KEGGAnalysis), or not respectively.
OutputID	"KEGG Gene ID"	OutputID is a string to indicate the kind of ID to convert input genomic analysis entries. The default is "KEGG Gene ID" consistently with use of the "pathway" database as the default genomic analysis.
ResultsFormat	"URL"	ResultsFormat provides a choice of output format, the choices are: "URL": returns a URL of the pathway, "Figure": returns figure output(s) for the pathway, "Movie": in the case of series data returns a movie/animation of the series pathway snapshots.
SingleColorPlace	"bg"	SingleColorPlace selects in the case of a single identifier input whether to place the color to the foreground, ("fg") or background ("bg" set by default).
Species	"human"	The Species option specifies the species considered in the calculation.

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StandardHighlight	{"fg" –> RGBColor[1, 0, 0], "bg" –> RGBColor[0.5, 0.7, 1]}	StandardHighlight provides a list of rules for setting the highlight colors for the IDs represented in the pathway (when no intensities are provided). The list specifies color rules for foregroung, "fg", and background, "bg", respectively. The colors must be provided as RGBColor[] specification.

Examples (46)

Basic Examples (8)

We first load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

MathIOmica (https://mathiomica.org), *by G. Mias Lab.*

Let's find the pathway on KEGG with accession "path:hsa04064":

In[2]:=
```
keggVisualExample1URL = KEGGPathwayVisual["path:hsa04064"]
```

Out[2]= ⟨| Pathway → path:hsa04064, Results → {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064} |⟩

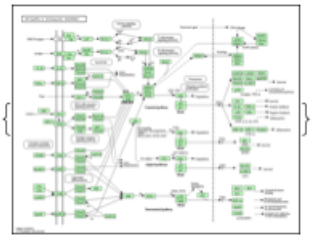
We can open the result URL in a browser:

In[3]:=
```
SystemOpen[keggVisualExample1URL["Results"][[1]]]
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can also download a figure for a pathway:

In[2]:=
```
keggVisualExample1Figure = KEGGPathwayVisual["path:hsa04064", ResultsFormat → "Figure"]
```

Out[2]= ⟨| Pathway → path:hsa04064, Results → {  } |⟩

We can zoom in, either manually or by setting the ImageSize:

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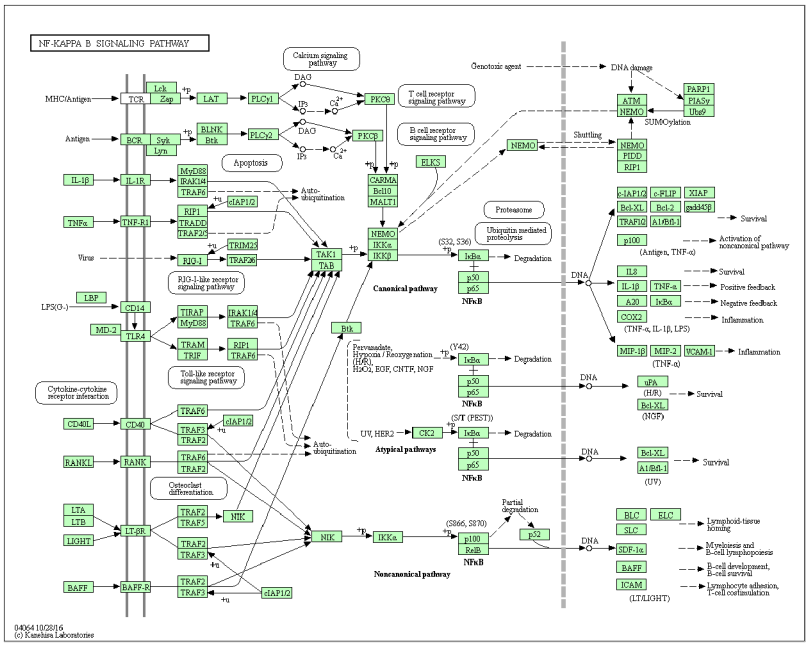
In[3]:=
```
Show[keggVisualExample1Figure["Results"][[1]], ImageSize → 500]
```

Out[3]=



In[1]:=
```
Needs["MathIOmica`"]
```

Let us find the pathway on KEGG with accession "path:hsa04064" and highlight three members of the pathway:

In[2]:=
```
keggVisualExampleHighlighted = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}]
```

Out[2]=
```
⟨|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|⟩
```

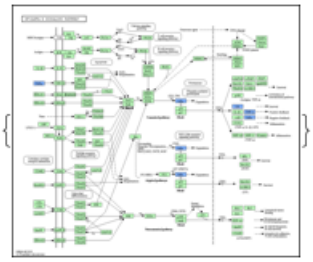
We can open the figure in the system browser online:

In[3]:=
```
SystemOpen[keggVisualExampleHighlighted["Results"][[1]]]
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can also download the figure programmatically:

In[2]:=
```
keggVisualExampleHighlightedFigure =
 KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}, ResultsFormat → "Figure"]
```

Out[2]= ⟨|Pathway → path:hsa04064, Results → {  }|⟩

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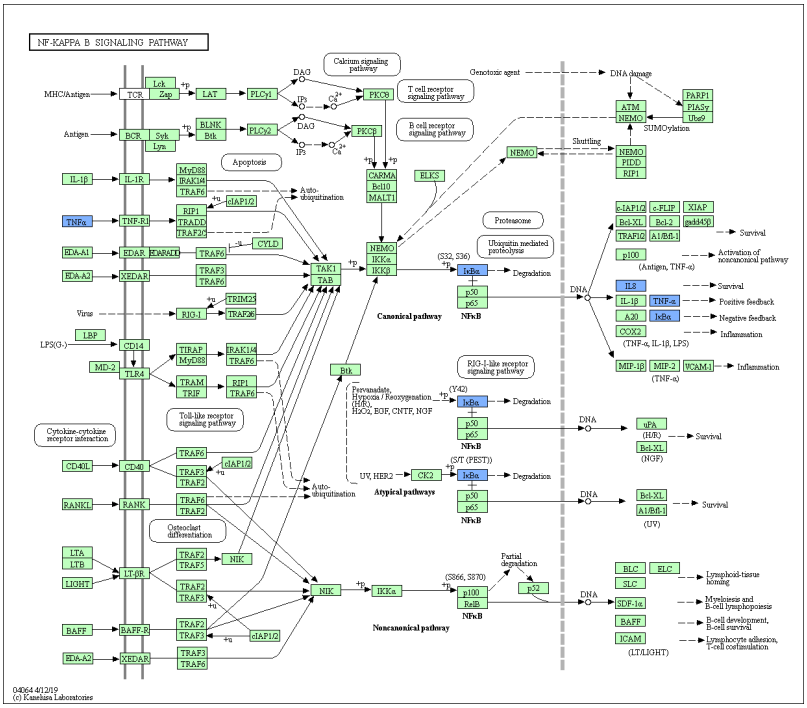
In[3]:=
```
Show[keggVisualExampleHighlightedFigure["Results"][[1]], ImageSize → 500]
```

Out[3]=



In[1]:=
```
Needs["MathIOmica`"]
```

The data can contain multiple omics information, that will be colored differently in backgrounds and foregrounds:

In[2]:=
```
keggVisualHighlightedMultiURL = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}}]
```

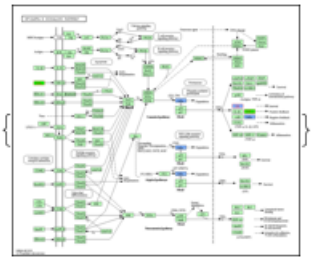
Out[2]=
```
⟨|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2300ff00%2C%23ff0000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23ff0000%0D%0A}|⟩
```

We can open the figure in the system browser online:

In[3]:=
```
SystemOpen[keggVisualHighlightedMultiURL["Results"][[1]]]
```

Alternatively we can directly download and import the figure:

In[4]:=
```
keggVisualHighlightedMultiFigure = KEGGPathwayVisual["path:hsa04064", MemberSet →
   {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}}, ResultsFormat → "Figure"]
```

Out[4]= ⟨|Pathway → path:hsa04064, Results → {  }|⟩

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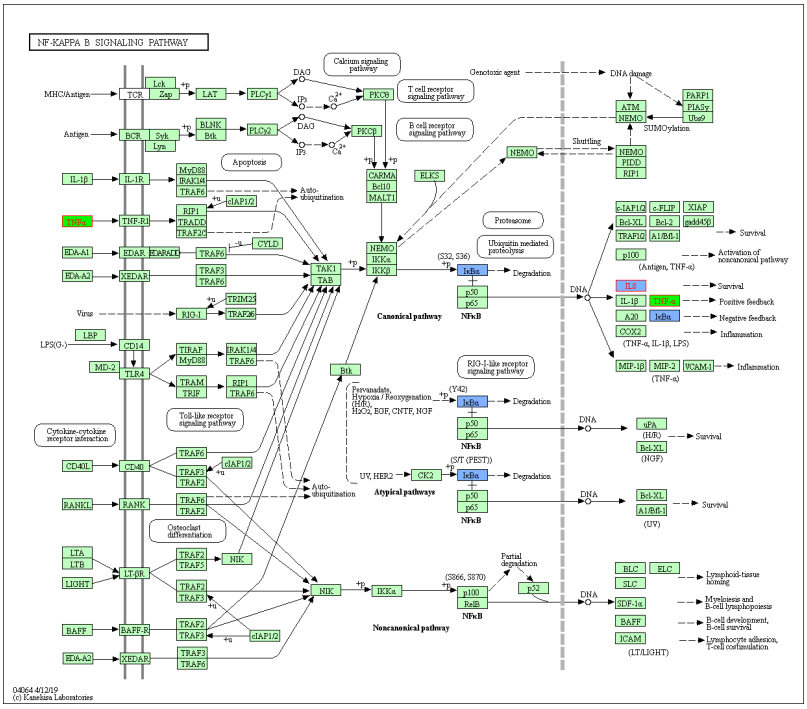
We can see that protein data has different foregrounds, RNA data different backgrounds, and if both are represent (e.g. IL8 in this example) we have both superimposed (N.B. colors can be manipulated by the options):

In[5]:=
```
Show[keggVisualHighlightedMultiFigure["Results"][[1]], ImageSize → 500]
```

Out[5]=



In[1]:=
```
Needs["MathIOmica`"]
```

We can provide intensities for the data: here is an example with a single intensity provided

In[2]:=
```
keggVisualIntensity = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {"TNF", "NFKBIA", "IL8"}, Intensities → <| "TNF" → 0.2, "NFKBIA" → -0.2, "IL8" → 0.8|>]
```

Out[2]=
```
<|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23b24d4d%2C%23000000%0D
    %0Ahsa%3A4792+%234d4db2%2C%23000000%0D%0Ahsa%3A3576+%23ff0000%2C%23000000%0D%0A}|>
```

We can open the figure in the system browser online:

In[3]:=
```
SystemOpen[keggVisualIntensity["Results"][[1]]]
```

Or we can view it as an imported figure:

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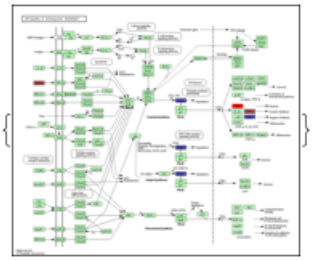
In[4]:=
```
keggVisualIntensityFigure = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → 0.2, "NFKBIA" → -0.2, "IL8" → 0.8|>, ResultsFormat → "Figure"]
```

Out[4]= ⟨|Pathway → path:hsa04064, Results → {  }|⟩

In[1]:=
```
Needs["MathIOmica`"]
```

If multiple data points are included for Intensities, a figure is generated for each corresponding position snapshot across data. For example, looking at data with three intensities (e.g. three timepoints) we can generate a pathway at each point:

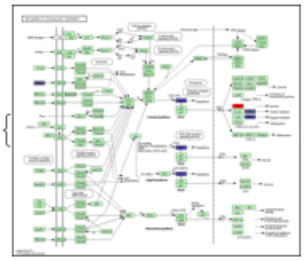
In[2]:=
```
keggVisualIntensitiesURL = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → { -0.1, 0.3, 0.4}, "NFKBIA" → { -0.2, 0.3, 0.2}, "IL8" → {0.8, 0.3, Missing[]}|>]
```

Out[2]= ⟨|Pathway → path:hsa04064, Results →
{https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23666699%2C%23000000%0D%0Ahsa%3A4792+%234d4db2%2C%23000000%0D%0Ahsa%3A3576+%23ff0000%2C%23000000%0D%0A,
https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23cc3333%2C%23000000%0D%0Ahsa%3A4792+%23cc3333%2C%23000000%0D%0Ahsa%3A3576+%23cc3333%2C%23000000%0D%0A,
https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23e51a1a%2C%23000000%0D%0Ahsa%3A4792+%23b24d4d%2C%23000000%0D%0Ahsa%3A3576+%23666666%2C%23000000%0D%0A}|⟩

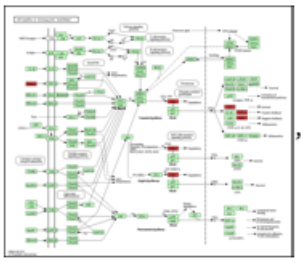
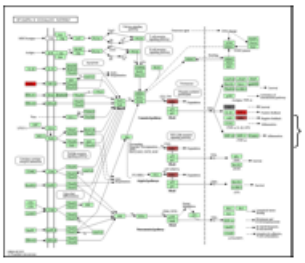
The results has three URLs corresponding to each set that may be used in a browser.

We can also import all the figures:

In[3]:=
```
keggVisualIntensitiesFigures = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → { -0.1, 0.3, 0.4}, "NFKBIA" → { -0.2, 0.3, 0.2}, "IL8" → {0.8, 0.3, Missing[]}|>,
  ResultsFormat → "Figure"]
```

⟨|Pathway → path:hsa04064, Results → {  ,

Out[3]=

 ,  }|⟩

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Intensities marked as Missing[] are shown in grey by default.

These figures can also be exported as a .mov movie file in the current directory (the default format and save location can be changed with the options, please further below for details):

```
In[4]:= Directory[]

In[5]:= keggVisualIntensitiesMovie = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
          Intensities → <| "TNF" → { -0.1, 0.3, 0.4}, "NFKBIA" → { -0.2, 0.3, 0.2}, "IL8" → {0.8, 0.3, Missing[]}|>,
          ResultsFormat → "Movie"]

Out[5]= <|Pathway → path:hsa04064, Results → path_hsa04064.mov|>
```

The "Results" value indicates the name of the movie file.

```
In[1]:= Needs["MathIOmica`"]
```

Multi-omics datasets with both "RNA" and "Protein" data can be represented as well with series Intensities provided:

```
In[2]:= keggVisualMultiomicIntensitiesURLs = KEGGPathwayVisual["path:hsa04064",
          MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}},
          Intensities → <| {"TNF", "Protein"} → {-0.2, 0.1, -0.4, .3} , {"NFKBIA", "RNA"} → {-0.2, -0.4, -0.3, -0.2},
            {"IL8", "RNA"} → {0.3, 0.1, 0.1, Missing[]}, {"IL8", "Protein"} → {0.1, Missing[], 0.2, 0.1}|>]

Out[2]= <|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2300ff00%2C%234d4db2%0D
            %0Ahsa%3A4792+%234d4db2%2C%23000000%0D%0Ahsa%3A3576+%23cc3333%2C%23996666%0D%0A,
           https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2300ff00%2C%23996666%0D
            %0Ahsa%3A4792+%231919e6%2C%23000000%0D%0Ahsa%3A3576+%23996666%2C%23666666%0D%0A,
           https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2300ff00%2C%231919e6%0D
            %0Ahsa%3A4792+%233333cc%2C%23000000%0D%0Ahsa%3A3576+%23996666%2C%23b24d4d%0D%0A,
           https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2300ff00%2C%23cc3333%0D
            %0Ahsa%3A4792+%234d4db2%2C%23000000%0D%0Ahsa%3A3576+%23666666%2C%23996666%0D%0A}|>
```

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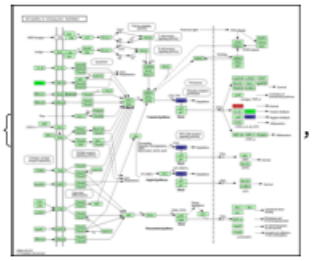
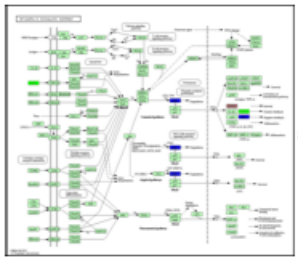
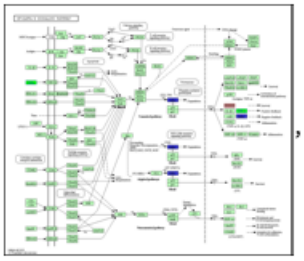
In[3]:=
```
keggVisualMultiomicIntensitiesFigures = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}},
  Intensities → <| {"TNF", "Protein"} → {-0.2, 0.1, -0.4, .3} ,
    {"NFKBIA", "RNA"} → {-0.2, -0.4, -0.3, -0.2}, {"IL8", "RNA"} → {0.3, 0.1, 0.1, Missing[]},
    {"IL8", "Protein"} → {0.1, Missing[], 0.2, 0.1}|>, ResultsFormat → "Figure"]
```

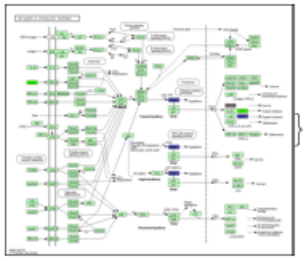
Out[3]=

```
⟨| Pathway → path:hsa04064,
  Results → {
```









We note here that the color choice can be adjusted using various options.

Options (38)

AnalysisType (1)

In[1]:=
```
Needs["MathIOmica`"]
```

AnalysisType provides a selection for the type of analysis to perform. "Genomic" analysis (default) uses gene identifier based pathway visualization. "Molecular" analysis uses molecular analysis map visualization.

Let us consider a molecular analysis mapping compounds to the insulin signaling pathway (path:map04910)

In[2]:=
```
keggVisualMolecular = KEGGPathwayVisual["path:map04910",
  MemberSet → {"cpd:C00031", "cpd:C00369", "cpd:C00575", "cpd:C05981"}, AnalysisType → "Molecular"]
```

Out[2]=
```
⟨| Pathway → path:map04910, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=map04910&multi_query=cpd%3AC00031+%2380b2ff%2C%23000000%0
    D%0Acpd%3AC00369+%2380b2ff%2C%23000000%0D%0Acpd%3AC00575+%2380b2ff%2C%23000000%0D%0Acpd%3AC05981+
    %2380b2ff%2C%23000000%0D%0A} |⟩
```

We can open the above URL in a browser, or we can instead import the figures:

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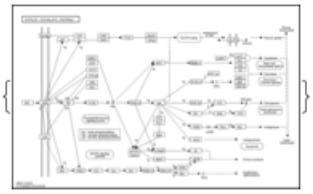
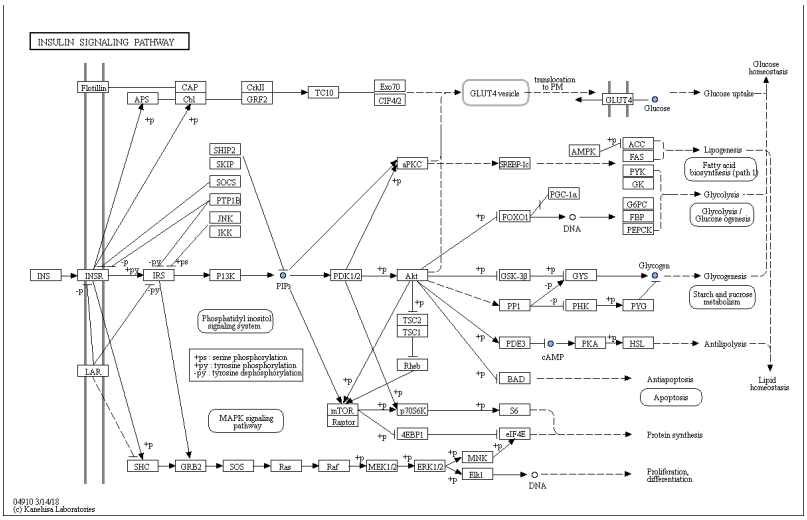
In[3]:=
```
keggVisualMolecularFigures =
 KEGGPathwayVisual["path:map04910", MemberSet → {"cpd:C00031", "cpd:C00369", "cpd:C00575", "cpd:C05981"},
  AnalysisType → "Molecular", ResultsFormat → "Figure"]
```

Out[3]= ⟨|Pathway → path:map04910, Results → {  }|⟩

In[4]:=
```
Show[keggVisualMolecularFigures["Results"][[1]], ImageSize → 500]
```

Out[4]=



AugmentDictionary (1)

In[1]:=
```
Needs["MathIOmica`"]
```

AugmentDictionary provides a choice whether or not to augment the current ConstantGeneDictionary variable or create a new one. In the example below gene dictionary already exists, and set a simple dictionary as an example (please note that this will reset your variable if you have one already created, so use with caution):

In[2]:=
```
ConstantGeneDictionary =
  ⟨|"humanExample" → ⟨|"UCSC ID" → {"uc001aaa.3", "uc010nxr.1", "uc010nxq.1", "uc001aal.1", "uc001aaq.2",
       "uc001aar.2", "uc001aau.3", "uc021oeh.1", "uc009vjk.2", "uc021oei.1", "uc010nxu.2", "uc001aax.1",
       "uc001abb.3", "uc001abp.2", "uc021oem.2", "uc009vjn.2", "uc009vjo.2", "uc031pjk.1", "uc031pjj.1",
       "uc001abu.1", "uc001abw.1", "uc031pjv.1", "uc031pkd.1", "uc031pkk.1", "uc031pkl.1"},
     "Gene Symbol" → {"DDX11L1", "DDX11L1", "DDX11L1", "OR4F5", "DQ597235", "DQ599768",
       "LOC100132062", "LOC100133331", "LOC100133331", "LOC388312", "OR4F29", "BC036251",
       "M37726", "LOC643837", "LOC643837", "LOC643837", "LOC643837", "LOC643837",
       "LOC643837", "AK056486", "SAMD11", "SAMD11", "SAMD11", "SAMD11", "SAMD11"}|⟩|⟩;
```

If we now run a standard analysis with the AugmentDictionary option set to True we have:

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In[3]:=
```
keggVisualAugmentDictionary =
 KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}, AugmentDictionary → True]
```

Out[3]=
```
<|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|>
```

We now check again the ConstantGeneDictionary :

In[4]:=
```
ConstantGeneDictionary
```

Out[4]=
```
<|humanExample →
  <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1, uc001aaq.2, uc001aar.2, uc001aau.3,
     uc021oeh.1, ⋯ 9 ⋯, uc031pjk.1, uc031pjj.1, uc001abu.1, uc001abw.1, uc031pjv.1,
     uc031pkd.1, uc031pkk.1, uc031pkl.1}, Gene Symbol → ⋯ 1 ⋯|>, human → ⋯ 1 ⋯|>
```

large output | show less | show more | show all | set size limit...

In[5]:=
```
Keys[ConstantGeneDictionary]
```

Out[5]=
```
{humanExample, human}
```

We see that this has augmented the previous dictionary with the "human" annotation used in the example. We now repeat with `AugmentDictionary` set to False:

In[6]:=
```
keggVisualAugmentDictionaryFalse =
 KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}, AugmentDictionary → False]
```

Out[6]=
```
<|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|>
```

We now check again the ConstantGeneDictionary to notice that the previous ConstantGeneDictionary has now been replaced with a new default one.

In[7]:=
```
ConstantGeneDictionary
```

Out[7]=
```
<|human → <|UCSC ID → {uc001aaa.3, uc010nxr.1, uc010nxq.1, uc001aal.1, uc001aaq.2, uc001aar.2, uc001aau.3,
     uc021oeh.1, uc009vjk.2, ⋯ 121565 ⋯, uc022cff.1, uc022cfk.1, uc031tkn.1, uc022cgh.1,
     uc022cha.1, uc022chb.1, uc022chc.1, uc022che.1, uc022cpe.1}, ⋯ 6 ⋯, ⋯ 1 ⋯|>|>
```

large output | show less | show more | show all | set size limit...

In[8]:=
```
Keys[ConstantGeneDictionary]
```

Out[8]=
```
{human}
```

BlendColors (1)

In[1]:=
```
Needs["MathIOmica`"]
```

BlendColors provides a list of colors to be used in coloring intensities provided and is used

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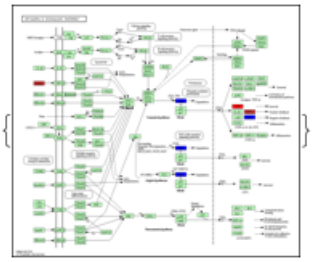
by the IntensityFunction option function as its first argument. The colors must be provided as RGBColor[] scheme specifications.

Let us first consider the default analysis, with the default color scheme:

In[2]:=
```
blendColorsDefault =
 {RGBColor[0, 0, 1], RGBColor[0, 0, 1], RGBColor[0.5, 0.5, 0.5], RGBColor[1, 0, 0], RGBColor[1, 0, 0]}
```

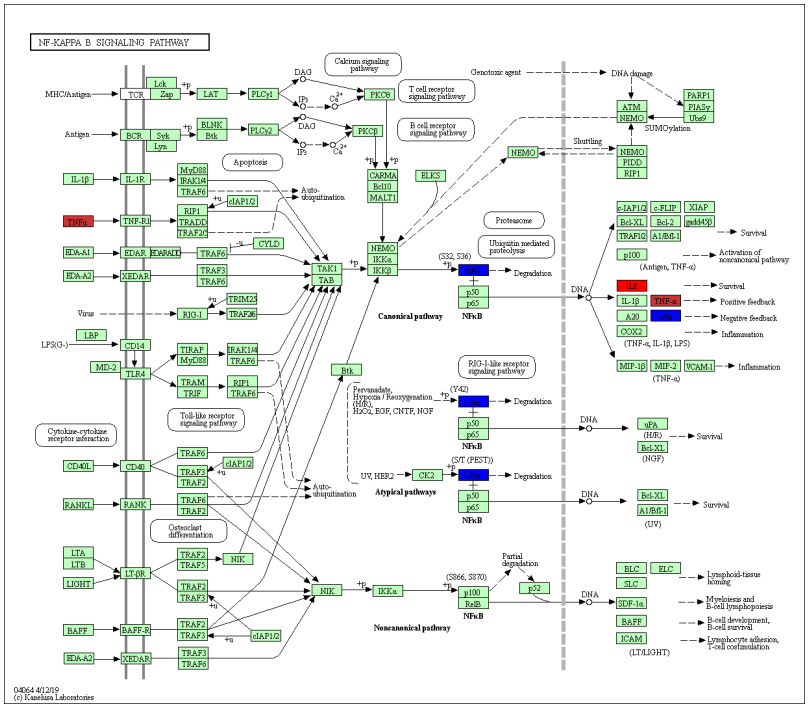
Out[2]= {■, ■, ■, ■, ■}

In[3]:=
```
keggVisualBlendColorsDefault = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {"TNF", "NFKBIA", "IL8"}, Intensities → <| "TNF" → 0.3, "NFKBIA" → -0.7, "IL8" → 0.8|>,
  ResultsFormat → "Figure", BlendColors → blendColorsDefault]
```

Out[3]= ⟨| Pathway → path:hsa04064, Results → {  } |⟩

In[4]:=
```
Show[keggVisualBlendColorsDefault["Results"][[1]], ImageSize → 500]
```

Out[4]=



Let us use a custom color scheme:

In[5]:=
```
blendColorsCustom = {RGBColor[1, 0.7, 0], RGBColor[0.5, 0.5, 0.5], RGBColor[0, 0.5, 1]}
```

Out[5]= {■, ■, ■}

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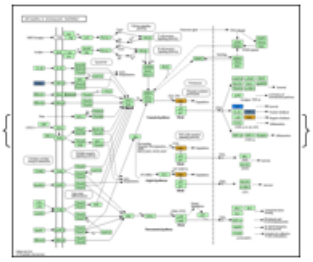
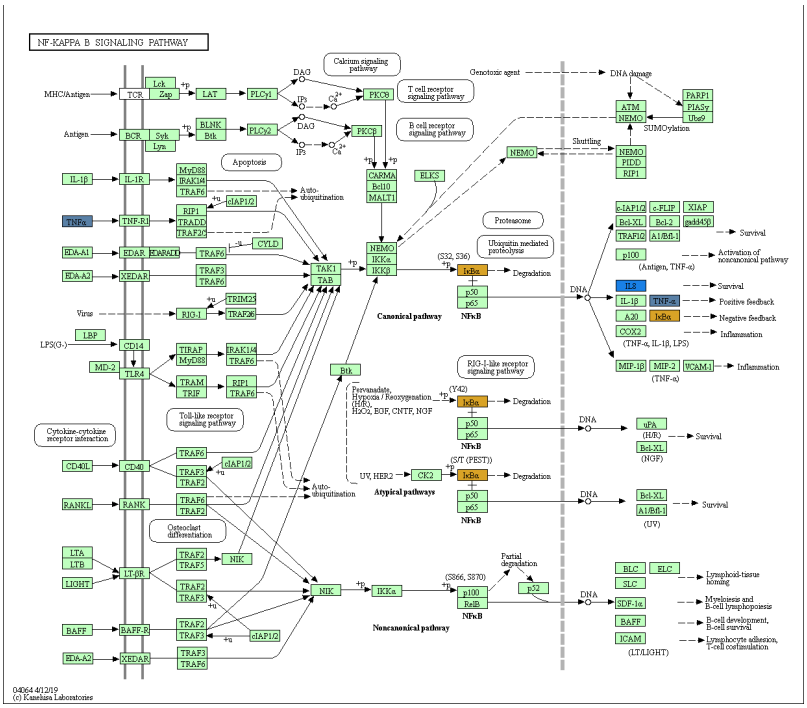
In[6]:=
```
keggVisualBlendColorsCustom = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {"TNF", "NFKBIA", "IL8"}, Intensities → <| "TNF" → 0.3, "NFKBIA" → -0.7, "IL8" → 0.8|>,
  ResultsFormat → "Figure", BlendColors → blendColorsCustom]
```

Out[6]= ⟨|Pathway → path:hsa04064, Results → {  }|⟩

In[7]:=
```
Show[keggVisualBlendColorsCustom["Results"][[1]], ImageSize → 500]
```

Out[7]=



ColorSelection (3)

In[1]:=
```
Needs["MathIOmica`"]
```

ColorSelection assigns foreground and background colors in the KEGG pathway through an association. The Keys point to labels for multi - omics data, and the values "bg" and "fg" can point to background and foreground representations respectively for each key.

As an example we can color "Protein" and "RNA" data as "fg" foreground or "bg" background colors:

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In[2]:=
```
keggVisualColorSelectionDefault = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}},
  Intensities → <| {"TNF", "Protein"} → 0.3 , {"NFKBIA", "RNA"} → 0.8, {"IL8", "RNA"} → -0.7,
    {"IL8", "Protein"} → -0.3|>, ColorSelection → <|"RNA" → "bg", "Protein" → "fg"|>]
```

Out[2]=
```
<|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2300ff00%2C%23cc3333%0D
    %0Ahsa%3A4792+%23ff0000%2C%23000000%0D%0Ahsa%3A3576+%230000ff%2C%233333cc%0D%0A}|>
```

In[3]:=
```
SystemOpen[keggVisualColorSelectionDefault["Results"][[1]]]
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can reverse background and foreground assignments:

In[2]:=
```
keggVisualColorSelectionDefaultReverse = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}},
  Intensities → <| {"TNF", "Protein"} → 0.3 , {"NFKBIA", "RNA"} → 0.8, {"IL8", "RNA"} → -0.7,
    {"IL8", "Protein"} → -0.3|>, ColorSelection → <|"RNA" → "fg", "Protein" → "bg"|>]
```

Out[2]=
```
<|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23cc3333%2C%23000000%0D
    %0Ahsa%3A4792+%2300ff00%2C%23ff0000%0D%0Ahsa%3A3576+%233333cc%2C%230000ff%0D%0A}|>
```

In[3]:=
```
SystemOpen[keggVisualColorSelectionDefaultReverse["Results"][[1]]]
```

In[1]:=
```
Needs["MathIOmica`"]
```

We can also adjust the keys to accommodate non-default labels for multi-omics IDs:

In[2]:=
```
keggVisualColorSelectionCustom = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {{"TNF", "Label2"}, {"NFKBIA", "Label1"}, {"IL8", "Label1"}, {"IL8", "Label2"}},
  Intensities → <| {"TNF", "Label2"} → 0.3 , {"NFKBIA", "Label1"} → 0.8, {"IL8", "Label1"} → -0.7,
    {"IL8", "Label2"} → -0.3|>, ColorSelection → <|"Label1" → "fg", "Label2" → "bg"|>]
```

Out[2]=
```
<|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23cc3333%2C%23000000%0D
    %0Ahsa%3A4792+%2300ff00%2C%23ff0000%0D%0Ahsa%3A3576+%233333cc%2C%230000ff%0D%0A}|>
```

In[3]:=
```
SystemOpen[keggVisualColorSelectionCustom["Results"][[1]]]
```

DefaultColors (2)

In[1]:=
```
Needs["MathIOmica`"]
```

DefaultColors provides a list of rules for setting the colors to be used as default values for the foreground "fg" and background "bg" respectively in the generated pathways. The colors must be provided as RGBColor[] specification.

The default setting is:

In[2]:=
```
defaultColorsValue = {"fg" -> RGBColor[0, 0, 0], "bg" -> RGBColor[0, 1, 0]}
```

Out[2]= {fg → ■, bg → ■}

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```
In[3]:= keggVisualDefaultColors = KEGGPathwayVisual["path:hsa04064",
          MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}},
          DefaultColors → defaultColorsValue]

Out[3]= ⟨|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2300ff00%2C%23ff0000%0D
            %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23ff0000%0D%0A}|⟩

In[4]:= SystemOpen[keggVisualDefaultColors["Results"][[1]]]
```

```
In[1]:= Needs["MathIOmica`"]
```

We can change the default setting to a custom selection:

```
In[2]:= defaultColorsCustom = {"fg" -> RGBColor[0, 1, 1], "bg" -> RGBColor[1, 1, 0]}

Out[2]= {fg → ■, bg → ■}

In[3]:= keggVisualDefaultColorsCustom = KEGGPathwayVisual["path:hsa04064",
          MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}},
          DefaultColors → defaultColorsCustom]

Out[3]= ⟨|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23ffff00%2C%23ff0000%0D
            %0Ahsa%3A4792+%2380b2ff%2C%2300ffff%0D%0Ahsa%3A3576+%2380b2ff%2C%23ff0000%0D%0A}|⟩

In[4]:= SystemOpen[keggVisualDefaultColorsCustom["Results"][[1]]]
```

ExportMovieOptions (2)

```
In[1]:= Needs["MathIOmica`"]
```

ExportMovieOptions provides options for the Export function used internally to export the pathway list when Intensities have been provided for a sequential series representation of data, e.g. time series.

```
In[2]:= defaultMovieOptions = {"FrameRate" → 1};
```

We can export the movie in the current directory (evaluate Directory[] if it is necessary to verify the current directory:

```
In[3]:= Directory[](*check current directory for output*)

In[4]:= keggVisualExportMovieOptionsDefault =
         KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
          Intensities → <| "TNF" → { -0.3, 0.3, -0.3, 0.3}, "NFKBIA" → { -0.2, 0.2, -0.2, 0.2},
            "IL8" → {0.8, 0.3, Missing[], 0.3}|>, ResultsFormat → "Movie", ExportMovieOptions → defaultMovieOptions ]
```

For example we can change a different frame rate:

```
In[1]:= customMovieOptions = {"VideoEncoding" → "MPEG-4 Video", "FrameRate" → 0.5};
```

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```
In[2]:= keggVisualExportMovieOptionsCustom =
  KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
   Intensities → <| "TNF" → { -0.3, 0.3, -0.3, 0.3}, "NFKBIA" → { -0.2, 0.2, -0.2, 0.2},
     "IL8" → {0.8, 0.3, Missing[], 0.3}|>, ResultsFormat → "Movie", ExportMovieOptions → customMovieOptions ]
```

```
File path_hsa04064.mov already exists. Please choose a
  different file name or rename/move existing file and retry.
```

FileExtend (1)

```
In[1]:= Needs["MathIOmica`"]
```

FileExtend provides a string to be appended to the file name if the ResultsFormat is set to "Movie". This choice may affect the Export automatic determination of file kind to export.

We can export to GIF format in the example below, and we also need to set the ExportMovieOptions to accommodate 4 images displaying two seconds each:

```
In[2]:= Directory[](*check current directory for output*)

In[3]:= keggVisualFileExtend = KEGGPathwayVisual["path:hsa04064",
   MemberSet → {"TNF", "NFKBIA", "IL8"}, Intensities → <| "TNF" → { -0.3, 0.3, -0.3, 0.3},
     "NFKBIA" → { -0.2, 0.2, -0.2, 0.2}, "IL8" → {0.8, 0.3, Missing[], 0.3}|>, ResultsFormat → "Movie",
   FileExtend → ".gif", ExportMovieOptions → {"ImageCount" → 4, "DisplayDurations" → 2} ]

Out[3]= <|Pathway → path:hsa04064, Results → path_hsa04064.gif|>
```

GeneDictionary (1)

```
In[1]:= Needs["MathIOmica`"]
```

GeneDictionary takes values that point to an existing variable to be used as a gene dictionary in annotations. By default, it is set to None and the default ConstantGeneDictionary is used.

```
In[2]:= keggVisualGeneDictionaryDefault =
  KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNFSF13B", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR",
     "LYN", "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4"}, GeneDictionary → None]

Out[2]= <|Pathway → path:hsa04064, Results →
   {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A10673+%2380b2ff%2C%23000000%0D
     %0Ahsa%3A1457+%2380b2ff%2C%23000000%0D%0Ahsa%3A1459+%2380b2ff%2C%23000000%0D%0Ahsa%3A1460+%2380
     b2ff%2C%23000000%0D%0Ahsa%3A4055+%2380b2ff%2C%23000000%0D%0Ahsa%3A4067+%2380b2ff%2C%23000000%0D%0
     Ahsa%3A4615+%2380b2ff%2C%23000000%0D%0Ahsa%3A4616+%2380b2ff%2C%23000000%0D%0Ahsa%3A472+%2380b2ff
     %2C%23000000%0D%0Ahsa%3A4790+%2380b2ff%2C%23000000%0D%0Ahsa%3A4791+%2380b2ff%2C%23000000%0D%0Ahsa
     %3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A51135+%2380b2ff%2C%23000000%0D%0A}|>

In[3]:= SystemOpen[keggVisualGeneDictionaryDefault["Results"][[1]]]
```

We can instead use a variable as a gene dictionary. For example suppose we have a rather restricted dictionary:

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In[4]:=
```
geneDictionaryExample =
  <|"human" → <|"UniProt ID" → {"P19838", "B4DUJ4", "O15111", "Q9NWZ3", "P19838", "J3KQ87", "P58753-2",
      "P67870", "P19838", "Q9NWZ3", "O15111", Missing[], "P68400", "Q99836-3", "B4DUJ4", "Q9NWZ3",
      "P67870", "Q9NWZ3", "P19838", "Q9Y275", "B4DUJ4", Missing[], "B4DUJ4", "Q15750", "O15111",
      "P67870", Missing[], "P19838-3", "O15111", "F5GXE7", "P25963", "P19838-2", "Q9NWZ3",
      "P07948", "Q6P7P1", "B4DUJ4", Missing[], "Q9NWZ3", "O15111", Missing[], "P67870", "J3KQJ6",
      "P25963", "Q99836-3", "H0YDU7", "D3DR86", "B4DUJ4", "Q9NWZ3", "P19838-3", "O15111",
      Missing[], "H0YDU7", "P25963", "B4DUJ4", "B4DUJ4", "B4DUJ4", "Q99836-4", "P68400", "B4DUJ4",
      Missing[], "P19838", Missing[], "B4DUJ4", "O15111", "P19838", "P68400", Missing[],
      "Q9NWZ3", "P19838-3", "O75293", "O15111", "Q9NWZ3", Missing[], "P67870", "P58753",
      "O75293", "Q96RJ3", "P67870", "B4DUJ4", "O15111", "P19838", "P19838", "P25963", "Q9NWZ3",
      "P19838-2", "O15111", "P25963", "Q9NWZ3", Missing[], Missing[], "P19838-2", "B4DUJ4",
      "Q9NWZ3", "O15111", "J3KQJ6", "Q15750-2", Missing[], "P68400", "B4DUJ4", "P19838-3"},
    "Gene Symbol" → {"NFKB1", "CSNK2B", "CHUK", "IRAK4", "NFKB1", "MYD88", "TIRAP", "CSNK2B",
      "NFKB1", "IRAK4", "CHUK", "CSNK2B", "CSNK2A1", "MYD88", "CSNK2B", "IRAK4", "CSNK2B", "IRAK4",
      "NFKB1", "TNFSF13B", "CSNK2B", "CSNK2B", "CSNK2B", "TAB1", "CHUK", "CSNK2B", "ATM", "NFKB1",
      "CHUK", "LTBR", "NFKBIA", "NFKB1", "IRAK4", "LYN", "ATM", "CSNK2B", "ATM", "IRAK4", "CHUK",
      "CSNK2B", "CSNK2B", "MYD88", "NFKBIA", "MYD88", "ATM", "NFKB2", "CSNK2B", "IRAK4", "NFKB1", "CHUK",
      "CSNK2B", "ATM", "NFKBIA", "CSNK2B", "CSNK2B", "CSNK2B", "MYD88", "CSNK2A1", "CSNK2B", "ATM",
      "NFKB1", "CSNK2B", "CSNK2B", "CHUK", "NFKB1", "CSNK2A1", "CSNK2A2", "IRAK4", "NFKB1", "GADD45B",
      "CHUK", "IRAK4", "TNFSF13B", "CSNK2B", "TIRAP", "GADD45B", "TNFRSF13C", "CSNK2B", "CSNK2B",
      "CHUK", "NFKB1", "NFKB1", "NFKBIA", "IRAK4", "NFKB1", "CHUK", "NFKBIA", "IRAK4", "CSNK2A2",
      "ATM", "NFKB1", "CSNK2B", "IRAK4", "CHUK", "MYD88", "TAB1", "ATM", "CSNK2A1", "CSNK2B", "NFKB1"},
    "KEGG Gene ID" → {"4790", "1460", "1147", "51135", "4790", "4615", "114609", "1460", "4790",
      "51135", "1147", "1460", "1457", "4615", "1460", "51135", "1460", "51135", "4790", "10673",
      "1460", "1460", "1460", "10454", "1147", "1460", "472", "4790", "1147", "4055", "4792", "4790",
      "51135", "4067", "472", "1460", "472", "51135", "1147", "1460", "1460", "4615", "4792",
      "4615", "472", "4791", "1460", "51135", "4790", "1147", "1460", "472", "4792", "1460", "1460",
      "1460", "4615", "1457", "1460", "472", "4790", "1460", "1460", "1147", "4790", "1457", "1459",
      "51135", "4790", "4616", "1147", "51135", "10673", "1460", "114609", "4616", "115650", "1460",
      "1460", "1147", "4790", "4790", "4792", "51135", "4790", "1147", "4792", "51135", "1459",
      "472", "4790", "1460", "51135", "1147", "4615", "10454", "472", "1457", "1460", "4790"}|>|>;
```

In[5]:=
```
keggVisualGeneDictionaryCustom =
 KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNFSF13B", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN",
    "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4"}, GeneDictionary → geneDictionaryExample]
```

Out[5]=
```
<|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A10673+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A1457+%2380b2ff%2C%23000000%0D%0Ahsa%3A1459+%2380b2ff%2C%23000000%0D%0Ahsa%3A1460+%2380
    b2ff%2C%23000000%0D%0Ahsa%3A4055+%2380b2ff%2C%23000000%0D%0Ahsa%3A4067+%2380b2ff%2C%23000000%0D%0
    Ahsa%3A4615+%2380b2ff%2C%23000000%0D%0Ahsa%3A4616+%2380b2ff%2C%23000000%0D%0Ahsa%3A472+%2380b2ff
    %2C%23000000%0D%0Ahsa%3A4790+%2380b2ff%2C%23000000%0D%0Ahsa%3A4791+%2380b2ff%2C%23000000%0D%0Ahsa
    %3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A51135+%2380b2ff%2C%23000000%0D%0A}|>
```

In[6]:=
```
SystemOpen[keggVisualGeneDictionaryCustom["Results"][[1]]]
```

GetGeneDictionaryOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

GetGeneDictionaryOptions values specify a list of options that will be passed to the internal GetGeneDictionary function. For example, we can re-import the gene dictionary from online:

In[2]:=
```
keggVisualGetGeneDictionaryOptions = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {"TNF", "NFKBIA", "IL8"}, GetGeneDictionaryOptions → {ImportDirectly → True}]
```

Out[2]=
```
<|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|>
```

InputID (1)

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```
In[1]:= Needs["MathIOmica`"]
```

The InputID option specifies the kind of identifiers/accessions used as input when identifiers are provided through setting the MemberSet values.

For example if we already know we are using official Gene Symbol as an identifier we may specify this directly:

```
In[2]:= keggVisualExampleInputID =
  KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}, InputID → {"Gene Symbol"}]

Out[2]= <|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|>
```

Intensities (1)

```
In[1]:= Needs["MathIOmica`"]
```

Intensities may be used to provide a set of intensities that will be used for coloring components of the pathway. The intensities are provided as an association for each ID as single values, or as a list of values in the case of series data:

<|ID$_1$ → {intensity list for ID$_1$},
ID$_2$ → {intensity list for ID$_2$}, ...,
ID$_N$ → {intensity list for ID$_N$}|>.

Intensities must be scaled from -1 to 1, or selected such that the IntensityFunction can convert them to a number between 0 to 1.

Intensities can be provided as single values:

```
In[2]:= keggVisualIntensity = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {"TNF", "NFKBIA", "IL8"}, Intensities → <| "TNF" → 0.2, "NFKBIA" → -0.2, "IL8" → 0.8|>]

Out[2]= <|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23b24d4d%2C%23000000%0D
    %0Ahsa%3A4792+%234d4db2%2C%23000000%0D%0Ahsa%3A3576+%23ff0000%2C%23000000%0D%0A}|>
```

Intensities can be also be provided as a list of values (e.g. corresponding to time series measurements):

```
In[3]:= keggVisualIntensitiesFigures = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → { -0.1, 0.3, 0.4}, "NFKBIA" → { -0.2, 0.3, 0.2}, "IL8" → {0.8, 0.3, Missing[]}|>]

Out[3]= <|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23666699%2C%23000000%0D
    %0Ahsa%3A4792+%234d4db2%2C%23000000%0D%0Ahsa%3A3576+%23ff0000%2C%23000000%0D%0A,
   https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23cc3333%2C%23000000%0D
    %0Ahsa%3A4792+%23cc3333%2C%23000000%0D%0Ahsa%3A3576+%23cc3333%2C%23000000%0D%0A,
   https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23e51a1a%2C%23000000%0D
    %0Ahsa%3A4792+%23b24d4d%2C%23000000%0D%0Ahsa%3A3576+%23666666%2C%23000000%0D%0A}|>
```

IntensityFunction (1)

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```
In[1]:= Needs["MathIOmica`"]
```

IntensityFunction is a function of two arguments that allows customization of the coloring for the intensities. The IntensityFunction value can be any function which outputs a color, I(#1,#2), (*where#1 is the BlendColors option value, and #2 is an intensity vector, that has values typically ranging from [-1,1].

The default intensity function is:

```
In[2]:= defaultIntensityFunction = (Blend[#1, (#2 + 1) / 2] &);

In[3]:= keggVisualIntensityFunction = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
          Intensities → <| "TNF" → 0.2, "NFKBIA" → -0.2, "IL8" → 0.8|>, IntensityFunction → defaultIntensityFunction]

Out[3]= ⟨|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23b24d4d%2C%23000000%0D
            %0Ahsa%3A4792+%234d4db2%2C%23000000%0D%0Ahsa%3A3576+%23ff0000%2C%23000000%0D%0A}|⟩
```

As another example let's assume the values for intensities range from 0 to 10. Then we can adjust these either directly or by setting the Intensity function, for example by dividing each input by 10:

```
In[4]:= customIntensityFunction = (Blend[#1, #2 / 10] &);

In[5]:= keggVisualIntensityFunctionCustom = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
          Intensities → <| "TNF" → 6, "NFKBIA" → 4, "IL8" → 9|>, IntensityFunction → customIntensityFunction]

Out[5]= ⟨|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23b24c4c%2C%23000000%0D
            %0Ahsa%3A4792+%234c4cb2%2C%23000000%0D%0Ahsa%3A3576+%23ff0000%2C%23000000%0D%0A}|⟩

In[6]:= SystemOpen[keggVisualIntensityFunctionCustom["Results"][[1]]]
```

KEGGAnalysisAssignerOptions (1)

```
In[1]:= Needs["MathIOmica`"]
```

The KEGGAnalysisAssignerOptions option specifies a list of options that will be passed to the internal KEGGAnalysisAssigner function.

For example, we can restrict import new KEGG pathways/maps assignments:

```
In[2]:= keggVisualKEGGAnalysisAssignerOptions = KEGGPathwayVisual["path:hsa04064",
          MemberSet → {"TNF", "NFKBIA", "IL8"}, KEGGAnalysisAssignerOptions → {ImportDirectly → True}]

Out[2]= ⟨|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
            %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|⟩
```

KEGGDatabase (1)

```
In[1]:= Needs["MathIOmica`"]
```

KEGGDatabase value indicates which KEGG database to use as the target database. The default is to use the pathway database:

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In[2]:=
```
keggVisualKEGGDatabaseDefault =
 KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}, KEGGDatabase → "pathway"]
```

Out[2]=
```
⟨|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|⟩
```

KEGGMolecular (1)

In[1]:=
```
Needs["MathIOmica`"]
```

KEGGMolecular specifies which database to use for molecular analysis. The default is the compound database ("cpd").

In[2]:=
```
keggVisualMolecular =
 KEGGPathwayVisual["path:map04910", MemberSet → {"cpd:C00031", "cpd:C00369", "cpd:C00575", "cpd:C05981"},
  AnalysisType → "Molecular", KEGGMolecular → "cpd"]
```

Out[2]=
```
⟨|Pathway → path:map04910, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=map04910&multi_query=cpd%3AC00031+%2380b2ff%2C%23000000%0
    D%0Acpd%3AC00369+%2380b2ff%2C%23000000%0D%0Acpd%3AC00575+%2380b2ff%2C%23000000%0D%0Acpd%3AC05981+
    %2380b2ff%2C%23000000%0D%0A}|⟩
```

In[3]:=
```
SystemOpen[keggVisualMolecular["Results"][[1]]]
```

KEGGOrganism (1)

In[1]:=
```
Needs["MathIOmica`"]
```

KEGGOrganism indicates which organism (org) to use for "Genomic" type of analysis. The default is human analysis org = "hsa".

In[2]:=
```
keggVisualKEGGOrganismDefault =
 KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}, KEGGOrganism → "hsa"]
```

Out[2]=
```
⟨|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|⟩
```

MathIOmicaDataDirectory (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value point to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

In[2]:=
```
KEGGPathwayVisual["path:hsa04064",
 MemberSet → {"TNF", "NFKBIA", "IL8"}, MathIOmicaDataDirectory → FileNameJoin[
   Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]
```

Out[2]=
```
⟨|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|⟩
```

MemberSet (3)

In[1]:=
```
Needs["MathIOmica`"]
```

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MemberSet selects which members of the pathway are to be considered. The choices are:

All: return the pathway only:

```
In[2]:= keggVisualMemberSetAll = KEGGPathwayVisual["path:hsa04064", MemberSet → All]
Out[2]= <|Pathway → path:hsa04064, Results → {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064}|>
```

```
In[1]:= Needs["MathIOmica`"]
```

MemberSet value can be a {list of identifiers} that will be highlighted:

```
In[2]:= keggVisualMemberSetList =
         KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}, MemberSet → All]
Out[2]= <|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
            %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|>
```

```
In[1]:= Needs["MathIOmica`"]
```

ORA can be set to True or False depending on whether the input is from an over representation analysis (e.g. output from KEGGAnalysis), or not respectively. If ORA is set to True the MemberSet list must be the output from an over representation analysis, and the identifiers will be selected from the last list, second sublist.

```
In[2]:= keggVisualMemberSetListORA =
         KEGGPathwayVisual["path:hsa04064", MemberSet → {{3.2795703206253904`*^-37, 2.623656256500312`*^-35, True},
            {25, 93, 7086, 21}, {"NF-kappa B signaling pathway - Homo sapiens (human)",
             {{"TAB1"}, {"TNFSF13B"}, {"MALT1"}, {"TIRAP"}, {"CHUK"}, {"TNFRSF13C"}, {"PARP1"},
              {"CSNK2A1"}, {"CSNK2A2"}, {"CSNK2B"}, {"LTBR"}, {"LYN"}, {"MYD88"}, {"GADD45B"},
              {"ATM"}, {"NFKB1"}, {"NFKB2"}, {"NFKBIA"}, {"IRAK4"}, {"PIAS4"}, {"PLAU"}}}}, ORA → True]
Out[2]= <|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A10454+%2380b2ff%2C%23000000%0D
            %0Ahsa%3A10673+%2380b2ff%2C%23000000%0D%0Ahsa%3A10892+%2380b2ff%2C%23000000%0D%0Ahsa%3A114609+
            %2380b2ff%2C%23000000%0D%0Ahsa%3A1147+%2380b2ff%2C%23000000%0D%0Ahsa%3A115650+%2380b2ff%2C
            %23000000%0D%0Ahsa%3A142+%2380b2ff%2C%23000000%0D%0Ahsa%3A1457+%2380b2ff%2C%23000000%0D%0Ahsa%3
            A1459+%2380b2ff%2C%23000000%0D%0Ahsa%3A1460+%2380b2ff%2C%23000000%0D%0Ahsa%3A4055+%2380b2ff%2C
            %23000000%0D%0Ahsa%3A4067+%2380b2ff%2C%23000000%0D%0Ahsa%3A4615+%2380b2ff%2C%23000000%0D%0Ahsa%3
            A4616+%2380b2ff%2C%23000000%0D%0Ahsa%3A472+%2380b2ff%2C%23000000%0D%0Ahsa%3A4790+%2380b2ff%2C
            %23000000%0D%0Ahsa%3A4791+%2380b2ff%2C%23000000%0D%0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3
            A51135+%2380b2ff%2C%23000000%0D%0Ahsa%3A51588+%2380b2ff%2C%23000000%0D%0Ahsa%3A5328+%2380b2ff%2C
            %23000000%0D%0A}|>
```

```
In[3]:= SystemOpen[keggVisualMemberSetListORA["Results"][[1]]]
```

MissingValueColor (1)

```
In[1]:= Needs["MathIOmica`"]
```

MissingValueColor provides a color to be used when Intensities are provided to represent values that are tagged as Missing[]. The color must be provided as RGBColor[] specification.

```
In[2]:= RGBColor[0.4, 0.4, 0.4]
Out[2]= ■
```

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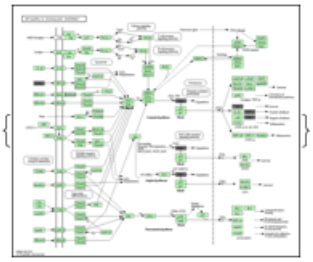
In[3]:=
```
keggVisualMissingColorDefault = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → Missing[], "NFKBIA" → Missing[], "IL8" → Missing[] |>,
  MissingValueColor → RGBColor[0.4, 0.4, 0.4], ResultsFormat → "Figure"]
```

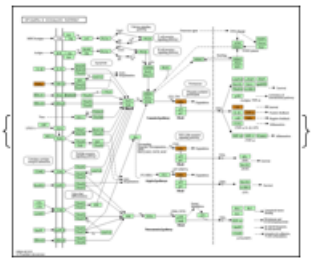
Out[3]= ⟨| Pathway → path:hsa04064, Results → {  } |⟩

We can change the color to a custom value:

In[4]:=
```
customMissingValueColor = RGBColor[0.8, 0.5, 0.1]
```

Out[4]= ■

In[5]:=
```
keggVisualMissingColorCustom = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → Missing[], "NFKBIA" → Missing[], "IL8" → Missing[] |>,
  MissingValueColor → customMissingValueColor, ResultsFormat → "Figure"]
```

Out[5]= ⟨| Pathway → path:hsa04064, Results → {  } |⟩

MolecularInputID (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MolecularInputID is a string list to indicate the kind of ID to use for the input molecule entries. The default is {"cpd"}:

In[2]:=
```
keggVisualMolecularInputID =
 KEGGPathwayVisual["path:map04910", MemberSet → {"cpd:C00031", "cpd:C00369", "cpd:C00575", "cpd:C05981"},
  AnalysisType → "Molecular", MolecularInputID → {"cpd"}]
```

Out[2]= ⟨| Pathway → path:map04910, Results →
{https://www.kegg.jp/kegg-bin/show_pathway?map=map04910&multi_query=cpd%3AC00031+%2380b2ff%2C%23000000%0D%0Acpd%3AC00369+%2380b2ff%2C%23000000%0D%0Acpd%3AC00575+%2380b2ff%2C%23000000%0D%0Acpd%3AC05981+%2380b2ff%2C%23000000%0D%0A} |⟩

MolecularOutputID (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MolecularOutputID is a string to indicate the kind of ID to convert input molecule entries. The default is "cpd" consistently with use of the "cpd" database as the default molecular analysis.

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In[2]:=
```
keggVisualMolecularOutputID =
 KEGGPathwayVisual["path:map04910", MemberSet → {"cpd:C00031", "cpd:C00369", "cpd:C00575", "cpd:C05981"},
  AnalysisType → "Molecular", MolecularOutputID → "cpd"]
```

Out[2]=
```
<|Pathway → path:map04910, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=map04910&multi_query=cpd%3AC00031+%2380b2ff%2C%23000000%0
    D%0Acpd%3AC00369+%2380b2ff%2C%23000000%0D%0Acpd%3AC00575+%2380b2ff%2C%23000000%0D%0Acpd%3AC05981+
    %2380b2ff%2C%23000000%0D%0A}|>
```

MolecularSpecies (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MolecularSpecies specifies the kind of molecular input. The default is "compound":

In[2]:=
```
keggVisualMolecularSpecies =
 KEGGPathwayVisual["path:map04910", MemberSet → {"cpd:C00031", "cpd:C00369", "cpd:C00575", "cpd:C05981"},
  AnalysisType → "Molecular", MolecularSpecies → "compound"]
```

Out[2]=
```
<|Pathway → path:map04910, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=map04910&multi_query=cpd%3AC00031+%2380b2ff%2C%23000000%0
    D%0Acpd%3AC00369+%2380b2ff%2C%23000000%0D%0Acpd%3AC00575+%2380b2ff%2C%23000000%0D%0Acpd%3AC05981+
    %2380b2ff%2C%23000000%0D%0A}|>
```

MovieFilePath (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MovieFilePath indicates the path (including file name) where if ResultsFormat is set to "Movie" the movie generated will be saved. The default value None will generate a file named after the pathway with extension set by the FileExtend option in the current directory.

In[2]:=
```
Directory[]
```

Out[2]=
```
/Users/george
```

In[3]:=
```
keggVisualMovieFilePathDefault = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → { -0.3, 0.3, -0.3, 0.3}, "NFKBIA" → { -0.2, 0.2, -0.2, 0.2},
    "IL8" → {0.8, 0.3, Missing[], 0.3}|>, ResultsFormat → "Movie" , MovieFilePath → None]
```

```
File path_hsa04064.mov already exists. Please choose a
  different file name or rename/move existing file and retry.
```

We could for example export the file to the $UserDocumentDirectory:

In[4]:=
```
customFileLocation = FileNameJoin[Flatten[{FileNameSplit[$UserDocumentsDirectory], "exampleName.mov"}]]
```

Out[4]=
```
/Users/george/Documents/exampleName.mov
```

The above path will depend on the operating system and user. We can now generate the movie/animation to be saved at the custom file location by setting the `MovieFilePath`:

In[5]:=
```
keggVisualMovieFilePathDefault = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → { -0.3, 0.3, -0.3, 0.3}, "NFKBIA" → { -0.2, 0.2, -0.2, 0.2},
    "IL8" → {0.8, 0.3, Missing[], 0.3}|>, ResultsFormat → "Movie" , MovieFilePath → customFileLocation]
```

Out[5]=
```
<|Pathway → path:hsa04064, Results → /Users/george/Documents/exampleName.mov|>
```

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In[6]:=
```
SystemOpen[keggVisualMovieFilePathDefault["Results"][[1]]]
```

Part: Part specification /Users/george/Documents/exampleName.mov[[1]] is longer than depth of object.

Out[6]=
```
SystemOpen[/Users/george/Documents/exampleName.mov[[1]]]
```

NonUCSC (1)

In[1]:=
```
Needs["MathIOmica`"]
```

NonUCSC option set to False assumes UCSC browser was used in determining an internal GeneDictionary used in ID translations where the KEGG identifiers for genes are number strings (e.g. 4790).

The NonUCSC option can be set to True if standard KEGG accessions are used in a user provided GeneDictionary variable, in the form OptionValue[KEGGOrganism] <>":"<>"number string", e.g. "hsa:4790"

We consider the following limited non UCSC generated dictionary as a simple example:

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```
In[2]:= nonUCSCGeneDictionary =
  <|"human" → <|"UCSC ID" → {"uc002lwb.2", "uc002lwb.2", "uc002lwb.2", "uc002lwc.1", "uc002lwc.1",
      "uc002lwc.1", "uc001pkb.1", "uc001pkb.1", "uc001pkb.1", "uc009yxr.1", "uc009yxr.1", "uc009yxr.1",
      "uc001pke.2", "uc001pke.2", "uc001pke.2", "uc001pkg.1", "uc001pkg.1", "uc001pkg.1", "uc009yxt.1",
      "uc009yxt.1", "uc009yxt.1", "uc001pkf.3", "uc001pkf.3", "uc001pkf.3", "uc001pkc.1", "uc001pkc.1",
      "uc001pkc.1", "uc001pkd.4", "uc001pkd.4", "uc001pkd.4", "uc009yxs.1", "uc009yxs.1", "uc009yxs.1",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc001kvb.4", "uc001kvb.4", "uc001kvd.4", "uc001kvd.4",
      "uc001kva.4", "uc001kva.4", "uc009xxc.4", "uc009xxc.4", "uc010qqk.2", "uc010qqk.2", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001rnu.3", "uc001rnu.3", "uc001rnu.3", "uc001rnu.3",
      "uc001rnu.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnx.3",
      "uc001rnx.3", "uc001rnx.3", "uc001rnx.3", "uc001rnx.3", "uc001rny.3", "uc001rny.3", "uc001rny.3",
      "uc001rny.3", "uc001rny.3", "uc010sky.1", "uc010sky.1", "uc010sky.1", "uc010sky.1", "uc010sky.1",
      "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnw.3", "uc001rnw.3",
      "uc001rnw.3", "uc001rnw.3", "uc001rnw.3", "uc002lzg.3", "uc002lzg.3", "uc002lzg.3", "uc002lzg.3",
      "uc010qkw.2", "uc001jwa.3", "uc010qkx.2", "uc001jwb.3", "uc001jwc.3", "uc009xrq.1"},
    "Gene Symbol" → {"GADD45B", "GADD45B", "GADD45B", "GADD45B", "GADD45B", "GADD45B", "ATM",
      "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM",
      "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB2",
      "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKBIA",
      "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA",
      "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "IRAK4", "IRAK4",
      "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4",
      "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4",
      "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4",
      "IRAK4", "PIAS4", "PIAS4", "PIAS4", "PIAS4", "PLAU", "PLAU", "PLAU", "PLAU", "PLAU", "PLAU"},
    "KEGG Gene ID" → {"hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:472",
      "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472",
      "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472",
      "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791",
      "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792",
      "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792",
      "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51588", "hsa:51588", "hsa:51588",
      "hsa:51588", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328"}|>|>;
```

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We can use this in the analysis:

```
In[3]:= keggVisualNonUCSC = KEGGPathwayVisual["path:hsa04064",
          MemberSet → {"ATM", "NFKBIA"} , GeneDictionary → nonUCSCGeneDictionary, NonUCSC → True]
Out[3]= ⟨|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A472+%2380b2ff%2C%23000000%0D%0
            Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0A}|⟩

In[4]:= SystemOpen[keggVisualNonUCSC["Results"][[1]]]
```

ORA (1)

```
In[1]:= Needs["MathIOmica`"]
```

ORA can be set to True or False depending on whether the input is from an over representation analysis (e.g. output from KEGGAnalysis), or not respectively. If ORA is set to True the MemberSet list must be the output from an over representation analysis, and the identifiers will be selected from the last list, second sublist.

```
In[2]:= keggVisualORA = KEGGPathwayVisual["path:hsa04064",
          MemberSet → {{2.6971348540311576`*^-11, 1.0788539416124631`*^-9, True}, {25, 204, 7086, 11},
            {"Epstein-Barr virus infection - Homo sapiens (human)", {{"TAB1"}, {"CHUK"}, {"CSNK2A1"}, {"CSNK2A2"},
              {"CSNK2B"}, {"LYN"}, {"NFKB1"}, {"NFKB2"}, {"NFKBIA"}, {"POLR3B"}, {"POLR3A"}}}}, ORA → True]
Out[2]= ⟨|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A10454+%2380b2ff%2C%23000000%0D
            %0Ahsa%3A1147+%2380b2ff%2C%23000000%0D%0Ahsa%3A1457+%2380b2ff%2C%23000000%0D%0Ahsa%3A1459+%2380
            b2ff%2C%23000000%0D%0Ahsa%3A1460+%2380b2ff%2C%23000000%0D%0Ahsa%3A4067+%2380b2ff%2C%23000000%0D%0
            Ahsa%3A4790+%2380b2ff%2C%23000000%0D%0Ahsa%3A4791+%2380b2ff%2C%23000000%0D%0Ahsa%3A4792+%2380b2ff
            %2C%23000000%0D%0Ahsa%3A55703+%2380b2ff%2C%23000000%0D%0Ahsa%3A11128+%2380b2ff%2C%23000000%0D%0A}
           |⟩
```

With ORA set to False, the MemberSet must be a list of identifiers:

```
In[3]:= keggVisualMemberSetListORAFalse =
         keggVisualMemberSetListORA = KEGGPathwayVisual["path:hsa05169", MemberSet → {"TAB1", "TNFSF13B",
             "MALT1", "TIRAP", "CHUK", "TNFRSF13C", "PARP1", "CSNK2A1", "CSNK2A2", "CSNK2B", "LTBR", "LYN",
             "MYD88", "GADD45B", "ATM", "NFKB1", "NFKB2", "NFKBIA", "IRAK4", "PIAS4", "PLAU"}, ORA → False]
Out[3]= ⟨|Pathway → path:hsa05169, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa05169&multi_query=hsa%3A10454+%2380b2ff%2C%23000000%0D
            %0Ahsa%3A1147+%2380b2ff%2C%23000000%0D%0Ahsa%3A4067+%2380b2ff%2C%23000000%0D%0Ahsa%3A4615+%2380
            b2ff%2C%23000000%0D%0Ahsa%3A4616+%2380b2ff%2C%23000000%0D%0Ahsa%3A4790+%2380b2ff%2C%23000000%0D%0
            Ahsa%3A4791+%2380b2ff%2C%23000000%0D%0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A51135+%2380
            b2ff%2C%23000000%0D%0A}|⟩

In[4]:= SystemOpen[keggVisualMemberSetListORAFalse["Results"][[1]]]
```

OutputID (1)

```
In[1]:= Needs["MathIOmica`"]
```

OutputID is a string to indicate the kind of ID to convert input genomic analysis entries. The default is "KEGG Gene ID" consistently with use of the "pathway" database as the default genomic analysis.

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```
In[2]:= keggVisualOutputIDDefault =
         KEGGPathwayVisual["path:hsa04064", MemberSet → {"ATM", "NFKBIA"} , OutputID → "KEGG Gene ID"]
Out[2]= ⟨|Pathway → path:hsa04064, Results →
          {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A472+%2380b2ff%2C%23000000%0D%0
             Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0A}|⟩
```

We could be using an input gene dictionary where the label for the output is named differently, e.g. "kgene" below:

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```
In[3]:= exampleGeneDictionary =
  <|"human" → <|"UCSC ID" → {"uc002lwb.2", "uc002lwb.2", "uc002lwb.2", "uc002lwc.1", "uc002lwc.1",
      "uc002lwc.1", "uc001pkb.1", "uc001pkb.1", "uc001pkb.1", "uc009yxr.1", "uc009yxr.1", "uc009yxr.1",
      "uc001pke.2", "uc001pke.2", "uc001pke.2", "uc001pkg.1", "uc001pkg.1", "uc001pkg.1", "uc009yxt.1",
      "uc009yxt.1", "uc009yxt.1", "uc001pkf.3", "uc001pkf.3", "uc001pkf.3", "uc001pkc.1", "uc001pkc.1",
      "uc001pkc.1", "uc001pkd.4", "uc001pkd.4", "uc001pkd.4", "uc009yxs.1", "uc009yxs.1", "uc009yxs.1",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2", "uc011cep.2",
      "uc011cep.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2", "uc011ceq.2",
      "uc011ceq.2", "uc011ceq.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc011cer.2",
      "uc011cer.2", "uc011cer.2", "uc011cer.2", "uc001kvb.4", "uc001kvb.4", "uc001kvd.4", "uc001kvd.4",
      "uc001kva.4", "uc001kva.4", "uc009xxc.4", "uc009xxc.4", "uc010qqk.2", "uc010qqk.2", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001wtf.4",
      "uc001wtf.4", "uc001wtf.4", "uc001wtf.4", "uc001rnu.3", "uc001rnu.3", "uc001rnu.3", "uc001rnu.3",
      "uc001rnu.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnt.3", "uc001rnx.3",
      "uc001rnx.3", "uc001rnx.3", "uc001rnx.3", "uc001rnx.3", "uc001rny.3", "uc001rny.3", "uc001rny.3",
      "uc001rny.3", "uc001rny.3", "uc010sky.1", "uc010sky.1", "uc010sky.1", "uc010sky.1", "uc010sky.1",
      "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnv.3", "uc001rnw.3", "uc001rnw.3",
      "uc001rnw.3", "uc001rnw.3", "uc001rnw.3", "uc002lzg.3", "uc002lzg.3", "uc002lzg.3", "uc002lzg.3",
      "uc010qkw.2", "uc001jwa.3", "uc010qkx.2", "uc001jwb.3", "uc001jwc.3", "uc009xrq.1"},
    "Gene Symbol" → {"GADD45B", "GADD45B", "GADD45B", "GADD45B", "GADD45B", "GADD45B", "ATM",
      "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM",
      "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "ATM", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1",
      "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB1", "NFKB2",
      "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKB2", "NFKBIA",
      "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA",
      "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "NFKBIA", "IRAK4", "IRAK4",
      "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4",
      "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4",
      "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4", "IRAK4",
      "IRAK4", "PIAS4", "PIAS4", "PIAS4", "PIAS4", "PLAU", "PLAU", "PLAU", "PLAU", "PLAU", "PLAU"},
    "kgene" → {"hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:4616", "hsa:472",
      "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472",
      "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472",
      "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:472", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790", "hsa:4790",
      "hsa:4790", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4791",
      "hsa:4791", "hsa:4791", "hsa:4791", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792",
      "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792",
      "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:4792", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135",
      "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51135", "hsa:51588", "hsa:51588", "hsa:51588",
      "hsa:51588", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328", "hsa:5328"}|>|>;
```

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In[4]:=
```
keggVisualOutputIDCustom = KEGGPathwayVisual["path:hsa04064", MemberSet → {"ATM", "NFKBIA"} ,
  GeneDictionary → exampleGeneDictionary, NonUCSC → True, OutputID → "kgene"]
```

Out[4]=
```
⟨|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A472+%2380b2ff%2C%23000000%0D%0
    Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0A}|⟩
```

In[5]:=

ResultsFormat (3)

In[1]:=
```
Needs["MathIOmica`"]
```

ResultsFormat provides a choice of output format, the choices are:

`ResultsFormat → "URL"` returns a URL of the pathway. For example:

In[2]:=
```
keggVisualResultsFormatDefault = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → { -0.1, 0.3, 0.4}, "NFKBIA" → { -0.2, 0.3, 0.2}, "IL8" → {0.8, 0.3, Missing[]}|>,
  ResultsFormat → "URL"]
```

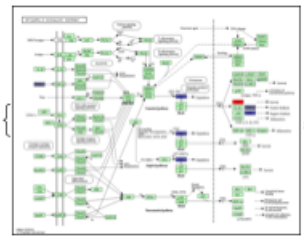
Out[2]=
```
⟨|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23666699%2C%23000000%0D
    %0Ahsa%3A4792+%234d4db2%2C%23000000%0D%0Ahsa%3A3576+%23ff0000%2C%23000000%0D%0A,
   https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23cc3333%2C%23000000%0D
    %0Ahsa%3A4792+%23cc3333%2C%23000000%0D%0Ahsa%3A3576+%23cc3333%2C%23000000%0D%0A,
   https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%23e51a1a%2C%23000000%0D
    %0Ahsa%3A4792+%23b24d4d%2C%23000000%0D%0Ahsa%3A3576+%23666666%2C%23000000%0D%0A}|⟩
```

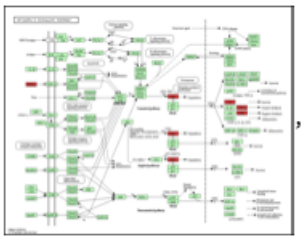
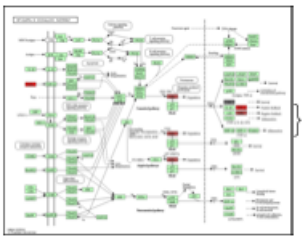
In[1]:=
```
Needs["MathIOmica`"]
```

`ResultsFormat → "Figure"` returns figure output(s) for the pathway

In[2]:=
```
keggVisualResultsFormatFigure = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → { -0.1, 0.3, 0.4}, "NFKBIA" → { -0.2, 0.3, 0.2}, "IL8" → {0.8, 0.3, Missing[]}|>,
  ResultsFormat → "Figure"]
```

Out[2]=

⟨|Pathway → path:hsa04064, Results → {  ,

 ,  }|⟩

In[1]:=
```
Needs["MathIOmica`"]
```

Setting `ResultsFormat → "Movie"` in the case of series data returns a

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movie/animation of the series pathway snapshots. The default is to save under the pathway name in the present working directory:

In[2]:=
```
Directory[]
```

In[3]:=
```
keggVisualResultsFormatMovie = KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"},
  Intensities → <| "TNF" → { -0.1, 0.3, 0.4}, "NFKBIA" → { -0.2, 0.3, 0.2}, "IL8" → {0.8, 0.3, Missing[]}|>,
  ResultsFormat → "Movie"]
```

Out[3]=
```
<| Pathway → path:hsa04064, Results → path_hsa04064.mov |>
```

SingleColorPlace (1)

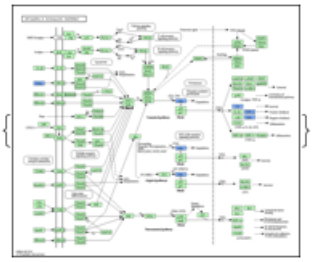
In[1]:=
```
Needs["MathIOmica`"]
```

SingleColorPlace selects in the case of a single identifier input whether to place the color to the foreground, ("fg") or background ("bg" set by default).

Let us look at the default placement in the background:

In[2]:=
```
keggVisualSingleColorPlaceDefault = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {"TNF", "NFKBIA", "IL8"}, SingleColorPlace → "bg", ResultsFormat → "Figure"]
```

Out[2]= ⟨| Pathway → path:hsa04064, Results → {



} |⟩

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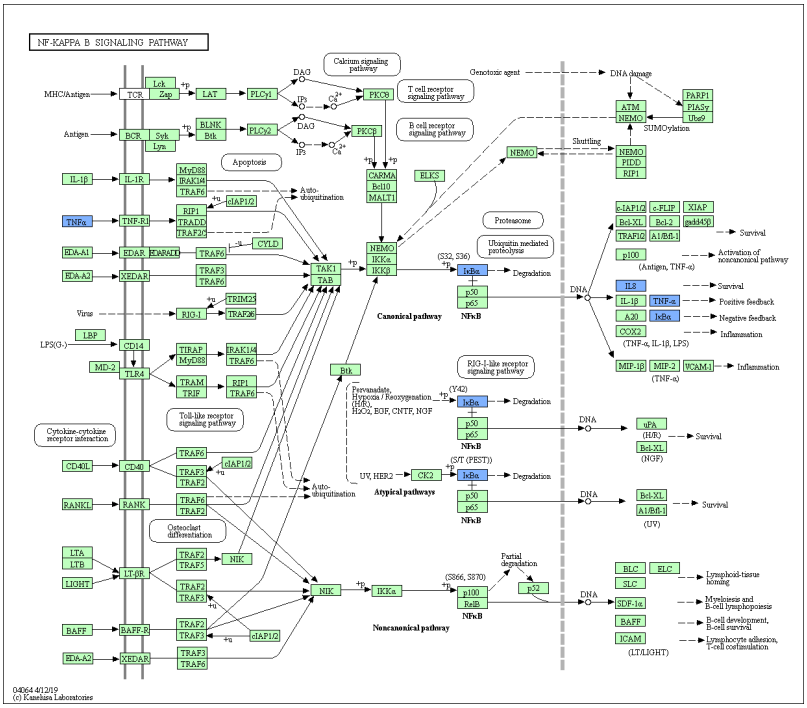
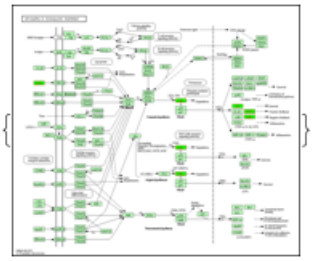
In[3]:=
```
Show[keggVisualSingleColorPlaceDefault["Results"][[1]], ImageSize → 500]
```

Out[3]=



We can instead color the foreground:

In[4]:=
```
keggVisualSingleColorPlaceFg = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {"TNF", "NFKBIA", "IL8"}, SingleColorPlace → "fg", ResultsFormat → "Figure"]
```

Out[4]= ⟨|Pathway → path:hsa04064, Results → {  }|⟩

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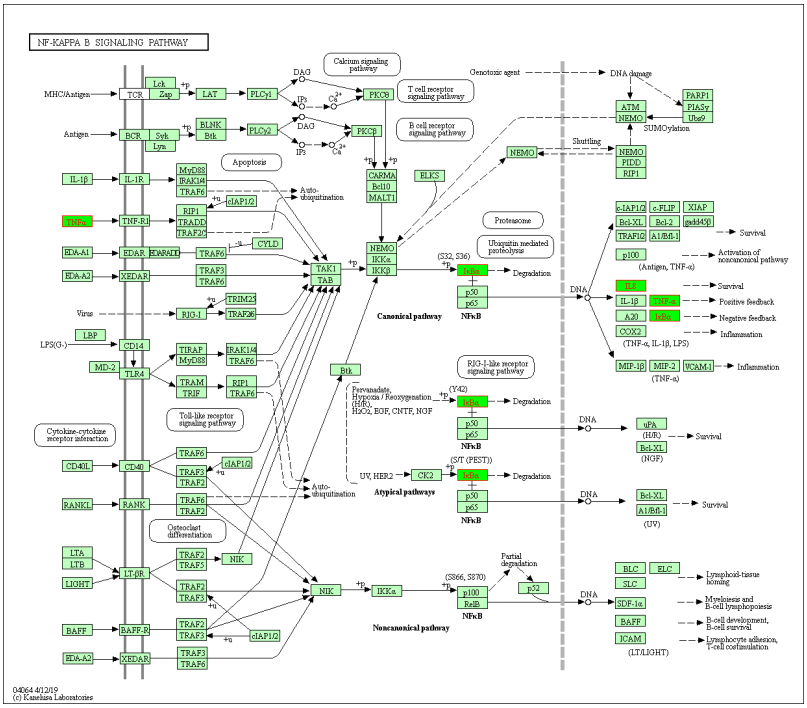
In[5]:=
```
Show[keggVisualSingleColorPlaceFg["Results"][[1]], ImageSize → 500]
```

Out[5]=



Species (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The Species option specifies the species considered in the calculation. The default implementation is "human":

In[2]:=
```
keggVisualSpecies =
 KEGGPathwayVisual["path:hsa04064", MemberSet → {"TNF", "NFKBIA", "IL8"}, Species → "human"]
```

Out[2]=
```
⟨|Pathway → path:hsa04064, Results →
  {https://www.kegg.jp/kegg-bin/show_pathway?map=hsa04064&multi_query=hsa%3A7124+%2380b2ff%2C%23000000%0D
    %0Ahsa%3A4792+%2380b2ff%2C%23000000%0D%0Ahsa%3A3576+%2380b2ff%2C%23000000%0D%0A}|⟩
```

StandardHighlight (1)

In[1]:=
```
Needs["MathIOmica`"]
```

StandardHighlight provides a list of rules for setting the highlight colors for the IDs represented in the pathway (when no intensities are provided). The list specifies color rules for foreground, "fg", and background, "bg", respectively. The colors must be provided as RGBColor[] specification.

The default setting is:

In[2]:=
```
defaultStandardHighlight = {"fg" → RGBColor[1, 0, 0], "bg" → RGBColor[0.5, 0.7, 1]}
```

Out[2]= {fg → ■, bg → ■}

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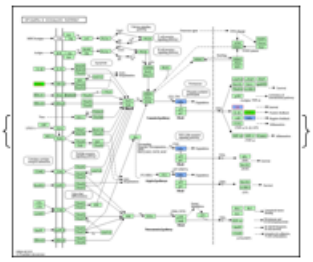
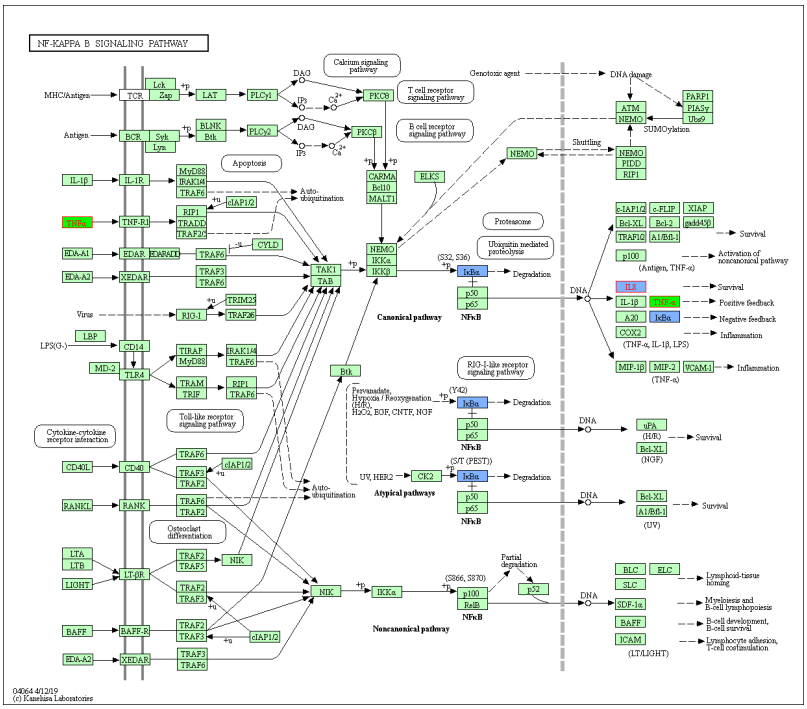
In[3]:=
```
keggVisualStandardHighlightDefault = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}},
  StandardHighlight → defaultStandardHighlight, ResultsFormat → "Figure"]
```

Out[3]= ⟨|Pathway → path:hsa04064, Results → {  }|⟩

In[4]:=
```
Show[keggVisualStandardHighlightDefault["Results"][[1]], ImageSize → 500]
```

Out[4]=



We can change the default colors. For example:

In[5]:=
```
RGBColor[0, 0.6, 0.9]
```

Out[5]= ■

In[6]:=
```
customStandardHighlight = {"fg" → RGBColor[1, 1, 0], "bg" → RGBColor[1, 0.4, 0.4]}
```

Out[6]= {fg → ■, bg → ■}

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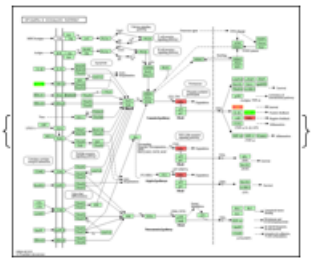
In[7]:=
```
keggVisualStandardHighlightCustom = KEGGPathwayVisual["path:hsa04064",
  MemberSet → {{"TNF", "Protein"}, {"NFKBIA", "RNA"}, {"IL8", "RNA"}, {"IL8", "Protein"}},
  StandardHighlight → customStandardHighlight, ResultsFormat → "Figure"]
```

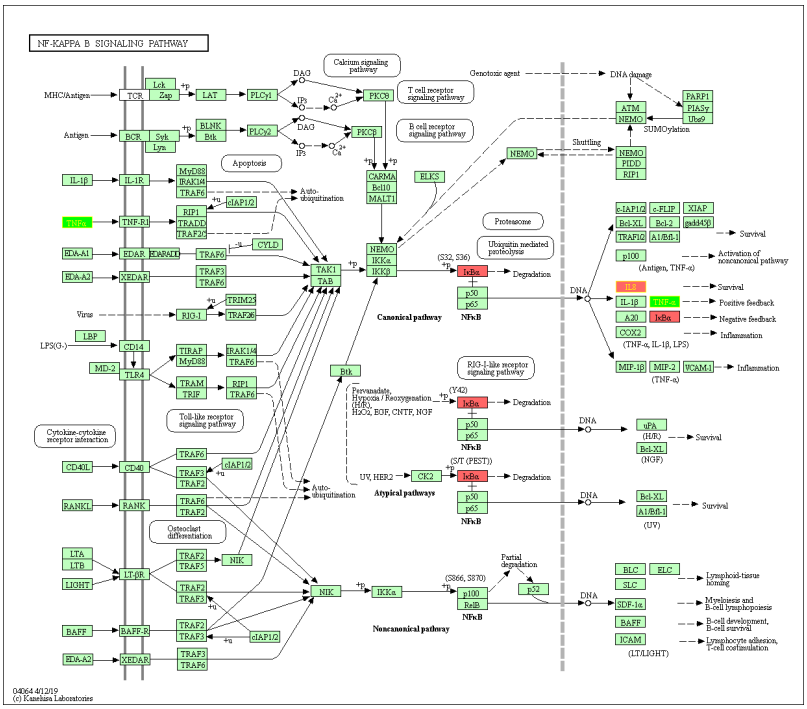
Out[7]= ⟨|Pathway → path:hsa04064, Results → {



}|⟩

In[8]:=
```
Show[keggVisualStandardHighlightCustom["Results"][[1]], ImageSize → 500]
```

Out[8]=



See Also

EnrichmentReportExport ▪ **GeneTranslation** ▪ **GetGeneDictionary** ▪ **GOAnalysis** ▪ **KEGGAnalysis** ▪ **KEGGAnalysisAssigner** ▪ **KEGGDictionary** ▪ **MassDictionary** ▪ **MassMatcher** ▪ **OBOGODictionary** ▪ **TimeSeriesClusters** ▪ **UCSCBrowserSQL**

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- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ URL ▾

LabelFunction

`LabelFunction`
LabelFunction is an option for BootstrapGeneral indicating which function to use to generate the labels for the simulated data.

Details

- LabelFunction is an option for BootstrapGeneral indicating which function to use to generate the labels for the simulated data. In BootstrapGeneral the `LabelFunction` variable must be function that take only one input, namely the sampling (i.e. number of samples created).

See Also

BootstrapGeneral

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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ListIndex

`ListIndex`
is an option for MathIOmica functions, such as Applier that allows selection of which list to use in the association or OmicsObject input or output values.

Details

- ListIndex allows the selection of a list (e.g. in an OmicsObject internal value) to be used by various functions, (e.g. FilteringFunction).

See Also

Applier ▪ **ApplierList** ▪ **ComponentIndex** ▪ **FilteringFunction** ▪ **MeasurementApplier** ▪ **OmicsObject** ▪ **Returner**

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LombScargle

LombScargle[*data*, *setTimes*]
calculates the Lomb–Scargle power spectrum for time series *data* that runs over specified *setTimes*.

Details

- LombScargle[*data*, *setTimes*] calculates a Lomb-Scargle based power spectrum of a dataset over a set of specified times (with possibly unevenly sampling). It takes as input:

data	Time series (data as a list; list may be the value of a single key in an association). The series may include Missing data points. Data may be entered as list of N signal intensities corresponding one–to–one to the N setTimes with Missing inserted appropriately if the data is absent, $\{X_1 = X(t_1), X_2 = X(t_2), \ldots, X_N = X(t_N)\}$. Alternatively, the data may be a list of pairs of values $\{\{t_1,X_1\},\{t_2,X_2\},\ldots,\{t_N,X_N\}\}$ for only existing measurements.
setTimes	A complete set of all possible N times during which data could have been collected in the window of the experiment, including times for which no data was collected, $\{t_1, t_2, \ldots, t_N\}$.

- LombScargle returns a list of {frequency list, intensity list} of the corresponding n frequencies (typically n = Floor[N / 2] as discussed below) and intensities.
- The following options can be given:

FrequenciesOnly	False	Whether to return only the computation frequencies. An association of frequencies "f" ordered from low to high by index i is returned in the form <|"f1" → frequency_1, "f2" → frequency_2, ..., "fi" → frequency_i,..., "fn" → frequency_n|>
NormalizeIntensities	False	Whether the intensities list should be normalized or not.

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OversamplingRate	1	Rate at which to oversample the time series using zero–padding.
PairReturn	False	Whether data should be returned as {frequency list,intensity list} or as pairs: {{frequency1,intensity1}, {frequency2, intensity2},...,{frequencyN,intensityN}.
UpperFrequencyFactor	1	Value ≥ 1, by which to scale the upper Nyquist cutoff frequency and increase spectral resolution.

- The data has to be in the order that the set times appear. In general the data are list of time series signal values, e.g. $\{X_1 = X(t_1), X_2 = X(t_2), \ldots, X_N = X(t_N)\}$ over a list of ordered sampling times, where $t_1 < t_2 < \ldots < t_N$. Note that $\{t_1, t_2, \ldots, t_N\}$ is necessarily a subset of the input *setTimes*, since any time point during which data was collected is necessarily a possible time point during which it could have been collected.

Background

- In order to calculate the periodogram spectra, first a frequency-dependent phase angle $\theta(f) = \frac{1}{2}\text{ArcTan}\left[\left(\frac{\sum \text{Sin}(4\pi f t_i)}{\sum \text{Cos}(4\pi f t_i)}\right)\right]$ is calculated where the sum is over $i = 1, 2, 3, \ldots, N$ time points.
  With $\theta(f)$, the periodogram $P_x(f) = \frac{1}{2\sigma_x^2}\left\{\frac{\left[\sum (x(t_i)-\bar{x})\text{Cos}(2\pi f t_i - \theta(f))\right]^2}{\sum \text{Cos}^2(2\pi f t_i - \theta(f))} + \frac{\left[\sum (x(t_i)-\bar{x})\text{Sin}(2\pi f t_i - \theta(f))\right]^2}{\sum \text{Sin}^2(2\pi f t_i - \theta(f))}\right\}$ where σ_x^2 is the variance of the time series, and again, sums are over the $i = 1, 2, 3, \ldots, N$ time points. Note the centering the data by subtracting off the mean $\bar{x}$ of the time series. The complete time window of the experiment is defined by the range of $\{t_{complete}\}$, $t_{window} = \text{Max}[\{t_{complete}\}] - \text{Min}[\{t_{complete}\}]$. From this time window, the Nyquist frequency is defined to be $f_{Nyq} = \frac{N}{2}\frac{N}{N-1}\frac{1}{t_{window}}$, and a given UpperFrequencyFactor ≥ 1 sets the cutoff frequency f_{cutoff} for calculation by $\frac{f_{cutoff}}{f_{Nyq}} = \text{UpperFrequencyFactor}$.

- The frequency grid sampled when calculating the Lomb-Scargle power spectrum is $\{f_0, f_1 = f_0 + \Delta f, f_2 = f_0 + 2\Delta f, \ldots, f_{cutoff}\}$, where $f_0 = \frac{N}{N-1}\frac{1}{t_{window}}$, $f_{cutoff} = \frac{N}{2} * \text{Scaling}_{cutoff} * f_0$, and $\Delta f = \frac{f_{cutoff} - f_0}{\text{OversamplingRate} * \left(\text{Floor}\left(\frac{N}{2}\right) - 1\right)}$, where $\text{Floor}\left(\frac{N}{2}\right)$ rounds to the lowest integer, and the OversamplingRate controls the frequency mesh size and spectral resolution.

References

- Lomb, N.R, Least-squares frequency analysis of unequally spaced data, Astrophysics and Space Science 39 (2) : 447–462 (1976). External link: http://dx.doi.org/10.1007/BF00648343.
- Scargle, J.D., Studies in astronomical time series analysis II - Statistical aspects of spectral analysis of unevenly spaced data, Astrophysical Journal 263 : 835 (1982). External link: http://dx.doi.org/10.1086/160554.

Examples (10)

Basic Examples (4)

Package Dependencies (1)

First we load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

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General Example: Noisy Sinusoidal Data (1)

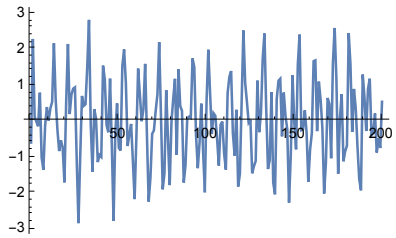
We consider the following noisy measurement:

In[1]:=
```
dataLombScargleExample1 = Table[{n, Sin[0.1*2 π n ] + Sin[0.25*2 π n] + RandomReal[{-1, 1}]}, {n, 0, 200}];
```

The data is pairs of values for the ith point $\{t_i, X_i\}$. A plot of the data looks like:

In[2]:=
```
ListLinePlot[dataLombScargleExample1]
```

Out[2]=



We obtain a list of periodogram frequencies and intensities:

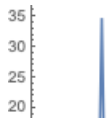
In[3]:=
```
dataLombScarglePeriodogram = LombScargle[dataLombScargleExample1, Range[0, 200]]
```

Out[3]=
```
{{0.005025, 0.0100754, 0.0151258, 0.0201761, 0.0252265, 0.0302769, 0.0353273, 0.0403777, 0.045428, 0.0504784,
  0.0555288, 0.0605792, 0.0656295, 0.0706799, 0.0757303, 0.0807807, 0.0858311, 0.0908814, 0.0959318,
  0.100982, 0.106033, 0.111083, 0.116133, 0.121184, 0.126234, 0.131284, 0.136335, 0.141385, 0.146436,
  0.151486, 0.156536, 0.161587, 0.166637, 0.171688, 0.176738, 0.181788, 0.186839, 0.191889, 0.196939,
  0.20199, 0.20704, 0.212091, 0.217141, 0.222191, 0.227242, 0.232292, 0.237342, 0.242393, 0.247443,
  0.252494, 0.257544, 0.262594, 0.267645, 0.272695, 0.277745, 0.282796, 0.287846, 0.292897, 0.297947,
  0.302997, 0.308048, 0.313098, 0.318148, 0.323199, 0.328249, 0.3333, 0.33835, 0.3434, 0.348451, 0.353501,
  0.358552, 0.363602, 0.368652, 0.373703, 0.378753, 0.383803, 0.388854, 0.393904, 0.398955, 0.404005,
  0.409055, 0.414106, 0.419156, 0.424206, 0.429257, 0.434307, 0.439358, 0.444408, 0.449458, 0.454509,
  0.459559, 0.464609, 0.46966, 0.47471, 0.479761, 0.484811, 0.489861, 0.494912, 0.499962, 0.505013},
 {0.404298, 0.00210275, 0.0942125, 0.0748646, 0.0663814, 0.0658068, 0.0915162, 0.113575,
  0.00641422, 0.219869, 0.14415, 0.152305, 0.179954, 0.0527938, 0.15753, 0.0900466, 0.179191,
  2.17543, 1.42221, 34.7614, 0.829275, 0.249408, 0.51088, 0.432199, 0.0402742, 0.806919, 0.190798,
  0.916989, 0.420114, 0.0345335, 0.0930855, 0.297033, 0.6691, 0.52593, 0.263783, 0.070414,
  0.00335504, 0.0910968, 0.258793, 0.381283, 0.050921, 0.0778359, 0.00549298, 0.519531, 0.0889353,
  0.176237, 0.134712, 3.45326, 14.4433, 16.2136, 1.38012, 0.689129, 0.576828, 0.593918, 0.152049,
  0.0106348, 0.0178817, 0.64424, 0.583515, 0.641604, 0.512644, 0.0835693, 1.47448, 0.0843249,
  0.0501894, 0.116205, 0.140858, 0.658514, 0.219186, 0.0288231, 0.285657, 0.146449, 0.00755994,
  0.116471, 0.337773, 0.196072, 0.0559808, 0.0661482, 0.597321, 1.16398, 0.0556676, 0.0102993,
  0.0955497, 0.0234931, 0.0485152, 0.197377, 0.0941688, 0.0266502, 0.219751, 0.187101, 0.0223984,
  1.00659, 0.270763, 0.0732352, 0.0673942, 0.36816, 0.335401, 0.158245, 0.317757, 0.156636}}
```

If we plot the periodogram we see two peaks corresponding to the right frequencies:

In[4]:=
```
ListLinePlot[Transpose[dataLombScarglePeriodogram], PlotRange → Full]
```

Out[4]=



The LombScargle function can also take a list of data, provided this is in the same order as the supplied times:

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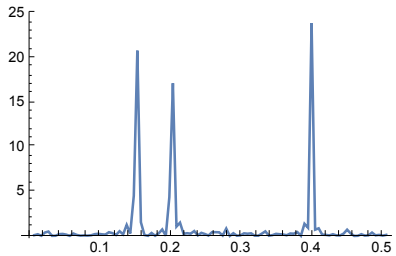
In[5]:=
```
dataLombScargleExample2 =
  Table[Sin[0.15*2 π n ] + Sin[0.2*2 π n] + Sin[0.4*2 π n] + RandomReal[{-1, 1}], {n, 0, 200}];
```

In[6]:=
```
dataLombScarglePeriodogram2 = LombScargle[dataLombScargleExample2, Range[0, 200]];
```

A plot the periodogram we see peaks corresponding to the frequencies corresponding to the example signal:

In[7]:=
```
ListLinePlot[Transpose[dataLombScarglePeriodogram2], PlotRange → Full]
```

Out[7]=


Let's consider a sample with missing data. First we generate a data list:

In[8]:=
```
dataLombScargleExample3a = Table[Cos[0.2*2 π n ] + Sin[0.1*2 π n], {n, 0, 100}];
```

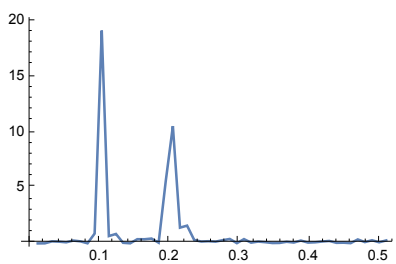
We next introduce missing data at random integer positions, say 10 points missing :

In[9]:=
```
dataLombScargleExample3aMissing =
 Nest[ReplacePart[#, RandomInteger[{1, 100}] → Missing[]] &, dataLombScargleExample3a, 10]
```

Out[9]=
```
{1., 0.896802, 0.14204, 0.14204, 0.896802, 1., -0.278768, -1.76007, -1.76007, Missing[], 1., 0.896802,
 0.14204, 0.14204, 0.896802, 1., -0.278768, -1.76007, -1.76007, -0.278768, Missing[], 0.896802, 0.14204,
 0.14204, 0.896802, 1., -0.278768, -1.76007, Missing[], -0.278768, 1., 0.896802, 0.14204, 0.14204,
 0.896802, 1., -0.278768, -1.76007, -1.76007, -0.278768, 1., 0.896802, 0.14204, 0.14204, 0.896802, 1.,
 -0.278768, -1.76007, -1.76007, -0.278768, 1., 0.896802, 0.14204, 0.14204, 0.896802, 1., Missing[],
 -1.76007, -1.76007, -0.278768, 1., 0.896802, 0.14204, 0.14204, 0.896802, Missing[], -0.278768, Missing[],
 -1.76007, -0.278768, 1., 0.896802, 0.14204, Missing[], 0.896802, 1., -0.278768, Missing[], -1.76007,
 -0.278768, Missing[], 0.896802, 0.14204, 0.14204, Missing[], 1., -0.278768, -1.76007, -1.76007,
 -0.278768, 1., 0.896802, 0.14204, 0.14204, 0.896802, 1., -0.278768, -1.76007, -1.76007, -0.278768, 1.}
```

In[10]:=
```
dataLombScarglePeriodogram3a = LombScargle[dataLombScargleExample3aMissing, Range[0, 100]];
```

In[11]:=
```
ListLinePlot[Transpose[dataLombScarglePeriodogram3a], PlotRange → Full]
```

Out[11]=


Instead of data tagged Missing we may have an unevenly sampled dataset provided as pairs of data. We consider a similar example:

In[12]:=
```
dataLombScargleExample3b = Table[{n, Cos[0.2*2 π n ] + Sin[0.1*2 π n]}, {n, 0, 100}];
```

Let's sample 90 points:

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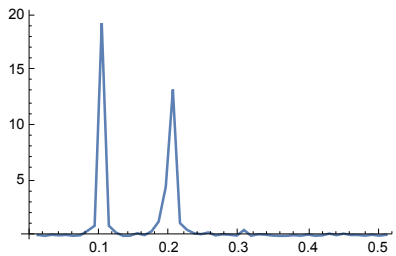
In[13]:=
```
dataLombScargleExample3bUneven = RandomSample[dataLombScargleExample3b, 90];
```

In[14]:=
```
dataLombScarglePeriodogram3b = LombScargle[dataLombScargleExample3bUneven, Range[0, 100]]
```

Out[14]=
```
{{0.0101, 0.0203031, 0.0305061, 0.0407092, 0.0509122, 0.0611153, 0.0713184, 0.0815214, 0.0917245, 0.101928,
  0.112131, 0.122334, 0.132537, 0.14274, 0.152943, 0.163146, 0.173349, 0.183552, 0.193755, 0.203958,
  0.214161, 0.224364, 0.234567, 0.24477, 0.254973, 0.265177, 0.27538, 0.285583, 0.295786, 0.305989,
  0.316192, 0.326395, 0.336598, 0.346801, 0.357004, 0.367207, 0.37741, 0.387613, 0.397816, 0.408019,
  0.418222, 0.428426, 0.438629, 0.448832, 0.459035, 0.469238, 0.479441, 0.489644, 0.499847, 0.51005},
 {0.0873388, 0.0125412, 0.104331, 0.0546728, 0.0940658, 0.0103549, 0.0636274, 0.463177, 0.919345,
  19.2839, 0.923514, 0.303791, 0.00752519, 0.0235442, 0.240654, 0.0711411, 0.414454, 1.29746, 4.43544,
  13.2603, 1.15927, 0.545528, 0.232457, 0.1622, 0.316315, 0.045352, 0.149017, 0.106985, 0.0341472, 0.535388,
  0.019016, 0.150042, 0.114676, 0.0343877, 0.00390789, 0.0117821, 0.067252, 0.0203344, 0.12462, 0.0176683,
  0.0488025, 0.211483, 0.0701024, 0.205517, 0.0843844, 0.0865547, 0.0258031, 0.106551, 0.0240134, 0.103065}}
```

In[15]:=
```
ListLinePlot[Transpose[dataLombScarglePeriodogram3b], PlotRange → Full]
```

Out[15]=



The data could also have been provided as an association

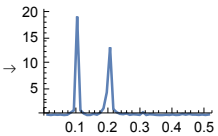
In[16]:=
```
dataLombScargleExample3c = <|"Unevenly Sampled data" → dataLombScargleExample3bUneven|>;
```

In[17]:=
```
dataLombScarglePeriodogram3c = LombScargle[dataLombScargleExample3c, Range[0, 100]]
```

Out[17]=
```
<|Unevenly Sampled data →
  {{0.0101, 0.0203031, 0.0305061, 0.0407092, 0.0509122, 0.0611153, 0.0713184, 0.0815214, 0.0917245,
    0.101928, 0.112131, 0.122334, 0.132537, 0.14274, 0.152943, 0.163146, 0.173349, 0.183552,
    0.193755, 0.203958, 0.214161, 0.224364, 0.234567, 0.24477, 0.254973, 0.265177,
    0.27538, 0.285583, 0.295786, 0.305989, 0.316192, 0.326395, 0.336598, 0.346801,
    0.357004, 0.367207, 0.37741, 0.387613, 0.397816, 0.408019, 0.418222, 0.428426,
    0.438629, 0.448832, 0.459035, 0.469238, 0.479441, 0.489644, 0.499847, 0.51005},
   {0.0873388, 0.0125412, 0.104331, 0.0546728, 0.0940658, 0.0103549, 0.0636274, 0.463177,
    0.919345, 19.2839, 0.923514, 0.303791, 0.00752519, 0.0235442, 0.240654, 0.0711411,
    0.414454, 1.29746, 4.43544, 13.2603, 1.15927, 0.545528, 0.232457, 0.1622, 0.316315,
    0.045352, 0.149017, 0.106985, 0.0341472, 0.535388, 0.019016, 0.150042, 0.114676, 0.0343877,
    0.00390789, 0.0117821, 0.067252, 0.0203344, 0.12462, 0.0176683, 0.0488025, 0.211483,
    0.0701024, 0.205517, 0.0843844, 0.0865547, 0.0258031, 0.106551, 0.0240134, 0.103065}}|>
```

In[18]:=
```
Query[All, ListLinePlot[Transpose[#], PlotRange → Full] &]@dataLombScarglePeriodogram3c
```

Out[18]= ⟨|Unevenly Sampled data →



|⟩

Linear Signal Examples (1)

Below are some examples of the Lomb-Scargle power spectrum for linear signal:

In[1]:=
```
timeSetLinear = Transpose[{Range[1, 100, 1], Range[1, 100, 1]}];
```

In[2]:=
```
lineLS = LombScargle[timeSetLinear, Range[1, 100, 1]];
```

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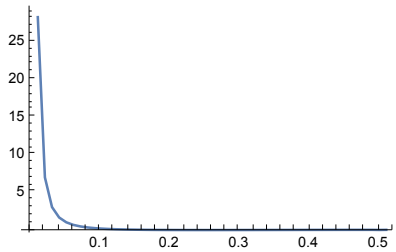
Below are some examples of the Lomb-Scargle power spectrum for linear signal:

In[3]:=
```
ListLinePlot[Transpose[lineLS], PlotRange → All]
```

Out[3]=


Here we create a function to generate some randomly sampled linear time series:

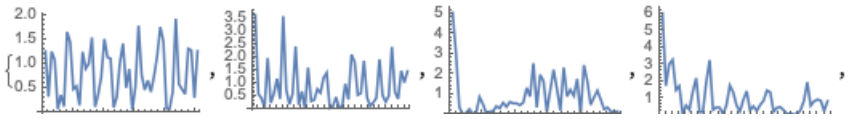
In[4]:=
```
timeSeriesLine[n_] := SortBy[RandomSample[Transpose[{Range[1, 100, 1], Range[1, 100, 1]}], n], First];
```

And also a function to generate the periodograms pairs:

In[5]:=
```
lineUnevenLS[n_] := LombScargle[timeSeriesLine[n] , Range[1, 100, 1], PairReturn → True] ;
```

Here is an assortment of randomly sampled periodograms from a linear series:

In[6]:=
```
ListLinePlot[lineUnevenLS[#], PlotRange → All] & /@ Range[5, 100, 5]
```

Out[6]=


Random Noise Examples (1)

Below are some examples of the Lomb-Scargle power spectrum for random noise:

In[1]:=
```
randomListExample = RandomReal[{-1, 1}, 100]
```

Out[1]=
```
{0.612117, -0.562518, 0.483396, -0.750512, -0.102579, -0.943674, 0.737527, -0.114387, 0.957514, -0.00437979,
 -0.421305, 0.209572, -0.0413869, -0.331315, 0.360671, -0.0242141, 0.779983, 0.765956, -0.996563,
 -0.098822, -0.160774, -0.638535, 0.865786, -0.723629, 0.95057, -0.491773, -0.564529, -0.319216,
 -0.25944, -0.222426, -0.459888, 0.525539, -0.0106817, -0.892003, -0.666769, -0.442718, 0.988761,
 -0.588773, -0.325857, -0.0121365, 0.363509, -0.501496, 0.399009, -0.988848, 0.583305, 0.0364649,
 -0.756267, 0.233415, 0.820643, -0.906347, -0.64526, -0.0656929, -0.226665, -0.445206, 0.562796,
 0.031319, 0.0535337, 0.765316, 0.810443, 0.227095, 0.163018, 0.337737, 0.0479837, -0.612613,
 0.337028, -0.173746, 0.81551, -0.260765, 0.729616, 0.726796, 0.682503, 0.948432, 0.842703,
 0.199995, -0.693807, 0.0341889, -0.317115, -0.232587, 0.500895, -0.735931, -0.866864, 0.936714,
 0.738743, -0.617008, 0.870873, -0.465819, -0.646301, -0.76299, -0.893036, 0.542074, 0.337383,
 0.876064, 0.870399, -0.0924157, -0.257027, 0.917818, -0.285887, 0.0425464, 0.180429, 0.467722}
```

The data looks like :

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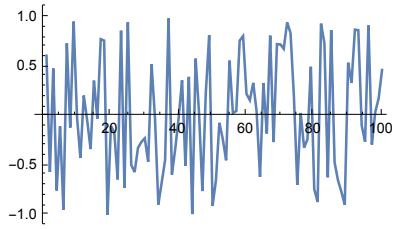
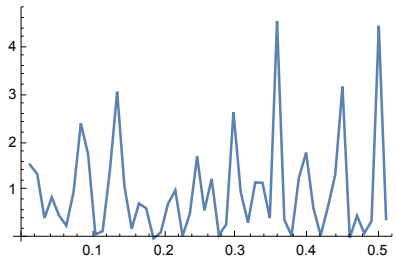
In[2]:=
```
ListLinePlot[randomListExample]
```

Out[2]=


The Lomb Scargle transformation gives:

In[3]:=
```
randomListLombScargle =
  LombScargle[Transpose[{Range[1, 100], randomListExample}], Range[1, 100], PairReturn → True];
```

In[4]:=
```
ListLinePlot[randomListLombScargle, PlotRange → All]
```

Out[4]=


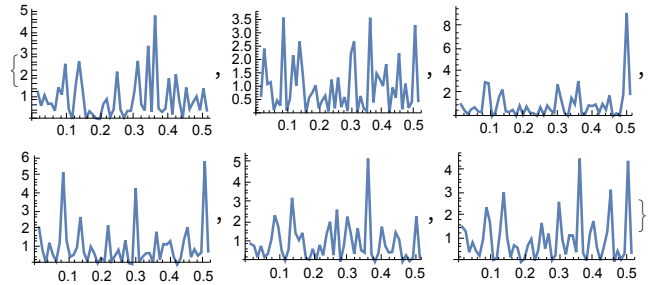
We can also remove data to see how the periodogram performs with missing data/uneven sampling:

In[5]:=
```
timeSeriesRandomSample[n_] :=
  SortBy[RandomSample[Transpose[{Range[1, 100], randomListExample}], n], First];
```

In[6]:=
```
randomUnevenLombScargle[n_] := LombScargle[timeSeriesRandomSample[n], Range[1, 100, 1], PairReturn → True] ;
```

We plot the periodograms with 50-100 points sampled in steps of 10:

In[7]:=
```
ListLinePlot[randomUnevenLombScargle[#], PlotRange → All] & /@ Range[50, 100, 10]
```

Out[7]=


Options (5)

FrequenciesOnly (1)

In[1]:=
```
Needs["MathIOmica`"]
```

FrequenciesOnly is an option that is by default set to False, of whether to return an association for the frequencies used in the computation only.

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In[2]:=
```
dataLombScargleExampleC = Table[Sin[0.05 * 2 π n ], {n, 0, 100}]
```

Out[2]=
```
{0., 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785, 0.309017, 1.22465×10^-16,
 -0.309017, -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017,
 -2.44929×10^-16, 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785,
 0.309017, 3.67394×10^-16, -0.309017, -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017,
 -0.587785, -0.309017, -4.89859×10^-16, 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057,
 0.809017, 0.587785, 0.309017, 6.12323×10^-16, -0.309017, -0.587785, -0.809017, -0.951057, -1.,
 -0.951057, -0.809017, -0.587785, -0.309017, -7.34788×10^-16, 0.309017, 0.587785, 0.809017, 0.951057,
 1., 0.951057, 0.809017, 0.587785, 0.309017, 8.57253×10^-16, -0.309017, -0.587785, -0.809017,
 -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017, -9.79717×10^-16, 0.309017, 0.587785,
 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785, 0.309017, 1.10218×10^-15, -0.309017,
 -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017, -1.22465×10^-15}
```

In[3]:=
```
LombScargle[dataLombScargleExampleC, Range[0, 100], FrequenciesOnly → True]
```

Out[3]=
```
<|f1 → 0.0101, f2 → 0.0203031, f3 → 0.0305061, f4 → 0.0407092, f5 → 0.0509122, f6 → 0.0611153, f7 → 0.0713184,
 f8 → 0.0815214, f9 → 0.0917245, f10 → 0.101928, f11 → 0.112131, f12 → 0.122334, f13 → 0.132537, f14 → 0.14274,
 f15 → 0.152943, f16 → 0.163146, f17 → 0.173349, f18 → 0.183552, f19 → 0.193755, f20 → 0.203958,
 f21 → 0.214161, f22 → 0.224364, f23 → 0.234567, f24 → 0.24477, f25 → 0.254973, f26 → 0.265177,
 f27 → 0.27538, f28 → 0.285583, f29 → 0.295786, f30 → 0.305989, f31 → 0.316192, f32 → 0.326395,
 f33 → 0.336598, f34 → 0.346801, f35 → 0.357004, f36 → 0.367207, f37 → 0.37741, f38 → 0.387613,
 f39 → 0.397816, f40 → 0.408019, f41 → 0.418222, f42 → 0.428426, f43 → 0.438629, f44 → 0.448832,
 f45 → 0.459035, f46 → 0.469238, f47 → 0.479441, f48 → 0.489644, f49 → 0.499847, f50 → 0.51005|>
```

NormalizeIntensities (1)

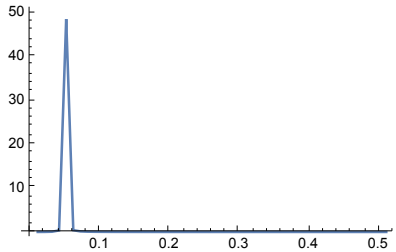
In[1]:=
```
Needs["MathIOmica`"]
```

NormalizeIntensities is an option that is by default set to False, of whether to normalize the intensity list for the periodogram.

In[2]:=
```
dataLombScargleExampleC = Table[Sin[0.05 * 2 π n ], {n, 0, 100}];
```

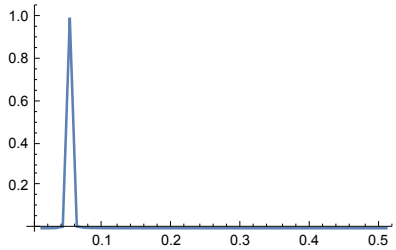
In[3]:=
```
ListLinePlot[Transpose[LombScargle[dataLombScargleExampleC, Range[0, 100]]], PlotRange → All]
```

Out[3]=



In[4]:=
```
ListLinePlot[Transpose[LombScargle[dataLombScargleExampleC, Range[0, 100], NormalizeIntensities → True]],
 PlotRange → All]
```

Out[4]=



OversamplingRate (1)

In[1]:=
```
Needs["MathIOmica`"]
```

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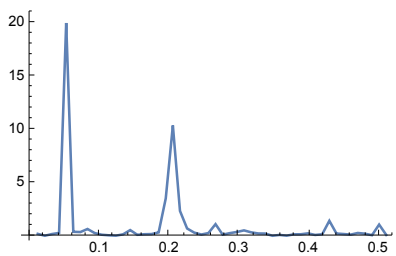
OversamplingRate takes values ≥ 1 by which to over-sample the time series with zero-padding. The default value is 1. We consider the following data:

In[2]:=
```
dataLombScargleExampleA = Table[{n, Sin[0.05*2 π n] + Sin[0.2*2 π n] + RandomReal[{-1, 1}]}, {n, 0, 100}]
```

Out[2]=
```
{{0, -0.417122}, {1, 0.647454}, {2, 2.07699}, {3, 0.739363}, {4, -0.18859}, {5, 0.74991},
 {6, 2.15956}, {7, 2.04931}, {8, 0.271593}, {9, 0.243813}, {10, -0.39953}, {11, 0.548378},
 {12, -0.918894}, {13, -2.30368}, {14, -1.57146}, {15, -1.35442}, {16, 0.601639}, {17, 0.0303234},
 {18, -0.963566}, {19, -0.714985}, {20, 0.0903895}, {21, 2.228}, {22, 0.819503}, {23, 0.109342},
 {24, 0.298824}, {25, 0.807742}, {26, 1.4149}, {27, 0.562726}, {28, 0.537843}, {29, -0.494252},
 {30, 0.830551}, {31, 0.083339}, {32, 0.628102}, {33, -1.97616}, {34, -2.25556}, {35, -1.64238},
 {36, 0.357692}, {37, -0.202561}, {38, -1.63419}, {39, -1.94739}, {40, -0.969832}, {41, 0.504889},
 {42, 2.08509}, {43, -0.0462768}, {44, -0.087973}, {45, 0.965544}, {46, 0.993837}, {47, 1.37432},
 {48, 0.697977}, {49, -0.687883}, {50, -0.794537}, {51, 1.01564}, {52, 0.863967}, {53, -1.76368},
 {54, -1.42616}, {55, -1.87409}, {56, -0.737071}, {57, -0.961874}, {58, -0.29848}, {59, -1.37093},
 {60, -0.924828}, {61, 0.313134}, {62, 1.30907}, {63, 0.0895472}, {64, -0.158025}, {65, 1.40837},
 {66, 2.093}, {67, 1.48575}, {68, 0.806283}, {69, -1.30998}, {70, -0.448431}, {71, -0.171351},
 {72, 0.914291}, {73, -1.91749}, {74, -2.30472}, {75, -1.07337}, {76, -0.980176}, {77, 0.250428},
 {78, -0.800775}, {79, -1.688}, {80, -0.485097}, {81, 1.54828}, {82, 1.6818}, {83, -0.654648},
 {84, 0.626648}, {85, 0.836846}, {86, 2.45704}, {87, 0.578129}, {88, 0.771643}, {89, -1.15092},
 {90, 0.772406}, {91, -0.320853}, {92, -0.323623}, {93, -0.469155}, {94, -1.97176},
 {95, -0.383042}, {96, 0.661678}, {97, -1.13831}, {98, -1.77358}, {99, -2.11201}, {100, 0.0758466}}
```

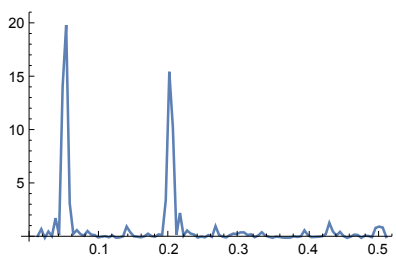
A plot with of the periodogram with no oversampling looks like:

In[3]:=
```
ListLinePlot[LombScargle[dataLombScargleExampleA,
  Range[0, 100], PairReturn → True, OversamplingRate → 1], PlotRange → All]
```

Out[3]=


Oversampling by a factor of 2 makes the periodogram look smoother in this case:

In[4]:=
```
ListLinePlot[LombScargle[dataLombScargleExampleA,
  Range[0, 100], PairReturn → True, OversamplingRate → 2], PlotRange → All]
```

Out[4]=


PairReturn (1)

In[1]:=
```
Needs["MathIOmica`"]
```

PairReturn is an option that is by default set to False, of whether to return pairs of frequencies and intensities, or a list of frequencies and a corresponding list of intensities for

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a periodogram.

In[2]:=
```
dataLombScargleExampleC = Table[Sin[0.05*2 π n ], {n, 0, 100}]
```

Out[2]=
```
{0., 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785, 0.309017, 1.22465×10^-16,
 -0.309017, -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017,
 -2.44929×10^-16, 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785,
 0.309017, 3.67394×10^-16, -0.309017, -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017,
 -0.587785, -0.309017, -4.89859×10^-16, 0.309017, 0.587785, 0.809017, 0.951057, 1., 0.951057,
 0.809017, 0.587785, 0.309017, 6.12323×10^-16, -0.309017, -0.587785, -0.809017, -0.951057, -1.,
 -0.951057, -0.809017, -0.587785, -0.309017, -7.34788×10^-16, 0.309017, 0.587785, 0.809017, 0.951057,
 1., 0.951057, 0.809017, 0.587785, 0.309017, 8.57253×10^-16, -0.309017, -0.587785, -0.809017,
 -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017, -9.79717×10^-16, 0.309017, 0.587785,
 0.809017, 0.951057, 1., 0.951057, 0.809017, 0.587785, 0.309017, 1.10218×10^-15, -0.309017,
 -0.587785, -0.809017, -0.951057, -1., -0.951057, -0.809017, -0.587785, -0.309017, -1.22465×10^-15}
```

In[3]:=
```
LombScargle[dataLombScargleExampleC, Range[0, 100], PairReturn → False]
```

Out[3]=
```
{{0.0101, 0.0203031, 0.0305061, 0.0407092, 0.0509122, 0.0611153, 0.0713184, 0.0815214, 0.0917245, 0.101928,
  0.112131, 0.122334, 0.132537, 0.14274, 0.152943, 0.163146, 0.173349, 0.183552, 0.193755, 0.203958,
  0.214161, 0.224364, 0.234567, 0.24477, 0.254973, 0.265177, 0.27538, 0.285583, 0.295786, 0.305989,
  0.316192, 0.326395, 0.336598, 0.346801, 0.357004, 0.367207, 0.37741, 0.387613, 0.397816, 0.408019,
  0.418222, 0.428426, 0.438629, 0.448832, 0.459035, 0.469238, 0.479441, 0.489644, 0.499847, 0.51005},
 {0.00086406, 0.0105129, 0.0518424, 0.351756, 48.5163, 0.399966, 0.126309, 0.0647705, 0.040398,
  0.0279618, 0.0206294, 0.015884, 0.0126072, 0.0102345, 0.00845305, 0.00707688, 0.00598916, 0.00511308,
  0.00439627, 0.0038019, 0.00330339, 0.00288112, 0.0025203, 0.00220963, 0.00194032, 0.00170546, 0.00149955,
  0.00131815, 0.00115767, 0.00101517, 0.000888251, 0.000774896, 0.000673446, 0.000582516, 0.000500943,
  0.000427754, 0.000362132, 0.000303395, 0.000250967, 0.000204372, 0.000163212, 0.00012716, 0.0000959483,
  0.0000693619, 0.0000472322, 0.0000294309, 0.0000158671, 6.48661×10^-6, 0.000730289, 1.24654×10^-7}}
```

In[4]:=
```
LombScargle[dataLombScargleExampleC, Range[0, 100], PairReturn → True]
```

Out[4]=
```
{{0.0101, 0.00086406}, {0.0203031, 0.0105129}, {0.0305061, 0.0518424}, {0.0407092, 0.351756},
 {0.0509122, 48.5163}, {0.0611153, 0.399966}, {0.0713184, 0.126309}, {0.0815214, 0.0647705},
 {0.0917245, 0.040398}, {0.101928, 0.0279618}, {0.112131, 0.0206294}, {0.122334, 0.015884},
 {0.132537, 0.0126072}, {0.14274, 0.0102345}, {0.152943, 0.00845305}, {0.163146, 0.00707688},
 {0.173349, 0.00598916}, {0.183552, 0.00511308}, {0.193755, 0.00439627}, {0.203958, 0.0038019},
 {0.214161, 0.00330339}, {0.224364, 0.00288112}, {0.234567, 0.0025203}, {0.24477, 0.00220963},
 {0.254973, 0.00194032}, {0.265177, 0.00170546}, {0.27538, 0.00149955}, {0.285583, 0.00131815},
 {0.295786, 0.00115767}, {0.305989, 0.00101517}, {0.316192, 0.000888251}, {0.326395, 0.000774896},
 {0.336598, 0.000673446}, {0.346801, 0.000582516}, {0.357004, 0.000500943}, {0.367207, 0.000427754},
 {0.37741, 0.000362132}, {0.387613, 0.000303395}, {0.397816, 0.000250967}, {0.408019, 0.000204372},
 {0.418222, 0.000163212}, {0.428426, 0.00012716}, {0.438629, 0.0000959483}, {0.448832, 0.0000693619},
 {0.459035, 0.0000472322}, {0.469238, 0.0000294309}, {0.479441, 0.0000158671},
 {0.489644, 6.48661×10^-6}, {0.499847, 0.000730289}, {0.51005, 1.24654×10^-7}}
```

UpperFrequencyFactor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

UpperFrequencyFactor takes values ≥ 1, by which to scale the upper Nyquist cutoff frequency and increase spectral resolution. It is recommended to set UpperFrequencyFactor close to 1. The default value is 1.

We consider the following example data:

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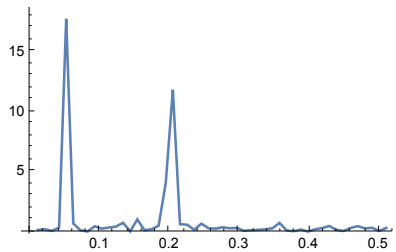
In[2]:=
```
dataLombScargleExampleB = Table[{n, Cos[0.05*2 π n ] + Cos[0.2*2 π n] + RandomReal[{-1, 1}]}, {n, 0, 100}]
```

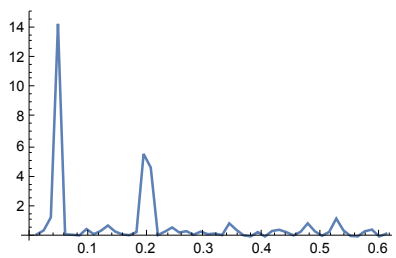
Out[2]=
```
{{0, 1.06758}, {1, 0.727809}, {2, -0.953679}, {3, 0.633537}, {4, -0.114898}, {5, 0.00615653},
 {6, -0.0842653}, {7, -0.831092}, {8, -1.49906}, {9, -0.741235}, {10, -0.817988}, {11, -1.62208},
 {12, -1.15314}, {13, -1.12631}, {14, 0.66192}, {15, 0.801535}, {16, 0.22197}, {17, 0.389082},
 {18, 0.893067}, {19, 1.2575}, {20, 2.39195}, {21, 2.02083}, {22, -0.0937002}, {23, -1.15719},
 {24, 0.485197}, {25, 0.688054}, {26, 0.717518}, {27, -2.37672}, {28, -0.80762}, {29, -0.446339},
 {30, -0.174637}, {31, -1.19861}, {32, -0.635418}, {33, -1.04121}, {34, -0.7398}, {35, 0.0342453},
 {36, -0.103795}, {37, -0.00421787}, {38, -0.502615}, {39, 0.946425}, {40, 2.99407},
 {41, 1.67436}, {42, -0.342592}, {43, -0.954558}, {44, -0.104282}, {45, 0.191607}, {46, 0.627982},
 {47, -0.42089}, {48, -1.62726}, {49, 0.217836}, {50, 0.0674613}, {51, -1.33451}, {52, -1.8543},
 {53, -1.98045}, {54, -0.4476}, {55, 0.115394}, {56, 0.622043}, {57, -0.334614}, {58, -0.966055},
 {59, 2.22324}, {60, 1.70022}, {61, 0.605191}, {62, 0.180938}, {63, -0.791251}, {64, 1.25072},
 {65, 1.30222}, {66, 0.486173}, {67, -2.26968}, {68, -1.79858}, {69, -1.52864}, {70, 0.694478},
 {71, -0.450693}, {72, -1.87546}, {73, -0.44933}, {74, -0.533488}, {75, 0.169709}, {76, 0.292892},
 {77, -0.45598}, {78, -0.52884}, {79, 1.56686}, {80, 2.16812}, {81, 1.8167}, {82, -0.797465},
 {83, -0.563426}, {84, -0.36773}, {85, 1.38058}, {86, -0.689093}, {87, -1.10104}, {88, -2.48725},
 {89, -1.26494}, {90, 0.0271144}, {91, -0.921098}, {92, -2.19054}, {93, -0.715192}, {94, 0.855395},
 {95, 0.710821}, {96, 0.0306188}, {97, -1.16671}, {98, 0.170233}, {99, 0.378105}, {100, 2.02868}}
```

In[3]:=
```
ListLinePlot[LombScargle[dataLombScargleExampleB,
  Range[0, 100], PairReturn → True, UpperFrequencyFactor → 1], PlotRange → All]
```

Out[3]=


Changing the upper Nyquist frequency has a direct effect on the periodogram:

In[4]:=
```
ListLinePlot[LombScargle[dataLombScargleExampleB,
  Range[0, 100], PairReturn → True, UpperFrequencyFactor → 1.2], PlotRange → All]
```

Out[4]=


Properties & Relations (1)

The inbuilt Periodogram function also gives similar results to a LombScargle function for a series that is evenly sampled without missing data. The results agree to each other up to normalization factors.

In calculating the Autocorrelation as an inverse Fourier transform of a periodogram a modified version of the LombScargle function is used, named InverseAutocovariance .

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See Also

Autocorrelation ▪ **InverseAutocovariance** ▪ **TimeSeriesClassification**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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LowValueTag

LowValueTag[*omicsObject*, *valueCutoff*]
takes an *omicsObject* and tags values in specified position as Missing[] based on provided *valueCutoff*.

Details

- LowValueTag[*omicsObject*, *valueCutoff*] takes an *omicsObject* and tags values in specified position as Missing[] based on provided *valueCutoff*. The function takes two inputs:

omicsObject	OmicsObject (or similar association) from which values will be tagged.
valueCutoff	Cutoff selection used in tagging low values that are less than or equal to this cutoff.

- LowValueTag returns a modified OmicsObject that replaces the values at the original location that are tagged with Missing[] or a specific value depending on the options provided.
- The following options can be given:

ComponentIndex	1	Selection of which component of a list to use in the association or OmicsObject input values.
ListIndex	1	Selection of which list to use in the association or OmicsObject input values.
OtherReplacement	_Missing :> Missing[]	Replacement rule for any other kind of replacement in the data.
ValueReplacement	Missing[]	Value that specifies how tagged data points will be replaced.

- Using the default options, LowValueTag replaces values tagged in the first list, first component of the input OmicsAssociation.
- LowValueTag can be used to tag values that are indistinguishable from noise levels as Missing, i.e. essentially not detected.

Examples (6)

Basic Examples (1)

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First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

Let' s consider the OmicsObject:

```
In[2]:= omicsObjectExampleTag = <|
    "7" → ⟨|{"FAM138A"} → {{0}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} → {{2.73998`}, {"OK"}},
      {"DDX11L1"} → {{6.75461`}, {"OK"}}, {"WASH7P"} → {{11.8883`}, {"OK"}}|⟩,
    "9" → ⟨|{"FAM138A"} → {{0.00257233`}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} →
       {{5.15563`}, {"OK"}}, {"DDX11L1"} → {{3.57627`}, {"OK"}}, {"WASH7P"} → {{11.93`}, {"OK"}}|⟩,
    "11" → ⟨|{"FAM138A"} → {{0}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} → {{5.71829`}, {"OK"}},
      {"DDX11L1"} → {{3.24942`}, {"OK"}}, {"WASH7P"} → {{10.4902`}, {"OK"}}|⟩,
    "14" → ⟨|{"FAM138A"} → {{0.00429509`}, {"OK"}}, {"OR4F5"} → {{0}, {"OK"}}, {"LOC729737"} →
       {{2.38838`}, {"OK"}}, {"DDX11L1"} → {{3.58037`}, {"OK"}}, {"WASH7P"} → {{9.0819`}, {"OK"}}|⟩|⟩;
```

We can tag values less than 1:

```
In[3]:= LowValueTag[omicsObjectExampleTag, 5 ]

Out[3]= <|7 → <|{FAM138A} → {{Missing[]}, {OK}}, {OR4F5} → {{Missing[]}, {OK}},
      {LOC729737} → {{Missing[]}, {OK}}, {DDX11L1} → {{6.75461}, {OK}}, {WASH7P} → {{11.8883}, {OK}}|>,
    9 → <|{FAM138A} → {{Missing[]}, {OK}}, {OR4F5} → {{Missing[]}, {OK}}, {LOC729737} → {{5.15563}, {OK}},
      {DDX11L1} → {{Missing[]}, {OK}}, {WASH7P} → {{11.93}, {OK}}|>,
    11 → <|{FAM138A} → {{Missing[]}, {OK}}, {OR4F5} → {{Missing[]}, {OK}}, {LOC729737} → {{5.71829}, {OK}},
      {DDX11L1} → {{Missing[]}, {OK}}, {WASH7P} → {{10.4902}, {OK}}|>,
    14 → <|{FAM138A} → {{Missing[]}, {OK}}, {OR4F5} → {{Missing[]}, {OK}}, {LOC729737} → {{Missing[]}, {OK}},
      {DDX11L1} → {{Missing[]}, {OK}}, {WASH7P} → {{9.0819}, {OK}}|>|>
```

Options (4)

ComponentIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

ComponentIndex allows selection of which component of the selected list to filter on from the OmicsObject. Let's consider the following OmicsObject:

```
In[2]:= omicsObjectMultiComponent =
   ⟨|"FirstSample" → ⟨|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
      {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
      {"Measurement5"} → Missing[]|⟩, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
      {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
      {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
    "ThirdSample" → ⟨|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
      {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
      {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|⟩|⟩;
```

Let's tag values from the first list, on the second component being ≤ 2:

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```
In[3]:= LowValueTag[omicsObjectMultiComponent, 2, ListIndex → 1, ComponentIndex → 2]

Out[3]= <|FirstSample → <|{Measurement1} → {{0.8, Missing[]}, {17, True}},
          {Measurement2} → Missing[], {Measurement3} → {{0.5, 4.}, {2, False}},
          {Measurement4} → {{0.2, 3.}, {5, True}}, {Measurement5} → Missing[]|>,
        SecondSample → <|{Measurement1} → {{0.7, Missing[]}, {15, True}},
          {Measurement2} → {{0.7, Missing[]}, {12, True}}, {Measurement3} → {{0.3, Missing[]}, {11, False}},
          {Measurement4} → {{0.3, 3.}, {6, True}}, {Measurement5} → {{0.6, 3.}, {10, True}}|>,
        ThirdSample → <|{Measurement1} → {{0.9, Missing[]}, {16, True}},
          {Measurement2} → {{0.3, 5.}, {11, True}}, {Measurement3} → {{0.4, 6.}, {8, False}},
          {Measurement4} → {{0.3, Missing[]}, {7, True}}, {Measurement5} → Missing[]|>|>
```

ListIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

ListIndex allows selection of which list to filter on (list 1 or 2 in a typical OmicsObject contain data or metadata). The default is set to 1.

We consider the following data:

```
In[2]:= omicsObjectMultiComponent =
          <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
            {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
            {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
            {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
            {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
          "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
            {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
            {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>|>;
```

In this example, we can tag the measurement (first list, ListIndex→1, first component), tagging values less than than 0.5 (these are relative intensity.

```
In[3]:= LowValueTag[omicsObjectMultiComponent, 0.5, ListIndex → 1, ComponentIndex → 1]

Out[3]= <|FirstSample → <|{Measurement1} → {{0.8, 2}, {17, True}},
          {Measurement2} → Missing[], {Measurement3} → {{Missing[], 4}, {2, False}},
          {Measurement4} → {{Missing[], 3}, {5, True}}, {Measurement5} → Missing[]|>,
        SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement2} → {{0.7, 1}, {12, True}},
          {Measurement3} → {{Missing[], 2}, {11, False}},
          {Measurement4} → {{Missing[], 3}, {6, True}}, {Measurement5} → {{0.6, 3}, {10, True}}|>,
        ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}}, {Measurement2} → {{Missing[], 5}, {11, True}},
          {Measurement3} → {{Missing[], 6}, {8, False}},
          {Measurement4} → {{Missing[], 2}, {7, True}}, {Measurement5} → Missing[]|>|>
```

We repeat this for the first component in the second list, for a cutoff of 8:

```
In[4]:= LowValueTag[omicsObjectMultiComponent, 8, ListIndex → 2, ComponentIndex → 1]

Out[4]= <|FirstSample → <|{Measurement1} → {{0.8, 2}, {17., True}},
          {Measurement2} → Missing[], {Measurement3} → {{0.5, 4}, {Missing[], False}},
          {Measurement4} → {{0.2, 3}, {Missing[], True}}, {Measurement5} → Missing[]|>,
        SecondSample → <|{Measurement1} → {{0.7, 1}, {15., True}}, {Measurement2} → {{0.7, 1}, {12., True}},
          {Measurement3} → {{0.3, 2}, {11., False}}, {Measurement4} → {{0.3, 3}, {Missing[], True}},
          {Measurement5} → {{0.6, 3}, {10., True}}|>, ThirdSample → <|{Measurement1} → {{0.9, 2}, {16., True}},
          {Measurement2} → {{0.3, 5}, {11., True}}, {Measurement3} → {{0.4, 6}, {Missing[], False}},
          {Measurement4} → {{0.3, 2}, {Missing[], True}}, {Measurement5} → Missing[]|>|>
```

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OtherReplacement (1)

```
In[1]:= Needs["MathIOmica`"]
```

OtherReplacement allows us to set a delayed replacement rule for any value in conjunction with the low value tagging at the same position. We use our example OmicsObject

```
In[2]:= omicsObjectMultiComponent =
  <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
     {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
     {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
     {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
     {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
   "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
     {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
     {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[""]|>|>;
```

We tag values from the first list, first component, ≤ 0.6 and also replace all 0.8 values with the text "High Value":

```
In[3]:= LowValueTag[omicsObjectMultiComponent, 0.6, OtherReplacement → 0.8 :> "High Value"]

Out[3]= <|FirstSample → <|{Measurement1} → {{High Value, 2}, {17, True}},
     {Measurement2} → Missing[], {Measurement3} → {{Missing[], 4}, {2, False}},
     {Measurement4} → {{Missing[], 3}, {5, True}}, {Measurement5} → Missing[]|>,
   SecondSample → <|{Measurement1} → {{0.7, 1}, {15, True}}, {Measurement2} → {{0.7, 1}, {12, True}},
     {Measurement3} → {{Missing[], 2}, {11, False}}, {Measurement4} → {{Missing[], 3}, {6, True}},
     {Measurement5} → {{Missing[], 3}, {10, True}}|>,
   ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}}, {Measurement2} → {{Missing[], 5}, {11, True}},
     {Measurement3} → {{Missing[], 6}, {8, False}},
     {Measurement4} → {{Missing[], 2}, {7, True}}, {Measurement5} → Missing[]|>|>
```

ValueReplacement (1)

```
In[1]:= Needs["MathIOmica`"]
```

ValueReplacement allows us to select what value will be replacing the tagged low data. The default value is Missing[]. We consider again an example OmicsObject

```
In[2]:= omicsObjectMultiComponent =
  <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
     {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
     {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
     {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
     {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
   "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
     {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
     {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>|>;
```

We tag values from the first list, first component, ≤ 5, setting them to "Tagged":

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```
In[3]:= LowValueTag[omicsObjectMultiComponent, 5, ValueReplacement → "Tagged"]
```

```
Out[3]= <|FirstSample → <|{Measurement1} → {{Tagged, 2}, {17, True}},
    {Measurement2} → Missing[], {Measurement3} → {{Tagged, 4}, {2, False}},
    {Measurement4} → {{Tagged, 3}, {5, True}}, {Measurement5} → Missing[]|>,
  SecondSample → <|{Measurement1} → {{Tagged, 1}, {15, True}},
    {Measurement2} → {{Tagged, 1}, {12, True}}, {Measurement3} → {{Tagged, 2}, {11, False}},
    {Measurement4} → {{Tagged, 3}, {6, True}}, {Measurement5} → {{Tagged, 3}, {10, True}}|>,
  ThirdSample → <|{Measurement1} → {{Tagged, 2}, {16, True}},
    {Measurement2} → {{Tagged, 5}, {11, True}}, {Measurement3} → {{Tagged, 6}, {8, False}},
    {Measurement4} → {{Tagged, 2}, {7, True}}, {Measurement5} → Missing[]|>|>
```

Properties & Relations (1)

LowValueTag is used to replace values with a tag, usually Missing[], in an association. No keys are removed. This is related to FilteringFunction that allows removal of data based on a filter.

FilterMissing may be used to filter and remove Missing[] values from an OmicsObject.

See Also

FilteringFunction ▪ **FilterMissing** ▪ **OmicsObject** ▪ **OmicsObjectCreator**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

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- MathIOmicaGuide
- MathIOmicaOverview

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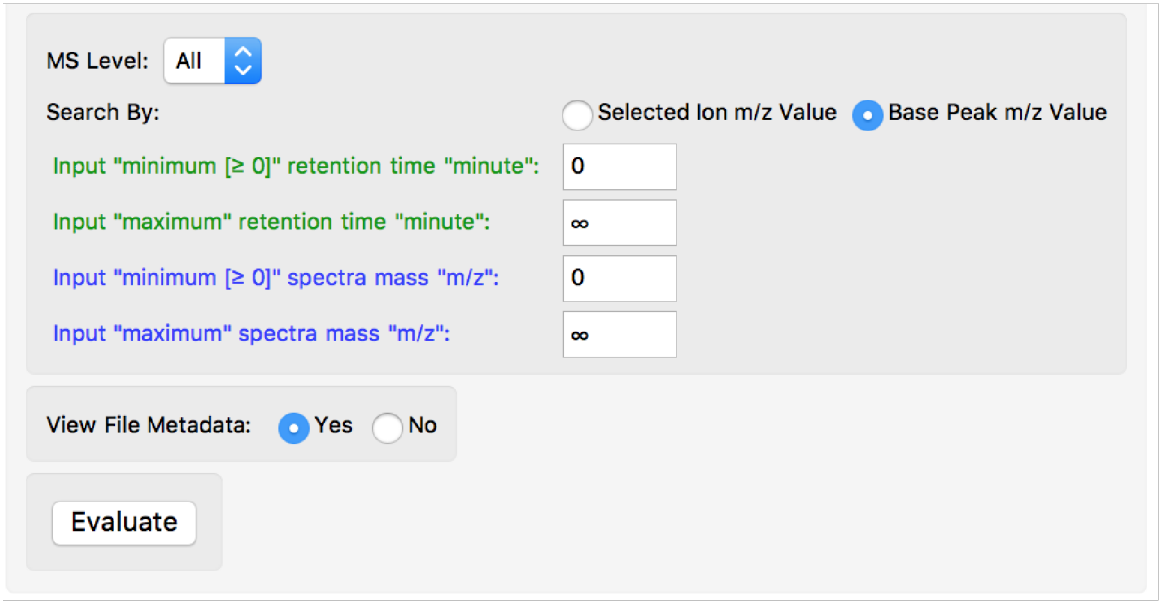
MSViewer

`MSViewer[file]`
is a spectrum viewer for mass spectrometry .mzXML or .mzML data, in the provided *file* path.

Details

- `MSViewer[file]` is a spectrum viewer for mass spectrometry current format .mzml data (or legacy .mzxml), in the provided *file* path.
- MSViewer provides an Interpretation interactive interfaces to view multi-MS mass spectrometry data.
- Data is streamed by the function to facilitate faster lookups.
- The *file* path is optional. If no file is provided, a file selector allows the user to point to the file they require.
- Two interpretation screens will appear in sequence based on selections followed by the output.
- The first interpretation screen will appear as:



- The choices corresponding to items in the first interpretation that can be made are:

Item in first Interpretation screen	Selection Choice
MS Level	Select what level of MS to be included for choices of spectra to see (e.g. MS 1, MS/MS or MS2, etc...).

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Search By :	Search by selected ion m/z Value for filtering or for Base peak m/z value in a spectrum. If "Selected ion m/z Value" is chosen MS Level should be chosen > 1.
Input minimum retention time	Numeric selection of minimum retention time to search for in spectra.
Input maximum retention time	Numeric selection of maximum retention time to search for in spectra.
Input minimum spectra mass	Minimum mass to be searched (for choice of mass selected by item "Search By:" selection.
Input maximum spectra mass	Maximum mass to be searched (for choice of mass selected by item "Search By:" selection.
View File Metadata	Select whether or not to display file metadata in the next interpretation output.
Evaluate	Pressing the "Evaluate" button will display the next interpretation based on the selections made.

- The second Interpretation screen will have the following form:

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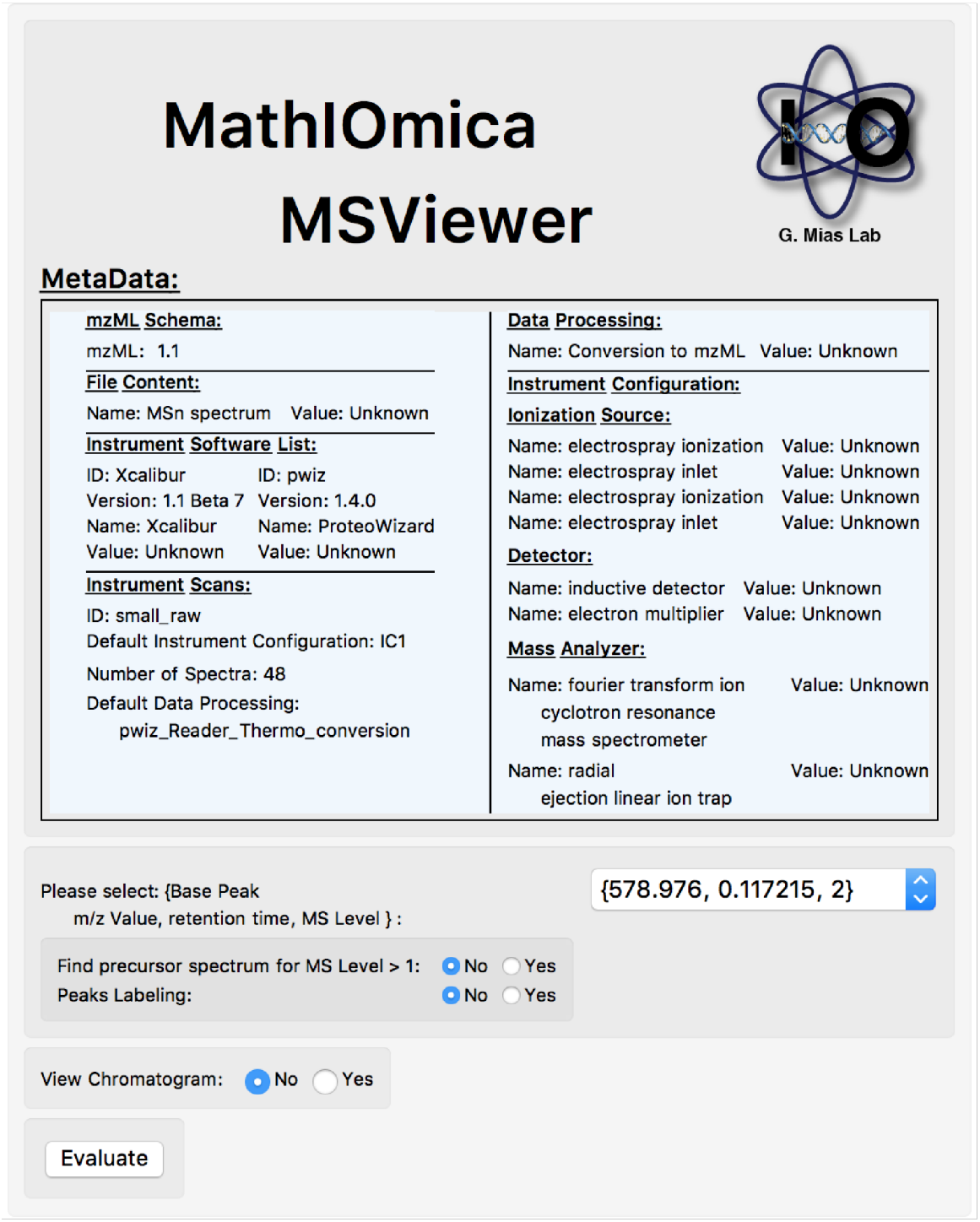

- The MetaData provides information regarding the run directly obtained from the file.
- The following selections may be made for the second Interpretation screen:

Item in second Interpretation screen	Selection Choice
Base Peak	Select from a menu masses corresponding to the filtering selections of the first interpretation. The general format for these choices is {m/z Value, retention time, MS level}.

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Find precursor for MS Level > 1	Select whether or not to display precursor spectra for MS Level > 1 selections of Base Peak item.
Peaks Labeling	Select whether or not to label peaks (appears on pointer hover over peak). This can be resource and time intensive if the spectra are dense and is not recommended for large files.
View Chromatogram	Whether or not to output the chromatogram.
Evaluate	Pressing the "Evaluate" button will display the spectra for the selections made in the second Interpretation screen.

- The following options can be given for the MSViewer function:

MathIOmicaDataDirectory	If[! DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]	MathIOmicaDataDirectory option value points to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.
PSImsOBOFile	"psi–ms.obo.txt"	PSImsOBOFile points to an Open Biomedical Ontologies (OBO) file for the mass spectromety information found in the ConstantMathIOmicaDataDirectory.
VocabularyVariable	None	VocabularyVariable provides a vocabulary variable to use for mass spectrometry vocabularies in lieu of using the PSImsOBOFile option. The content should have the form of an OBO file imported as lines: Import[filename,"Lines"].

References

- Derived controlled vocabularies and the .mzml example file were obtained from the HUPO Proteomics Standards Initiative Mass Spectrometry Standards Working Group and HUPO Proteomics Standards Initiative Proteomics Informatics Working Group, https://github.com/HUPO–PSI/psi–ms–CV/blob/master/psi–ms.obo and http://www.psidev.info/mzml_1_0_0%20 . (access date 8/22/2016) respectively.

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- The example file was converted from .raw format using Proteowizard *:*

- *A cross-platform toolkit for mass spectrometry and proteomics.* Chambers, M.C., MacLean, B., Burke, R., Amode, D., Ruderman, D.L., Neumann, S., Gatto, L., Fischer, B., Pratt, B., Egertson, J., Hoff, K., Kessner, D., Tasman, N., Shulman, N., Frewen, B., Baker, T.A., Brusniak, M.-Y., Paulse, C., Creasy, D., Flashner, L., Kani, K., Moulding, C., Seymour, S.L., Nuwaysir, L.M., Lefebvre, B., Kuhlmann, F., Roark, J., Rainer, P., Detlev, S., Hemenway, T., Huhmer, A., Langridge, J., Connolly, B., Chadick, T., Holly, K., Eckels, J., Deutsch, E.W., Moritz, R.L., Katz, J.E., Agus, D.B., MacCoss, M., Tabb, D.L. & Mallick, P. Nature Biotechnology 30, 918-920 (2012).

Examples (5)

Basic Examples (2)

Example mzML file format (1)

We first load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

As a first example we consider an .mzML example file. We can employ MSViewer[] without an argument to navigate to a file. Instead we will provide an exact location with the file name at:

In[2]:=
```
exampleMzml = FileNameJoin[{ConstantMathIOmicaExamplesDirectory, "small.pwiz.1.1.mzML"}]
```

(Note that the exact path on your system will not likely match the directory path as shown below).

We call MSViewer with the file path. In the first Interpretation we will select MS Level 2 spectra, for retention times 0 to 20 minutes, and m/z values of 800 to 900 for for "Selected Ion m/z Value". In the second Interpretation we will select the "811.41`" m/z value and "0.149755`" retention time MS2 spectrum, selecting to view the chromatogram as well as the precursor spectra:

In[3]:=
```
MSViewer[exampleMzml]
```

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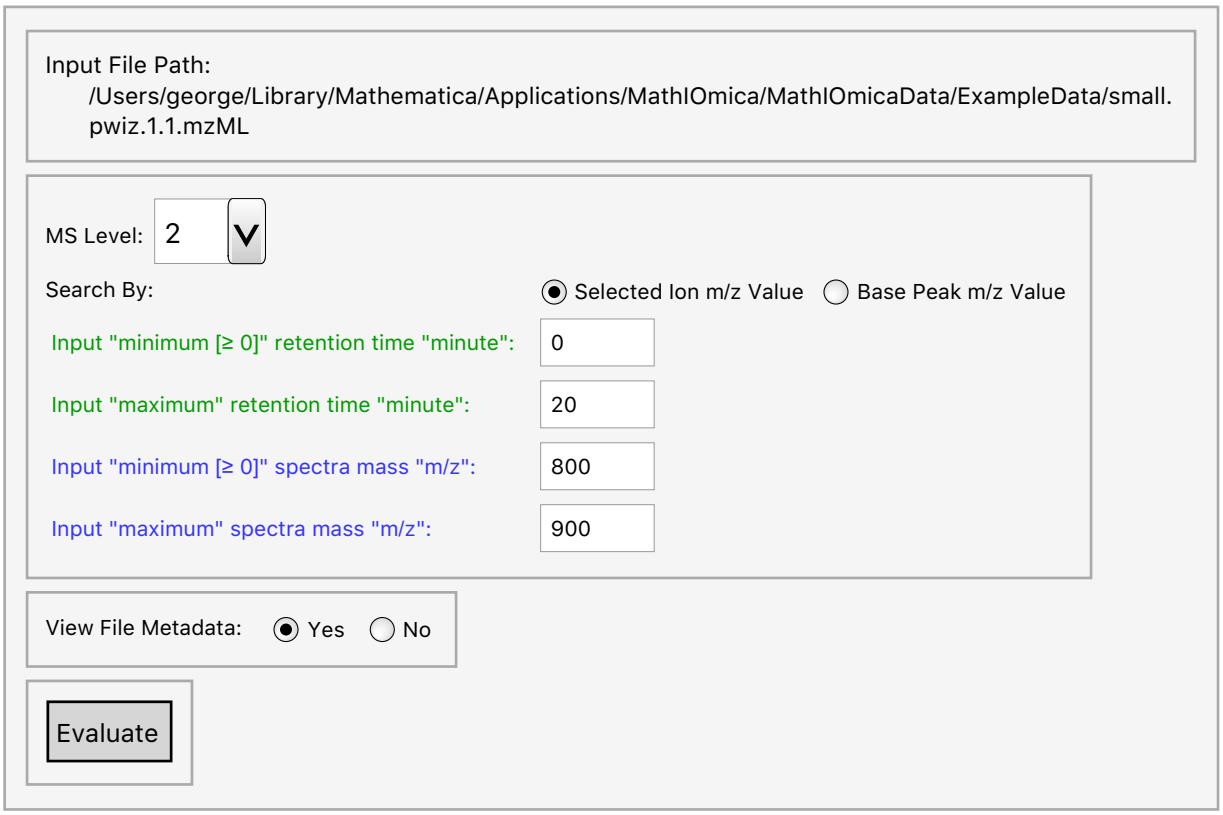
In[4]:=



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In[5]:=

MathIOmica MSViewer

G. Mias Lab

MetaData:

mzML Schema:

mzML: 1.1

File Content:

Name: MSn spectrum Value: Unknown

Instrument Software List:

ID: Xcalibur	ID: pwiz
Version: 1.1 Beta 7	Version: 1.4.0
Name: Xcalibur	Name: ProteoWizard
Value: Unknown	Value: Unknown

Instrument Scans:

ID: small_raw
Default Instrument Configuration: IC1
Number of Spectra: 48
Default Data Processing:
pwiz_Reader_Thermo_conversion

Data Processing:

Name: Conversion to mzML Value: Unknown

Instrument Configuration:

Ionization Source:

Name: electrospray ionization Value: Unknown
Name: electrospray inlet Value: Unknown
Name: electrospray ionization Value: Unknown
Name: electrospray inlet Value: Unknown

Detector:

Name: inductive detector Value: Unknown
Name: electron multiplier Value: Unknown

Mass Analyzer:

Name: fourier transform ion cyclotron resonance mass spectrometer Value: Unknown
Name: radial ejection linear ion trap Value: Unknown

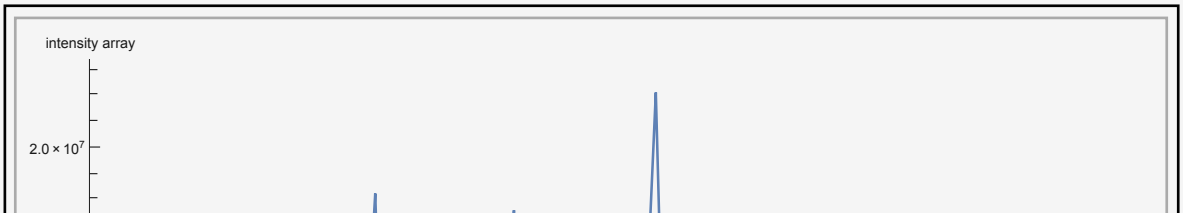
Please select: {Selected Ion m/z Value, retention time, MS Level } : {811.41`, 0.149755`, 2}

Find precursor spectrum for MS Level > 1: ○ No ◉ Yes
Peaks Labeling: ◉ No ○ Yes

View Chromatogram: ○ No ◉ Yes

Evaluate

Chromatogram "TIC":



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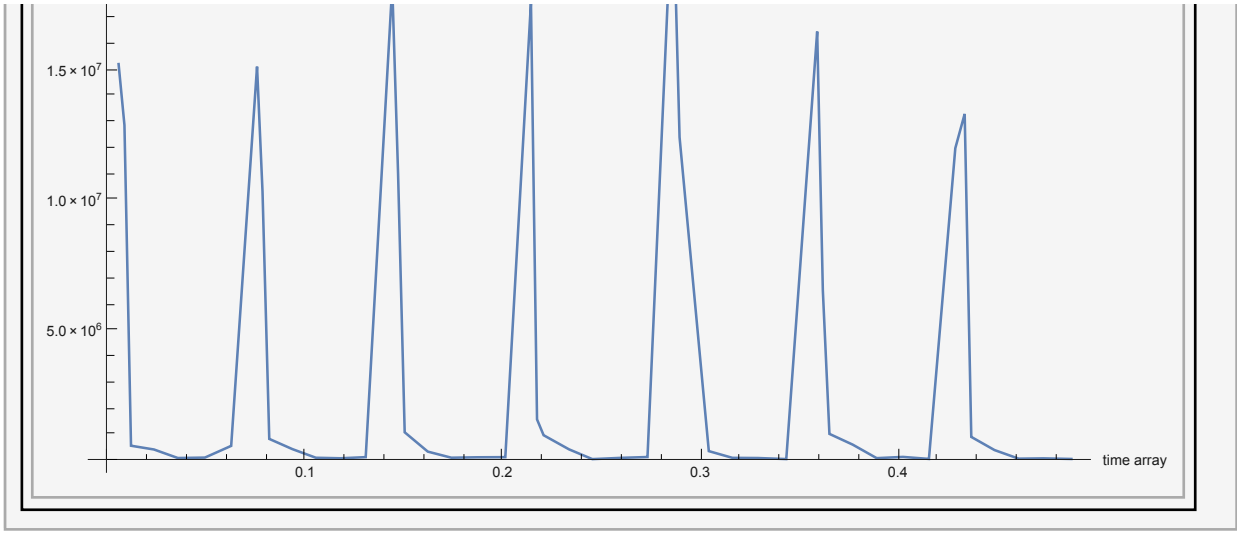
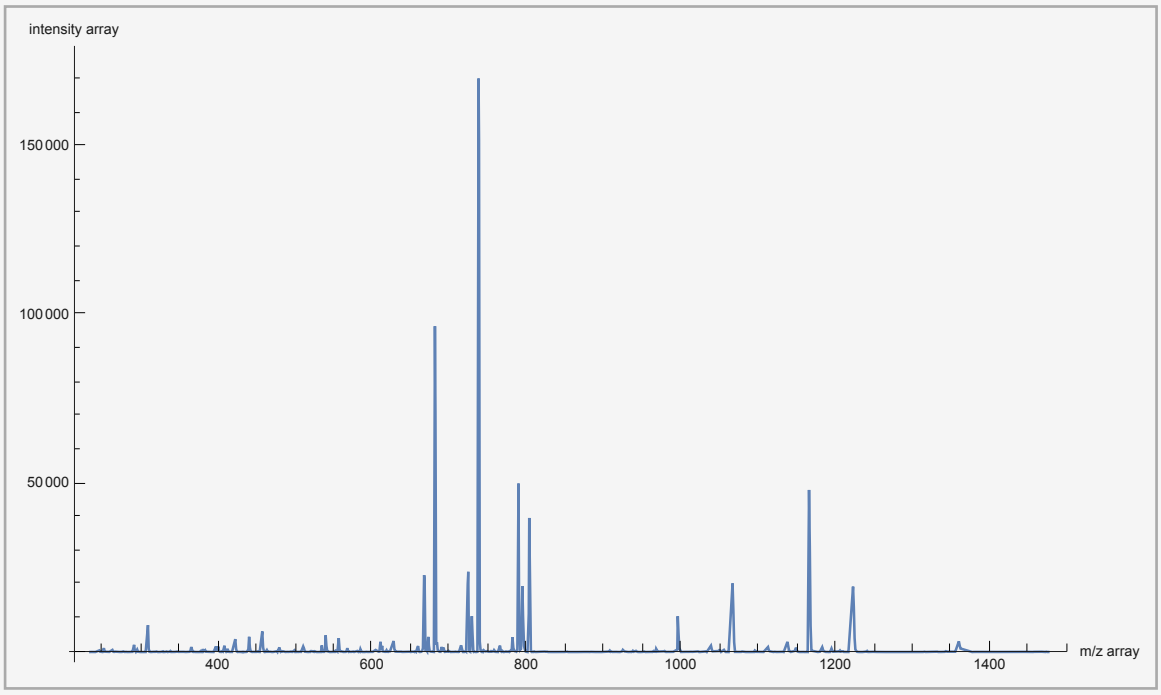
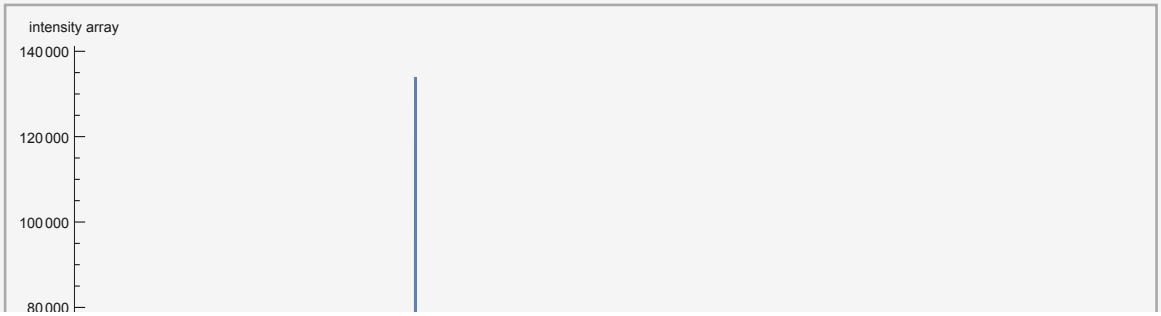


Out[5]=

base peak m/z value	ms level value	scan start time value	selected ion m/z value	spectrum representation	ionization mode
736.4835205078125	2	0.149755	811.40999999999997	centroid spectrum	positive scan



base peak m/z value	ms level value	scan start time value	spectrum representation	ionization mode
811.0909423828125	1	0.14640833333333333	profile spectrum	positive scan



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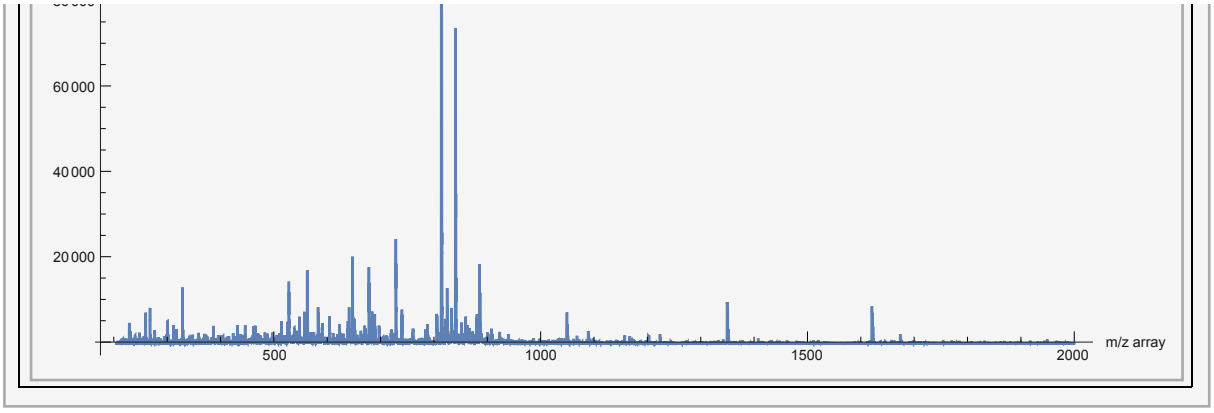


Example mzXML file format (1)

In[1]:=
```
Needs["MathIOmica`"]
```

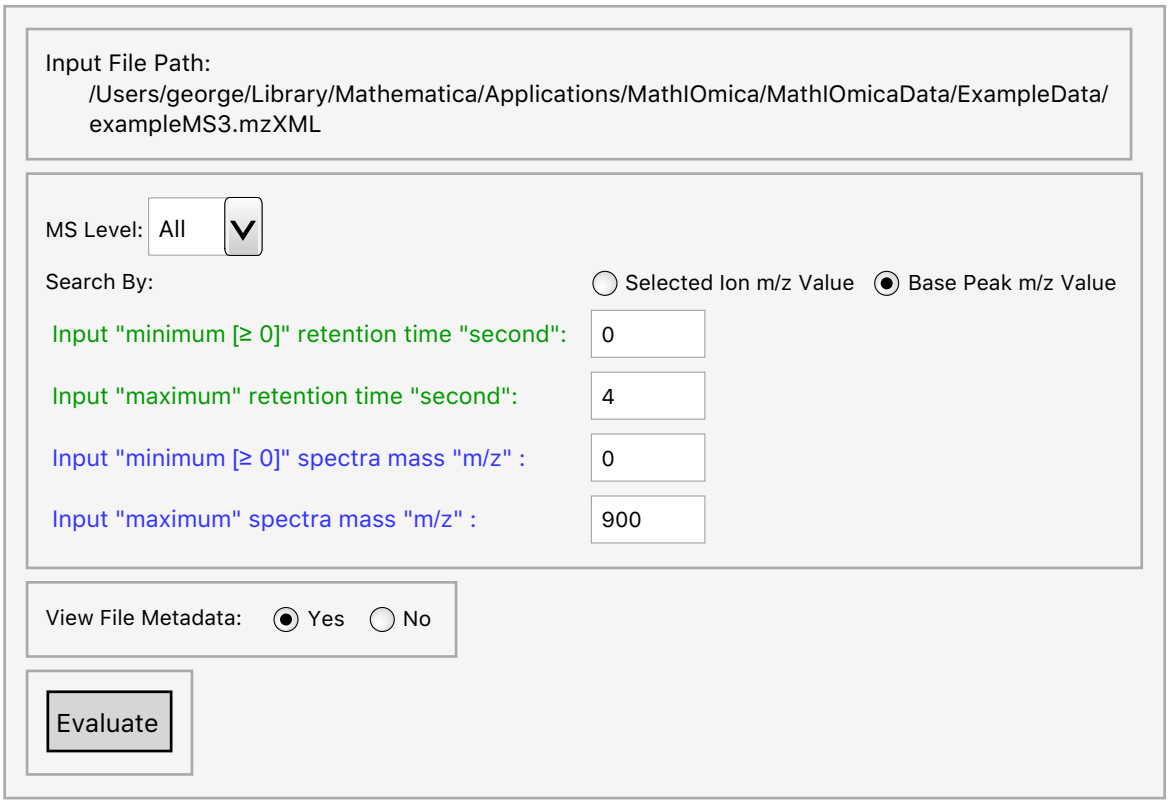
As a second example we consider an .mzXML example file. The file is provided at:

In[2]:=
```
exampleMzxml = FileNameJoin[{ConstantMathIOmicaExamplesDirectory, "exampleMS3.mzXML"}]
```

We select MS Level 3, and also view the precursor data for base peak selection {"808.427","3.3643",3}

In[3]:=
```
MSViewer[exampleMzxml]
```

In[4]:=



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In[5]:=

MathIOmica MSViewer

G. Mias Lab

MetaData:

mzXML Schema:

mzXML: 3.1

MS Run:

Scan Count: 52
Start Time: 0.3692
End Time: 17.6921

Instrument:

MS–Manufacturer:	Thermo Finnigan
MS–Model:	unknown
MS–Ionisation:	NSI
MS–Analyzer:	FTMS
MS–Detector:	unknown

Instrument Software:

Type: acquisition
Name: Xcalibur
Version: 2.6.0

Data Processing Software:

Type: conversion
Name: ReAdW
Version: 4.3.1(build Sep 9 2009 12:30:29)

Data Processing Operation

Name: Unknown
Value: Unknown
Type: Unknown

Please select: {Base Peak m/z Value, retention time, MS Level } : {808.427`, 3.3643`, 3}

Find precursor spectrum for MS Level > 1: ○ No ◉ Yes
Peaks Labeling: ◉ No ○ Yes

Evaluate

spectrum representation	ms level value	ionization mode	scan start time value	base peak m/z value	selected ion m/z value
profile spectrum	3	positive scan	3.3643	808.427	816.92663574

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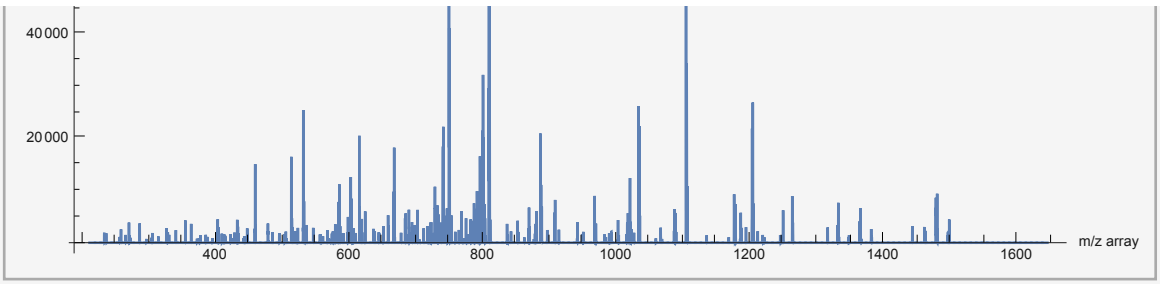
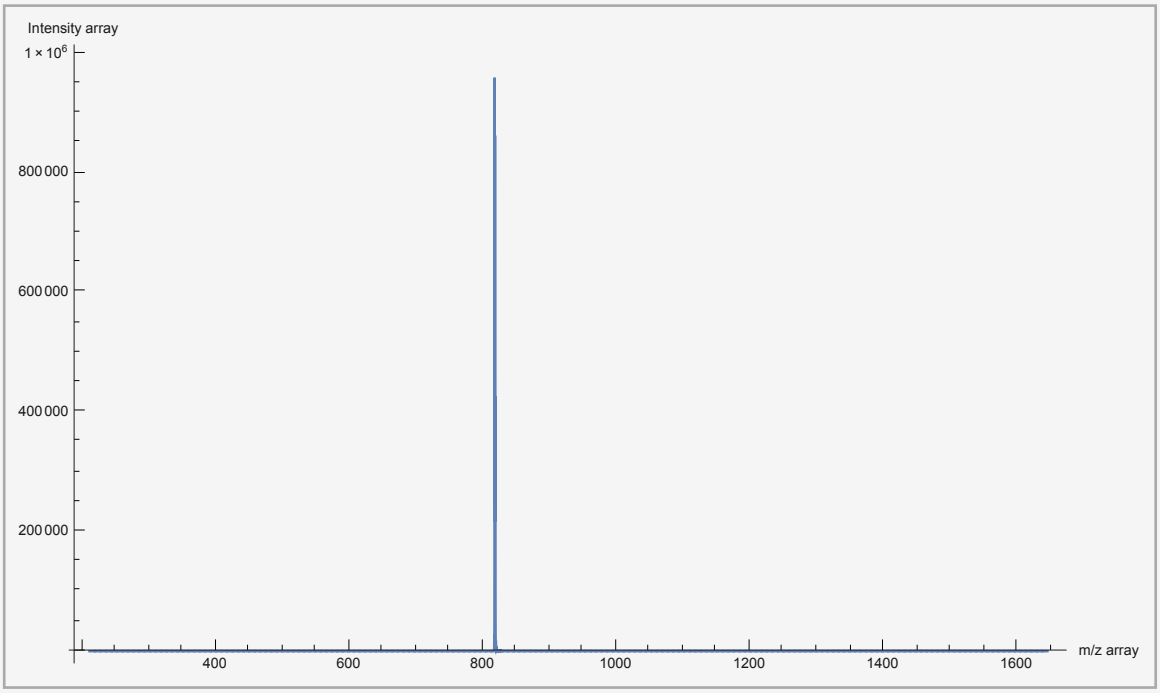
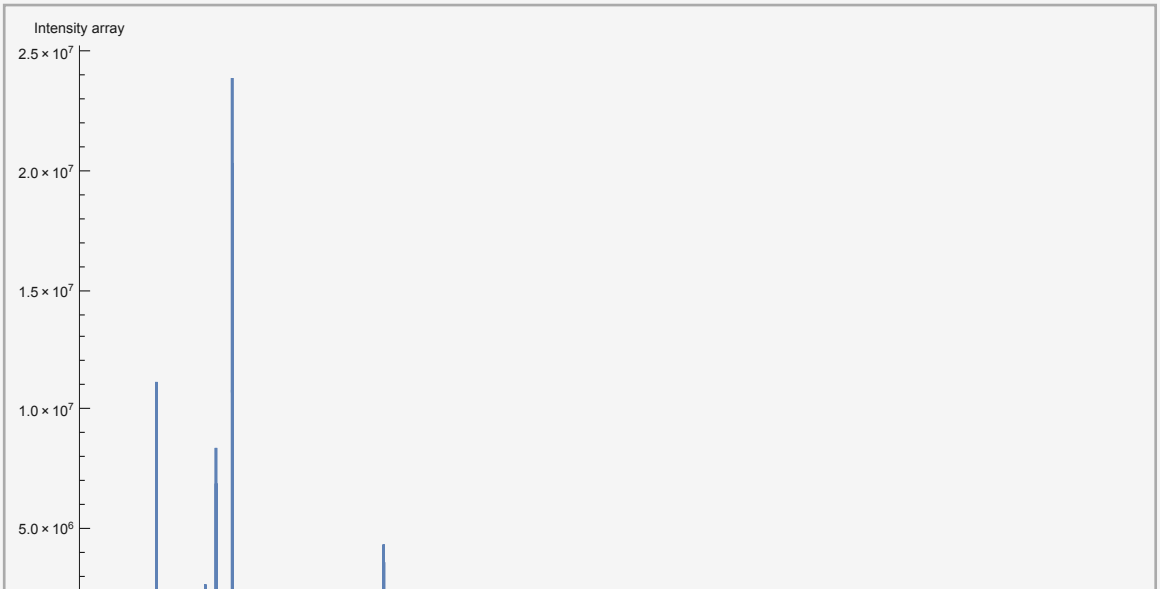


spectrum representation	ms level value	ionization mode	scan start time value	base peak m/z value	selected ion m/z value
profile spectrum	2	positive scan	3.1935	816.927	816.92932129

Out[5]=



spectrum representation	ms level value	ionization mode	scan start time value	base peak m/z value
profile spectrum	1	positive scan	2.0311	544.955



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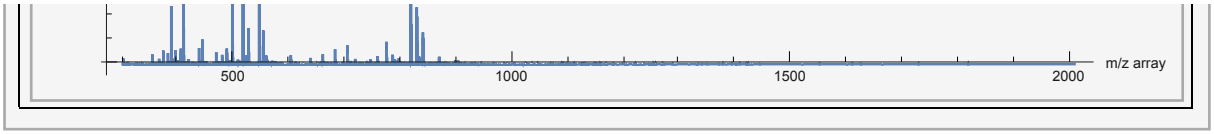


Options (3)

MathIOmicaDataDirectory (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value points to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

We consider an .mzML example file:

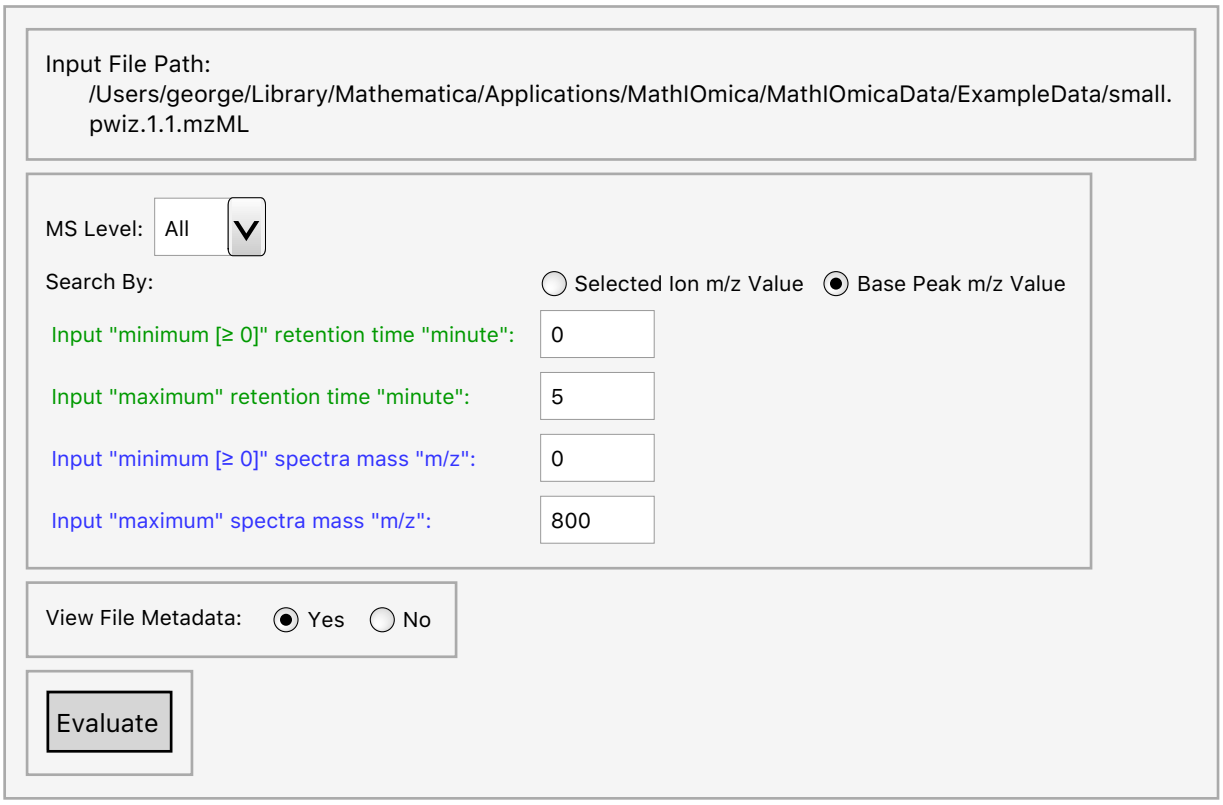
In[2]:=
```
exampleMzml = FileNameJoin[{ConstantMathIOmicaExamplesDirectory, "small.pwiz.1.1.mzML"}]
```

We can set the MathIOmicaDataDirectory explicitly to its default location:

In[3]:=
```
exampleDirectory = ConstantMathIOmicaDataDirectory
```

In[4]:=
```
MSViewer[exampleMzml, MathIOmicaDataDirectory → exampleDirectory]
```

In[5]:=



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In[6]:=

MathIOmica MSViewer

G. Mias Lab

MetaData:

mzML Schema:

mzML: 1.1

File Content:

Name: MSn spectrum Value: Unknown

Instrument Software List:

ID: Xcalibur	ID: pwiz
Version: 1.1 Beta 7	Version: 1.4.0
Name: Xcalibur	Name: ProteoWizard
Value: Unknown	Value: Unknown

Instrument Scans:

ID: small_raw

Default Instrument Configuration: IC1

Number of Spectra: 48

Default Data Processing:
pwiz_Reader_Thermo_conversion

Data Processing:

Name: Conversion to mzML Value: Unknown

Instrument Configuration:

Ionization Source:

Name: electrospray ionization Value: Unknown
Name: electrospray inlet Value: Unknown
Name: electrospray ionization Value: Unknown
Name: electrospray inlet Value: Unknown

Detector:

Name: inductive detector Value: Unknown
Name: electron multiplier Value: Unknown

Mass Analyzer:

Name: fourier transform ion cyclotron resonance mass spectrometer Value: Unknown

Name: radial ejection linear ion trap Value: Unknown

Please select: {Base Peak m/z Value, retention time, MS Level } :

{578.97607421875`, 0.11721500000000001`,

Find precursor spectrum for MS Level > 1: ◉ No ○ Yes
Peaks Labeling: ◉ No ○ Yes

View Chromatogram: ◉ No ○ Yes

Evaluate

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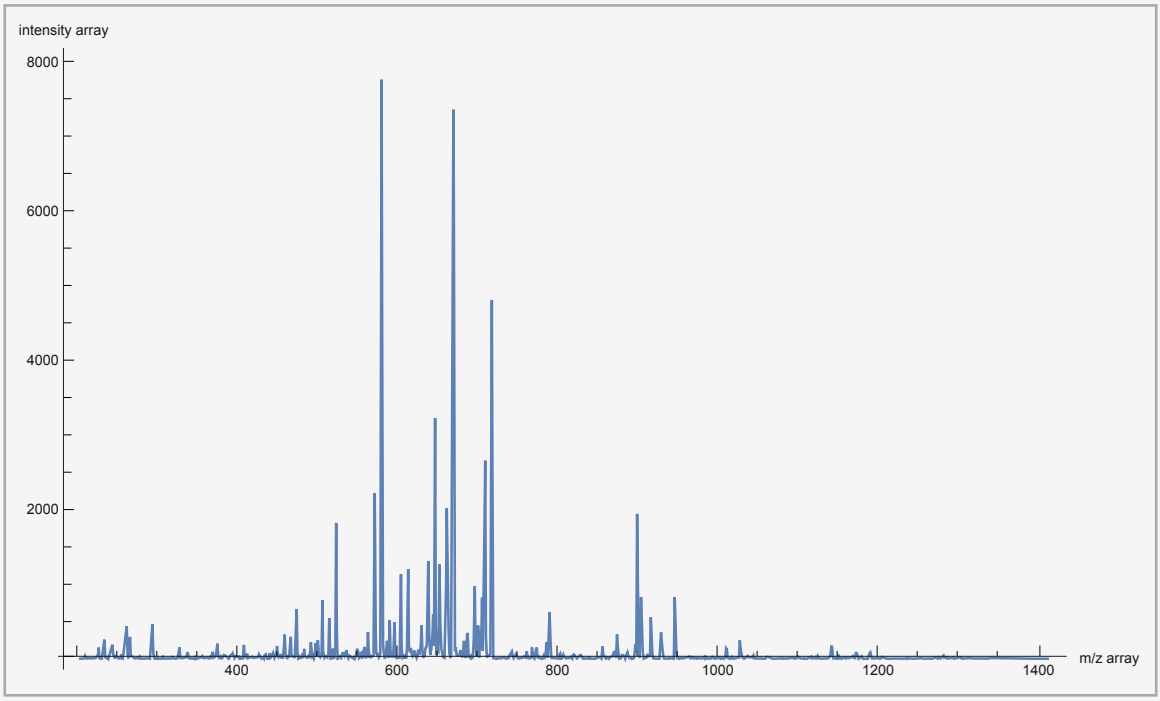
Out[6]=

base peak m/z value	ms level value	scan start time value	selected ion m/z value	spectrum representation	ionization mode
578.97607421875	2	0.11721500000000001	725.23000000000002	centroid spectrum	positive scan



PSImsOBOFile (1)

In[1]:=
```
Needs["MathIOmica`"]
```

PSImsOBOFile points to an Open Biomedical Ontologies (OBO) file for the mass spectrometry information found in the ConstantMathIOmicaDataDirectory.

We consider an .mzML example file:

In[2]:=
```
exampleMzml = FileNameJoin[{ConstantMathIOmicaExamplesDirectory, "small.pwiz.1.1.mzML"}]
```

We can set the PSImsOBOFile explicitly to its default name:

In[3]:=
```
examplePSImsOBOFile = "psi-ms.obo.txt";
```

In[4]:=
```
MSViewer[exampleMzml, PSImsOBOFile → examplePSImsOBOFile]
```

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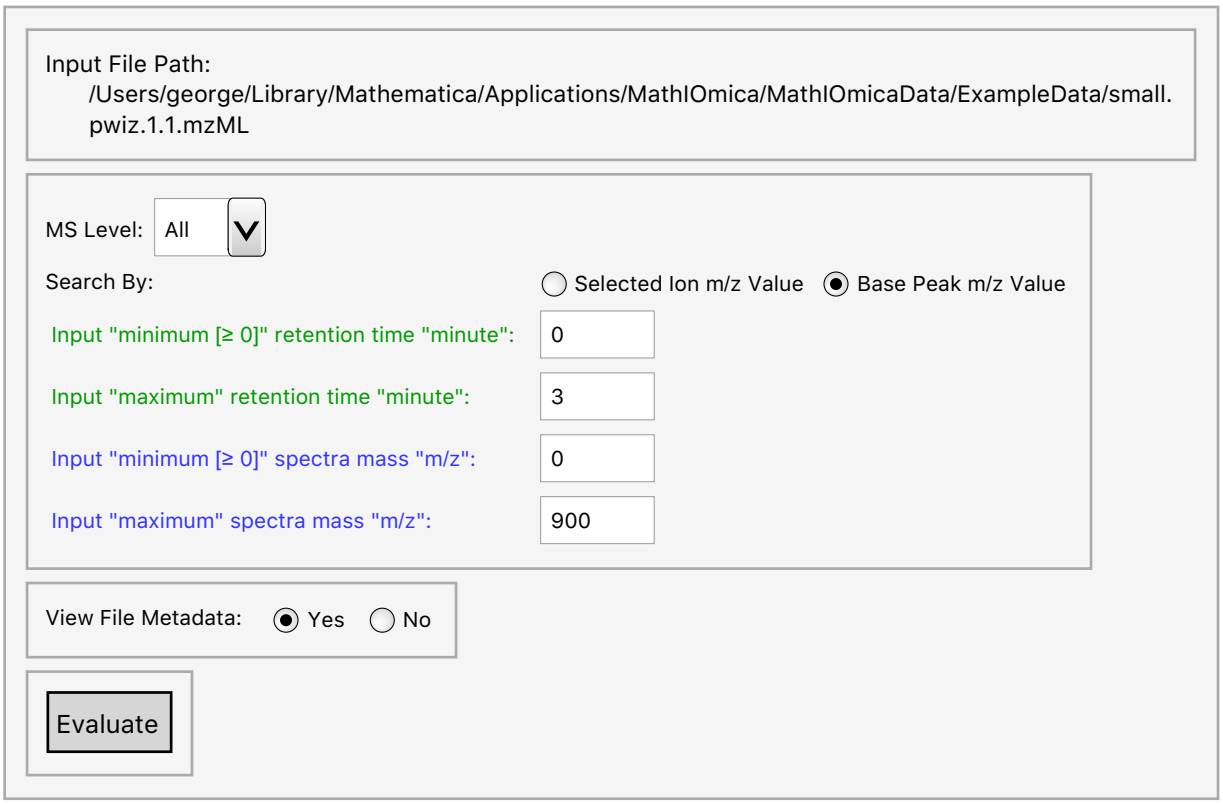
In[5]:=



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In[6]:=

MathIOmica MSViewer

G. Mias Lab

MetaData:

mzML Schema:

mzML: 1.1

File Content:

Name: MSn spectrum Value: Unknown

Instrument Software List:

ID: Xcalibur	ID: pwiz
Version: 1.1 Beta 7	Version: 1.4.0
Name: Xcalibur	Name: ProteoWizard
Value: Unknown	Value: Unknown

Instrument Scans:

ID: small_raw

Default Instrument Configuration: IC1

Number of Spectra: 48

Default Data Processing:
pwiz_Reader_Thermo_conversion

Data Processing:

Name: Conversion to mzML Value: Unknown

Instrument Configuration:

Ionization Source:

Name: electrospray ionization Value: Unknown
Name: electrospray inlet Value: Unknown
Name: electrospray ionization Value: Unknown
Name: electrospray inlet Value: Unknown

Detector:

Name: inductive detector Value: Unknown
Name: electron multiplier Value: Unknown

Mass Analyzer:

Name: fourier transform ion cyclotron resonance mass spectrometer Value: Unknown

Name: radial ejection linear ion trap Value: Unknown

Please select: {Base Peak m/z Value, retention time, MS Level } :

{578.97607421875`, 0.11721500000000001`,

Find precursor spectrum for MS Level > 1: ◉ No ○ Yes
Peaks Labeling: ◉ No ○ Yes

View Chromatogram: ◉ No ○ Yes

Evaluate

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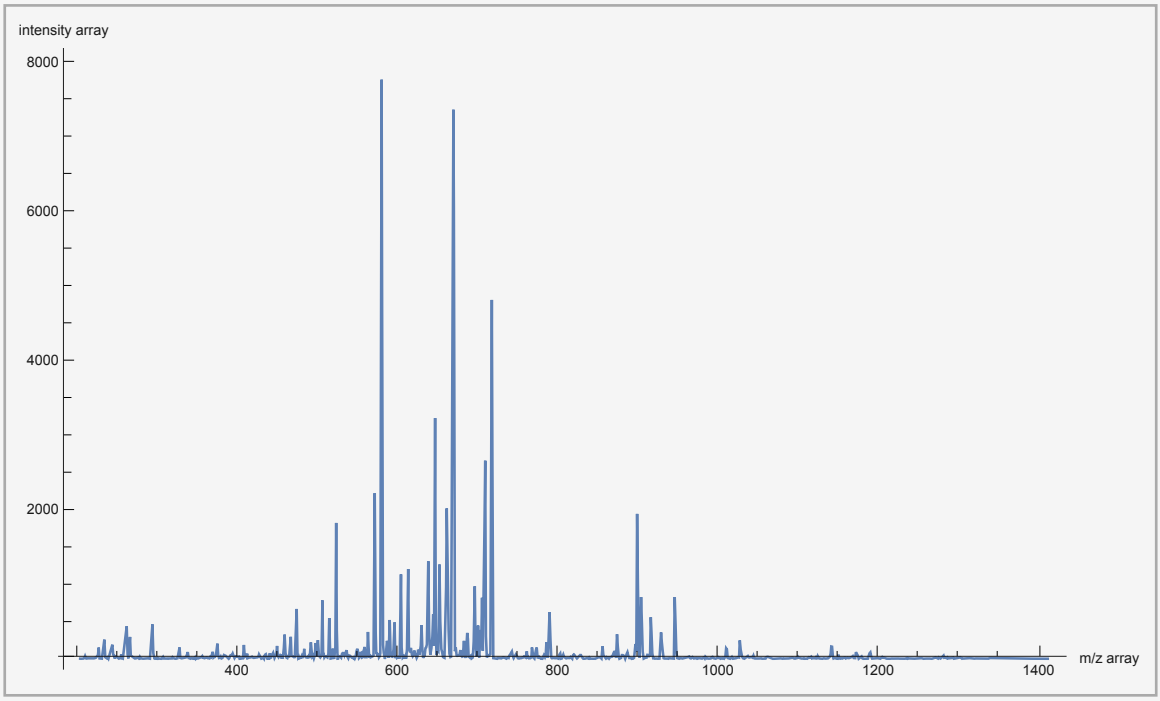
Out[6]=

base peak m/z value	ms level value	scan start time value	selected ion m/z value	spectrum representation	ionization mode
578.97607421875	2	0.11721500000000001	725.23000000000002	centroid spectrum	positive scan



VocabularyVariable (1)

In[1]:=
```
Needs["MathIOmica`"]
```

VocabularyVariable provides a vocabulary variable to use for mass spectrometry vocabularies in lieu of using the PSImsOBOFile option. The content should have the form of an OBO file imported as lines: Import[filename,"Lines"].

We consider an .mzML example file:

In[2]:=
```
exampleMzml = FileNameJoin[{ConstantMathIOmicaExamplesDirectory, "small.pwiz.1.1.mzML"}]
```

Let us suppose we are directly importing an OBO file. For this example we import the actual file at the ConstantMathIOmicaDataDirectory location as lines:

In[3]:=
```
exampleVocabularyVariable =
 Import[FileNameJoin[{ConstantMathIOmicaDataDirectory, "psi-ms.obo.txt"}], "Lines"]
```

Out[3]=
```
{format-version: 1.2, data-version: 4.0.1, date: 15:07:2016 14:16,
 ··· 17 649 ···, name: protein group-level result list statistic,
 def: "Attrbiute of an entire list of protein groups." [PSI:PI],
 is_a: MS:1002405 ! protein group-level result list attribute}
```

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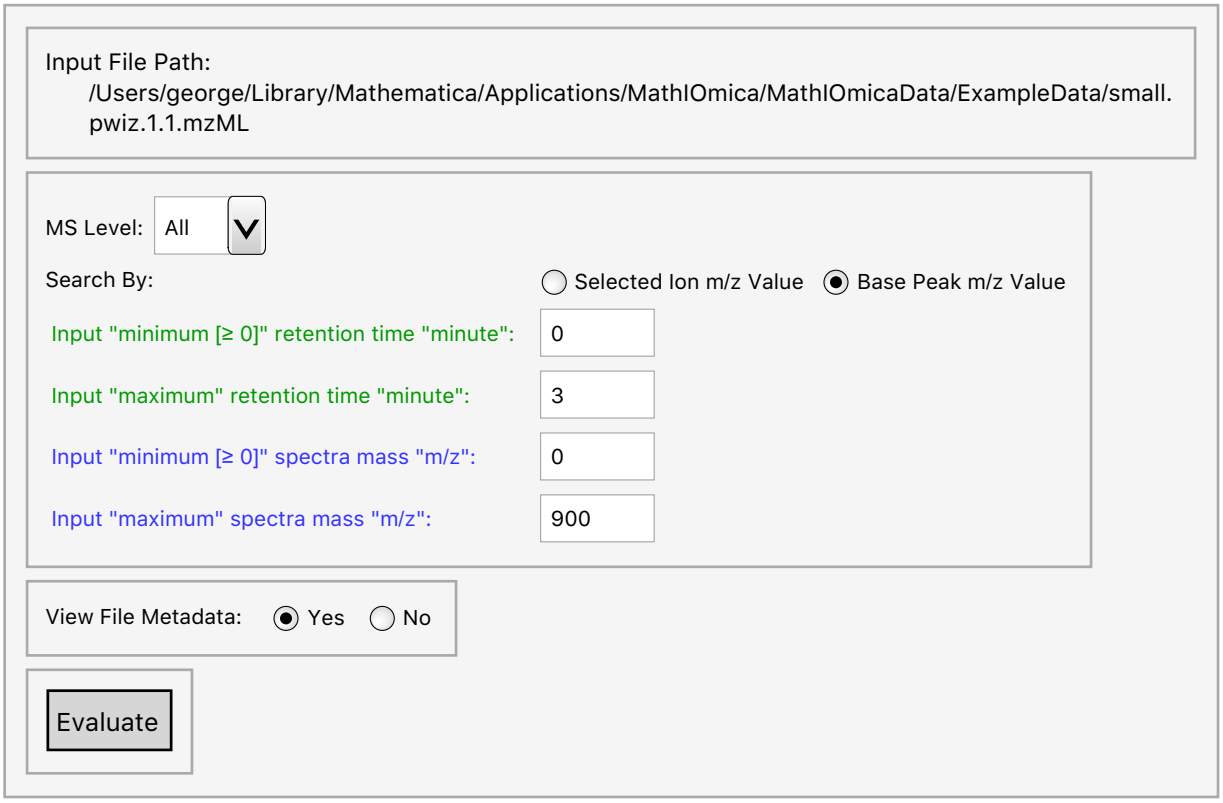
We can set the VocabularyVariable explicitly:

In[4]:=
```
MSViewer[exampleMzml, VocabularyVariable → exampleVocabularyVariable]
```

In[5]:=



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In[6]:=

MathIOmica MSViewer

G. Mias Lab

MetaData:

mzML Schema:

mzML: 1.1

File Content:

Name: MSn spectrum Value: Unknown

Instrument Software List:

ID: Xcalibur	ID: pwiz
Version: 1.1 Beta 7	Version: 1.4.0
Name: Xcalibur	Name: ProteoWizard
Value: Unknown	Value: Unknown

Instrument Scans:

ID: small_raw
Default Instrument Configuration: IC1
Number of Spectra: 48
Default Data Processing:
pwiz_Reader_Thermo_conversion

Data Processing:

Name: Conversion to mzML Value: Unknown

Instrument Configuration:

Ionization Source:

Name: electrospray ionization Value: Unknown
Name: electrospray inlet Value: Unknown
Name: electrospray ionization Value: Unknown
Name: electrospray inlet Value: Unknown

Detector:

Name: inductive detector Value: Unknown
Name: electron multiplier Value: Unknown

Mass Analyzer:

Name: fourier transform ion cyclotron resonance mass spectrometer Value: Unknown
Name: radial ejection linear ion trap Value: Unknown

Please select: {Base Peak m/z Value, retention time, MS Level } :

{578.97607421875`, 0.11721500000000001`,

Find precursor spectrum for MS Level > 1: ◉ No ○ Yes
Peaks Labeling: ◉ No ○ Yes

View Chromatogram: ◉ No ○ Yes

Evaluate

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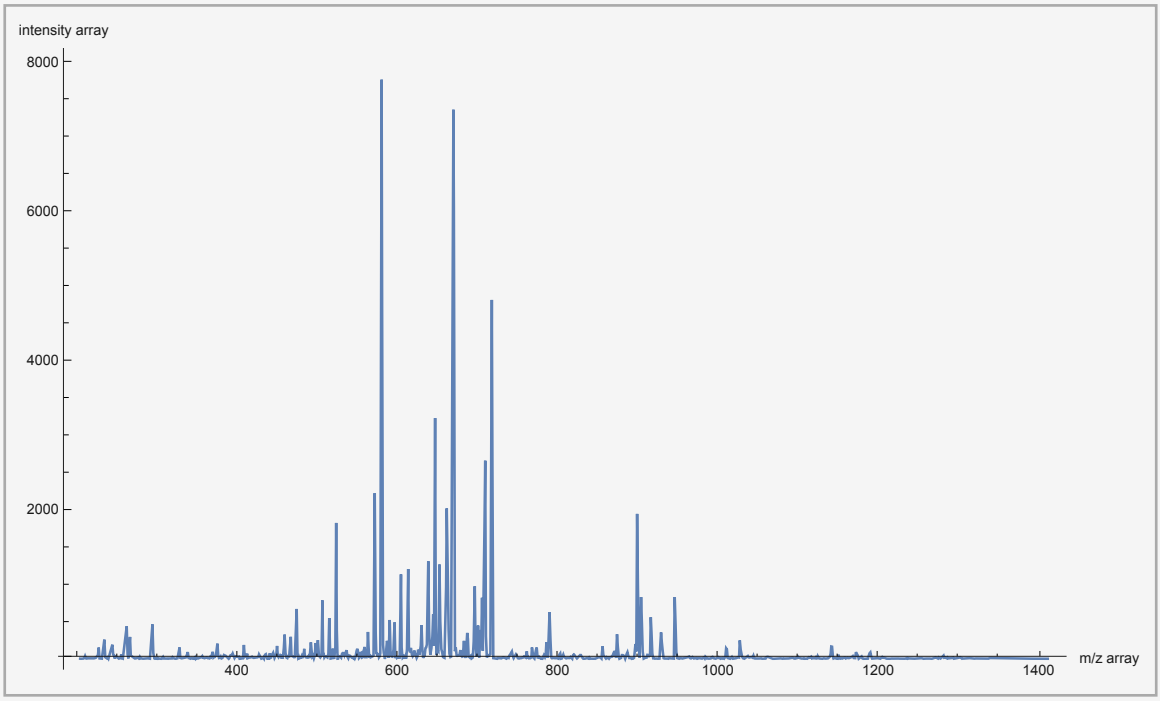
Out[6]=

base peak m/z value	ms level value	scan start time value	selected ion m/z value	spectrum representation	ionization mode
578.97607421875	2	0.11721500000000001	725.23000000000002	centroid spectrum	positive scan



See Also

OBOGODictionary

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

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Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾

URL ▾

MassDictionary

```
MassDictionary[]
```
loads MathIOmica's current mass dictionary.

Details

- `MassDictionary[]` loads MathIOmica's current mass dictionary from the MathIOmica data directory. In general, we may have N molecular species, with the jth molecular species having m_j identifiers labeled ID_{jk}, each associated to a mass (by default monoisotopic) $mass_{jk}$, then the dictionary has the following format:

- $$\begin{aligned}&\text{massDictionary} = <|\text{MolecularSpecies}_1 \to <|\ ID_{11} \to mass_{11},\\ &\quad ID_{12} \to mass_{12},\ \ldots,\ ID_{1k} \to mass_{1k},\ \ldots,\ ID_{1m_1} \to mass_{1m_1}\ |>,\\ &\ \text{MolecularSpecies}_2 \to <|\ ID_{21} \to mass_{21},\\ &\quad ID_{22} \to mass_{22},\ \ldots,\ ID_{2k} \to mass_{2k},\ \ldots,\ ID_{1m_2} \to mass_{2m_2}\ |>,\\ &\ \ldots,\\ &\ \text{MolecularSpecies}_j \to <|\ ID_{j1} \to mass_{j1},\\ &\quad ID_{j2} \to mass_{j2},\ \ldots,\ ID_{jk} \to mass_{jk},\ \ldots,\ ID_{jm_j} \to mass_{jm_j}\ |>,\\ &\ \ldots,\\ &\ \text{MolecularSpecies}_N \to <|\ ID_{11} \to mass_{N1},\\ &\quad ID_{N2} \to mass_{N2},\ \ldots,\ ID_{Nk} \to mass_{Nk},\ \ldots,\ ID_{Nm_N} \to mass_{Nm_N}\ |>\\ &\ |>\end{aligned}$$

- The current MathIOmica mass dictionary has mass annotations for KEGG compound IDs (i.e. MolecularSpecies="cpd").

- The following options can be given:

MathIOmicaDataDirectory	`If[!DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]`	MathIOmicaDataDirectory option specifies the directory where the default MathIOmica package data are stored. By default the option is set to create the standard directory if it does not exist already.

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Examples (2)

Basic Examples (1)

First we need to load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

In[2]:=
```
MassDictionary[]
```

Out[2]=
```
<| cpd → <| cpd:C00001 → 18.0106, cpd:C00002 → 506.996,
   cpd:C00003 → 664.117, cpd:C00004 → 665.125, cpd:C00005 → 745.091, ··· 15 235 ···,
   cpd:C21168 → 182.022, cpd:C21169 → 437.231, cpd:C21173 → 2360.34, cpd:C21174 → 1967.98 |> |>
```

large output | show less | show more | show all | set size limit...

Options (1)

MathIOmicaDataDirectory (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value points to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

In[2]:=
```
MassDictionary[MathIOmicaDataDirectory → FileNameJoin[
   Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]
```

Out[2]=
```
<| cpd → <| cpd:C00001 → 18.0106, cpd:C00002 → 506.996, cpd:C00003 → 664.117, cpd:C00004 → 665.125,
   ··· 15 236 ···, cpd:C21168 → 182.022, cpd:C21169 → 437.231, cpd:C21173 → 2360.34, cpd:C21174 → 1967.98 |> |>
```

large output | show less | show more | show all | set size limit...

See Also

GeneTranslation ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGDictionary** ▪ **KEGGPathwayVisual** ▪ **MassMatcher** ▪ **OBOGODictionary** ▪ **OmicsObjectUniqueMassConverter** ▪ **TimeSeriesClusters** ▪ **UCSCBrowserSQL**

Tutorials

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- MathIOmica Tutorial
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- MathIOmica Guide

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- MathIOmicaOverview

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MassMatcher

`MassMatcher[data, accuracy]`
assigns putative mass identification to input data based on monoisotopic mass (using MathIOmica's mass dictionary), using the accuracy in parts per million.

Details

- MassMatcher[data, accuracy] assigns a putative mass identification to input data based on monoisotopic mass in grams (using MathIOmica's mass dictionary), using the accuracy in parts per million (10^{-6}). It returns a list of matched accessions for the input mass.
- The following options can be given:

MassDictionaryVariable	None	MassDictionaryVariable can provide a mass dictionary variable. If set to None, MathIOmica's inbuilt mass dictionary (MassDictionary) will be loaded and used. For i species, each having m_i possible annotations (kinds of IDs) for n_i entities each (e.g. corresponding to n_i genes) the format for the variable is schematically: $<\|\text{Species}_1 \to <\|$ Kind of $\text{ID}_{11} \to$ {accessions list_{11} of length n_1}, Kind of $\text{ID}_{12} \to$ {accessions list_{12} of length n_1}, ..., Kind of $\text{ID}_{1\,m_1} \to$ {accessions $\text{list}_{1\,m_1}$ of length n_1}$\|>$, $\text{Species}_2 \to <\|$Kind of $\text{ID}_{21} \to$ {accessions list_{21} of length n_2}, Kind of $\text{ID}_{22} \to$ {accessions list_{22} of length n_2}, ...,

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		Kind of $ID_{2\,m_2}$ → {accessions $list_{2\,m_2}$ of length n_2} |>, ..., $Species_i$ → <| Kind of ID_{i1} → {accessions $list_{i2}$ of length n_i}, Kind of ID_{i2} → {accessions $list_{12}$ of length n_i}, ..., Kind of ID_{im_i} → {accessions $list_{12}$ of length n_i} |> |>
MolecularSpecies	"cpd"	MolecularSpecies specifies the kind of molecular input. The default is using KEGG compounds, returning KEGG "cpd" identifiers using MathIOmica's mass dictionary.

Examples (3)

Basic Examples (1)

First we need to load the MathIOmica package:

```
In[1]:= Needs["MathIOmica`"]
```

Let us match mass 18.010565 grams using accuracy 2 x10^{-6}:

```
In[2]:= massMatch1 = MassMatcher[18.010565, 2]
Out[2]= {cpd:C00001}
```

If we had a different (in this case more inaccurate mass), we also need to change the accuracy to get any matches:

```
In[3]:= massMatch2 = MassMatcher[54.1, 10 000]
Out[3]= {cpd:C05985, cpd:C16450}
```

We can actually obtain an annotation using KEGGDictionary

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In[4]:=
```
dictionaryCpd = KEGGDictionary[KEGGQuery1 → "cpd", KEGGQuery2 → ""]
```

Out[4]=
```
<|cpd:C00001 → H2O; Water, cpd:C00002 → ATP; Adenosine 5'-triphosphate, cpd:C00003 →
  NAD+; NAD; Nicotinamide adenine dinucleotide; DPN; Diphosphopyridine nucleotide; Nadide; beta-NAD+,
  ··· 17 740 ···, cpd:C21270 → Gentamicin C2a, cpd:C21273 → Benfluralin|>
```

large output | show less | show more | show all | set size limit...

We can directly query our results in both cases:

In[5]:=
```
Query[massMatch1]@dictionaryCpd
```

Out[5]=
```
<|cpd:C00001 → H2O; Water|>
```

In[6]:=
```
Query[massMatch2]@dictionaryCpd
```

Out[6]=
```
<|cpd:C05985 → 2-Propynal; 2-Propyn-1-al; Propiolaldehyde, cpd:C16450 → 1,3-Butadiene|>
```

Options (2)

MassDictionaryVariable (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MassDictionaryVariable can provide a mass dictionary variable. If set to None, MathIOmica's inbuilt mass dictionary (MassDictionary) will be loaded and used. We consider the following dictionary (note that the key for the MolecularSpecies is still the default "cpd" for compound):

In[2]:=
```
dictionaryNamedCpd = <|"cpd" → <|"2-Oxohept-3-enedioate; 2-Oxohept-3-ene-1,7-dioate" → 172.037173`,
      "2-Succinylbenzoate; o-Succinylbenzoate; Succinylbenzoate" → 222.052823`,
      "3'-O-(4-Benzoyl)benzoyl ATP; BzATP" → 715.048175`,
      "(4S,6S)-cis-Carveol" → 152.120115`, "5-Fluorodeoxyuridine monophosphate" → 326.03153`,
      "6beta-Hydroxy-D-homo-17a-oxaandrost-4-ene-3,17-dione" → 318.183109`,
      "7-Hydroxy-2-acetamidofluorene; N-(7-Hydroxy-9H-fluoren-2-yl)acetamide" → 239.094629`,
      "Aerophobin 2" → 502.980378`, "Arg-vasopressin; Argipressin; 8-L-Arginine vasopressin; AVP; ADH" →
       1083.437855`, "Atractyloside C" → 400.246103`, "Bentazone-sodium" → 262.038808`,
      "Chlorodibromomethane; Dibromochloromethane" → 205.813352`, "Conocurvone" → 952.382263`,
      "Cromakalim" → 286.131742`, "Halomon; 6-Bromo-3-(bromomethyl)-7-methyl-2,3,7-trichloro-1-octene" →
       397.860608`, "Integerrimine" → 335.173273`, "Nornitrogen mustard" → 141.011205`,
      "Orchinol; 9,10-Dihydro-5,7-dimethoxyphenanthren-2-ol" → 256.109944`, "Oxygen; O2" → 31.989829`,
      "Precorrin 2; Dihydrosirohydrochlorin" → 864.306531`, "Propanoylagmatine; Propionylagmatine" →
       186.148061`, "Sarisan" → 192.078644`, "Sempervirine" → 272.131349`,
      "UDP-2-acetamido-2-deoxy-alpha-D-ribo-hex-3-uluronate; UDP-3-keto-GlcNAcA" → 619.045184`,
      "Uncarine B; Formosamine" → 368.173607`|>|>;
```

Let us search for mass 31.9898grams with accuracy 3×10^{-6}:

In[3]:=
```
MassMatcher[31.9898, 3, MassDictionaryVariable → dictionaryNamedCpd]
```

Out[3]=
```
{Oxygen; O2}
```

MolecularSpecies (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MolecularSpecies specifies the kind of molecular input. The default is using KEGG

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compounds, returning KEGG "cpd" identifiers using MathIOmica's mass dictionary. We consider the following limited mass dictionary in which the dictionary has the MolecularSpecies association as "NamedCompound":

```
In[2]:= dictionaryNamed = <|"NamedCompound" → <|"2-Oxohept-3-enedioate; 2-Oxohept-3-ene-1,7-dioate" → 172.037173`,
      "2-Succinylbenzoate; o-Succinylbenzoate; Succinylbenzoate" → 222.052823`,
      "3'-O-(4-Benzoyl)benzoyl ATP; BzATP" → 715.048175`,
      "(4S,6S)-cis-Carveol" → 152.120115`, "5-Fluorodeoxyuridine monophosphate" → 326.03153`,
      "6beta-Hydroxy-D-homo-17a-oxaandrost-4-ene-3,17-dione" → 318.183109`,
      "7-Hydroxy-2-acetamidofluorene; N-(7-Hydroxy-9H-fluoren-2-yl)acetamide" → 239.094629`,
      "Aerophobin 2" → 502.980378`, "Arg-vasopressin; Argipressin; 8-L-Arginine vasopressin; AVP; ADH" →
       1083.437855`, "Atractyloside C" → 400.246103`, "Bentazone-sodium" → 262.038808`,
      "Chlorodibromomethane; Dibromochloromethane" → 205.813352`, "Conocurvone" → 952.382263`,
      "Cromakalim" → 286.131742`, "Halomon; 6-Bromo-3-(bromomethyl)-7-methyl-2,3,7-trichloro-1-octene" →
       397.860608`, "Integerrimine" → 335.173273`, "Nornitrogen mustard" → 141.011205`,
      "Orchinol; 9,10-Dihydro-5,7-dimethoxyphenanthren-2-ol" → 256.109944`, "Oxygen; O2" → 31.989829`,
      "Precorrin 2; Dihydrosirohydrochlorin" → 864.306531`, "Propanoylagmatine; Propionylagmatine" →
       186.148061`, "Sarisan" → 192.078644`, "Sempervirine" → 272.131349`,
      "UDP-2-acetamido-2-deoxy-alpha-D-ribo-hex-3-uluronate; UDP-3-keto-GlcNAcA" → 619.045184`,
      "Uncarine B; Formosamine" → 368.173607`|>|>;
```

Let us search for mass 502.98 with accuracy 2×10^{-6}:

```
In[3]:= MassMatcher[502.98, 2, MassDictionaryVariable → dictionaryNamed, MolecularSpecies → "NamedCompound"]
Out[3]= {Aerophobin 2}
```

See Also

GeneTranslation ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGDictionary** ▪ **KEGGPathwayVisual** ▪ **MassDictionary** ▪ **OmicsObjectUniqueMassConverter** ▪ **OBOGODictionary** ▪ **TimeSeriesClusters**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

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Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾ URL ▾

MatrixClusters

`MatrixClusters[data]`
performs hierarchical clustering in both dimensions of the provided data matrix.

Details

- MatrixClusters[data] takes as input series data matrices (i.e. a list of lists) and performs clustering of the data in both the horizontal and vertical directions to identify groups based on similarities between the input series rows and columns. The form of the input data is either a list of list, or an association of classes and members, where each member label corresponds to a row naming, and its values correspond to row data of the matrix. In this case the data has the form:

- $$\begin{aligned}\texttt{data} = \\ &\langle|\ \texttt{Class}_1 \to \langle|\texttt{Member}_{11} \to \{\texttt{data vector}_{11}\},\ \texttt{Member}_{12} \to \{\texttt{data vector}_{12}\},\ \ldots,\ \texttt{Member}_{1\,m_1} \to \{\texttt{data vector}_{1\,n_1}\}|\rangle, \\ &\ \texttt{Class}_2 \to \langle|\texttt{Member}_{21} \to \{\texttt{data vector}_{21}\},\ \texttt{Member}_{22} \to \{\texttt{data vector}_{22}\},\ \ldots,\ \texttt{Member}_{2\,n_2} \to \{\texttt{data vector}_{2\,n_2}\}|\rangle,\ \ldots, \\ &\ \texttt{Class}_M \to \langle|\texttt{Member}_{M1} \to \{\texttt{data vector}_{M1}\},\ \texttt{Member}_{M2} \to \{\texttt{data vector}_{M2}\},\ \ldots,\ \texttt{Member}_{Mn_1} \to \{\texttt{data vector}_{Mn_M}\}|\rangle|\rangle\end{aligned}$$

- Each class M is comprised of matrix data with n rows of data. All vectors for each class have to be the same size, i.e. if for a class M and a vector j, $L_{Mj} = \texttt{Length}[\{\texttt{data vector}_{Mj}\}]$, $L_{M1} == L_{M2} == \ldots == L_{Mj} == L_{Mn_M} \equiv L_M$, and hence the corresponding matrix has dimensions $n_M \times L_M$.

- We note that in the cases where only one class of data is being considered, the input can also be provided as a list of associations, or a single association, or a list of associations, or a single list of lists.

- A two-dimensional hierarchical clustering of the data is performed in each dimension (separately in horizontal and vertical directions), using the data rows and columns for the corresponding horizontal and vertical clustering respectively.

- The number of groups in each dimension are automatically determined by using internally the "Silhouette" (default) or "Gap" as "SignificanceTest" methods (see also Partitioning Data into Clusters).

- The result is grouping of the data based on similarity, and in each class it denoted as H:G#, or V:G#, where H and V refer to horizontal and vertical dimensions respectively, and G# denotes the group index based on the clustering For example H:G2 denotes the 2ndg group of horizontal clusters.

- The output is always an association of associations, providing a summary of the two dimensional clustering results for each class provided in the input. The output has the form:

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```
output =
 <| Class1 → <|"RowCluster" → cluster object1,
    "ColumnCluster" → cluster object1,
    "RowSplitClusters" → {RowSplitCluster11, RowSplitCluster12 ...},
    "ColumnSplitClusters" → {ColumnSplitCluster11, ColumnSplitCluster12 ...},
    "GroupAssociationsRows" → <|"H:G1" → {member list for horizontal group 1 labeled "H:G1"},
      "H:G2" → {member list for horizontal G2}, ...,
      "H:Gn1" → {member list for horizontal Gn1}|>,
    "GroupAssociationsColumns" → <|"V:G1" → {member list for vertical group 1 labeled "V:G1"},
      "V:G2" → {member list for vertical G2}, ...,
      "V:Gm1" → {member list for vertical Gm1}|>|>,
  Class2 → <|"RowCluster" → cluster object2,
    "ColumnCluster" → cluster object2,
    "RowSplitClusters" → {RowSplitCluster21, RowSplitCluster22 ...},
    "ColumnSplitClusters" → {ColumnSplitCluster21, ColumnSplitCluster22 ...},
    "GroupAssociationsRows" → <|"H:G1" → {member list for horizontal G1},
      "H:G2" → {member list for horizontal G2}, ...,
      "H:Gn2" → {member list for horizontal Gn2}|>,
    "GroupAssociationsColumns" → <|"V:G1" → {member list for vertical G1},
      "V:G2" → {member list for vertical G2}, ...,
      "V:Gm2" → {member list for vertical Gm2}|>|>,
  ...,
  Class2 → <|"RowCluster" → cluster object2,
    "ColumnCluster" → cluster object2,
    "RowSplitClusters" → {RowSplitCluster21, RowSplitCluster22 ...},
    "ColumnSplitClusters" → {ColumnSplitCluster21, ColumnSplitCluster22 ...},
    "GroupAssociationsRows" → <|"H:G1" → {member list for horizontal G1},
      "H:G2" → {member list for horizontal G2}, ...,
      "H:Gn2" → {member list for horizontal Gn2}|>,
    "GroupAssociationsColumns" → <|"V:G1" → {member list for vertical G1},
      "V:G2" → {member list for vertical G2}, ...,
      "V:Gm2" → {member list for vertical Gm2}|>|>
 |>
```

- The keys of the output correspond to the following properties related to the two dimensional clustering results:

"RowCluster"	Cluster generated for similarity between the rows.
"ColumnCluster"	Cluster generated for similarity between the columns.
"RowSplitClusters"	Clusters resulting from splitting the initial row cluster (reported by key "RowCluster") into groups using the SignificanceCriterion to determine the number of clusters.
"ColumnSplitClusters"	Clusters resulting from splitting the initial column cluster (reported by key "RowCluster") into groups using the SignificanceCriterion to determine the number of clusters.
"GroupAssociationsRows"	Association denoting membership of each initial row data label to groups generated by the clustering.
"GroupAssociationsColumns"	Association denoting membership of each column data original position index (or label if provided) to groups generated by the clustering.

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- The following options can be given:

ClusterLabeling	""	Additional label to append to each cluster being computed to prepend to the inbuilt H:G♯ or V:G♯ labeling.
ColumnLabels	{}	Labels for the columns of the input data matrix.
DataTransforms	{Identity, Identity}	Transformations to be applied to the input matrix data for clustering, in the form {transformation for horizontal, transformation for vertical}.
DendrogramPlotOptions	{{}, {}}	Options passed to the DendrogramPlot function used internally to generate the dendrograms, provided in the form {option list for horizontal clustering dendrograms,option list for vertical clustering dendrograms}.
DistanceFunction	EuclideanDistance	Distance function(s) to be used in calculating the similarities between different series in each dimension of clustering. Can be provided as a single function (same for both horizontal and vertical clusters) or a list {distance function horizontal clustering, distance function for vertical clustering}.
LinkageMeasure	"Average"	Which linkage measure(s) to use in computing fusion coefficients. Can be provided as a single value (same for both horizontal and vertical clusters) or a list {linkage for horizontal clustering, linkage function for vertical clustering}.
MissingSubstitution	Missing[] → 0	Substitution rule for Missing (or other pattern) of data.
PrintDendrograms	False	Option to print dendrograms for the clustering computed.
ReturnDendrograms	False	Option to return the dendrograms as output.
SignificanceCriterion	"Silhouette"	Method used in determining the number of groups in each dimension of clustering. Can be provided as a single value (same for both horizontal and vertical clusters) or a list {singificance criterion method for horizontal clustering,singificance criterion method for vertical clustering}.

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SimilarityVectors	{}	Similarity vectors to be used for clustering. It is provided as a list {list/association of similarity vectors for horizontal clustering, list/association of similarity vectors for vertical clustering}. The choice of list/association for the form of the similarity vectors is based on the input data, i.e. the form has to match the form of the input data. If the vector is {} then the input data is used as the similarity vectors (default).
SingleAssociationLabel	"1"	Label to use in case a list is provided to name the class of data produced.

- For a given set of series, Mathematica provides various measures of distance similarity, DistanceAndSimilarityMeasures. Three of the most common measures are the the EuclideanDistance, CorrelationDistance, and the CosineDistance.
- EuclideanDistance (default for both dimensions in MatrixClusters), uses the Euclidean distance between two arbitrary vectors U and V as $d_{euc}(U, V) = (\sum_i (U_i - V_i)^2)^{1/2}$, i.e. the Pythagorean distance between two vectors.
- CorrelationDistance measures the correlation distance between two arbitrary vectors U and V, as $d_{corr}(U, V) = 1 - \frac{(U - \langle U \rangle) \cdot (V - \langle V \rangle)}{\| U - \langle U \rangle \| \| V - \langle V \rangle \|}$ where * here denotes a dot product, <> denotes an average, and || || denotes a norm.
- The CosineDistance between two arbitrary vectors U and V is $d_{cos}(U, V) = 1 - \frac{U \cdot V}{\| U \| \| V \|}$. It is equal to the correlation distance in the case that the averages of U and V are zero.
- For two clusters A and B, the average linkage fusion coefficient between the two clusters is defined to be $L(A,B) = \frac{1}{|A|} \frac{1}{|B|} \sum_{a_i \in A} \sum_{b_j \in B} d(a_i, b_j)$, and thus a larger fusion coefficient means the two clusters are more well-separated. So, when deciding how to optimally cluster a given set of variables into two subsets, one chooses the partition such that the average linkage fusion coefficient is maximized, and this is the optimal partitioning of this group of data into two separate clusters.
- If using serial data (e.g. from time series) it is best to maintain the order of the data, and use TimeSeriesClusters or TimeSeriesSingleClusters instead of `MatrixClusters`.

Examples (13)

Basic Examples (1)

First we need to load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

We consider the following example, with three classes of data:

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```
In[2]:= dataClusterExample =
  <| "Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <| "Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <| "Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
```

We can obtain a data clustering for each class:

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In[3]:=
```
exampleClustering = MatrixClusters[dataClusterExample]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[3]=
```
<|Class1 → <|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>, Class2 → <|RowCluster →
   Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + Sqrt[2]), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
     Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
   {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + Sqrt[2]), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|>,
 Class3 → <|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
     2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
      Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
  RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
     {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
     Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
    {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
     6, 2.75455, 4, 1], 4}, GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|>|>
```

Let's take a look at the keys for the classification:

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In[4]:=
```
Query[All, Keys]@exampleClustering
```

Out[4]=
```
<|Class1 → {RowCluster, ColumnCluster, RowSplitClusters,
   ColumnSplitClusters, GroupAssociationsRows, GroupAssociationsColumns},
 Class2 → {RowCluster, ColumnCluster, RowSplitClusters, ColumnSplitClusters, GroupAssociationsRows,
   GroupAssociationsColumns}, Class3 → {RowCluster, ColumnCluster, RowSplitClusters,
   ColumnSplitClusters, GroupAssociationsRows, GroupAssociationsColumns}|>
```

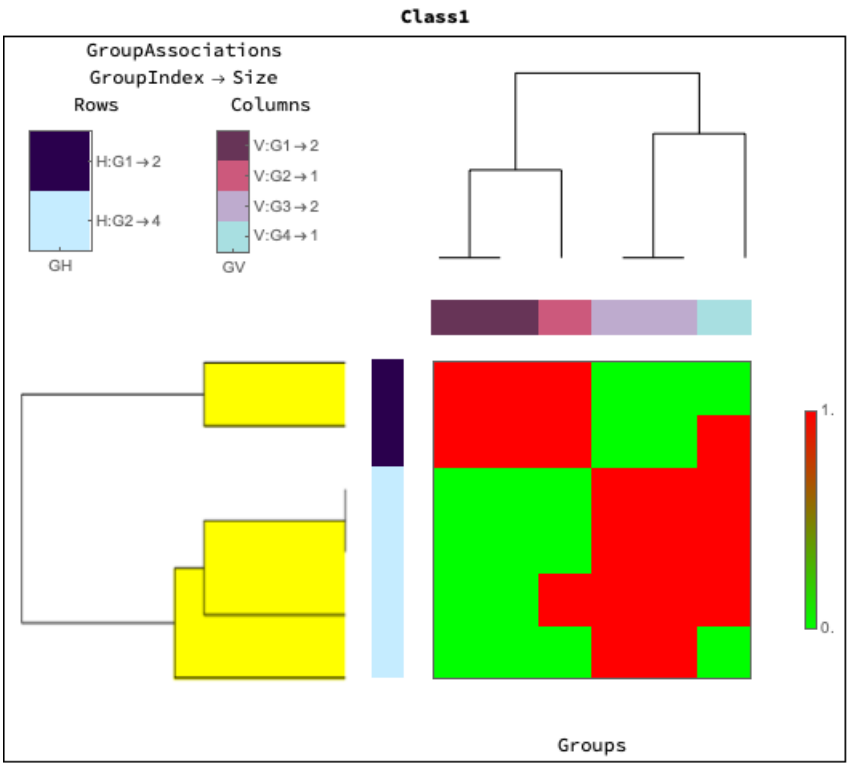
We can obtain the membership for each classification, for example in Class 1:

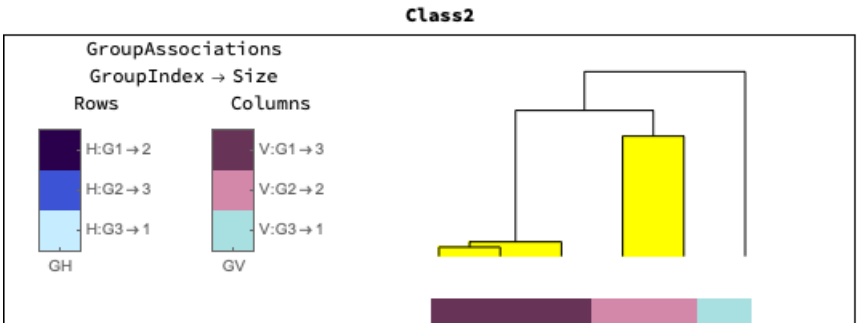
In[5]:=
```
Query["Class1",{"GroupAssociationsRows","GroupAssociationsColumns"}]@exampleClustering
```

Out[5]=
```
<|GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
 GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>
```

We can also generate heatmaps and dendrograms for all the classes using MatrixDendrogramsHeatmaps:

In[6]:=
```
MatrixDendrogramsHeatmaps[exampleClustering]
```





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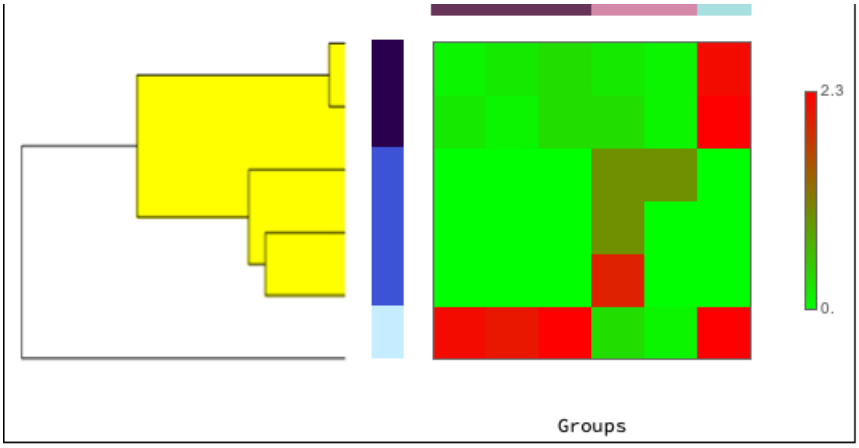
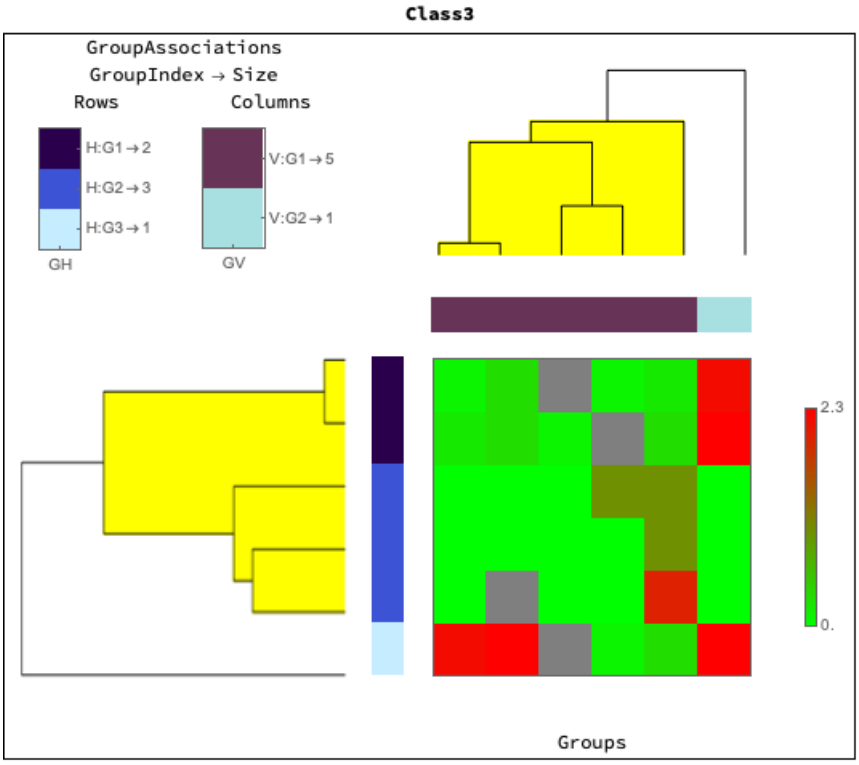
Out[6]=





The MatrixClusters function can also work with data from classes presented as a list of associations. Using the example above:

In[7]:=
```
Values@dataClusterExample
```

Out[7]=
```
{<|A → {1, 1, 1, 0, 0, 0}, B → {1, 1, 1, 1, 0, 0}, C → {0, 0, 0, 1, 1, 1},
  D → {0, 0, 1, 1, 1, 1}, E → {0, 0, 0, 0, 1, 1}, F → {0, 0, 0, 1, 1, 1}|>,
 <|a → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, b → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3}, c → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3},
  d → {0, 0, 0, 0, 0, 1}, e → {0, 0, 0, 0, 0, 2}, f → {0, 0, 0, 0, 1, 1}|>,
 <|a → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, b → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
  c → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, d → {0, 0, 0, 0, 0, 1},
  e → {0, 0, Missing[], 0, 0, 2}, f → {0, 0, 0, 0, 1, 1}|>}
```

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In[8]:=
```
MatrixClusters[Values@dataClusterExample]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[8]=
```
<|1 → <|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>, 2 → <|RowCluster →
   Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + Sqrt[2]), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
     Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
   {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + Sqrt[2]), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|>,
 3 → <|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
     2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
      Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
  RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
     {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
     Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
    {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
     6, 2.75455, 4, 1], 4}, GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|>|>
```

The MatrixClusters function can also work with data from a single class presented as an association. Using the example above :

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In[9]:=
```
dataClusterExample["Class1"]
```

Out[9]=
```
<|A → {1, 1, 1, 0, 0, 0}, B → {1, 1, 1, 1, 0, 0}, C → {0, 0, 0, 1, 1, 1},
 D → {0, 0, 1, 1, 1, 1}, E → {0, 0, 0, 0, 1, 1}, F → {0, 0, 0, 1, 1, 1}|>
```

In[10]:=
```
MatrixClusters[dataClusterExample["Class1"]]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

Out[10]=
```
<|1 → <|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>|>
```

In addition the MatrixClusters function can also work with data from a single matrix (list of lists). Using again the example above :

In[11]:=
```
Values[dataClusterExample["Class1"]]
```

Out[11]=
```
{{1, 1, 1, 0, 0, 0}, {1, 1, 1, 1, 0, 0}, {0, 0, 0, 1, 1, 1},
 {0, 0, 1, 1, 1, 1}, {0, 0, 0, 0, 1, 1}, {0, 0, 0, 1, 1, 1}}
```

In[12]:=
```
MatrixClusters[Values[dataClusterExample["Class1"]]]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Out[12]=
```
<|1 → <|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → 1, {1, 1, 1, 1, 0, 0} → 2, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → 6, {0, 0, 0, 1, 1, 1} → 3, 0, 1, 1], {0, 0, 1, 1, 1, 1} → 4, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → 5, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → 1, {1, 1, 1, 1, 0, 0} → 2, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → 6, {0, 0, 0, 1, 1, 1} → 3, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → 4, 1, 2, 1], {0, 0, 0, 0, 1, 1} → 5, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {1, 2}, H:G2 → {6, 3, 4, 5}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>|>
```

Options (12)

ClusterLabeling (1)

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```
In[1]:= Needs["MathIOmica`"]
```

ClusterLabeling provides a way to add a prepend text to all the cluster groups named.

```
In[2]:= dataClusterExample =
  <|"Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <|"Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <|"Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
```

The default text is "" and so nothing is appended to the class names:

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In[3]:=
```
exampleClustering = MatrixClusters[dataClusterExample]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[3]=
```
<|Class1 → <|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>, Class2 → <|RowCluster →
   Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + Sqrt[2]), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
     Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
   {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + Sqrt[2]), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|>,
 Class3 → <|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
     2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
      Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
  RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
     {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
     Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
    {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
     6, 2.75455, 4, 1], 4}, GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|>|>
```

In[4]:=
```
Query["Class1", {"GroupAssociationsRows", "GroupAssociationsColumns"}]@exampleClustering
```

Out[4]=
```
<|GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
 GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>
```

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Let's now append text, "AppendedText_" to each group label:

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In[5]:=
```
exampleClusteringLabels = MatrixClusters[dataClusterExample, ClusterLabeling → "AppendedText_"]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[5]=
```
⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + √2), 3, 1], 1/2 (1/2 (√5 + √6) + 1/2 (1/2 (2 + √5) + 1/2 (√5 + √6))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, √2, 2, 1], 1/2 (1/2 (2 + √3) + 1/2 (√5 + √6)), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + √2), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|AppendedText_H:G1 → {A, B}, AppendedText_H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|AppendedText_V:G1 → {1, 2}, AppendedText_V:G2 → {3},
    AppendedText_V:G3 → {6, 5}, AppendedText_V:G4 → {4}|>|⟩, Class2 → ⟨|RowCluster →
   Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + √2), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
      Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
   {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + √2), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
  GroupAssociationsRows → <|AppendedText_H:G1 → {a, b}, AppendedText_H:G2 → {f, d, e},
    AppendedText_H:G3 → {c}|>, GroupAssociationsColumns →
   <|AppendedText_V:G1 → {1, 2, 3}, AppendedText_V:G2 → {6, 5}, AppendedText_V:G3 → {4}|>|⟩,
 Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
     2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
      Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
  RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
     {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
     Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
    {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
     6, 2.75455, 4, 1], 4}, GroupAssociationsRows →
   <|AppendedText_H:G1 → {a, b}, AppendedText_H:G2 → {f, d, e}, AppendedText_H:G3 → {c}|>,
  GroupAssociationsColumns → <|AppendedText_V:G1 → {1, 3, 2, 5, 6}, AppendedText_V:G2 → {4}|>|⟩|⟩
```

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In[6]:=
```
Query["Class1", {"GroupAssociationsRows", "GroupAssociationsColumns"}]@exampleClusteringLabels
```

Out[6]=
```
<|GroupAssociationsRows → <|AppendedText_H:G1 → {A, B}, AppendedText_H:G2 → {F, C, D, E}|>,
 GroupAssociationsColumns →
  <|AppendedText_V:G1 → {1, 2}, AppendedText_V:G2 → {3}, AppendedText_V:G3 → {6, 5}, AppendedText_V:G4 → {4}|>|>
```

ColumnLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ColumnLabels allows us to provide labels for the columns of the input data matrix. The default setting uses the position index for each column as a label to refer to the columns (e.g. when reporting group membership in "GroupAssociationsColumns":

In[2]:=
```
dataClusterExample =
  <|"Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <|"Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <|"Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
exampleClustering = MatrixClusters[dataClusterExample]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

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```
Out[2]= ⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
      Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
      {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
    ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
      Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
    RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
    ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
    GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|⟩, Class2 → ⟨|RowCluster →
     Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
       Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
        1/2 (1 + Sqrt[2]), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
       Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
     {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + Sqrt[2]), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
     {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
    GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|⟩,
   Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
       Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
      2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
     {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
     {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
       6, 2.75455, 4, 1], 4}, GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

```
In[3]:= Query[All, {"GroupAssociationsColumns"}]@exampleClustering
```

```
Out[3]= <|Class1 → <|GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>,
  Class2 → <|GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|>,
  Class3 → <|GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|>|>
```

We can provide labels for each class (note that if provided the labels must be given for all classes):

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In[4]:=
```
exampleClusteringColumnLabels = MatrixClusters[dataClusterExample, ColumnLabels →
   {{"I", "II", "III", "IV", "V", "VI"}, {"Column1", "Column2", "Column3", "Column4", "Column5", "Column6"},
    {"Column1", "Column2", "Column3", "Column4", "Column5", "Column6"}}]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[4]=
```
⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
      Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
      {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + √2), 3, 1], 1/2 (1/2 (√5 + √6) + 1/2 (1/2 (2 + √5) + 1/2 (√5 + √6))), 2, 4],
    ColumnCluster → Cluster[Cluster[Cluster[I, II, 0, 1, 1], III, 1, 2, 1],
      Cluster[Cluster[VI, V, 0, 1, 1], IV, √2, 2, 1], 1/2 (1/2 (2 + √3) + 1/2 (√5 + √6)), 3, 3],
    RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + √2), 3, 1]},
    ColumnSplitClusters → {Cluster[I, II, 0, 1, 1], III, Cluster[VI, V, 0, 1, 1], IV},
    GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
    GroupAssociationsColumns → <|V:G1 → {I, II}, V:G2 → {III}, V:G3 → {VI, V}, V:G4 → {IV}|>|⟩,
  Class2 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2], 2.60285, 2, 3],
      {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1], ColumnCluster →
     Cluster[Cluster[Cluster[Cluster[Column1, Column2, 0.173205, 1, 1], Column3, 0.272474, 2, 1],
       Cluster[Column6, Column5, 2.2561, 1, 1], 2.73873, 3, 2], Column4, 3.4654, 5, 1], RowSplitClusters →
     {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + √2), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c},
    ColumnSplitClusters → {Cluster[Cluster[Column1, Column2, 0.173205, 1, 1], Column3, 0.272474, 2, 1],
      Cluster[Column6, Column5, 2.2561, 1, 1], Column4},
    GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>, GroupAssociationsColumns →
     <|V:G1 → {Column1, Column2, Column3}, V:G2 → {Column6, Column5}, V:G3 → {Column4}|>|⟩,
  Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
      2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[Column1, Column3, 0.244949, 1, 1], Cluster[
       Column2, Column5, 1.01489, 1, 1], 2.32763, 2, 2], Column6, 2.75455, 4, 1], Column4, 3.81399, 5, 1],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + √2), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
    ColumnSplitClusters → {Cluster[Cluster[Cluster[Column1, Column3, 0.244949, 1, 1],
       Cluster[Column2, Column5, 1.01489, 1, 1], 2.32763, 2, 2], Column6, 2.75455, 4, 1], Column4},
    GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
    GroupAssociationsColumns → <|V:G1 → {Column1, Column3, Column2, Column5, Column6}, V:G2 → {Column4}|>|⟩|⟩
```

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In[5]:=
```
Query[All, {"GroupAssociationsColumns"}]@exampleClusteringColumnLabels
```

Out[5]=
```
<|Class1 → <|GroupAssociationsColumns → <|V:G1 → {I, II}, V:G2 → {III}, V:G3 → {VI, V}, V:G4 → {IV}|>|>,
 Class2 → <|GroupAssociationsColumns →
    <|V:G1 → {Column1, Column2, Column3}, V:G2 → {Column6, Column5}, V:G3 → {Column4}|>|>, Class3 →
  <|GroupAssociationsColumns → <|V:G1 → {Column1, Column3, Column2, Column5, Column6}, V:G2 → {Column4}|>|>|>
```

DataTransforms (1)

In[1]:=
```
Needs["MathIOmica`"]
```

Data transforms provides transformation functions that may be applied to either the vertical or horizontal direction to transform the similarity vectors (by default the input data) used in classifying the data. The default is `DataTransforms → {Identity, Identity}`, i.e. no transform is applied

In[2]:=
```
dataClusterExample1 =
  <|"Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>|>;
exampleClustering1 = MatrixClusters[dataClusterExample1]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Out[2]=
```
⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
      Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
      {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
    ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
      Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
    RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
    ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
    GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|⟩|⟩
```

For example let's transform the data by standardizing in the horizontal direction, and taking the norm in the vertical direction:

In[3]:=
```
exampleClusteringTransformed =
 MatrixClusters[dataClusterExample1, DataTransforms → {Standardize, Normalize}]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Out[3]=
```
⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A,
      {1, 1, 1, 1, 0, 0} → B, Sqrt[3 (Sqrt[5/6] - Sqrt[5/3]/2)^2 + (Sqrt[5/6] + Sqrt[5/3]/2)^2 + 2 (-Sqrt[5/6] + Sqrt[5/3])^2], 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
```

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$$\{0, 0, 1, 1, 1, 1\} \to D, \sqrt{3\left(\sqrt{\frac{5}{6}} - \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + \left(\sqrt{\frac{5}{6}} + \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 2\left(-\sqrt{\frac{5}{6}} + \sqrt{\frac{5}{3}}\right)^2}, 2, 1\Big],$$

$$\{0, 0, 0, 0, 1, 1\} \to E, \frac{1}{2}\left(\sqrt{5} + \sqrt{3\left(\sqrt{\frac{5}{6}} - \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + \left(\sqrt{\frac{5}{6}} + \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 2\left(-\sqrt{\frac{5}{6}} + \sqrt{\frac{5}{3}}\right)^2}\right), 3, 1\Big],$$

$$\frac{1}{2}\left(\frac{1}{2}\left(2\sqrt{5} + \sqrt{\left(\sqrt{\frac{5}{6}} - \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 3\left(\sqrt{\frac{5}{6}} + \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 2\left(\sqrt{\frac{5}{6}} + \sqrt{\frac{5}{3}}\right)^2} + \right.\right.$$

$$\frac{1}{2}\left(\frac{1}{2}\left(2\sqrt{5} + \sqrt{\left(\sqrt{\frac{5}{6}} - \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 3\left(\sqrt{\frac{5}{6}} + \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 2\left(\sqrt{\frac{5}{6}} + \sqrt{\frac{5}{3}}\right)^2} + \right.\right.$$

$$\left.\left.\left.\frac{1}{2}\left(\sqrt{15} + \sqrt{\left(\sqrt{\frac{5}{6}} - \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 3\left(\sqrt{\frac{5}{6}} + \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 2\left(\sqrt{\frac{5}{6}} + \sqrt{\frac{5}{3}}\right)^2}\right)\right)\right), 2, 4\Big],$$

$$\text{ColumnCluster} \to \text{Cluster}\Big[\text{Cluster}\Big[\text{Cluster}[1, 2, 0, 1, 1], 3, \sqrt{\frac{1}{3} + 2\left(\frac{1}{\sqrt{2}} - \frac{1}{\sqrt{3}}\right)^2}, 2, 1\Big],$$

$$\text{Cluster}\Big[\text{Cluster}[6, 5, 0, 1, 1], 4, \frac{1}{\sqrt{2}}, 2, 1\Big],$$

$$\frac{1}{2}\left(\frac{1}{2}\left(\sqrt{2} + \sqrt{\frac{17}{12} + \left(-\frac{1}{2} + \frac{1}{\sqrt{3}}\right)^2}\right) + \frac{1}{2}\left(\sqrt{\frac{5}{4} + \left(-\frac{1}{2} + \frac{1}{\sqrt{2}}\right)^2} + \sqrt{\frac{5}{6} + 2\left(-\frac{1}{2} + \frac{1}{\sqrt{3}}\right)^2}\right)\right), 3, 3\Big],$$

$$\text{RowSplitClusters} \to \Big\{\text{Cluster}\Big[\{1, 1, 1, 0, 0, 0\} \to A, \{1, 1, 1, 1, 0, 0\} \to B,$$

$$\sqrt{3\left(\sqrt{\frac{5}{6}} - \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + \left(\sqrt{\frac{5}{6}} + \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 2\left(-\sqrt{\frac{5}{6}} + \sqrt{\frac{5}{3}}\right)^2}, 1, 1\Big],$$

$$\text{Cluster}\Big[\text{Cluster}\Big[\text{Cluster}[\{0, 0, 0, 1, 1, 1\} \to F, \{0, 0, 0, 1, 1, 1\} \to C, 0, 1, 1],$$

$$\{0, 0, 1, 1, 1, 1\} \to D, \sqrt{3\left(\sqrt{\frac{5}{6}} - \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + \left(\sqrt{\frac{5}{6}} + \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 2\left(-\sqrt{\frac{5}{6}} + \sqrt{\frac{5}{3}}\right)^2}, 2, 1\Big],$$

$$\{0, 0, 0, 0, 1, 1\} \to E, \frac{1}{2}\left(\sqrt{5} + \sqrt{3\left(\sqrt{\frac{5}{6}} - \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + \left(\sqrt{\frac{5}{6}} + \frac{\sqrt{\frac{5}{3}}}{2}\right)^2 + 2\left(-\sqrt{\frac{5}{6}} + \sqrt{\frac{5}{3}}\right)^2}\right), 3, 1\Big]\Big\},$$

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```
ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|> |> |>
```

DendrogramPlotOptions (1)

```
In[1]:= Needs["MathIOmica`"]
```

DendrogramPlotOptions provides options for an internal DendrogramPlot in the case where either the PrintDendrograms or ReturnDendrograms option values are set to True. The options are provided as two lists {{options for horizontal cluster dendrograms},{options for vertical cluster dendrograms}}, and the default is {{},{}}.

```
In[2]:= dataClusterExample =
  <| "Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <| "Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <| "Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
```

For example, we can plot horizontal cluster dendrograms as blue and oriented from the left, and vertical cluster dendrograms as red:

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In[3]:=
```
exampleClustering = MatrixClusters[dataClusterExample, ReturnDendrograms → True,
  DendrogramPlotOptions → {{PlotStyle → Blue, Orientation → Left}, {PlotStyle → Red}}]
```

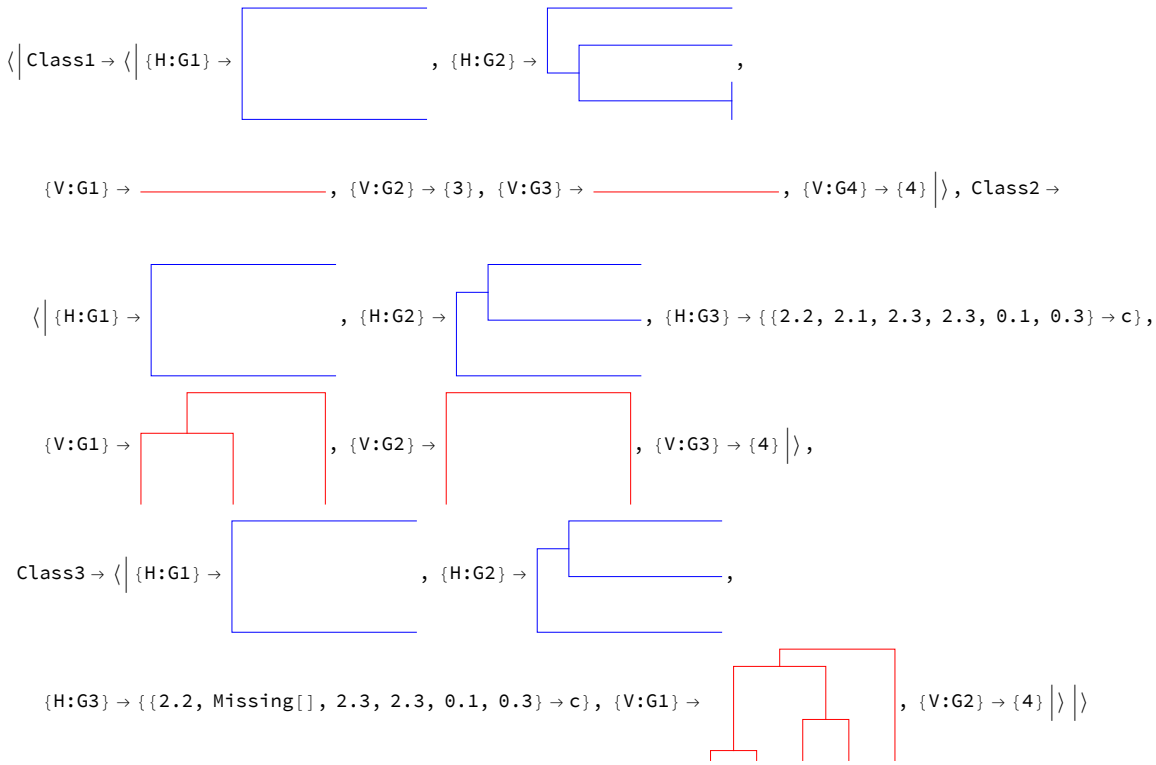
Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[3]=



DistanceFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

DistanceFunction values select the distance function(s) to be used in calculating the similarities between different series in each dimension of clustering. It can be provided as a single function (same for both horizontal and vertical clusters) or a list {distance function horizontal clustering, distance function for vertical clustering}.

In[2]:=
```
dataClusterExample =
  <| "Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <| "Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <| "Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
```

The default value for DistanceFunction is EuclideanDistance, which is implemented in both directions:

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In[3]:=
```
exampleClustering = MatrixClusters[dataClusterExample, DistanceFunction → EuclideanDistance]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[3]=
```
⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + √2), 3, 1], 1/2 (1/2 (√5 + √6) + 1/2 (1/2 (2 + √5) + 1/2 (√5 + √6))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, √2, 2, 1], 1/2 (1/2 (2 + √3) + 1/2 (√5 + √6)), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + √2), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|⟩, Class2 → ⟨|RowCluster →
   Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + √2), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
     Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
   {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + √2), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|⟩,
 Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
     2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
      Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
  RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
     {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
     Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
    {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
     6, 2.75455, 4, 1], 4}, GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

We can provide separate values for each direction,

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In[4]:=
```
exampleClusteringDistances =
 MatrixClusters[dataClusterExample, DistanceFunction → {CorrelationDistance, EuclideanDistance}]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

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```
Out[4]= ⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1 - 1/√2, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1/2 (2 - √2), 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1/2 + 1/2 (2 - √2)), 3, 1],
      1/2 (1/2 (3 + 1/√2) + 1/2 (1/2 (5/2 + 1/√2) + 1/2 (3 + 1/√2)))), 2, 4],
    ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
      Cluster[Cluster[6, 5, 0, 1, 1], 4, √2, 2, 1], 1/2 (1/2 (2 + √3) + 1/2 (√5 + √6)), 3, 3],
    RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1 - 1/√2, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1/2 (2 - √2), 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1/2 + 1/2 (2 - √2)), 3, 1]},
    ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
    GroupAssociationsRows → ⟨|H:G1 → {A, B}, H:G2 → {F, C, D, E}|⟩,
    GroupAssociationsColumns → ⟨|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|⟩|⟩, Class2 →
   ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b,
        0.00386391, 1, 1], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 0.631295, 2, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
       Cluster[{0, 0, 0, 0, 0, 2} → e, {0, 0, 0, 0, 0, 1} → d, 0, 1, 1], 1/2 (2 - 2 √(2/5)), 1, 2], 1.51806, 3, 3],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
       Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
     {Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.00386391, 1, 1],
       {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 0.631295, 2, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
       Cluster[{0, 0, 0, 0, 0, 2} → e, {0, 0, 0, 0, 0, 1} → d, 0, 1, 1], 1/2 (2 - 2 √(2/5)), 1, 2]},
    ColumnSplitClusters → {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
      Cluster[6, 5, 2.2561, 1, 1], 4}, GroupAssociationsRows → ⟨|H:G1 → {a, b, c}, H:G2 → {f, e, d}|⟩,
    GroupAssociationsColumns → ⟨|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|⟩|⟩,
   Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.00426849, 1, 1], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c,
       0.48175, 2, 1], Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, Missing[], 0, 0, 2} → e,
       {0, 0, 0, 0, 0, 1} → d, 0, 1, 1], 1/2 (2 - 2 √(2/5)), 1, 2], 1.37649, 3, 3],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1],
       2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1], RowSplitClusters →
     {Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b,
       0.00426849, 1, 1], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 0.48175, 2, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, Missing[], 0, 0, 2} → e, {0, 0, 0, 0, 0, 1} → d, 0, 1, 1],
       1/2 (2 - 2 √(2/5)), 1, 2]}, ColumnSplitClusters →
     {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
       6, 2.75455, 4, 1], 4}, GroupAssociationsRows → ⟨|H:G1 → {a, b, c}, H:G2 → {f, e, d}|⟩,
    GroupAssociationsColumns → ⟨|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|⟩|⟩|⟩
```

LinkageMeasure (1)

```
In[1]:= Needs["MathIOmica`"]
```

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LinkageMeasure values select what Linkage to use in computing fusion coefficients. The value can be provided as a single value (same for both horizontal and vertical clusters) or a list {linkage for horizontal clustering, linkage function for vertical clustering}.

In[2]:=
```
dataClusterExample =
 <| "Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
    "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
  <| "Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
     "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
     "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
  <| "Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
     "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
     "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>
```

Out[2]=
```
<|Class1 → <|A → {1, 1, 1, 0, 0, 0}, B → {1, 1, 1, 1, 0, 0},
    C → {0, 0, 0, 1, 1, 1}, D → {0, 0, 1, 1, 1, 1}, E → {0, 0, 0, 0, 1, 1}, F → {0, 0, 0, 1, 1, 1}|>,
  Class2 → <|a → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, b → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
    c → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, d → {0, 0, 0, 0, 0, 1}, e → {0, 0, 0, 0, 0, 2}, f → {0, 0, 0, 0, 1, 1}|>,
  Class3 → <|a → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, b → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
    c → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, d → {0, 0, 0, 0, 0, 1},
    e → {0, 0, Missing[], 0, 0, 2}, f → {0, 0, 0, 0, 1, 1}|>|>
```

The default value for LinkageMeasure is "Average", which is implemented in both directions:

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In[3]:=
```
exampleClustering = MatrixClusters[dataClusterExample, LinkageMeasure → "Average"]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[3]=
```
⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|⟩, Class2 → ⟨|RowCluster →
   Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + Sqrt[2]), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
     Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
   {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + Sqrt[2]), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
  GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
  GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|⟩,
 Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
     2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
      Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
  RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
     {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
     Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
    {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
     6, 2.75455, 4, 1], 4}, GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
  GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

We can provide separate values for each direction,

In[4]:=
```
exampleClusteringLinkage = MatrixClusters[dataClusterExample, LinkageMeasure → {"Centroid", "Ward"}]
```

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Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

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```
Out[4]= ⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 4/9 + Sqrt[2]/3, 3, 1],
      -3/16 (4/9 + Sqrt[2]/3) + 1/4 (-1/4 + Sqrt[3/2] + Sqrt[5]/2) + 3/4 (-2/9 + 1/3 (3/4 + Sqrt[5]/2) + 2/3 (-1/4 + Sqrt[3/2] + Sqrt[5]/2)), 2, 4],
    ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 4/3, 2, 1],
      Cluster[Cluster[6, 5, 0, 1, 1], 4, 4 Sqrt[2]/3, 2, 1], 1/6 (4 - 4 Sqrt[2] + 2 Sqrt[3] + 4 Sqrt[5] + 8 Sqrt[6]), 3, 3],
    RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 4/9 + Sqrt[2]/3, 3, 1]},
    ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
    GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|⟩,
  Class2 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1], 1/4 + 1/Sqrt[2], 1, 2], 2.18612, 2, 3],
      {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 3.38915, 5, 1], ColumnCluster →
     Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.305564, 2, 1], 4, 4.23535, 3, 1],
      Cluster[6, 5, 2.2561, 1, 1], 5.07126, 4, 2], RowSplitClusters →
     {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
       1/4 + 1/Sqrt[2], 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
     {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.305564, 2, 1], 4, Cluster[6, 5, 2.2561, 1, 1]},
    GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {4}, V:G3 → {6, 5}|>|⟩,
  Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/4 + 1/Sqrt[2], 1, 2], 2.18176, 2, 3],
      {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 2.84532, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], 4, 3.73845, 2, 1],
      Cluster[Cluster[2, 5, 1.01489, 1, 1], 6, 2.82911, 2, 1], 5.29678, 3, 3],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/4 + 1/Sqrt[2], 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
    ColumnSplitClusters → {Cluster[1, 3, 0.244949, 1, 1], 4, Cluster[2, 5, 1.01489, 1, 1], 6},
    GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 3}, V:G2 → {4}, V:G3 → {2, 5}, V:G4 → {6}|>|⟩|⟩
```

MissingSubstitution (1)

```
In[1]:= Needs["MathIOmica`"]

In[2]:= Needs["MathIOmica`"]
```

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MissingSubstitution provides a substitution rule for Missing (or other pattern) of data.

```
In[3]:= dataClusterExampleMissing =
  <| "ExampleClass" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
     "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
     "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>;
```

The default value for MissingSubstitution is `Missing[] → 0`,

```
In[4]:= exampleClusteringMissingA =
  MatrixClusters[dataClusterExampleMissing, MissingSubstitution → (Missing[] → 0)]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

```
Out[4]= ⟨|ExampleClass → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
       2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + Sqrt[2]), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
    ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
    GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
    GroupAssociationsColumns → ⟨|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|⟩|⟩|⟩
```

We can replace for example with the value 1:

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In[5]:=
```
exampleClusteringMissingB =
 MatrixClusters[dataClusterExampleMissing, MissingSubstitution → (Missing[] → 1)]
```

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

Out[5]=
```
⟨|ExampleClass → ⟨|RowCluster → Cluster[
    Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b,
      1.28452, 1, 1], Cluster[Cluster[{0, 0, 0, 0, 1, 1} → f, {0, 0, 0, 0, 0, 1} → d, 1, 1, 1],
      {0, 0, Missing[], 0, 0, 2} → e, 1/2 (Sqrt[2] + Sqrt[3]), 2, 1], 2.84727, 2, 3],
    {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.53284, 5, 1], ColumnCluster →
   Cluster[Cluster[Cluster[Cluster[Cluster[1, 3, 1.02956, 1, 1], 2, 1.64888, 2, 1], 5, 2.21963, 3, 1],
     6, 2.56514, 4, 1], 4, 3.70718, 5, 1], RowSplitClusters →
   {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b,
     1.28452, 1, 1], Cluster[Cluster[{0, 0, 0, 0, 1, 1} → f, {0, 0, 0, 0, 0, 1} → d, 1, 1, 1],
     {0, 0, Missing[], 0, 0, 2} → e, 1/2 (Sqrt[2] + Sqrt[3]), 2, 1], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
   ColumnSplitClusters → {Cluster[Cluster[Cluster[Cluster[1, 3, 1.02956, 1, 1], 2, 1.64888, 2, 1],
      5, 2.21963, 3, 1], 6, 2.56514, 4, 1], 4},
   GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
   GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

PrintDendrograms (1)

In[1]:=
```
Needs["MathIOmica`"]
```

PrintDendrograms provides the option to print the associated dendrograms for the groupings (if the cluster contains more than 2 members). We consider the data:

In[2]:=
```
dataClusterExample =
  <| "Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <| "Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <| "Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
```

We now cluster the data and also print the dendrograms in the notebook :

In[3]:=
```
exampleClusteringDendrogramPrint = MatrixClusters[dataClusterExample, PrintDendrograms → True]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

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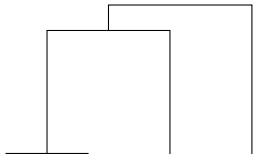
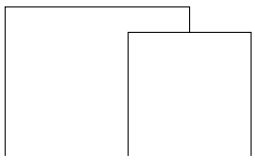
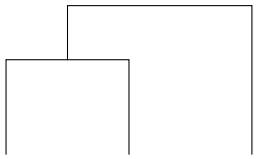
⟨|Class1 → ⟨|{H:G1} → ,

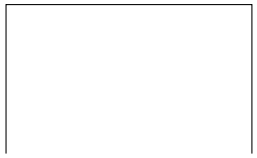
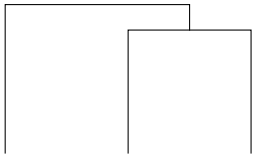
{H:G2} →  , {V:G1} → ,

{V:G2} → {3}, {V:G3} → , {V:G4} → {4} |⟩,

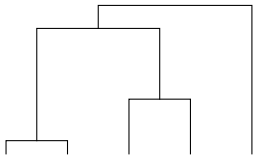
Class2 → ⟨|{H:G1} → , {H:G2} →  ,

{H:G3} → {{2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c},

{V:G1} →  , {V:G2} → , {V:G3} → {4} |⟩,

Class3 → ⟨|{H:G1} →  , {H:G2} →  ,

{H:G3} → {{2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},

{V:G1} →  , {V:G2} → {4} |⟩ |⟩

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```
Out[3]= ⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
      Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
      {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
    ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
      Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
    RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
    ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
    GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|⟩, Class2 → ⟨|RowCluster →
     Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
       Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
        1/2 (1 + Sqrt[2]), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
       Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
     {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + Sqrt[2]), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
     {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
    GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|⟩,
  Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
       Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
      2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
     {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
     {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
       6, 2.75455, 4, 1], 4}, GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

ReturnDendrograms (1)

```
In[1]:= Needs["MathIOmica`"]
```

ReturnDendrograms provides the option to return the dendrograms instead of the clustering information (if the cluster contains more than 2 members). We consider the data:

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```
In[2]:= dataClusterExample =
  <|"Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <|"Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <|"Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
```

We now cluster and return the dendrograms as output

SignificanceCriterion (1)

```
In[1]:= Needs["MathIOmica`"]
```

SignificanceCriterion provides an option for which method to use for determining the number of groups in each dimension of clustering. Can be provided as a single value (same for both horizontal and vertical clusters) or a list {singificance criterion method for horizontal clustering, singificance criterion method for vertical clustering}. We consider the data:

```
In[2]:= dataClusterExample =
  <|"Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <|"Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <|"Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>

Out[2]= <|Class1 → <|A → {1, 1, 1, 0, 0, 0}, B → {1, 1, 1, 1, 0, 0},
     C → {0, 0, 0, 1, 1, 1}, D → {0, 0, 1, 1, 1, 1}, E → {0, 0, 0, 0, 1, 1}, F → {0, 0, 0, 1, 1, 1}|>,
   Class2 → <|a → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, b → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
     c → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, d → {0, 0, 0, 0, 0, 1}, e → {0, 0, 0, 0, 0, 2}, f → {0, 0, 0, 0, 1, 1}|>,
   Class3 → <|a → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, b → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
     c → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, d → {0, 0, 0, 0, 0, 1},
     e → {0, 0, Missing[], 0, 0, 2}, f → {0, 0, 0, 0, 1, 1}|>|>
```

The default value for SignificanceCriterion is "Silhouette", which is implemented in both directions:

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In[3]:=
```
exampleSignificanceCriterion = MatrixClusters[dataClusterExample, SignificanceCriterion → "Silhouette"]
```

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[3]=
```
⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + √2), 3, 1], 1/2 (1/2 (√5 + √6) + 1/2 (1/2 (2 + √5) + 1/2 (√5 + √6))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, √2, 2, 1], 1/2 (1/2 (2 + √3) + 1/2 (√5 + √6)), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + √2), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|⟩, Class2 → ⟨|RowCluster →
   Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + √2), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
     Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
   {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + √2), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1], Cluster[6, 5, 2.2561, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|⟩,
 Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
     2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
      Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
  RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
     {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
     Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
    {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c}, ColumnSplitClusters →
   {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1], Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2],
     6, 2.75455, 4, 1], 4}, GroupAssociationsRows → <|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

We can provide separate values for each direction,

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In[4]:=
```
exampleClusteringLinkage = MatrixClusters[dataClusterExample, SignificanceCriterion → {"Silhouette", "Gap"}]
```

FindClusters: An internal error occured while evaluating FindClusters. Try different methods.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[4]=
```
⟨|Class1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1], Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2, 3}, V:G2 → {6, 5}, V:G3 → {4}|>|⟩, Class2 → ⟨|RowCluster →
   Cluster[Cluster[Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + Sqrt[2]), 1, 2], 2.60285, 2, 3], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c, 4.04224, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
     Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1], RowSplitClusters →
   {Cluster[{0.1, 0.2, 0.3, 2.2, 0.1, 0.2} → a, {0.2, 0.1, 0.3, 2.3, 0.1, 0.3} → b, 0.2, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, 0, 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + Sqrt[2]), 1, 2], {2.2, 2.1, 2.3, 2.3, 0.1, 0.3} → c},
  ColumnSplitClusters → {Cluster[Cluster[Cluster[Cluster[1, 2, 0.173205, 1, 1], 3, 0.272474, 2, 1],
      Cluster[6, 5, 2.2561, 1, 1], 2.73873, 3, 2], 4, 3.4654, 5, 1]},
  GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
  GroupAssociationsColumns → <|V:G1 → {1, 2, 3, 6, 5, 4}|>|⟩,
 Class3 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
      Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
     2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
  ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
      Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
  RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
     {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
    Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
     1/2 (1 + Sqrt[2]), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
  ColumnSplitClusters → {Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1]},
  GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
  GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6, 4}|>|⟩|⟩
```

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SimilarityVectors (1)

In[1]:=
```
Needs["MathIOmica`"]
```

SimilarityVectors provides a list of similarity vectors to be used for clustering purposes. It is provided as a list {list/association of similarity vectors for horizontal clustering, list/association of similarity vectors for vertical clustering}. The choice of list/association for the form of the similarity vectors is based on the input data, i.e. the form has to match the form of the input data.

We consider two classes that are the same in memberships:

In[2]:=
```
dataClusterA =
  <| "Class1a" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   "Class1b" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>|>;
```

As an example we provide exact similarity vectors for both horizontal and vertical clusters in case of a multiclass object:

In[3]:=
```
similarityVectorsA =
  {<|"Class1a" → <|"A" → {1, 1}, "B" → {1, 1}, "C" → {2, 2}, "D" → {2, 1}, "E" → {3, 1}, "F" → {1, 1}|>,
    "Class1b" → <|"A" → {1, 2}, "B" → {4, 4}, "C" → {1, 2}, "D" → {2, 1}, "E" → {3, 1}, "F" → {4, 5}|>|>, <|
    "Class1a" → <|1 → 1, 2 → 1, 3 → 3, 4 → 3, 5 → 3, 6 → 3|>,
    "Class1b" → <|1 → 1, 2 → 1, 3 → 2, 4 → 2, 5 → 3, 6 → 3|>|>};
```

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In[4]:=
```
exampleClusteringSimilarityVectors = MatrixClusters[dataClusterA, SimilarityVectors → similarityVectorsA]
```

Agglomerate: 4 ties have been detected; reordering input may produce a different result.

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

Agglomerate: 4 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

Out[4]=
```
⟨|Class1a → ⟨|RowCluster → Cluster[
    Cluster[{1, 1, 1, 0, 0, 0} → A, Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 0, 1, 1], 0, 1, 2],
    Cluster[{0, 0, 0, 0, 1, 1} → E, Cluster[{0, 0, 0, 1, 1, 1} → C, {0, 0, 1, 1, 1, 1} → D, 1, 1, 1],
     1/2 (1 + Sqrt[2]), 1, 2], 1/2 (2 + 1/2 (1 + Sqrt[2])), 3, 3], ColumnCluster → Cluster[Cluster[1, 2, 0, 1, 1],
    Cluster[6, Cluster[3, Cluster[4, 5, 0, 1, 1], 0, 1, 2], 0, 1, 3], 2, 2, 4], RowSplitClusters →
   {Cluster[{1, 1, 1, 0, 0, 0} → A, Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 0, 1, 1], 0, 1, 2],
    Cluster[{0, 0, 0, 0, 1, 1} → E, Cluster[{0, 0, 0, 1, 1, 1} → C, {0, 0, 1, 1, 1, 1} → D, 1, 1, 1],
     1/2 (1 + Sqrt[2]), 1, 2]}, ColumnSplitClusters →
   {Cluster[1, 2, 0, 1, 1], Cluster[6, Cluster[3, Cluster[4, 5, 0, 1, 1], 0, 1, 2], 0, 1, 3]},
  GroupAssociationsRows → <|H:G1 → {A, B, F}, H:G2 → {E, C, D}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {6, 3, 4, 5}|>|⟩,
 Class1b → ⟨|RowCluster → Cluster[Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
     Cluster[{0, 0, 1, 1, 1, 1} → D, {0, 0, 0, 0, 1, 1} → E, 1, 1, 1], 1/2 (Sqrt[2] + Sqrt[5]), 2, 2],
    Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 1, 1, 1],
    1/2 (1/2 (Sqrt[13] + 1/2 (Sqrt[10] + Sqrt[13])) + 1/2 (3 Sqrt[2] + 1/2 (2 Sqrt[5] + Sqrt[17]))), 4, 2], ColumnCluster →
   Cluster[Cluster[1, 2, 0, 1, 1], Cluster[Cluster[6, 5, 0, 1, 1], Cluster[3, 4, 0, 1, 1], 1, 2, 2], 3/2, 2, 4],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
    Cluster[{0, 0, 1, 1, 1, 1} → D, {0, 0, 0, 0, 1, 1} → E, 1, 1, 1],
    Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 1, 1, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], Cluster[6, 5, 0, 1, 1], Cluster[3, 4, 0, 1, 1]},
  GroupAssociationsRows → <|H:G1 → {A, C}, H:G2 → {D, E}, H:G3 → {B, F}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {6, 5}, V:G3 → {3, 4}|>|⟩|⟩
```

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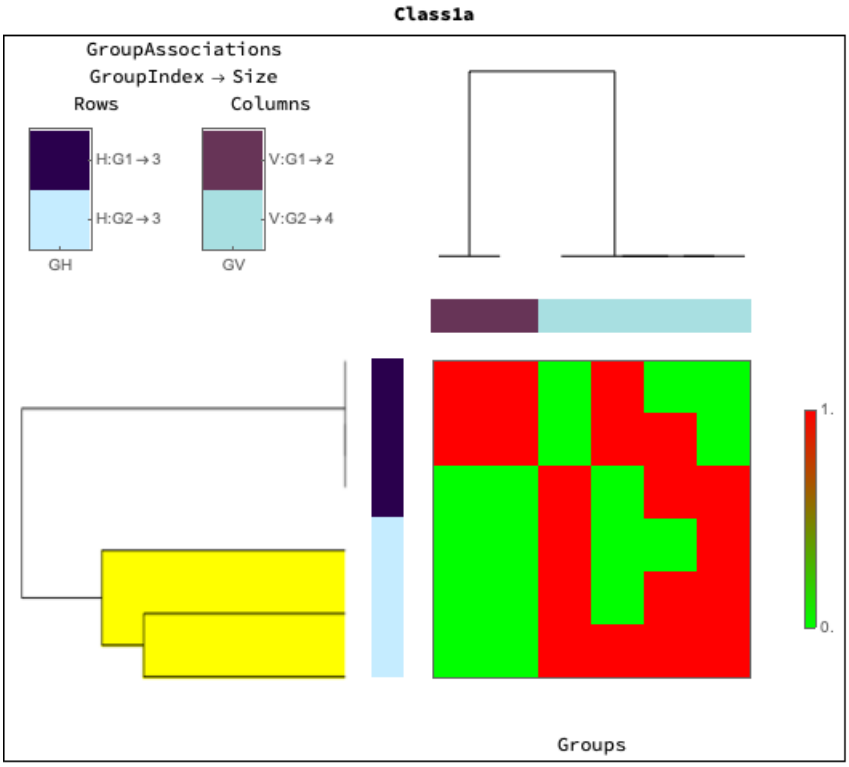
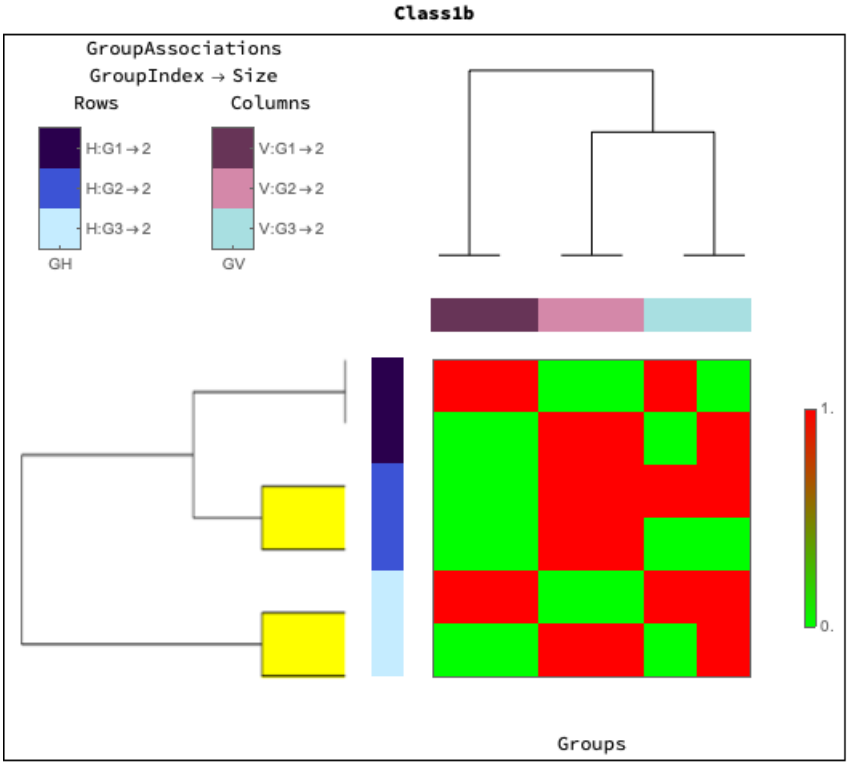
In[5]:=
```
MatrixDendrogramsHeatmaps[exampleClusteringSimilarityVectors]
```

Out[5]=





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The data could be presented as a list of associations:

```
In[6]:= Query[Values]@dataClusterA

Out[6]= {<|A → {1, 1, 1, 0, 0, 0}, B → {1, 1, 1, 1, 0, 0}, C → {0, 0, 0, 1, 1, 1}, D → {0, 0, 1, 1, 1, 1},
    E → {0, 0, 0, 0, 1, 1}, F → {0, 0, 0, 1, 1, 1}|>, <|A → {1, 1, 1, 0, 0, 0}, B → {1, 1, 1, 1, 0, 0},
    C → {0, 0, 0, 1, 1, 1}, D → {0, 0, 1, 1, 1, 1}, E → {0, 0, 0, 0, 1, 1}, F → {0, 0, 0, 1, 1, 1}|>}
```

The similarity vectors must be provided in the same format as the input data:

```
In[7]:= Query[Values]@similarityVectorsA

Out[7]= {{<|A → {1, 1}, B → {1, 1}, C → {2, 2}, D → {2, 1}, E → {3, 1}, F → {1, 1}|>,
    <|A → {1, 2}, B → {4, 4}, C → {1, 2}, D → {2, 1}, E → {3, 1}, F → {4, 5}|>},
   {<|1 → 1, 2 → 1, 3 → 3, 4 → 3, 5 → 3, 6 → 3|>, <|1 → 1, 2 → 1, 3 → 2, 4 → 2, 5 → 3, 6 → 3|>}}

In[8]:= exampleClusteringSimilarityVectorsListA =
  MatrixClusters[Query[Values]@dataClusterA, SimilarityVectors → Query[Values]@ similarityVectorsA]
```

Agglomerate: 4 ties have been detected; reordering input may produce a different result.

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

Agglomerate: 4 ties have been detected; reordering input may produce a different result.

General: Further output of Agglomerate::ties will be suppressed during this calculation.

```
Out[8]= ⟨|1 → ⟨|RowCluster → Cluster[
      Cluster[{1, 1, 1, 0, 0, 0} → A, Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 0, 1, 1], 0, 1, 2],
      Cluster[{0, 0, 0, 0, 1, 1} → E, Cluster[{0, 0, 0, 1, 1, 1} → C, {0, 0, 1, 1, 1, 1} → D, 1, 1, 1],
       1/2 (1 + Sqrt[2]), 1, 2], 1/2 (2 + 1/2 (1 + Sqrt[2])), 3, 3], ColumnCluster → Cluster[Cluster[1, 2, 0, 1, 1],
      Cluster[6, Cluster[3, Cluster[4, 5, 0, 1, 1], 0, 1, 2], 0, 1, 3], 2, 2, 4], RowSplitClusters →
     {Cluster[{1, 1, 1, 0, 0, 0} → A, Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 0, 1, 1], 0, 1, 2],
      Cluster[{0, 0, 0, 0, 1, 1} → E, Cluster[{0, 0, 0, 1, 1, 1} → C, {0, 0, 1, 1, 1, 1} → D, 1, 1, 1],
       1/2 (1 + Sqrt[2]), 1, 2]}, ColumnSplitClusters →
     {Cluster[1, 2, 0, 1, 1], Cluster[6, Cluster[3, Cluster[4, 5, 0, 1, 1], 0, 1, 2], 0, 1, 3]},
    GroupAssociationsRows → <|H:G1 → {A, B, F}, H:G2 → {E, C, D}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {6, 3, 4, 5}|>|⟩,
  2 → ⟨|RowCluster → Cluster[Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
       Cluster[{0, 0, 1, 1, 1, 1} → D, {0, 0, 0, 0, 1, 1} → E, 1, 1, 1], 1/2 (Sqrt[2] + Sqrt[5]), 2, 2],
      Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 1, 1, 1],
      1/2 (1/2 (Sqrt[13] + 1/2 (Sqrt[10] + Sqrt[13])) + 1/2 (3 Sqrt[2] + 1/2 (2 Sqrt[5] + Sqrt[17]))), 4, 2], ColumnCluster →
     Cluster[Cluster[1, 2, 0, 1, 1], Cluster[Cluster[6, 5, 0, 1, 1], Cluster[3, 4, 0, 1, 1], 1, 2, 2], 3/2, 2, 4],
    RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
      Cluster[{0, 0, 1, 1, 1, 1} → D, {0, 0, 0, 0, 1, 1} → E, 1, 1, 1],
      Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 1, 1, 1]},
    ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], Cluster[6, 5, 0, 1, 1], Cluster[3, 4, 0, 1, 1]},
    GroupAssociationsRows → <|H:G1 → {A, C}, H:G2 → {D, E}, H:G3 → {B, F}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {6, 5}, V:G3 → {3, 4}|>|⟩|⟩
```

The data could be presented as a single class presented as an association. Using the example above for "Class1a" only:

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```
In[9]:= dataClusterA["Class1a"]

Out[9]= <|A → {1, 1, 1, 0, 0, 0}, B → {1, 1, 1, 1, 0, 0}, C → {0, 0, 0, 1, 1, 1},
         D → {0, 0, 1, 1, 1, 1}, E → {0, 0, 0, 0, 1, 1}, F → {0, 0, 0, 1, 1, 1}|>
```

The similarity vectors are again provided in the same format as the input data:

```
In[10]:= Query[All, "Class1a"]@similarityVectorsA

Out[10]= {<|A → {1, 1}, B → {1, 1}, C → {2, 2}, D → {2, 1}, E → {3, 1}, F → {1, 1}|>, <|1 → 1, 2 → 1, 3 → 3, 4 → 3, 5 → 3, 6 → 3|>}

In[11]:= exampleClusteringSimilarityVectorsSingleA =
          MatrixClusters[dataClusterA["Class1a"], SimilarityVectors → Query[All, "Class1a"]@similarityVectorsA]
```

Agglomerate: 4 ties have been detected; reordering input may produce a different result.

Agglomerate: 4 ties have been detected; reordering input may produce a different result.

```
Out[11]= ⟨|1 → ⟨|RowCluster → Cluster[
            Cluster[{1, 1, 1, 0, 0, 0} → A, Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 0, 1, 1], 0, 1, 2],
            Cluster[{0, 0, 0, 0, 1, 1} → E, Cluster[{0, 0, 0, 1, 1, 1} → C, {0, 0, 1, 1, 1, 1} → D, 1, 1, 1],
             1/2 (1 + √2), 1, 2], 1/2 (2 + 1/2 (1 + √2)), 3, 3], ColumnCluster → Cluster[Cluster[1, 2, 0, 1, 1],
            Cluster[6, Cluster[3, Cluster[4, 5, 0, 1, 1], 0, 1, 2], 0, 1, 3], 2, 2, 4], RowSplitClusters →
           {Cluster[{1, 1, 1, 0, 0, 0} → A, Cluster[{1, 1, 1, 1, 0, 0} → B, {0, 0, 0, 1, 1, 1} → F, 0, 1, 1], 0, 1, 2],
            Cluster[{0, 0, 0, 0, 1, 1} → E, Cluster[{0, 0, 0, 1, 1, 1} → C, {0, 0, 1, 1, 1, 1} → D, 1, 1, 1],
             1/2 (1 + √2), 1, 2]}, ColumnSplitClusters →
           {Cluster[1, 2, 0, 1, 1], Cluster[6, Cluster[3, Cluster[4, 5, 0, 1, 1], 0, 1, 2], 0, 1, 3]},
          GroupAssociationsRows → <|H:G1 → {A, B, F}, H:G2 → {E, C, D}|>,
          GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {6, 3, 4, 5}|> |⟩ |⟩
```

In addition the MatrixClusters function can also work with data from a single matrix (list of lists). Using again the example above :

```
In[12]:= Values[dataClusterA["Class1a"]]

Out[12]= {{1, 1, 1, 0, 0, 0}, {1, 1, 1, 1, 0, 0}, {0, 0, 0, 1, 1, 1},
          {0, 0, 1, 1, 1, 1}, {0, 0, 0, 0, 1, 1}, {0, 0, 0, 1, 1, 1}}
```

The similarity vectors should again be provided in the same format as the input data:

```
In[13]:= Values@Query[All, "Class1a"]@similarityVectorsA

Out[13]= {{{1, 1}, {1, 1}, {2, 2}, {2, 1}, {3, 1}, {1, 1}}, {1, 1, 3, 3, 3, 3}}
```

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In[14]:=
```
exampleClusteringSimilarityVectorsList = MatrixClusters[{{1, 1, 1, 0, 0, 0},
   {1, 1, 1, 1, 0, 0}, {0, 0, 0, 1, 1, 1}, {0, 0, 1, 1, 1, 1}, {0, 0, 0, 0, 1, 1}, {0, 0, 0, 1, 1, 1}},
  SimilarityVectors → {{{1, 1}, {1, 1}, {2, 2}, {2, 1}, {3, 1}, {1, 1}}, {1, 1, 3, 3, 3, 3}}]
```

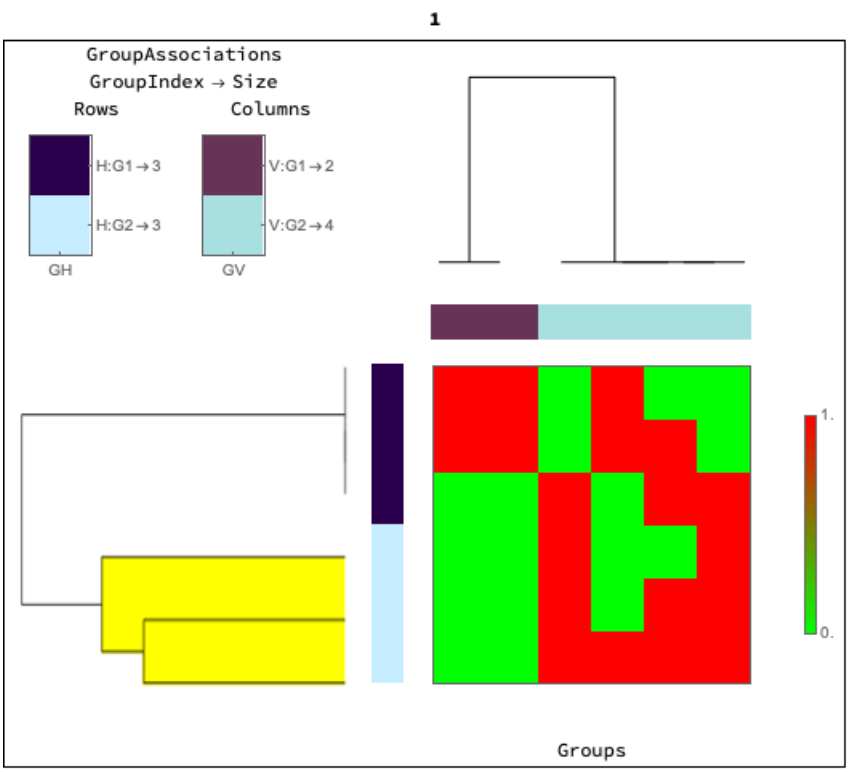
Agglomerate: 4 ties have been detected; reordering input may produce a different result.

Agglomerate: 4 ties have been detected; reordering input may produce a different result.

Out[14]=
```
⟨|1 → ⟨|RowCluster → Cluster[
    Cluster[{1, 1, 1, 0, 0, 0} → 1, Cluster[{1, 1, 1, 1, 0, 0} → 2, {0, 0, 0, 1, 1, 1} → 6, 0, 1, 1], 0, 1, 2],
    Cluster[{0, 0, 0, 0, 1, 1} → 5, Cluster[{0, 0, 0, 1, 1, 1} → 3, {0, 0, 1, 1, 1, 1} → 4, 1, 1, 1],
     1/2 (1 + √2), 1, 2], 1/2 (2 + 1/2 (1 + √2)), 3, 3], ColumnCluster → Cluster[Cluster[1, 2, 0, 1, 1],
    Cluster[6, Cluster[3, Cluster[4, 5, 0, 1, 1], 0, 1, 2], 0, 1, 3], 2, 2, 4], RowSplitClusters →
   {Cluster[{1, 1, 1, 0, 0, 0} → 1, Cluster[{1, 1, 1, 1, 0, 0} → 2, {0, 0, 0, 1, 1, 1} → 6, 0, 1, 1], 0, 1, 2],
    Cluster[{0, 0, 0, 0, 1, 1} → 5, Cluster[{0, 0, 0, 1, 1, 1} → 3, {0, 0, 1, 1, 1, 1} → 4, 1, 1, 1],
     1/2 (1 + √2), 1, 2]}, ColumnSplitClusters →
   {Cluster[1, 2, 0, 1, 1], Cluster[6, Cluster[3, Cluster[4, 5, 0, 1, 1], 0, 1, 2], 0, 1, 3]},
  GroupAssociationsRows → <|H:G1 → {1, 2, 6}, H:G2 → {5, 3, 4}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {6, 3, 4, 5}|>|>|>
```

In[15]:=
```
MatrixDendrogramsHeatmaps[exampleClusteringSimilarityVectorsList]
```

Out[15]=



SingleAssociationLabel (1)

In[1]:=
```
Needs["MathIOmica`"]
```

SingleAssociationLabel provides an option for what to label the class if a single class (or matrix) is provided as input in the form of a list. The default label is "1".

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In[2]:=
```
MatrixClusters[{{1, 1, 1, 0, 0, 0}, {1, 1, 1, 1, 0, 0},
  {0, 0, 0, 1, 1, 1}, {0, 0, 1, 1, 1, 1}, {0, 0, 0, 0, 1, 1}, {0, 0, 0, 1, 1, 1}}]
```

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Out[2]=
```
<|1 → <|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → 1, {1, 1, 1, 1, 0, 0} → 2, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → 6, {0, 0, 0, 1, 1, 1} → 3, 0, 1, 1], {0, 0, 1, 1, 1, 1} → 4, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → 5, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → 1, {1, 1, 1, 1, 0, 0} → 2, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → 6, {0, 0, 0, 1, 1, 1} → 3, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → 4, 1, 2, 1], {0, 0, 0, 0, 1, 1} → 5, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {1, 2}, H:G2 → {6, 3, 4, 5}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>|>
```

Let' s now label the class manually "First Class" :

In[3]:=
```
MatrixClusters[{{1, 1, 1, 0, 0, 0}, {1, 1, 1, 1, 0, 0}, {0, 0, 0, 1, 1, 1}, {0, 0, 1, 1, 1, 1},
  {0, 0, 0, 0, 1, 1}, {0, 0, 0, 1, 1, 1}}, SingleAssociationLabel → "First Class"]
```

Agglomerate: 1 ties have been detected; reordering input may produce a different result.

Agglomerate: 2 ties have been detected; reordering input may produce a different result.

Out[3]=
```
<|First Class → <|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → 1, {1, 1, 1, 1, 0, 0} → 2, 1, 1, 1], Cluster[
    Cluster[Cluster[{0, 0, 0, 1, 1, 1} → 6, {0, 0, 0, 1, 1, 1} → 3, 0, 1, 1], {0, 0, 1, 1, 1, 1} → 4, 1, 2, 1],
    {0, 0, 0, 0, 1, 1} → 5, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
  ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
    Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
  RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → 1, {1, 1, 1, 1, 0, 0} → 2, 1, 1, 1],
    Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → 6, {0, 0, 0, 1, 1, 1} → 3, 0, 1, 1],
      {0, 0, 1, 1, 1, 1} → 4, 1, 2, 1], {0, 0, 0, 0, 1, 1} → 5, 1/2 (1 + Sqrt[2]), 3, 1]},
  ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
  GroupAssociationsRows → <|H:G1 → {1, 2}, H:G2 → {6, 3, 4, 5}|>,
  GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|>|>
```

See Also

Autocorrelation ▪ **CreateTimeSeries** ▪ **LombScargle** ▪ **SeriesApplier** ▪ **SeriesCompare** ▪ **SeriesInternalCompare** ▪

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TimeExtractor ▪ TimeSeriesClassification ▪ TimeSeriesModelFit ▪ TimeSeriesClusters ▪ TimeSeriesSingleClusters

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

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- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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MatrixDendrogramHeatmap

MatrixDendrogramHeatmap[*data*]
generates dendrograms and heatmap plots for a matrix.

Details

- MatrixDendrogramHeatmap[*data*] generates a dendrogram and heatmap plot for matrix data clusters, typically the output of a single class of MatrixClusters . The input has the form of an association:

-
```
data = <|"RowCluster" → cluster object,
  "ColumnCluster" → cluster object,
  "RowSplitClusters" → {RowSplitCluster1, RowSplitCluster2 ...},
  "ColumnSplitClusters" → {ColumnSplitCluster1, ColumnSplitCluster2 ...},
  "GroupAssociationsRows" → <|"H:G1" → {member list for horizontal group 1 labeled "H:G1"},
    "H:G2" → {member list for horizontal group 2, labeled "H:G2"}, ...,
    "H:Gn" → {member list for horizontal group Gn}|>,
  "GroupAssociationsColumns" → <|"V:G1" → {member list for vertical group 1 labeled "V:G1"},
    "V:G2" → {member list for vertical G2, labeled G2}, ...,
    "V:Gm" → {member list for vertical group n, labeled Gm}|>
 |>
```

- The keys of the input have values that correspond to the following properties related to the two dimensional clustering for a single class results from MatrixClusters :

"RowCluster"	Cluster generated for similarity between the rows.
"ColumnCluster"	Cluster generated for similarity between the columns.
"RowSplitClusters"	Clusters resulting from splitting the initial row cluster (reported by key "RowCluster") into groups.
"ColumnSplitClusters"	Clusters resulting from splitting the initial column cluster (reported by key "RowCluster") into groups.
"GroupAssociationsRows"	Association denoting membership of each initial row data label to groups generated by the clustering.
"GroupAssociationsColumns"	Association denoting membership of each column data original position index (or label if provided) to groups generated by the clustering.

- The data can also be provided as a list with the corresponding values from the MatrixClusters clustering for a single classification class:

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```
data = { row cluster object,
  column cluster object,
  {RowSplitCluster1, RowSplitCluster2 ...},
  {ColumnSplitCluster1, ColumnSplitCluster2 ...},
  <|"H:G1" → {member list for horizontal group 1, labeled G1},
   "H:G2" → {member list for horizontal group 2, labeled G2}, ...,
   "H:Gn" → {member list for horizontal group n, labeled Gn}|>,
  <|"V:G1" → {member list for vertical group 1, labeled G1},
   "V:G2" → {member list for vertical group 2, labeled G2}, ...,
   "V:Gm" → {member list for vertical group n, labeled Gm}|>
 }
```

- The following options can be given:

ColorBlending	{CMYKColor[1, 0, 1, 0], CMYKColor[0, 1, 1, 0]}	Color scheme for the plot. The color list is passed to an internal Blend function to create a ColorFunction for an internal ArrayPlot function.
DendrogramColor	{RGBColor[1, 1, 0], RGBColor[1, 1, 0]}	Color list option for highlighting the dendrograms for the horizontal and vertical clusters respectively. If a single color is given instead of a list both dendrograms are colored the same.
FrameName	"Dendrogram and Heatmap"	Label for plot frame.
HorizontalAxisName	"Groups"	Label for the horizontal heatmap axis.
HorizontalLabels	None	Labels for horizontal axis for each column.
IndexColor	{"DeepSeaColors", "CandyColors"}	Color gradient list option for labeling the group horizontal and vertical groups respectively. If a single color gradient is given instead of a list both indexes use the same color scheme.
ImageSize	200	ImageSize is an option that specifies the overall size of an image to display for an object.
ScaleShift	None	Option to reset the blend of the colors used overall. The option is a real positive number, and is used as a multiplier for an internal Blend function's second argument.
VerticalLabels	None	Labels for vertical axis for each row.

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Examples (12)

Basic Examples (2)

First we need to load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

We consider the following example, with one set of data clustered:

In[2]:=
```
dataClusterExample1 =
   <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
   "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>;
exampleClustering1 = MatrixClusters[dataClusterExample1]
```

Out[2]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
      Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
      {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
    ColumnCluster → Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1],
      Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1], 1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3],
    RowSplitClusters → {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
      Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
        {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
    ColumnSplitClusters → {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4},
    GroupAssociationsRows → <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
    GroupAssociationsColumns → <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>|⟩|⟩
```

We can generate the corresponding clustering for the single class "1":

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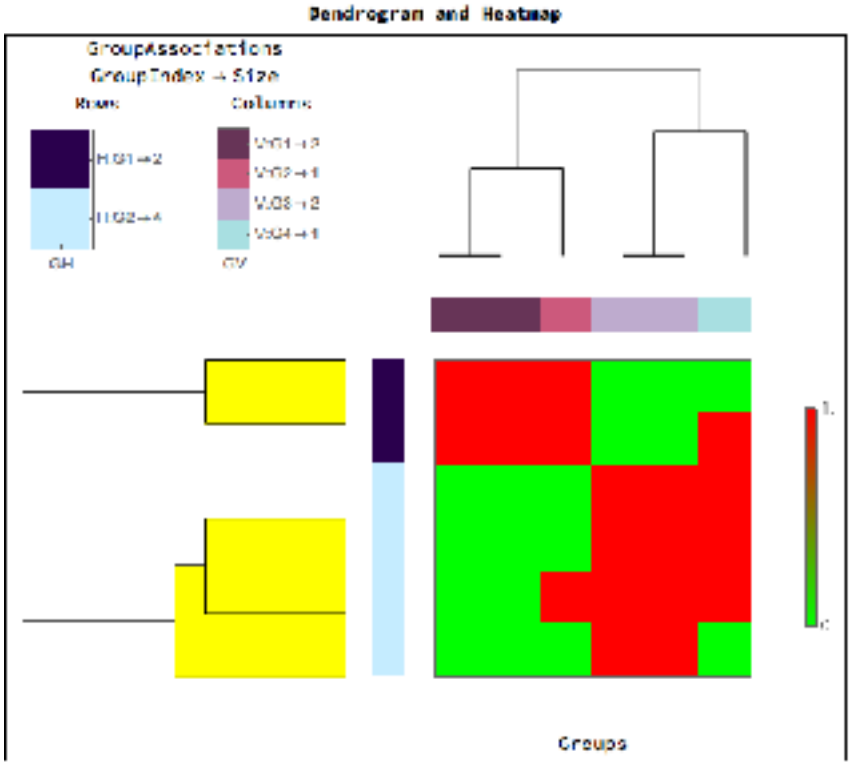
In[3]:=
```
MatrixDendrogramHeatmap[exampleClustering1["1"]]
```

Out[3]=



The dendrogram are represented on the left and on top for horizontal and vertical clusters respectively, and are highlighted to represent the grouping levels. The GH, GV, columns represent the grouping color indices in the horizontal and vertical reference bars respectively as generated by the clustering, and indicate also the number of elements in each correspoding group. For example above, in horizontal group 1, "H:G1" there are 2 members, and in vertical group 4 "V:G4" there is one member. We can extract the corresponding members from the input data :

In[4]:=
```
exampleClustering1["1", "GroupAssociationsRows", "H:G1"]
```

Out[4]= {A, B}

In[5]:=
```
DamerauLevenshteinDistance @@ {"A", "B"}
```

Out[5]= 1

In[6]:=
```
exampleClustering1["1", "GroupAssociationsColumns", "V:G4"]
```

Out[6]= {4}

We note that we could have provided the data as a list as well:

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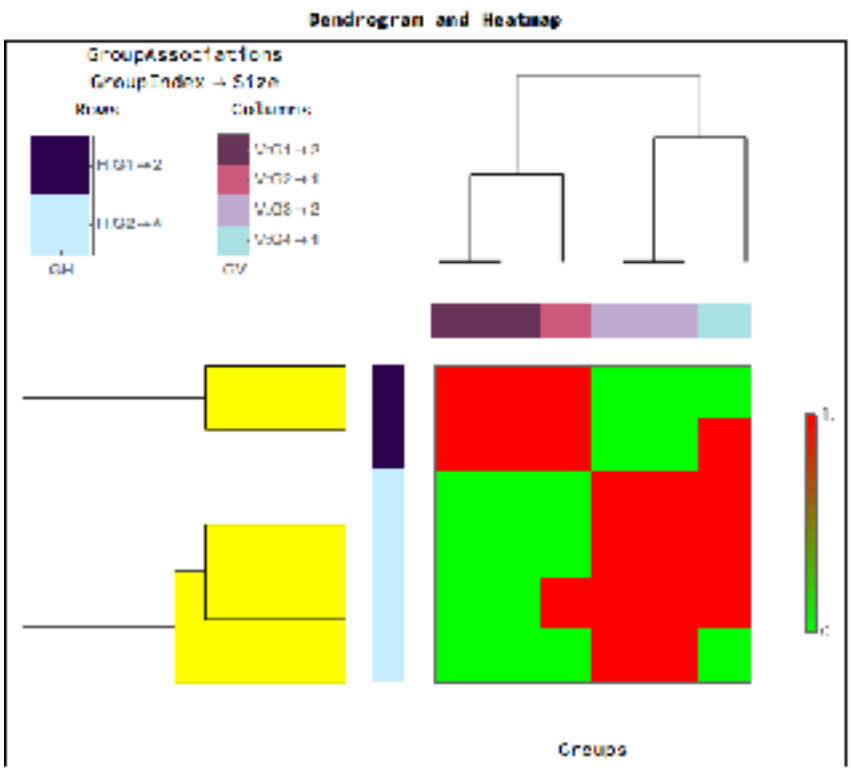
In[7]:=
```
exampleClusteringList = Values[exampleClustering1["1"]]
```

Out[7]=
```
{Cluster[Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1], Cluster[
   Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1], {0, 0, 1, 1, 1, 1} → D, 1, 2, 1],
   {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1], 1/2 (1/2 (Sqrt[5] + Sqrt[6]) + 1/2 (1/2 (2 + Sqrt[5]) + 1/2 (Sqrt[5] + Sqrt[6]))), 2, 4],
 Cluster[Cluster[Cluster[1, 2, 0, 1, 1], 3, 1, 2, 1], Cluster[Cluster[6, 5, 0, 1, 1], 4, Sqrt[2], 2, 1],
  1/2 (1/2 (2 + Sqrt[3]) + 1/2 (Sqrt[5] + Sqrt[6])), 3, 3], {Cluster[{1, 1, 1, 0, 0, 0} → A, {1, 1, 1, 1, 0, 0} → B, 1, 1, 1],
  Cluster[Cluster[Cluster[{0, 0, 0, 1, 1, 1} → F, {0, 0, 0, 1, 1, 1} → C, 0, 1, 1],
    {0, 0, 1, 1, 1, 1} → D, 1, 2, 1], {0, 0, 0, 0, 1, 1} → E, 1/2 (1 + Sqrt[2]), 3, 1]},
 {Cluster[1, 2, 0, 1, 1], 3, Cluster[6, 5, 0, 1, 1], 4}, <|H:G1 → {A, B}, H:G2 → {F, C, D, E}|>,
 <|V:G1 → {1, 2}, V:G2 → {3}, V:G3 → {6, 5}, V:G4 → {4}|>}
```

In[8]:=
```
MatrixDendrogramHeatmap[exampleClusteringList]
```

Out[8]=



In[1]:=
```
Needs["MathIOmica`"]
```

Data with missing values can be used in the clustering and subsequent plotting as well:

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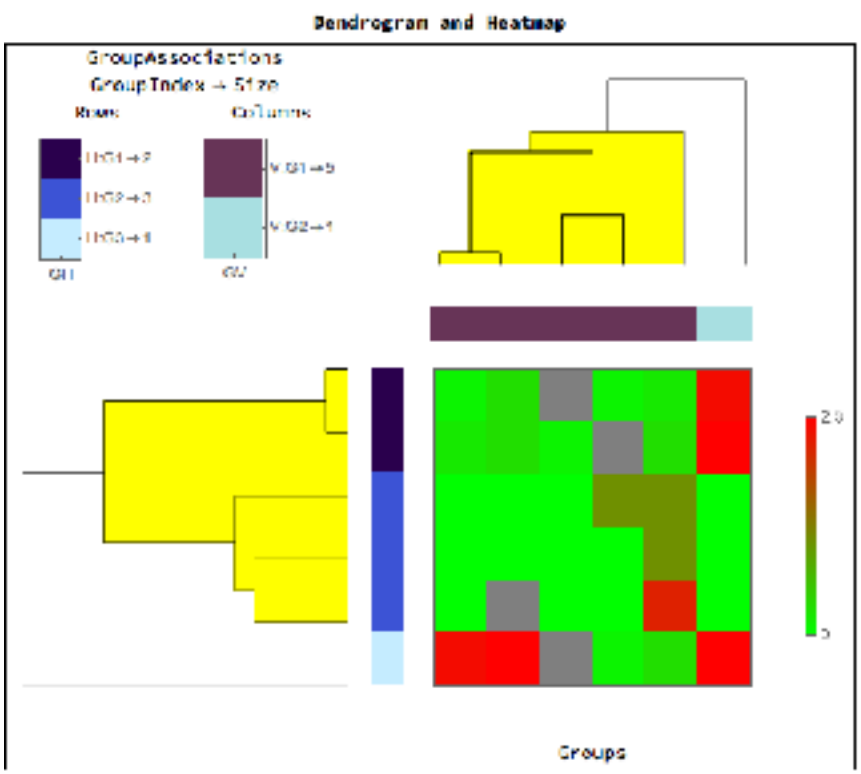
In[2]:=
```
dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
   "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
   "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
exampleClustering2 = MatrixClusters[dataClusterExample2]
```

Out[2]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
       2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + √2), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
    ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
    GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
    GroupAssociationsColumns → ⟨|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|⟩|⟩|⟩
```

Missing data are represented bye the grey squares.

In[3]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"]]
```

Out[3]=



Options (9)

ColorBlending (1)

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```
In[1]:= Needs["MathIOmica`"]
```

ColorBlending provides a list of colors to be used in the plot to create gradient effects. Named colors can be used as well.

We consider the following example, with one set of data clustered:

```
In[2]:= dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
    "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
    "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
 exampleClustering2 = MatrixClusters[dataClusterExample2]
```

```
Out[2]= ⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
       2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + Sqrt[2]), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
    ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
    GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
    GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

We can generate the corresponding clustering for the single class "1":

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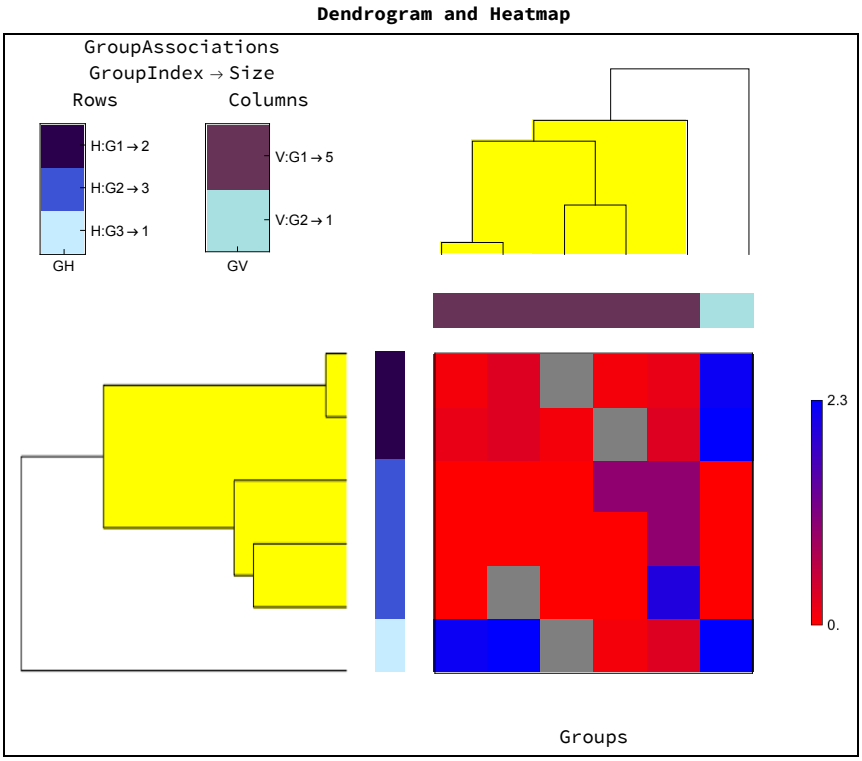
In[3]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], ColorBlending → {Red, Blue}]
```

Out[3]=



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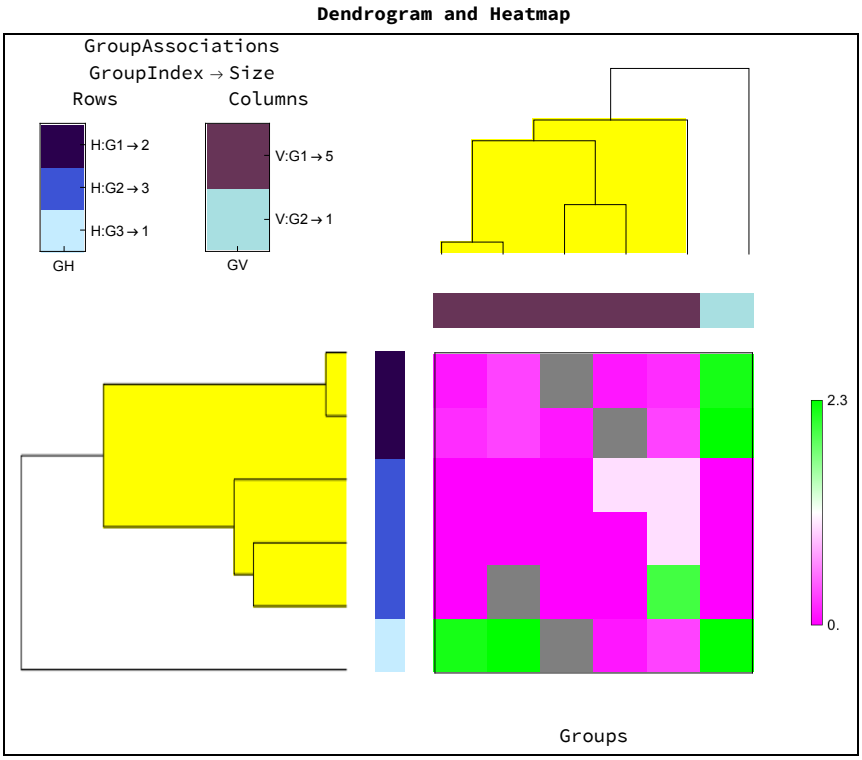
In[4]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"],
 ColorBlending → {RGBColor[1, 0, 1], White, CMYKColor[1, 0, 1, 0]}]
```

Out[4]=



DendrogramColor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

DendrogramColor takes a list of color values, for highlighting the dendrograms at the level where the groupings are called by the clustering in horizontal and vertical directions.

We consider the following example, with one set of data clustered:

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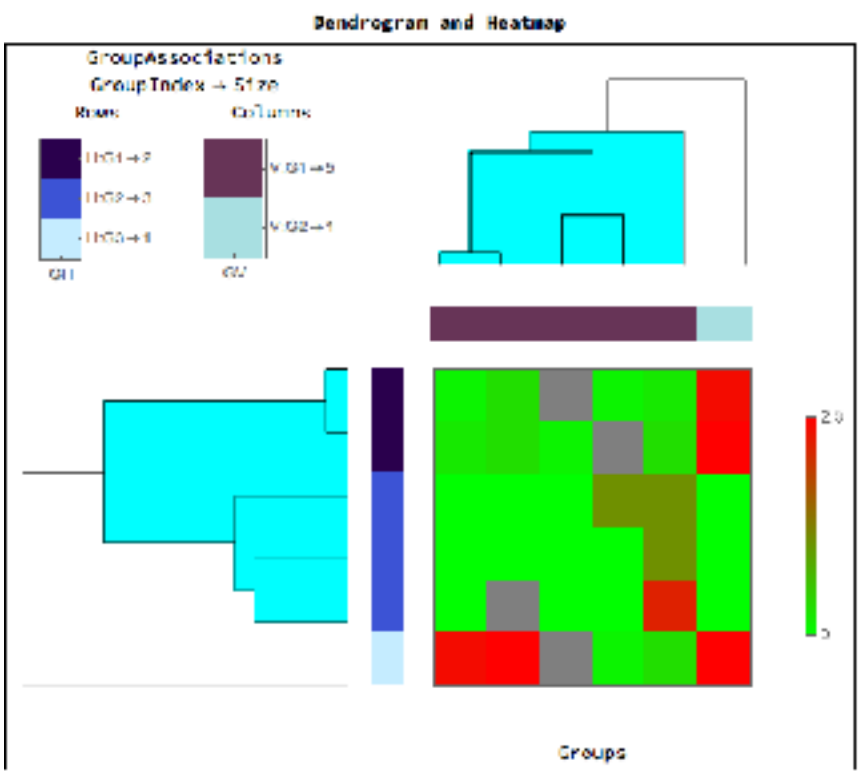
In[2]:=
```
dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
   "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
   "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
exampleClustering2 = MatrixClusters[dataClusterExample2]
```

Out[2]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
      2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
   ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
   RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + √2), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
   ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
   GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
   GroupAssociationsColumns → ⟨|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|⟩|⟩|⟩
```

We can generate the corresponding clustering for the single class "1". If a single color is given both dendrograms are colored the same:

In[3]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], DendrogramColor → Cyan]
```

Out[3]=



We can have different colors in each direction:

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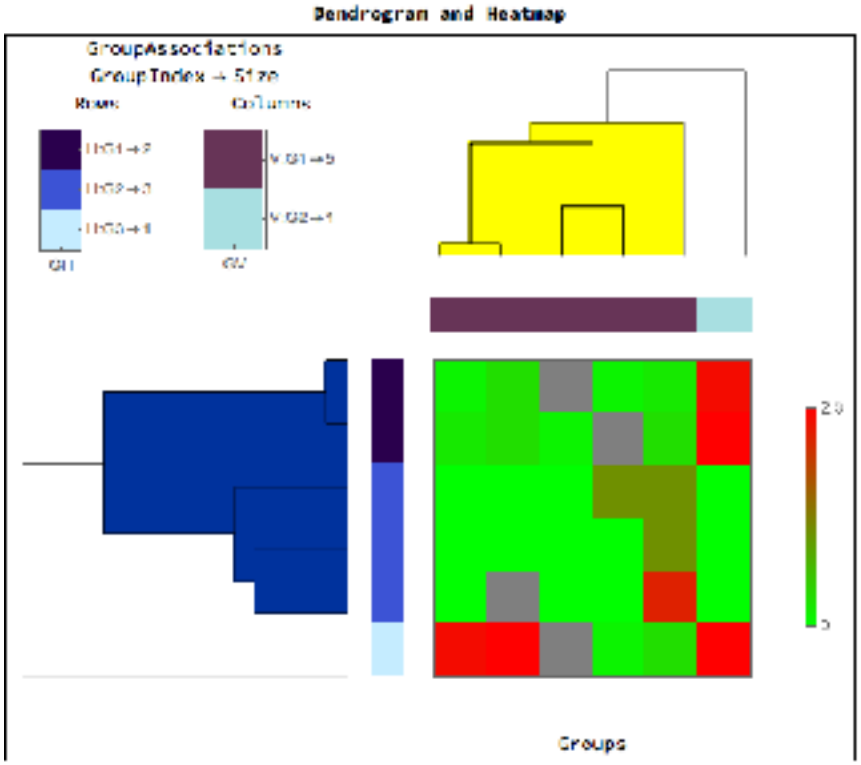
In[4]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], DendrogramColor → {CMYKColor[1, .7, .05, .35], Yellow}]
```

Out[4]=



FrameName (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The FrameName option let's us create a label for plot frame.

We consider the following example, with one set of data clustered:

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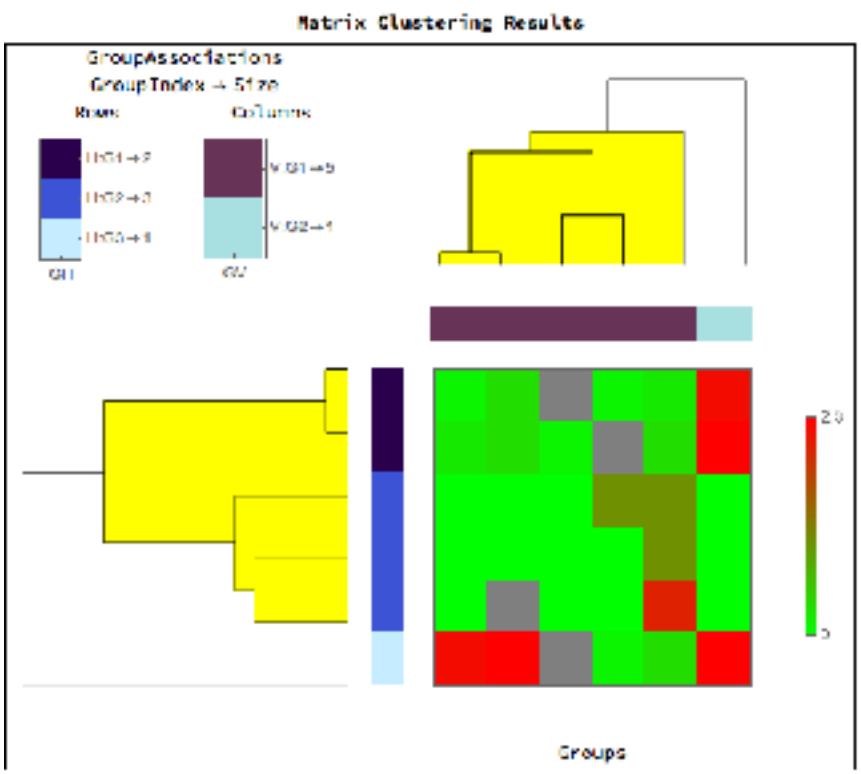
In[2]:=
```
dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
   "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
   "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
exampleClustering2 = MatrixClusters[dataClusterExample2]
```

Out[2]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
       2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
   ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
   RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + √2), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
   ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
   GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
   GroupAssociationsColumns → ⟨|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|⟩|⟩|⟩
```

In[3]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], FrameName → "Matrix Clustering Results"]
```

Out[3]=



HorizontalAxisName (1)

In[1]:=
```
Needs["MathIOmica`"]
```

HorizontalAxisName provides a label for the heatmap's horizontal axis.

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We consider the following example, with one set of data clustered:

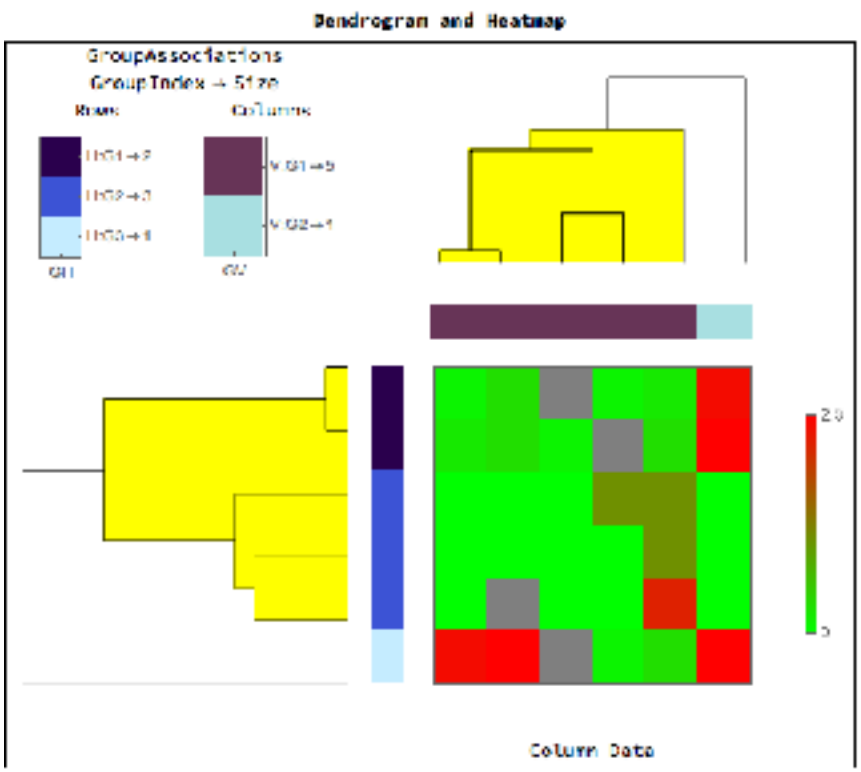
In[2]:=
```
dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
   "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
   "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
exampleClustering2 = MatrixClusters[dataClusterExample2]
```

Out[2]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
      2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
   ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
   RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + √2), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
   ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
   GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
   GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|> |⟩ |⟩
```

We can provide a custom horizontal axis name

In[3]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], HorizontalAxisName → "Column Data"]
```

Out[3]=



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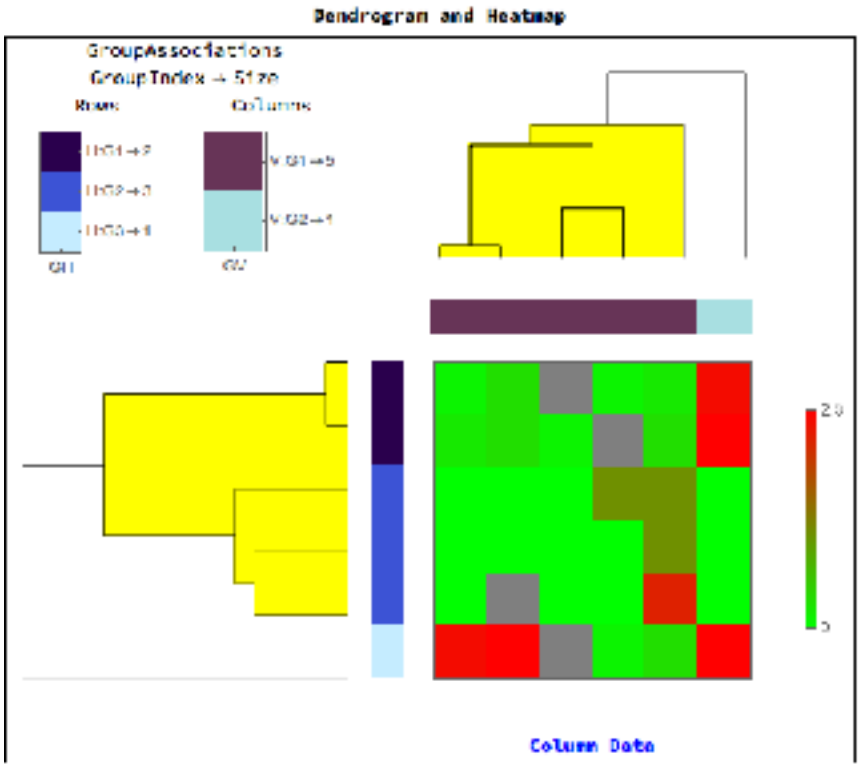
Styles can also be applied to the axis name:

In[4]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], HorizontalAxisName → Style["Column Data", {Bold, Blue}]]
```

Out[4]=



HorizontalLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

HorizontalLabels provides labels for the horizontal heatmap axis.

We consider the following example, with one set of data clustered:

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```
In[2]:= dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
          "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
          "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
        exampleClustering2 = MatrixClusters[dataClusterExample2]

Out[2]= ⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
            {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
            Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
           2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
        ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
            Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
        RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
           {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
          Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
           1/2 (1 + Sqrt[2]), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
        ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
            Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
        GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
        GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

We can extract the horizontal labels (i.e. clustering labels for the columns)

```
In[3]:= horizontalLabels = Flatten@Values@exampleClustering2["1", "GroupAssociationsColumns"]

Out[3]= {1, 3, 2, 5, 6, 4}
```

We can label each of the columns:

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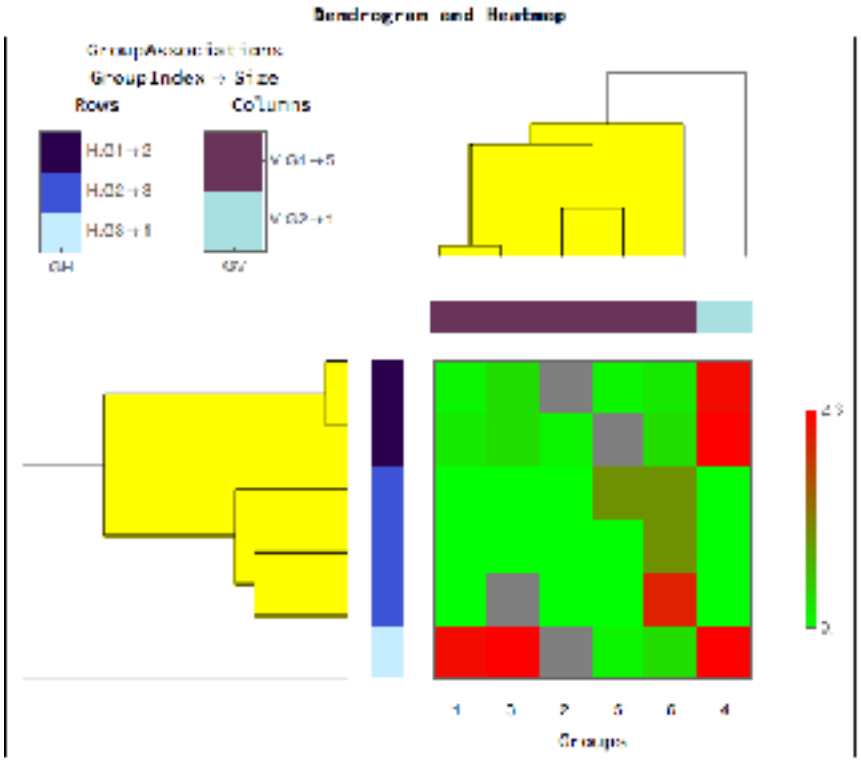
In[4]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], HorizontalLabels → horizontalLabels]
```

Out[4]=



IndexColor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

IndexColor allows us to chose the color gradients for labeling the group/subgroup index. Named Mathematica gradients can be used as well:

In[2]:=
```
ColorData["Gradients"]
```

Out[2]=
```
{AlpineColors, Aquamarine, ArmyColors, AtlanticColors, AuroraColors, AvocadoColors,
 BeachColors, BlueGreenYellow, BrassTones, BrightBands, BrownCyanTones, CandyColors, CherryTones,
 CMYKColors, CoffeeTones, DarkBands, DarkRainbow, DarkTerrain, DeepSeaColors, FallColors,
 FruitPunchColors, FuchsiaTones, GrayTones, GrayYellowTones, GreenBrownTerrain, GreenPinkTones,
 IslandColors, LakeColors, LightTemperatureMap, LightTerrain, MintColors, NeonColors, Pastel,
 PearlColors, PigeonTones, PlumColors, Rainbow, RedBlueTones, RedGreenSplit, RoseColors,
 RustTones, SandyTerrain, SiennaTones, SolarColors, SouthwestColors, StarryNightColors,
 SunsetColors, TemperatureMap, ThermometerColors, ValentineTones, WatermelonColors}
```

We consider the following example, with one set of data clustered:

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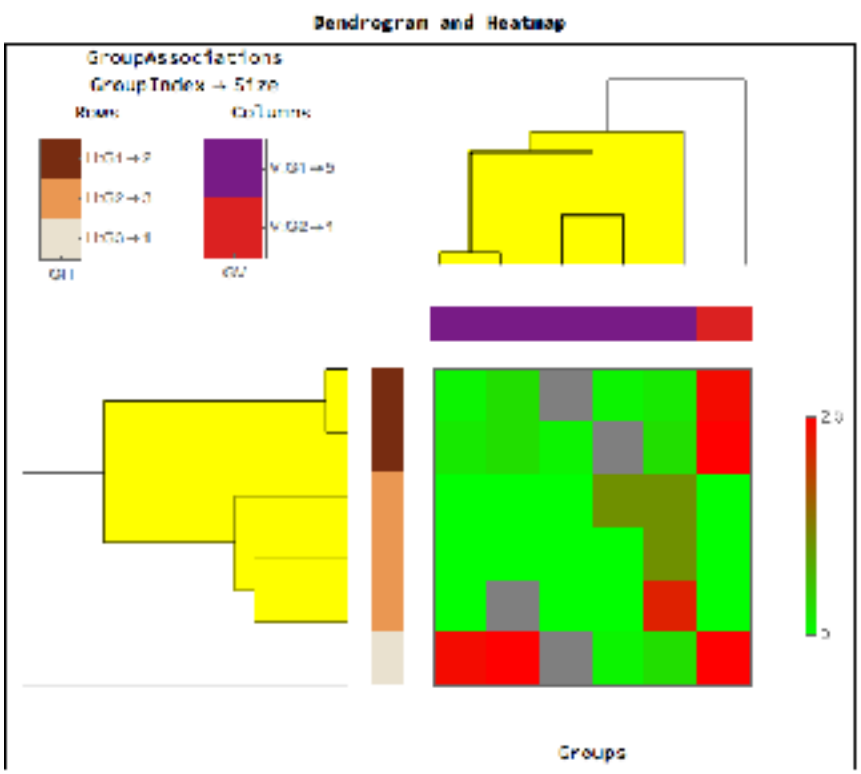
In[3]:=
```
dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
   "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
   "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
exampleClustering2 = MatrixClusters[dataClusterExample2]
```

Out[3]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
       2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + √2), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
    ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
    GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
    GroupAssociationsColumns → ⟨|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|⟩|⟩|⟩
```

We can generate the corresponding clustering for the single class "1", providing an index color list, corresponding to a color for the horizontal and vertical directions respectively :

In[4]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], IndexColor → {"SiennaTones", "Rainbow"}]
```

Out[4]=



If a single color scheme is provided then both indexes will be colored the same:

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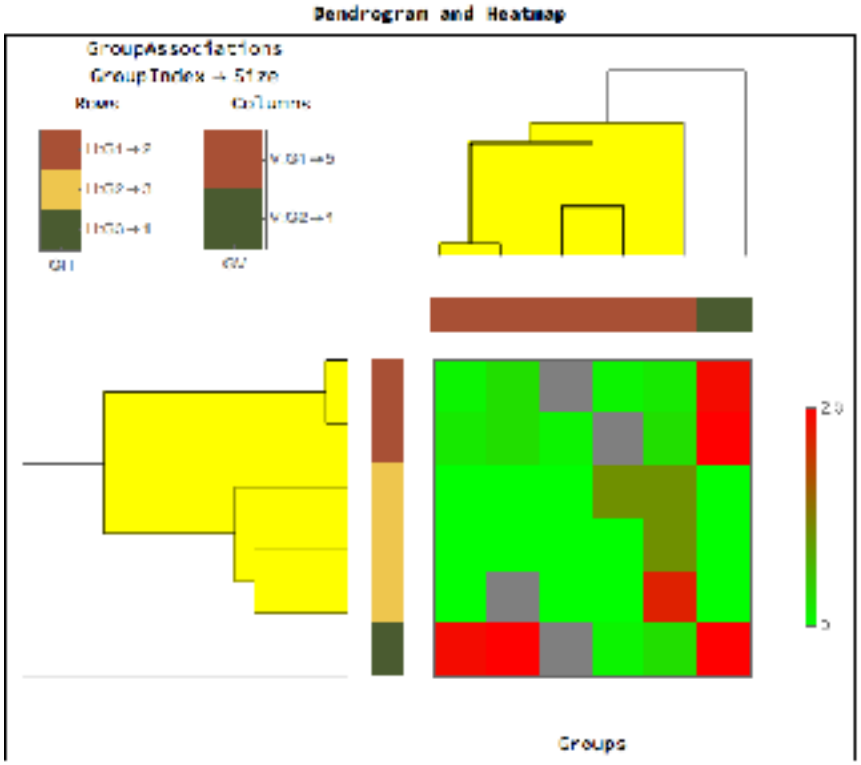
In[5]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], IndexColor → "SandyTerrain"]
```

Out[5]=



ImageSize (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ImageSize is an option that allows us to provide the overall size of the plots.

We consider the following example, with one set of data clustered:

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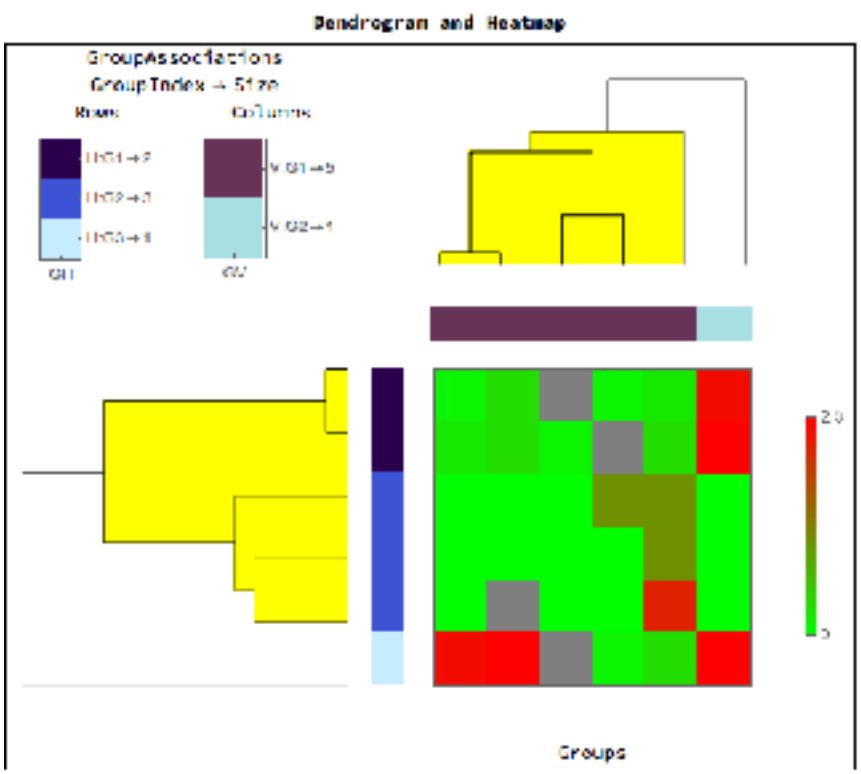
In[2]:=
```
dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
   "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
   "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
exampleClustering2 = MatrixClusters[dataClusterExample2]
```

Out[2]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
       2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
    ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
    RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + √2), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
    ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
        Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
    GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
    GroupAssociationsColumns → ⟨|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|⟩|⟩|⟩
```

We can change the image size (default is 200):

In[3]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], ImageSize → 200]
```

Out[3]=



ScaleShift (1)

In[1]:=
```
Needs["MathIOmica`"]
```

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ScaleShift provides a shift of overall color in a heatmap, allowing for overall adjustments if necessary.

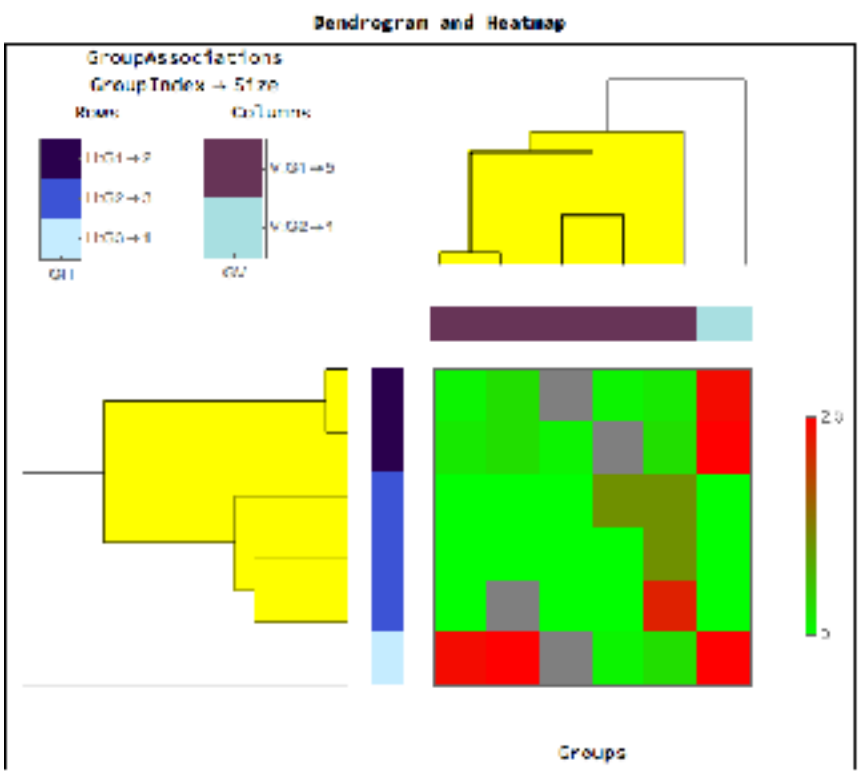
We consider the following example, with one set of data clustered:

In[2]:=
```
dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
   "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
   "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
exampleClustering2 = MatrixClusters[dataClusterExample2]
```

Out[2]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + √2), 1, 2],
      2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
   ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
   RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
      {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
     Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
      1/2 (1 + √2), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
   ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
   GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
   GroupAssociationsColumns → ⟨|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|⟩ |⟩ |⟩
```

In[3]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], ScaleShift → 1]
```

Out[3]=



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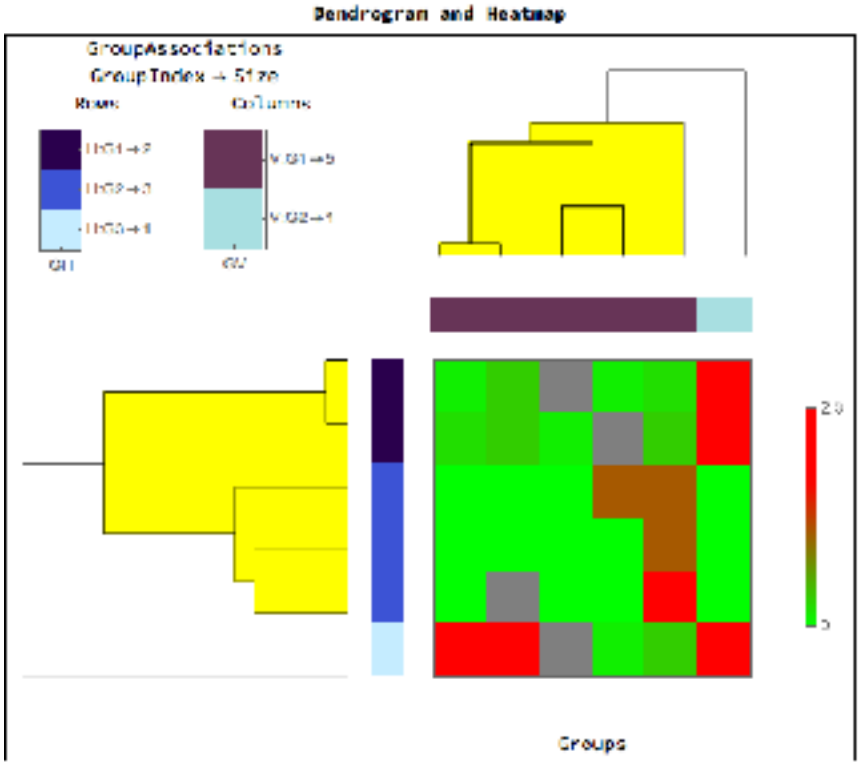
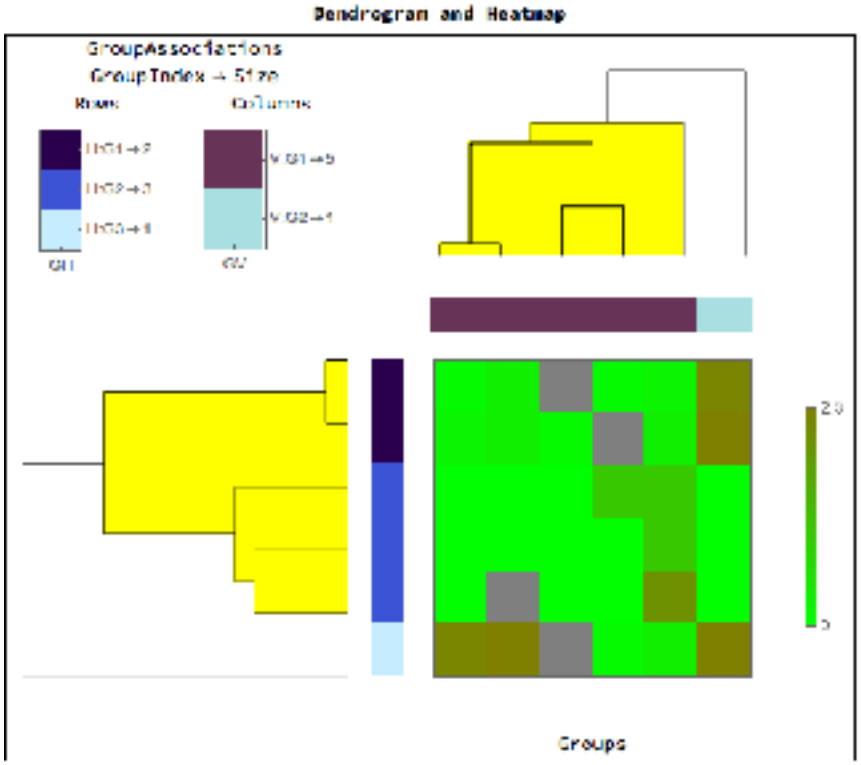
In[4]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], ScaleShift → 1.5]
```

Out[4]=



In[5]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], ScaleShift → 0.5]
```

Out[5]=



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VerticalLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

VerticalLabels provides labels for the vertical heatmap axis.

We consider the following example, with one set of data clustered:

In[2]:=
```
dataClusterExample2 = <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2},
   "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3}, "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3},
   "d" → {0, 0, 0, 0, 0, 1}, "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>;
exampleClustering2 = MatrixClusters[dataClusterExample2]
```

Out[2]=
```
⟨|1 → ⟨|RowCluster → Cluster[Cluster[Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
        {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1], Cluster[{0, 0, 0, 0, 1, 1} → f,
        Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1], 1/2 (1 + Sqrt[2]), 1, 2],
       2.60757, 2, 3], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c, 3.48988, 5, 1],
   ColumnCluster → Cluster[Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4, 3.81399, 5, 1],
   RowSplitClusters → {Cluster[{0.1, Missing[], 0.3, 2.2, 0.1, 0.2} → a,
       {0.2, 0.1, 0.3, 2.3, Missing[], 0.3} → b, 0.223607, 1, 1],
      Cluster[{0, 0, 0, 0, 1, 1} → f, Cluster[{0, 0, 0, 0, 0, 1} → d, {0, 0, Missing[], 0, 0, 2} → e, 1, 1, 1],
       1/2 (1 + Sqrt[2]), 1, 2], {2.2, Missing[], 2.3, 2.3, 0.1, 0.3} → c},
   ColumnSplitClusters → {Cluster[Cluster[Cluster[1, 3, 0.244949, 1, 1],
       Cluster[2, 5, 1.01489, 1, 1], 2.32763, 2, 2], 6, 2.75455, 4, 1], 4},
   GroupAssociationsRows → ⟨|H:G1 → {a, b}, H:G2 → {f, d, e}, H:G3 → {c}|⟩,
   GroupAssociationsColumns → <|V:G1 → {1, 3, 2, 5, 6}, V:G2 → {4}|>|⟩|⟩
```

We can extract the vertical labels in the clustering (i.e. the horizontal clustering results):

In[3]:=
```
verticalLabels = Flatten@Values@exampleClustering2["1", "GroupAssociationsColumns"]
```

Out[3]=
```
{1, 3, 2, 5, 6, 4}
```

We can label each of the columns:

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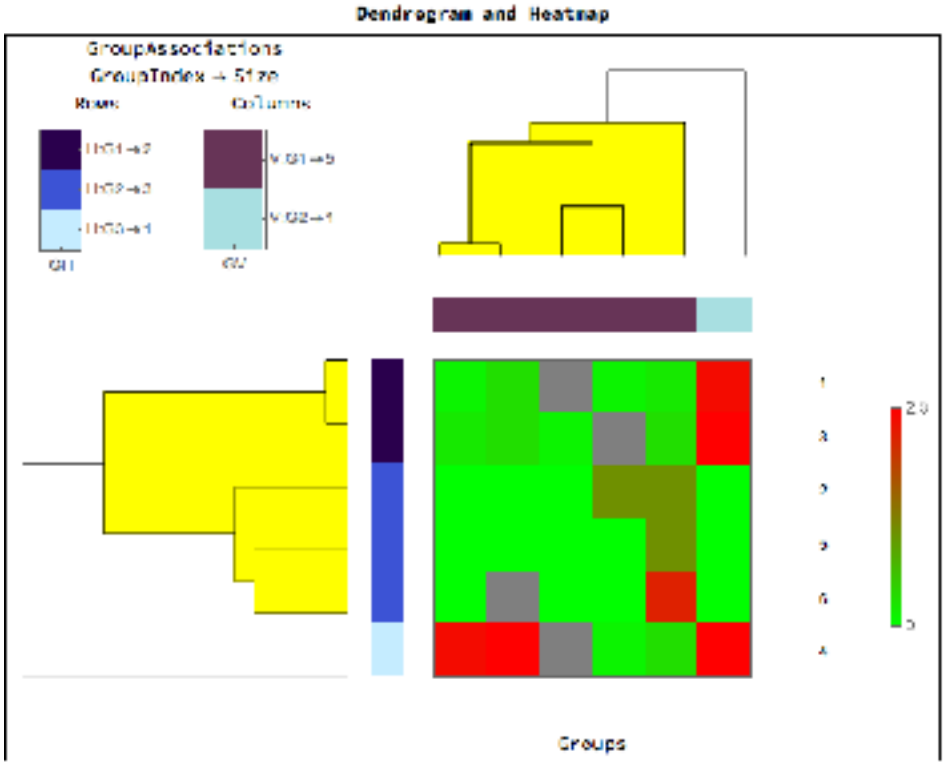
In[4]:=
```
MatrixDendrogramHeatmap[exampleClustering2["1"], VerticalLabels → verticalLabels]
```

Out[4]=



Properties & Relations (1)

MatrixDendrogramsHeatmaps uses `MatrixDendrogramHeatmap` repeatedly to plot multiple classes generated from clustering (e.g. by MatrixClusters).

See Also

Heatmapper ▪ **MatrixClusters** ▪ **MatrixDendrogramsHeatmaps** ▪ **TimeSeriesDendrogramHeatmap** ▪ **TimeSeriesDendrogramsHeatmaps** ▪ **TimeSeriesClusters** ▪ **TimeSeriesSingleClusters** ▪ **TimeSeriesSingleDendrogramHeatmap** ▪ **TimeSeriesSingleDendrogramsHeatmaps**

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Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾

URL ▾

MatrixDendrogramsHeatmaps

MatrixDendrogramsHeatmaps[*data*]
generates dendrograms and heatmap plots for a matrix, all classifications.

Details

- MatrixDendrogramsHeatmaps[*data*] generates dendrograms and associated heatmap plots for clustered matrix data, typically the output of all classes generated by implementing MatrixClusters . The input has the form of an association:

- data =

```
<| Class1 → <|"RowCluster" → cluster object1,
    "ColumnCluster" → cluster object1,
    "RowSplitClusters" → {RowSplitCluster11, RowSplitCluster12 ...},
    "ColumnSplitClusters" → {ColumnSplitCluster11, ColumnSplitCluster12 ...},
    "GroupAssociationsRows" → <|"H:G1" → {member list for horizontal group 1 labeled "H:G1"},
      "H:G2" → {member list for horizontal G2}, ...,
      "H:Gn1" → {member list for horizontal Gn1}|>,
    "GroupAssociationsColumns" → <|"V:G1" → {member list for vertical group 1 labeled "V:G1"},
      "V:G2" → {member list for vertical G2}, ...,
      "V:Gm1" → {member list for vertical Gm1}|>|>,
  Class2 → <|"RowCluster" → cluster object2,
    "ColumnCluster" → cluster object2,
    "RowSplitClusters" → {RowSplitCluster21, RowSplitCluster22 ...},
    "ColumnSplitClusters" → {ColumnSplitCluster21, ColumnSplitCluster22 ...},
    "GroupAssociationsRows" → <|"H:G1" → {member list for horizontal G1},
      "H:G2" → {member list for horizontal G2}, ...,
      "H:Gn2" → {member list for horizontal Gn2}|>,
    "GroupAssociationsColumns" → <|"V:G1" → {member list for vertical G1},
      "V:G2" → {member list for vertical G2}, ...,
      "V:Gm2" → {member list for vertical Gm2}|>|>,
  ...,
  Class2 → <|"RowCluster" → cluster object2,
    "ColumnCluster" → cluster object2,
    "RowSplitClusters" → {RowSplitCluster21, RowSplitCluster22 ...},
    "ColumnSplitClusters" → {ColumnSplitCluster21, ColumnSplitCluster22 ...},
    "GroupAssociationsRows" → <|"H:G1" → {member list for horizontal G1},
      "H:G2" → {member list for horizontal G2}, ...,
      "H:Gn2" → {member list for horizontal Gn2}|>,
    "GroupAssociationsColumns" → <|"V:G1" → {member list for vertical G1},
      "V:G2" → {member list for vertical G2}, ...,
      "V:Gm2" → {member list for vertical Gm2}|>|>
|>
```

- The keys of the input for each class have values that correspond to the following properties related to the two dimensional clustering for a single class results from MatrixClusters :

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"RowCluster"	Cluster generated for similarity between the rows.
"ColumnCluster"	Cluster generated for similarity between the columns.
"RowSplitClusters"	Clusters resulting from splitting the initial row cluster (reported by key "RowCluster") into groups.
"ColumnSplitClusters"	Clusters resulting from splitting the initial column cluster (reported by key "RowCluster") into groups.
"GroupAssociationsRows"	Association denoting membership of each initial row data label to groups generated by the clustering.
"GroupAssociationsColumns"	Association denoting membership of each column data original position index (or label if provided) to groups generated by the clustering.

- For each class a separate plot is generated: dendrograms are represented on the left and on top, and are highlighted to represent the grouping level. The "H:G" and "V:G" reference columns represent the groupings generated by the clustering in the horizontal and vertical directions respectively. The legend shows the corresponding groupings, and the number of elements in each group subgroup.
- The following options can be given:

FunctionOptions	{ImageSize –> 200}	Options list passed to the internal MatrixDendrogramHeatmap function.

Examples (3)

Basic Examples (1)

First we need to load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

We create, classify and cluster the following example, with three classes of data:

```
In[2]:= dataClusterExample =
  <| "Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <| "Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <| "Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
exampleClustering = MatrixClusters[dataClusterExample];
```

- We have multiple classes:

```
In[3]:= Keys[exampleClustering]
Out[3]= {Class1, Class2, Class3}
```

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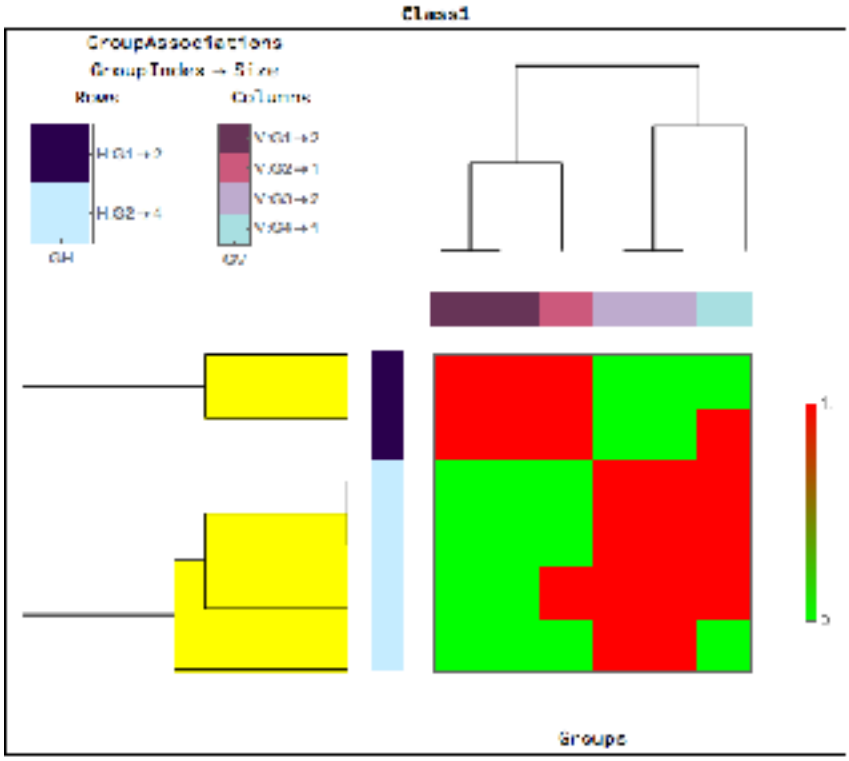
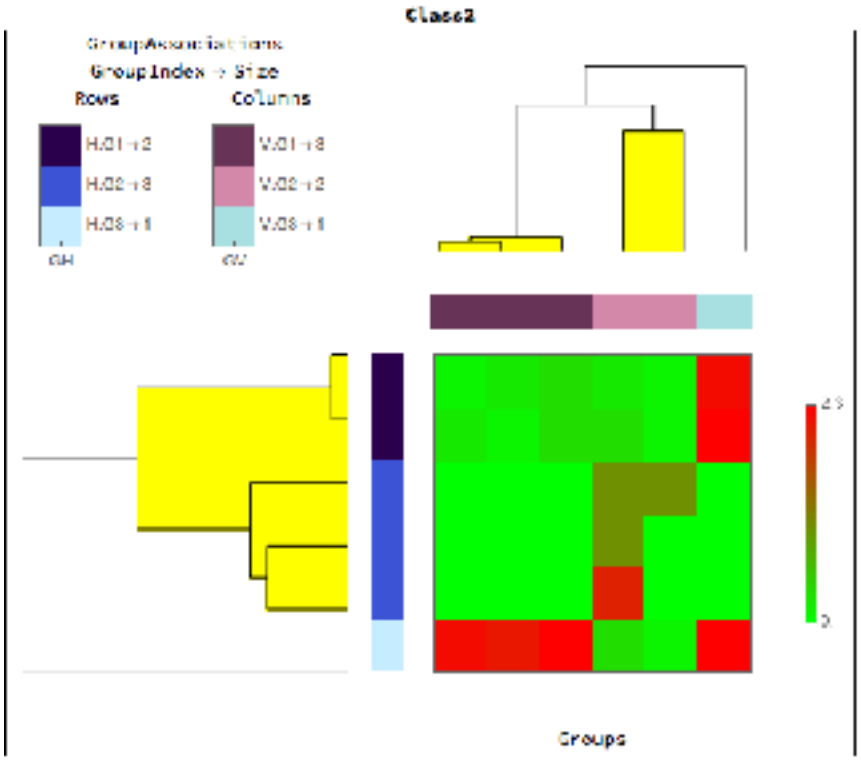
- To plot clustering results from all classes we use MatrixDendrogramsHeatmaps (note Missing[] values are shown as grey):

In[4]:=
```
MatrixDendrogramsHeatmaps[exampleClustering]
```

Out[4]=





Class3

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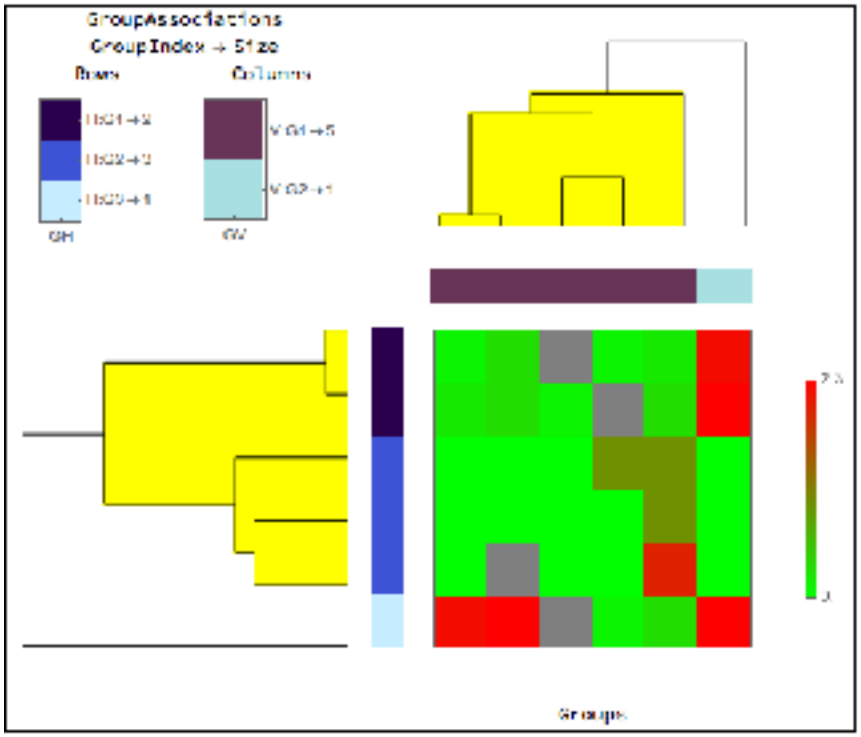

Options (1)

FunctionOptions (1)

```
In[1]:= Needs["MathIOmica`"]
```

FunctionOptions provides a list of options that are used by the internal MatrixDendrogramHeatmap functions that are used to generate the plots.

We create, classify and cluster the following example, with three classes of data:

```
In[2]:= dataClusterExample =
  <|"Class1" → <|"A" → {1, 1, 1, 0, 0, 0}, "B" → {1, 1, 1, 1, 0, 0}, "C" → {0, 0, 0, 1, 1, 1},
     "D" → {0, 0, 1, 1, 1, 1}, "E" → {0, 0, 0, 0, 1, 1}, "F" → {0, 0, 0, 1, 1, 1}|>,
   <|"Class2" → <|"a" → {0.1, 0.2, 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, 0.1, 0.3},
      "c" → {2.2, 2.1, 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, 0, 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>,
   <|"Class3" → <|"a" → {0.1, Missing[], 0.3, 2.2, 0.1, 0.2}, "b" → {0.2, 0.1, 0.3, 2.3, Missing[], 0.3},
      "c" → {2.2, Missing[], 2.3, 2.3, 0.1, 0.3}, "d" → {0, 0, 0, 0, 0, 1},
      "e" → {0, 0, Missing[], 0, 0, 2}, "f" → {0, 0, 0, 0, 1, 1}|>|>|>;
exampleClustering = MatrixClusters[dataClusterExample];
```

- We have multiple classes:

```
In[3]:= Keys[exampleClustering]
Out[3]= {Class1, Class2, Class3}
```

- To plot clustering results from all classes we use MatrixDendrogramsHeatmaps

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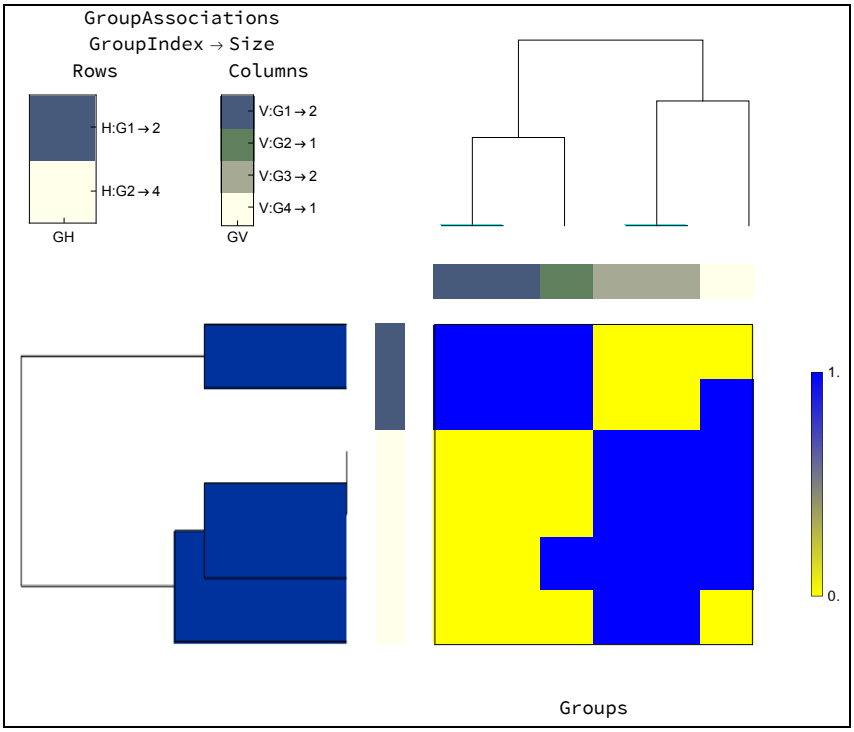
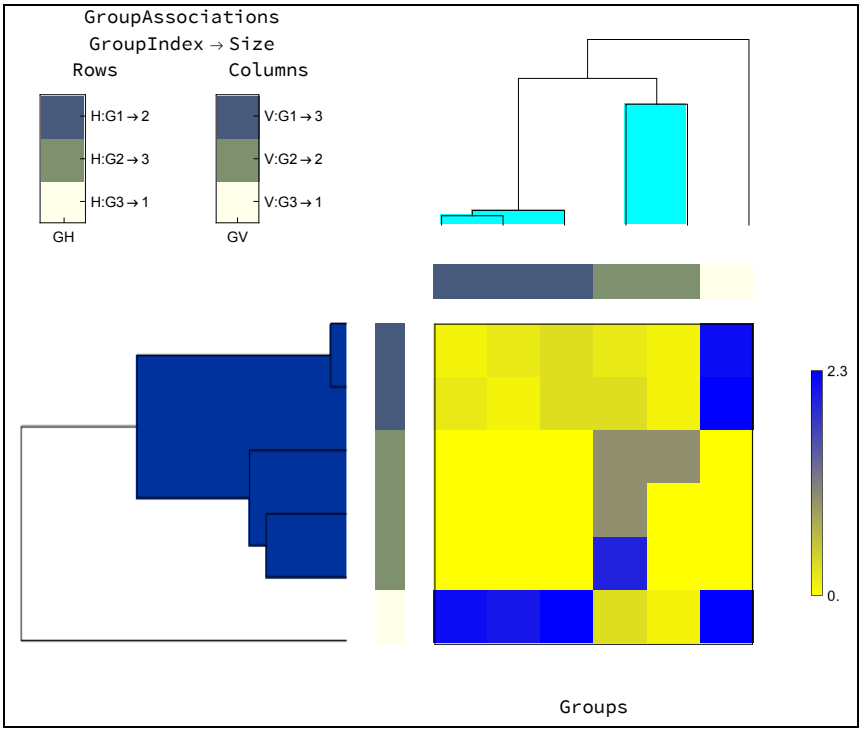
In[4]:=
```
MatrixDendrogramsHeatmaps[exampleClustering, FunctionOptions → {IndexColor → "AlpineColors",
  ColorBlending → {Yellow, Blue}, DendrogramColor → {CMYKColor[1, .7, .05, .35], Cyan}}]
```

Out[4]=

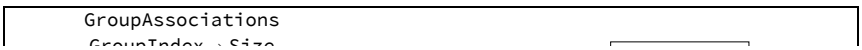
Class1



Class2



Class3



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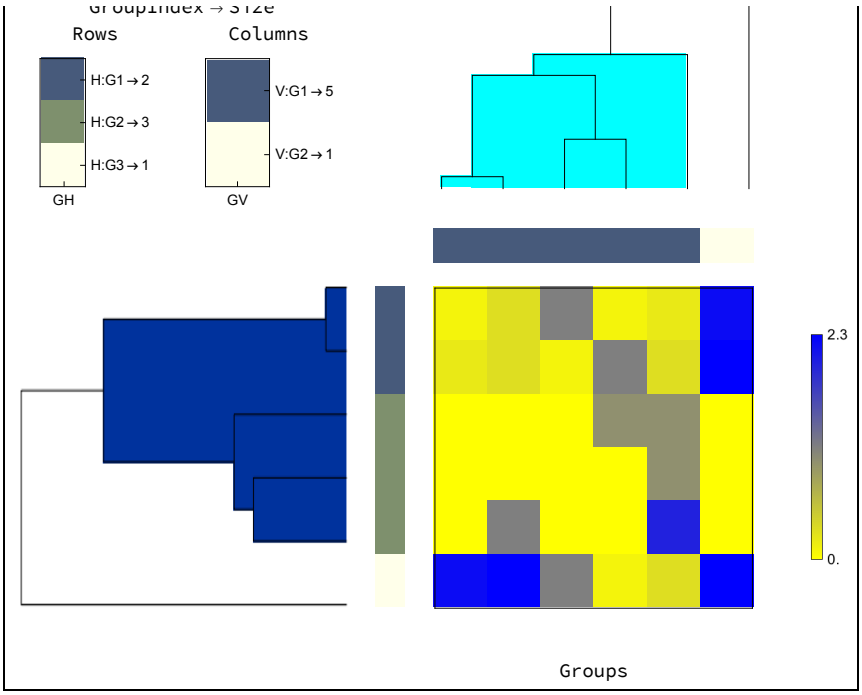

Properties & Relations (1)

MatrixDendrogramsHeatmaps uses MatrixDendrogramHeatmap repeatedly to plot multiple classes generated from clustering (e.g. by MatrixClusters).

See Also

Heatmapper ▪ **MatrixClusters** ▪ **MatrixDendrogramHeatmap** ▪ **TimeSeriesDendrogramHeatmap** ▪ **TimeSeriesDendrogramsHeatmaps** ▪ **TimeSeriesClusters** ▪ **TimeSeriesSingleClusters** ▪ **TimeSeriesSingleDendrogramHeatmap** ▪ **TimeSeriesSingleDendrogramsHeatmaps**

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MeasurementApplier

`MeasurementApplier[function, omicsObject]`
applies a *function* to the measurement list of an *omicsObject*, ignoring missing values.

Details

- `MeasurementApplier[function, omicsObject]` applies a *function* to measurement list (first list of the inner value) of an *omicsObject*, ignoring missing values. `MeasurementApplier` returns the calculated value as substituted for the measurement of the original input *omicsObject*.
- The following options can be given:

ComponentIndex	All	ComponentIndex is an option for MathIOmica functions, such as Applier, that allows selection of which component of a list to use in an association or OmicsObject input or output values.
IgnorePattern	_Missing	`IgnorePattern` is an option for `MeasurementApplier` specifying a pattern of values to delete prior to applying the function to the measurement list.
ListIndex	1	ListIndex is an option for MathIOmica functions, such as Applier that allows selection of which list to use in the association or OmicsObject input or output values.

Examples (4)

Basic Examples (1)

First we load the MathIOmica package:

```
In[1]:= Needs["MathIOmica`"]
```

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We consider the following example:

```
In[2]:= omicsObjectExample = <|"FirstSample" → <|{A0AVT1} → {{0.93, 0.94, 0}, {17}}, {A0MZ66} → {{1.06, 1, 1.0}, {9}},
          {A1A4S6} → {{1.03, Missing[], 0}, {11}}, {A1L0T0} → {{0, 0, Missing[]}, {4}}, {A0FGR8} → Missing[]|>,
        "SecondSample" → <|{A0AVT1} → {{1.0, 0, 1.2}, {17}}, {A0MZ66} → Missing[],
          {A1A4S6} → {{Missing[], Missing[], Missing[]}, {13}},
          {A1L0T0} → {{0, 0, 0}, {4}}, {A0FGR8} → {{3.1, 2, 1}, {24}}|>|>;
```

We use `MeasurementApplier` to calculate the median value of all measurements:

```
In[3]:= measurementApplierExampleMedian = MeasurementApplier[Median, omicsObjectExample]

Out[3]= <|FirstSample → <|{A0AVT1} → {{0.93}, {17}}, {A0MZ66} → {{1.}, {9}},
          {A1A4S6} → {{0.515}, {11}}, {A1L0T0} → {{0.}, {4}}, {A0FGR8} → Missing[]|>,
        SecondSample → <|{A0AVT1} → {{1.}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {Missing[], {13}},
          {A1L0T0} → {{0.}, {4}}, {A0FGR8} → {{2.}, {24}}|>|>
```

Options (3)

ComponentIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

ComponentIndex is an option for MathIOmica functions, such as Applier, that allows selection of which component of a list to use in an association or OmicsObject input or output values.

We consider the following example:

```
In[2]:= omicsObjectExample = <|"FirstSample" → <|{A0AVT1} → {{0.93, 0.94, 0}, {17}}, {A0MZ66} → {{1.06, 1, 1.0}, {9}},
          {A1A4S6} → {{1.03, Missing[], 0}, {11}}, {A1L0T0} → {{0, 0, Missing[]}, {4}}, {A0FGR8} → Missing[]|>,
        "SecondSample" → <|{A0AVT1} → {{1.0, 0, 1.2}, {17}}, {A0MZ66} → Missing[],
          {A1A4S6} → {{Missing[], Missing[], Missing[]}, {13}},
          {A1L0T0} → {{0, 0, 0}, {4}}, {A0FGR8} → {{3.1, 2, 1}, {24}}|>|>;
```

We use `MeasurementApplier` to calculate the median value of all measurements in the 2nd and 3rd component for the measurements:

```
In[3]:= measurementApplierComponentIndex = MeasurementApplier[Median, omicsObjectExample, ComponentIndex → {2, 3}]

Out[3]= <|FirstSample → <|{A0AVT1} → {{0.47}, {17}}, {A0MZ66} → {{1.}, {9}},
          {A1A4S6} → {{0.}, {11}}, {A1L0T0} → {{0.}, {4}}, {A0FGR8} → Missing[]|>,
        SecondSample → <|{A0AVT1} → {{0.6}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {Missing[], {13}},
          {A1L0T0} → {{0.}, {4}}, {A0FGR8} → {{1.5}, {24}}|>|>
```

IgnorePattern (1)

```
In[1]:= Needs["MathIOmica`"]
```

`IgnorePattern` is an option for `MeasurementApplier` specifying a pattern of values to delete prior to applying the function to the measurement list.

We consider the following example:

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```
In[2]:= omicsObjectExample = <|"FirstSample" → <|{A0AVT1} → {{0.93, 0.94, 0}, {17}}, {A0MZ66} → {{1.06, 1, 1.0}, {9}},
          {A1A4S6} → {{1.03, Missing[], 0}, {11}}, {A1L0T0} → {{0, 0, Missing[]}, {4}}, {A0FGR8} → Missing[]|>,
        "SecondSample" → <|{A0AVT1} → {{1.0, 0, 1.2}, {17}}, {A0MZ66} → Missing[],
          {A1A4S6} → {{Missing[], Missing[], Missing[]}, {13}},
          {A1L0T0} → {{0, 0, 0}, {4}}, {A0FGR8} → {{3.1, 2, 1}, {24}}|>|>;
```

We use `MeasurementApplier` to calculate the median value of all measurements, removing Missing and values of 1:

```
In[3]:= measurementApplierIgnorePattern =
         MeasurementApplier[Median, omicsObjectExample, IgnorePattern → _Missing | 1]

Out[3]= <|FirstSample → <|{A0AVT1} → {{0.93}, {17}}, {A0MZ66} → {{1.}, {9}},
          {A1A4S6} → {{0.515}, {11}}, {A1L0T0} → {{0.}, {4}}, {A0FGR8} → Missing[]|>,
        SecondSample → <|{A0AVT1} → {{1.}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {Missing[], {13}},
          {A1L0T0} → {{0.}, {4}}, {A0FGR8} → {{2.}, {24}}|>|>
```

We can add more components to the pattern to ignore:

```
In[4]:= measurementApplierIgnorePattern =
         MeasurementApplier[Median, omicsObjectExample, IgnorePattern → (Missing[] | 1 | 1.)]

Out[4]= <|FirstSample → <|{A0AVT1} → {{0.93}, {17}}, {A0MZ66} → {{1.06}, {9}},
          {A1A4S6} → {{0.515}, {11}}, {A1L0T0} → {{0.}, {4}}, {A0FGR8} → Missing[]|>,
        SecondSample → <|{A0AVT1} → {{0.6}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {Missing[], {13}},
          {A1L0T0} → {{0.}, {4}}, {A0FGR8} → {{2.55}, {24}}|>|>
```

ListIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

ListIndex is an option for MathIOmica functions, such as Applier that allows selection of which list to use in the association or OmicsObject input or output values.

We consider the following example:

```
In[2]:= omicsObjectExampleMetadata =
          <|"FirstSample" → <|{A0AVT1} → {{0.93, 0.94, 0}, {17, 11, 12}}, {A0MZ66} → {{1.06, 1, 1.0}, {9, 3, 1}},
            {A1A4S6} → {{1.03, Missing[], 0}, {11, 2, 1}}, {A1L0T0} → {{0, 0, Missing[]}, {4}},
            {A0FGR8} → Missing[]|>, "SecondSample" → <|{A0AVT1} → {{1.0, 0, 1.2}, {17, 11, 12}},
            {A0MZ66} → Missing[], {A1A4S6} → {{Missing[], Missing[], Missing[]}, {13, Missing[], 2}},
            {A1L0T0} → {{0, 0, 0}, {4, 3, Missing[]}}, {A0FGR8} → {{3.1, 2, 1}, {24, 2, Missing[]}}|>|>;
```

We use `MeasurementApplier` to calculate the median value of all measurements from the "Metadata" list and return this as the first "Measurement" list:

```
In[3]:= omicsObjectExampleMedian = MeasurementApplier[Median, omicsObjectExampleMetadata, ListIndex → 2]

Out[3]= <|FirstSample → <|{A0AVT1} → {{12.}, {17, 11, 12}}, {A0MZ66} → {{3.}, {9, 3, 1}},
          {A1A4S6} → {{2.}, {11, 2, 1}}, {A1L0T0} → {{4.}, {4}}, {A0FGR8} → Missing[]|>, SecondSample →
          <|{A0AVT1} → {{12.}, {17, 11, 12}}, {A0MZ66} → Missing[], {A1A4S6} → {{7.5}, {13, Missing[], 2}},
          {A1L0T0} → {{3.5}, {4, 3, Missing[]}}, {A0FGR8} → {{13.}, {24, 2, Missing[]}}|>|>
```

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See Also

Applier ▪ **ApplierList** ▪ **ComponentIndex** ▪ **FilteringFunction** ▪ **MeasurementApplier** ▪ **OmicsObject** ▪ **Returner**

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MissingDataCreator

`MissingDataCreator[data, setSamples]`
fills in Missing tags in a paired dataset for which the first component is not a member of a given sample list.

Details

- `MissingDataCreator[data, setSamples]` takes a set of paired data, compares the first components to a given list and returns a sorted series of second components with Missing tags introduced for missing points. MissingDataCreator takes as input:

data	Paired data, from which the first components will be compared to a given list.
setSamples	List against which the input data first components will be compared.

- MissingDataCreator can be used to construct series with missing points inserted, for example to use with LombScargle transformations when dealing with time series.

Examples (1)

Basic Examples (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

Let' s suppose we have the following data that came from serial measurements:

```
In[2]:= dataSeries = {{1, 4.2}, {3, 4.4}, {5, 4.1}};
```

If we expected to have a list where measurement were conducted from 1 through 7 for example:

```
In[3]:= timepointSet = {1, 2, 3, 4, 5, 6, 7};
```

then we can create the associated second component list:

```
In[4]:= dataSeriesFullMeasurements = MissingDataCreator[dataSeries, timepointSet]
Out[4]= {4.2, Missing[], 4.4, Missing[], 4.1, Missing[], Missing[]}
```

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The corresponding pairs would be:

```
In[5]:= Transpose[{timepointSet, dataSeriesFullMeasurements}]
Out[5]= {{1, 4.2}, {2, Missing[]}, {3, 4.4}, {4, Missing[]}, {5, 4.1}, {6, Missing[]}, {7, Missing[]}}
```

We can have for a example a set of measurements for different people, e.g. their height:

```
In[6]:= nameHeight = {{"John", 1.72}, {"Mary", 1.65}, {"Michael", 1.65}, {"Jane", 1.70}, {"Mark", 1.83}};
In[7]:= peopleList = {"Agnes", "Clarissa", "James", "Jason", "Jane", "John", "Laura", "Mary", "Michael", "Kirsten"};
```

The corresponding measurement to the people list would then be:

```
In[8]:= fullListHeights = MissingDataCreator[nameHeight, peopleList]
Out[8]= {Missing[], Missing[], Missing[], Missing[], 1.7, 1.72, Missing[], 1.65, 1.65, Missing[]}
```

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MissingReplacement

`MissingReplacement`
is an option for functions that handle missing data (e.g. EnlargeInnerAssociation) that indicates what value missing data should be globally assigned. .

Details

- MissingReplacement is an option for functions that handle missing data (e.g. EnlargeInnerAssociation) that indicates what value missing data should be globally assigned.

See Also

EnlargeInnerAssociation ▪ **EnlargeOuterAssociation**

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OBOGODictionary

`OBOGODictionary[]`
is an Open Biomedical Ontologies (OBO) Gene Ontology (GO) vocabulary dictionary generator.

Details

- `OBOGODictionary[]` generates a vocabulary dictionary (association) of Gene Ontology (GO) term to label based on Open Biomedical Ontologies (OBO) Gene Ontology (GO) information. The form of the output for n GO accessions is:

- output = <|GO : accession$_1$ → {description of GO : accession$_1$, GO : accession$_1$ category},
  GO : accession$_2$ → {description of GO : accession$_2$, GO : accession$_2$ category}, ...,
  GO : accession$_n$ → {description of GO : accession$_n$, GO : accession$_n$ category}
  |>

- The following options can be given:

FileURL	"http://purl.obolibrary.org/obo/go/go-basic.obo"	The FileURL option provides the location of the obo file in case this will be downloaded from the web.
ImportDirectly	False	ImportDirectly gives the option to import a new version of an OBO information file directly from the Gene Ontology consortium site to either replace the current version in the MathIOmica package data directory or add a new one (e.g. for a different species).
MathIOmicaDataDirectory	If[!DirectoryQ[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], CreateDirectory[FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]], FileNameJoin[Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]	MathIOmicaDataDirectory option specifies the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

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OBOFile	"goBasicObo.txt"	The OBOFile specifies the name of the file that will be used to construct the dictionary, or if not present saved when dowloaded from the web.

Examples (5)

Basic Examples (1)

First we need to load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

In[2]:=
```
goAnnotationExample = OBOGODictionary[]
```

Out[2]=
```
<|GO:0000001 → {mitochondrion inheritance, biological_process},
 GO:0000002 → {mitochondrial genome maintenance, biological_process},
 ··· 47 398 ···, GO:2001317 → {kojic acid biosynthetic process, biological_process}|>
```

large output | show less | show more | show all | set size limit...

For example, we query "GO:0033256":

In[3]:=
```
goAnnotationExample["GO:0033256"]
```

Out[3]=
```
{I-kappaB/NF-kappaB complex, cellular_component}
```

Options (4)

FileURL (1)

In[1]:=
```
Needs["MathIOmica`"]
```

FileURL provides the online location of the OBO file used in creating the GO annotation if importing directly from the web. Typically the GO consortium website provides an updated OBO file.

In[2]:=
```
OBOGODictionary[FileURL → "http://purl.obolibrary.org/obo/go/go-basic.obo", ImportDirectly → True]
```

Out[2]=
```
<|GO:0000001 → {mitochondrion inheritance, biological_process},
 GO:0000002 → {mitochondrial genome maintenance, biological_process},
 ··· 47 398 ···, GO:2001317 → {kojic acid biosynthetic process, biological_process}|>
```

large output | show less | show more | show all | set size limit...

ImportDirectly (1)

In[1]:=
```
Needs["MathIOmica`"]
```

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ImportDirectly gives the option to import a new version of an OBO information file directly from the Gene Ontology consortium site to either replace the current version in the MathIOmica package data directory or add a new one (e.g. for a different species).

In[2]:=
```
OBOGODictionary[ImportDirectly → True]
```

Out[2]=
```
⟨|GO:0000001 → {mitochondrion inheritance, biological_process},
 GO:0000002 → {mitochondrial genome maintenance, biological_process},
 ··· 47 398 ···, GO:2001317 → {kojic acid biosynthetic process, biological_process}|⟩
```

large output | show less | show more | show all | set size limit...

MathIOmicaDataDirectory (1)

In[1]:=
```
Needs["MathIOmica`"]
```

MathIOmicaDataDirectory option value points to the directory where the default MathIOmica package data is stored. By default the option is set to create the standard directory if it does not exist already.

In[2]:=
```
OBOGODictionary[MathIOmicaDataDirectory → FileNameJoin[
   Flatten[{FileNameSplit[$UserBaseDirectory], "Applications", "MathIOmica", "MathIOmicaData"}]]]
```

Out[2]=
```
⟨|GO:0000001 → {mitochondrion inheritance, biological_process},
 GO:0000002 → {mitochondrial genome maintenance, biological_process},
 ··· 47 398 ···, GO:2001317 → {kojic acid biosynthetic process, biological_process}|⟩
```

large output | show less | show more | show all | set size limit...

OBOFile (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The OBOFile specifies the name of the file in the MathIOmica package directory that will be used, or if not present saved when downloaded from the web.

In[2]:=
```
OBOGODictionary[OBOFile → "goBasicObo.txt"]
```

Out[2]=
```
⟨|GO:0000001 → {mitochondrion inheritance, biological_process},
 GO:0000002 → {mitochondrial genome maintenance, biological_process},
 ··· 47 398 ···, GO:2001317 → {kojic acid biosynthetic process, biological_process}|⟩
```

large output | show less | show more | show all | set size limit...

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See Also

GetGeneDictionary ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGPathwayVisual** ▪ **UCSCBrowserSQL**

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OmicsObject

`OmicsObject`
is a data format used in MathIOmica for indexing lists of measurements associated to different samples or timepoints.

Details

- In MathIOmica the calculations utilize what we term an omics object. An omics object has an external (outer) association to denote samples and an internal (inner) association for annotation. The main structure looks like:

- <|OuterLabel$_1$ → <|InnerLabel$_1$ → {{Measurements$_{11}$}, {Metadata$_{11}$}},
  InnerLabel$_2$ → {{Measurements$_{12}$}, {Metadata$_{12}$}},
  InnerLabel$_3$ → {{Measurements$_{13}$}, {Metadata$_{13}$}},
  ...,
  InnerLabel$_k$ → {{Measurements$_{1k}$}, {Metadata$_{1k}$}},
  ...,
  InnerLabel$_N$ → {{Measurements$_{1N}$}, {Metadata$_{1N}$}}|>,
  OuterLabel$_2$ → <|InnerLabel$_1$ → {{Measurements$_{21}$}, {Metadata$_{21}$}},
  InnerLabel$_2$ → {{Measurements$_{22}$}, {Metadata$_{22}$}},
  InnerLabel$_3$ → {{Measurements$_{23}$}, {Metadata$_{23}$}},
  ...,
  InnerLabel$_k$ → {{Measurements$_{2k}$}, {Metadata$_{2k}$}},
  ...,
  InnerLabel$_N$ → {{Measurements$_{2N}$}, {Metadata$_{2N}$}}|>,
  ...,
  OuterLabel$_j$ → <|InnerLabel$_1$ → {{Measurements$_{j1}$}, {Metadata$_{j1}$}},
  InnerLabel$_2$ → {{Measurements$_{j2}$}, {Metadata$_{j2}$}},
  InnerLabel$_3$ → {{Measurements$_{j3}$}, {Metadata$_{j3}$}},
  ...,
  InnerLabel$_k$ → {{Measurements$_{jk}$}, {Metadata$_{jk}$}},
  ...,
  InnerLabel$_N$ → {{Measurements$_{jN}$}, {Metadata$_{jN}$}}|>,
  ...,
  OuterLabel$_M$ → <|InnerLabel$_1$ → {{Measurements$_{M1}$}, {Metadata$_{M1}$}},
  InnerLabel$_2$ → {{Measurements$_{M2}$}, {Metadata$_{M2}$}},
  InnerLabel$_3$ → {{Measurements$_{M3}$}, {Metadata$_{M3}$}},
  ...,
  InnerLabel$_k$ → {{Measurements$_{Mk}$}, {Metadata$_{Mk}$}},
  ...,
  InnerLabel$_N$ → {{Measurements$_{MN}$}, {Metadata$_{MN}$}}|>
  |>

- In this example there are M outer labels, corresponding to M samples. Across the samples there are N inner labels (e.g. identifiers for genes/proteins), and the the inner labels are the same across samples. For a given j^{th} outer label, OuterLabel$_j$, the kth inner label, InnerLabel$_k$ has a value of the form: InnerLabel$_k$ → {{Measurements$_{jk}$}, {Metadata$_{jk}$}}.

- For any j^{th} outer label, OuterLabel$_j$, it is possible that the mth inner label, InnerLabel$_m$ is missing and takes a Missing[] value in the form InnerLabel$_m$ → Missing[]. This can happen if the measurement was not performed for the sample, or no value was recorded (e.g. mass spectrometry data).

- For example here is a list of 3 samples using protein identifiers (specifically, these are UniProt accessions). The measurements are relative intensities in this case and the metadata is the number of peptides per sample.

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```
<|FirstSample → <|{A0AVT1} → {{0.937}, {17}}, {A0MZ66} → {{1.059}, {9}},
   {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[]|>,
 SecondSample → <|{A0AVT1} → {{1.003}, {17}}, {A0MZ66} → Missing[],
   {A1A4S6} → {{0.779}, {11}}, {A1L0T0} → {{0.917}, {4}}, {A0FGR8} → {{0.921}, {24}}|>,
 ThirdSample → <|{A0AVT1} → {{1.064}, {19}}, {A0MZ66} → Missing[],
   {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {23}}|>|>
```

- The outer labels are strings, while the inner labels are typically lists of strings.

Examples (1)

Properties & Relations (1)

DataImporter, DataImporterDirect and DataImporterDirectLabeled, import data from external files to create omics objects. OmicsObjectCreator can be used to create an omics object from internal data.

An OmicsObject can be manipulated using Query as for regular data structures/associations, and additionally using specialized MathIOmica functions, such as Applier, ApplierList, ConstantAssociator EnlargeInnerAssociation, EnlargeOuterAssociation, Returner.

See Also

Applier ▪ **ApplierList** ▪ **ConstantAssociator** ▪ **CreateTimeSeries** ▪ **DataImporter** ▪ **DataImporterDirect** ▪ **DataImporterDirectLabeled** ▪ **EnlargeInnerAssociation** ▪ **EnlargeOuterAssociation** ▪ **FileSelector** ▪ **FilteringFunction** ▪ **FilterMissing** ▪ **LowValueTag** ▪ **OmicsObjectCreator** ▪ **OmicsObjectMerge** ▪ **OmicsObjectPairedMerge** ▪ **Returner**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

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- MathIOmicaOverview

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OmicsObjectCreator

OmicsObjectCreator[*outerLabels*, *innerLabels*, *measurements*, *metadata*]
creates an OmicsObject for use with MathIOmica.

Details

- In MathIOmica the calculations utilize what we term an OmicsObject. OmicsObjectCreator[*outerLabels*, *innerLabels*, *measurements*, *metadata*] allows the creation of an OmicsObject. It uses the following inputs:

outerLabels	Outer labels (keys) for the OmicsObject.
innerLabels	Inner labels (keys) for identifiers in the OmicsObject.
measurements	List of measurements for each inner label.
metadata	List of metadata for each label.

Examples (3)

Basic Examples (2)

We first need the MathIOmica package loaded.

In[1]:=
```
Needs["MathIOmica`"]
```

We can illustrate the structure of the OmicsObject with the following example:

In[2]:=
```
outerLabels = {"OuterLabel1", "OuterLabel2"};
innerLabels = {{"InnerLabel1", "InnerLabel2", "InnerLabel3", "InnerLabel4"},
  {"InnerLabel1", "InnerLabel2", "InnerLabel5"}};
measurements = {{{"Measurements11"}, {"Measurements12"}, {"Measurements13"}, {"Measurements14"}},
   {{"Measurements21"}, {"Measurements22"}, {"Measurements25"}}};
metadata = {{{"Metadata11"}, {"Metadata12"}, {"Metadata13"}, {"Metadata14"}},
   {{"Metadata21"}, {"Metadata22"}, {"Metadata25"}}};
```

In[3]:=
```
OmicsObjectCreator[outerLabels, innerLabels, measurements, metadata]
```

Out[3]=
```
<|OuterLabel1 → <|InnerLabel1 → {{Measurements11}, {Metadata11}},
   InnerLabel2 → {{Measurements12}, {Metadata12}}, InnerLabel3 → {{Measurements13}, {Metadata13}},
   InnerLabel4 → {{Measurements14}, {Metadata14}}, InnerLabel5 → Missing[]|>,
 OuterLabel2 → <|InnerLabel1 → {{Measurements21}, {Metadata21}}, InnerLabel2 → {{Measurements22}, {Metadata22}},
   InnerLabel3 → Missing[], InnerLabel4 → Missing[], InnerLabel5 → {{Measurements25}, {Metadata25}}|>|>
```

As another example let's assume we have three samples:

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```
In[1]:= outerLabelsSample = {"FirstSample", "SecondSample", "ThirdSample"};
```

For each sample we have identifiers for the proteins measured. Note that not all protein identifiers are in all samples.

```
In[2]:= proteinAccessions = {{{"A0AVT1"}, {"A0MZ66"}, {"A1A4S6"}, {"A1L0T0"}},
          {{"A0AVT1"}, {"A0FGR8"}, {"A1A4S6"}, {"A1L0T0"}}, {{"A0AVT1"}, {"A0FGR8"}, {"A1A4S6"}}};
```

We have relative intensities for each measurement:

```
In[3]:= intensities =
          {{{0.937}, {1.059}, {1.03}, {1.268}}, {{1.003}, {0.921}, {0.779}, {0.917}}, {{1.064}, {0.87}, {0.545}}};
```

In this example we also want to track the number of peptides identified as metadata.

```
In[4]:= numberOfPeptidesMetadata = {{{17}, {9}, {11}, {4}}, {{17}, {24}, {11}, {4}}, {{19}, {23}, {5}}};
```

We can now create our OmicsObject manually:

```
In[5]:= OmicsObjectCreator[outerLabelsSample, proteinAccessions, intensities, numberOfPeptidesMetadata]

Out[5]= <|FirstSample → <|{A0AVT1} → {{0.937}, {17}}, {A0MZ66} → {{1.059}, {9}},
            {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[]|>,
          SecondSample → <|{A0AVT1} → {{1.003}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.779}, {11}},
            {A1L0T0} → {{0.917}, {4}}, {A0FGR8} → {{0.921}, {24}}|>,
          ThirdSample → <|{A0AVT1} → {{1.064}, {19}}, {A0MZ66} → Missing[],
            {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {23}}|>|>
```

Properties & Relations (1)

DataImporter, DataImporterDirect and DataImporterDirectLabeled import data from external files to create an OmicsObject.

See Also

Applier ▪ **ApplierList** ▪ **DataImporter** ▪ **DataImporterDirect** ▪ **DataImporterDirectLabeled** ▪ **EnlargeInnerAssociation** ▪ **EnlargeOuterAssociation** ▪ **FileSelector** ▪ **OmicsObject** ▪ **Returner**

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OmicsObjectMerge

OmicsObjectMerge[{*omicsObject*$_1$, *omicsObject*$_2$, …}, *f*]

merges a list of OmicsObject components {omicsObject1,omicsObject2,…}, using the function f to combine values with the same inner and outer keys.

Details

- OmicsObjectMerge[{*omicsObject*$_1$, *omicsObject*$_2$, …}, *f*] can merge a list of multiple omics objects, where the function *f* is applied to lists of values that share the same inner and outer key. Non-matching keys, or missing Keys are replaced by Missing[].
- The following options can be given:

MissingTest	MemberQ[#1, __Missing | {{__Missing}, __} | {__Missing, __}] || Length[#1] < #2 &	MissingTest is an option for functions that merge OmicsObject components that specifies the test function used to assign a Missing[] value. The first input is the list of values with matched keys. The second input is the length of the input OmicsObject lists.
MissingReplacement	Missing[]	MissingReplacement is an option for functions that handle missing data that indicates what value missing data should be globally assigned.

Examples (3)

Basic Examples (1)

We first load MathIOmica:

In[1]:=
```
Needs["MathIOmica`"]
```

Let's consider the following two OmicsObject variables:

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```
In[2]:= object1 = <|"FirstSample" → <|{"Symbol1", "RNA"} → {{0.937}, {1, 1}},
          {"Symbol2", "RNA"} → {{1.059}, {1, 1}}, {"Symbol3", "RNA"} → {{1.03}, {1, 1}},
          {"Symbol4", "RNA"} → {{1.268}, {1, 1}}, {"Symbol5", "RNA"} → Missing[]|>,
        "SecondSample" → <|{"Symbol1", "RNA"} → {{1.003}, {1, 2}}, {"Symbol2", "RNA"} → Missing[],
          {"Symbol3", "RNA"} → {{0.779}, {1, 2}}, {"Symbol4", "RNA"} → {{0.917}, {1, 2}},
          {"Symbol5", "RNA"} → {{0.921}, {1, 2}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.064}, {1, 3}},
          {"Symbol2", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{0.545}, {1, 3}},
          {"Symbol4", "RNA"} → Missing[], {"Symbol5", "RNA"} → {{0.87}, {1, 3}}|>|>;
      object2 = <|"FirstSample" → <|{"Symbol1", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{1.03}, {2, 1}},
          {"Symbol4", "RNA"} → {{1.268}, {2, 1}}, {"Symbol5", "RNA"} → Missing[],
          {"Symbol6", "RNA"} → {{1.1}, {2, 1}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.003}, {2, 3}},
          {"Symbol3", "RNA"} → {{0.779}, {2, 3}}, {"Symbol4", "RNA"} → {{0.917}, {2, 3}},
          {"Symbol5", "RNA"} → {{0.921}, {2, 3}}, {"Symbol6", "RNA"} → {{1.1}, {2, 3}}|>, "FourthSample" →
         <|{"Symbol1", "RNA"} → {{1.064}, {2, 4}}, {"Symbol3", "RNA"} → {{0.545}, {2, 4}}, {"Symbol4", "RNA"} →
           Missing[], {"Symbol5", "RNA"} → {{0.87}, {2, 4}}, {"Symbol6", "RNA"} → {{1.1}, {2, 4}}|>|>;
      object3 = <|"FirstSample" → <|{"Symbol3", "RNA"} → {{1.03}, {3, 1}}, {"Symbol4", "RNA"} → {{1.268}, {3, 1}},
          {"Symbol5", "RNA"} → Missing[], {"Symbol6", "RNA"} → {{1.1}, {3, 1}}|>,
        "ThirdSample" → <|{"Symbol3", "RNA"} → {{0.779}, {3, 3}}, {"Symbol4", "RNA"} → {{0.917}, {3, 3}},
          {"Symbol5", "RNA"} → {{0.921}, {3, 3}}, {"Symbol6", "RNA"} → {{1.1}, {3, 3}}|>,
        "FourthSample" → <|{"Symbol3", "RNA"} → {{0.545}, {3, 4}}, {"Symbol4", "RNA"} → Missing[],
          {"Symbol5", "RNA"} → {{0.87}, {3, 4}}, {"Symbol6", "RNA"} → {{1.1}, {3, 4}}|>|>;
```

We now want to calculate the return the matched samples and matched symbols. We use Identity as the merging function to obtain a full list of the corresponding values:

```
In[3]:= OmicsObjectMerge[{object1, object2, object3}, Identity]

Out[3]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → {{{1.03}, {1, 1}}, {{1.03}, {2, 1}}, {{1.03}, {3, 1}}},
          {Symbol4, RNA} → {{{1.268}, {1, 1}}, {{1.268}, {2, 1}}, {{1.268}, {3, 1}}},
          {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
        SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>,
        ThirdSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → {{{0.545}, {1, 3}}, {{0.779}, {2, 3}}, {{0.779}, {3, 3}}}, {Symbol4, RNA} → Missing[],
          {Symbol5, RNA} → {{{0.87}, {1, 3}}, {{0.921}, {2, 3}}, {{0.921}, {3, 3}}}, {Symbol6, RNA} → Missing[]|>,
        FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

We can also use any function f that will act on the list of matched values:

```
In[4]:= OmicsObjectMerge[{object1, object2, object3}, f]

Out[4]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → f[{{{1.03}, {1, 1}}, {{1.03}, {2, 1}}, {{1.03}, {3, 1}}}],
          {Symbol4, RNA} → f[{{{1.268}, {1, 1}}, {{1.268}, {2, 1}}, {{1.268}, {3, 1}}}],
          {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
        SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>,
        ThirdSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → f[{{{0.545}, {1, 3}}, {{0.779}, {2, 3}}, {{0.779}, {3, 3}}}], {Symbol4, RNA} → Missing[],
          {Symbol5, RNA} → f[{{{0.87}, {1, 3}}, {{0.921}, {2, 3}}, {{0.921}, {3, 3}}}], {Symbol6, RNA} → Missing[]|>,
        FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

For a specific example, let's calculate get all values from the first Measurement value in the first input OmicsObject:

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```
In[5]:= OmicsObjectMerge[{object1, object2, object3}, (#[[All, 1]] &)]

Out[5]= <|FirstSample →
    <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} → {{1.03}, {1.03}, {1.03}},
     {Symbol4, RNA} → {{1.268}, {1.268}, {1.268}}, {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
  SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} → Missing[],
     {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>, ThirdSample →
    <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} → {{0.545}, {0.779}, {0.779}},
     {Symbol4, RNA} → Missing[], {Symbol5, RNA} → {{0.87}, {0.921}, {0.921}}, {Symbol6, RNA} → Missing[]|>,
  FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
     {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

Options (2)

MissingTest (1)

```
In[1]:= Needs["MathIOmica`"]
```

`MissingTest` is an option for functions that merge OmicsObject components that specifies the test function used to assign a Missing[] value. The first input is the list of values with matched keys. The second input is the length of the input OmicsObject lists. The function is applied to lists of inner values that share the same inner and outer keys. We consider here the following objects:

```
In[2]:= object1 = <|"FirstSample" → <|{"Symbol1", "RNA"} → {{0.937}, {1, 1}},
     {"Symbol2", "RNA"} → {{1.059}, {1, 1}}, {"Symbol3", "RNA"} → {{1.03}, {1, 1}},
     {"Symbol4", "RNA"} → {{1.268}, {1, 1}}, {"Symbol5", "RNA"} → Missing[]|>,
   "SecondSample" → <|{"Symbol1", "RNA"} → {{1.003}, {1, 2}}, {"Symbol2", "RNA"} → Missing[],
     {"Symbol3", "RNA"} → {{0.779}, {1, 2}}, {"Symbol4", "RNA"} → {{0.917}, {1, 2}},
     {"Symbol5", "RNA"} → {{0.921}, {1, 2}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.064}, {1, 3}},
     {"Symbol2", "RNA"} → {Missing[], {1, 3}}, {"Symbol3", "RNA"} → {{0.545}, {1, 3}},
     {"Symbol4", "RNA"} → Missing[], {"Symbol5", "RNA"} → {{0.87}, {1, 3}}|>|>;
 object2 = <|"FirstSample" → <|{"Symbol1", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{1.03}, {2, 1}},
     {"Symbol4", "RNA"} → {{1.268}, {2, 1}}, {"Symbol5", "RNA"} → Missing[],
     {"Symbol6", "RNA"} → {{1.1}, {2, 1}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.003}, {2, 3}},
     {"Symbol3", "RNA"} → {{0.779}, {2, 3}}, {"Symbol4", "RNA"} → {{0.917}, {2, 3}},
     {"Symbol5", "RNA"} → {{0.921}, {2, 3}}, {"Symbol6", "RNA"} → {{1.1}, {2, 3}}|>, "FourthSample" →
    <|{"Symbol1", "RNA"} → {{1.064}, {2, 4}}, {"Symbol3", "RNA"} → {{0.545}, {2, 4}}, {"Symbol4", "RNA"} →
      Missing[], {"Symbol5", "RNA"} → {{0.87}, {2, 4}}, {"Symbol6", "RNA"} → {{1.1}, {2, 4}}|>|>;
 object3 = <|"FirstSample" → <|{"Symbol3", "RNA"} → {{1.03}, {3, 1}}, {"Symbol4", "RNA"} → {{1.268}, {3, 1}},
     {"Symbol5", "RNA"} → Missing[], {"Symbol6", "RNA"} → {{1.1}, {3, 1}}|>,
   "ThirdSample" → <|{"Symbol3", "RNA"} → {{0.779}, {3, 3}}, {"Symbol4", "RNA"} → {{0.917}, {3, 3}},
     {"Symbol5", "RNA"} → {{0.921}, {3, 3}}, {"Symbol6", "RNA"} → {{1.1}, {3, 3}}|>,
   "FourthSample" → <|{"Symbol3", "RNA"} → {{0.545}, {3, 4}}, {"Symbol4", "RNA"} → Missing[],
     {"Symbol5", "RNA"} → {{0.87}, {3, 4}}, {"Symbol6", "RNA"} → {{1.1}, {3, 4}}|>|>;
```

The default `MissingTest` option value is a function that tests whether any of the matched entities have a Missing[] value, or if any one of them does not have a values list:

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```
In[3]:= OmicsObjectMerge[{object1, object2, object3}, Identity,
         MissingTest → ((MemberQ[#1, __Missing | {{__Missing}, __} | {__Missing, __}] || Length[#1] < #2) &)]

Out[3]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → {{{1.03}, {1, 1}}, {{1.03}, {2, 1}}, {{1.03}, {3, 1}}},
           {Symbol4, RNA} → {{{1.268}, {1, 1}}, {{1.268}, {2, 1}}, {{1.268}, {3, 1}}},
           {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
         SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>,
         ThirdSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → {{{0.545}, {1, 3}}, {{0.779}, {2, 3}}, {{0.779}, {3, 3}}}, {Symbol4, RNA} → Missing[],
           {Symbol5, RNA} → {{{0.87}, {1, 3}}, {{0.921}, {2, 3}}, {{0.921}, {3, 3}}}, {Symbol6, RNA} → Missing[]|>,
         FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
           {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

For another example, let's set the `MissingTest` to a function that also tests for any Measurement values across the OmicsObject inputs being merged having a value less than a constant, say 0.6:

```
In[4]:= valuesSmall = (MemberQ[#1, __Missing | {{__Missing}, __} | {__Missing, __}] ||
            Length[#1] < #2 || Count[#1[[All, 1, 1]], x_ /; x ≤ 0.6] ≥ 1 &);

In[5]:= OmicsObjectMerge[{object1, object2, object3}, Identity, MissingTest → valuesSmall]

Out[5]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → {{{1.03}, {1, 1}}, {{1.03}, {2, 1}}, {{1.03}, {3, 1}}},
           {Symbol4, RNA} → {{{1.268}, {1, 1}}, {{1.268}, {2, 1}}, {{1.268}, {3, 1}}},
           {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
         SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>,
         ThirdSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[],
           {Symbol5, RNA} → {{{0.87}, {1, 3}}, {{0.921}, {2, 3}}, {{0.921}, {3, 3}}}, {Symbol6, RNA} → Missing[]|>,
         FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
           {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

MissingReplacement (1)

```
In[1]:= Needs["MathIOmica`"]
```

`MissingReplacement` is an option for functions that handle missing data that indicates what value missing data should be globally assigned. We consider here the following two objects:

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```
In[2]:= object1 = <|"FirstSample" → <|{"Symbol1", "RNA"} → {{0.937}, {1, 1}},
          {"Symbol2", "RNA"} → {{1.059}, {1, 1}}, {"Symbol3", "RNA"} → {{1.03}, {1, 1}},
          {"Symbol4", "RNA"} → {{1.268}, {1, 1}}, {"Symbol5", "RNA"} → Missing[]|>,
        "SecondSample" → <|{"Symbol1", "RNA"} → {{1.003}, {1, 2}}, {"Symbol2", "RNA"} → Missing[],
          {"Symbol3", "RNA"} → {{0.779}, {1, 2}}, {"Symbol4", "RNA"} → {{0.917}, {1, 2}},
          {"Symbol5", "RNA"} → {{0.921}, {1, 2}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.064}, {1, 3}},
          {"Symbol2", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{0.545}, {1, 3}},
          {"Symbol4", "RNA"} → Missing[], {"Symbol5", "RNA"} → {{0.87}, {1, 3}}|>|>;
      object2 = <|"FirstSample" → <|{"Symbol1", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{1.03}, {2, 1}},
          {"Symbol4", "RNA"} → {{1.268}, {2, 1}}, {"Symbol5", "RNA"} → Missing[],
          {"Symbol6", "RNA"} → {{1.1}, {2, 1}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.003}, {2, 3}},
          {"Symbol3", "RNA"} → {{0.779}, {2, 3}}, {"Symbol4", "RNA"} → {{0.917}, {2, 3}},
          {"Symbol5", "RNA"} → {{0.921}, {2, 3}}, {"Symbol6", "RNA"} → {{1.1}, {2, 3}}|>, "FourthSample" →
         <|{"Symbol1", "RNA"} → {{1.064}, {2, 4}}, {"Symbol3", "RNA"} → {{0.545}, {2, 4}}, {"Symbol4", "RNA"} →
           Missing[], {"Symbol5", "RNA"} → {{0.87}, {2, 4}}, {"Symbol6", "RNA"} → {{1.1}, {2, 4}}|>|>;
      object3 = <|"FirstSample" → <|{"Symbol3", "RNA"} → {{1.03}, {3, 1}}, {"Symbol4", "RNA"} → {{1.268}, {3, 1}},
          {"Symbol5", "RNA"} → Missing[], {"Symbol6", "RNA"} → {{1.1}, {3, 1}}|>,
        "ThirdSample" → <|{"Symbol3", "RNA"} → {{0.779}, {3, 3}}, {"Symbol4", "RNA"} → {{0.917}, {3, 3}},
          {"Symbol5", "RNA"} → {{0.921}, {3, 3}}, {"Symbol6", "RNA"} → {{1.1}, {3, 3}}|>,
        "FourthSample" → <|{"Symbol3", "RNA"} → {{0.545}, {3, 4}}, {"Symbol4", "RNA"} → Missing[],
          {"Symbol5", "RNA"} → {{0.87}, {3, 4}}, {"Symbol6", "RNA"} → {{1.1}, {3, 4}}|>|>;
```

The default is to replace missing values with Missing[]:

```
In[3]:= OmicsObjectMerge[{object1, object2, object3}, Identity, MissingReplacement → Missing[]]

Out[3]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → {{{1.03}, {1, 1}}, {{1.03}, {2, 1}}, {{1.03}, {3, 1}}},
          {Symbol4, RNA} → {{{1.268}, {1, 1}}, {{1.268}, {2, 1}}, {{1.268}, {3, 1}}},
          {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
        SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>,
        ThirdSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → {{{0.545}, {1, 3}}, {{0.779}, {2, 3}}, {{0.779}, {3, 3}}}, {Symbol4, RNA} → Missing[],
          {Symbol5, RNA} → {{{0.87}, {1, 3}}, {{0.921}, {2, 3}}, {{0.921}, {3, 3}}}, {Symbol6, RNA} → Missing[]|>,
        FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

For another example, we replace the values with a string:

```
In[4]:= OmicsObjectMerge[{object1, object2, object3}, Identity, MissingReplacement → "Data Not Found"]

Out[4]= <|FirstSample → <|{Symbol1, RNA} → Data Not Found, {Symbol2, RNA} → Data Not Found,
          {Symbol3, RNA} → {{{1.03}, {1, 1}}, {{1.03}, {2, 1}}, {{1.03}, {3, 1}}},
          {Symbol4, RNA} → {{{1.268}, {1, 1}}, {{1.268}, {2, 1}}, {{1.268}, {3, 1}}},
          {Symbol5, RNA} → Data Not Found, {Symbol6, RNA} → Data Not Found|>,
        SecondSample → <|{Symbol1, RNA} → Data Not Found, {Symbol2, RNA} → Data Not Found,
          {Symbol3, RNA} → Data Not Found, {Symbol4, RNA} → Data Not Found, {Symbol5, RNA} → Data Not Found|>,
        ThirdSample → <|{Symbol1, RNA} → Data Not Found, {Symbol2, RNA} → Data Not Found,
          {Symbol3, RNA} → {{{0.545}, {1, 3}}, {{0.779}, {2, 3}}, {{0.779}, {3, 3}}},
          {Symbol4, RNA} → Data Not Found, {Symbol5, RNA} → {{{0.87}, {1, 3}}, {{0.921}, {2, 3}}, {{0.921}, {3, 3}}},
          {Symbol6, RNA} → Data Not Found|>,
        FourthSample → <|{Symbol1, RNA} → Data Not Found, {Symbol3, RNA} → Data Not Found,
          {Symbol4, RNA} → Data Not Found, {Symbol5, RNA} → Data Not Found, {Symbol6, RNA} → Data Not Found|>|>
```

See Also

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ConstantAssociator ▪ **DataImporter** ▪ **DataImporterDirect** ▪ **DataImporterDirectLabeled** ▪ **EnlargeInnerAssociation** ▪ **EnlargeOuterAssociation** ▪ **JoinNestedAssociations** ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **OmicsObjectPairedMerge**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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OmicsObjectPairedMerge

OmicsObjectPairedMerge[$omicsObject_1$, $omicsObject_2$]
merges pairwise omicsObject1 and omicsObject2 values that have the same inner and outer keys.

Details

- OmicsObjectPairedMerge[$omicsObject_1$, $omicsObject_2$] is designed to work two paired OmicObject data and merge them into a new OmicsObject.
- The input for OmicsObjectPairedMerge is two OmicsObject entities, $omicsObject_1$ and $omicsObject_2$ that are combined to generate the new OmicsObject. The inputs are matched on both inner and outer keys.
- The default output OmicsObject is set by the option FunctionForm, and has as output the difference in matched measurements between $omicsObject_1$ and $omicsObject_2$ for each matched outer label i and matched inner label j. Unmatched inner labels q are set to Missing[]. Similarly, all inner label values n for unmatched outer labels p are set to Missing[]. Schematically this is shown below:
-
```
<| ...,
  MatchedOuterLabel_i → <| ...,
     MatchedInnerLabel_j → {{(omicsObject_1 Measurement_ij) - (omicsObject_2 Measurement_ij)}, <|
        Metadata 1 -> {omicsObject_1 Metadata_ij}, Metadata 2 -> {omicsObject_2 Metadata_ij}|>}, ...,
     UnMatchedInnerLabel_q → Missing[], ...|>, ...,
  UnMatchedOuterLabel_p → <| ..., AnyInnerLabel_n → Missing[], ...|>, ...,
  ...|>
```
- The following options can be given:

FunctionForm	{#[[1, 1]] - #[[2, 1]], Association[Metadata 1 -> #[[1, 2]], Metadata 2 -> #[[2, 2]]]} &	FunctionForm is an option for OmicsObjectPairedMerge that specifies the function used in combining paired values from the two OmicsObject inputs. The function is applied to lists of inner values that share the same inner and out keys. The list entries for entries 1 and 2 matching have the following general form: {{{$Measurement_1$}, {$Metadata_1$}}, {{$Measurement_2$}, {$Metadata_2$}}},

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MissingTest	MemberQ[#, __Missing | {{__Missing}, __} | {__Missing, __}] || Length[#] < 2 &	MissingTest is an option for functions that merge OmicsObject components that specifies the test function used to assign a Missing[] value. The function is applied to lists of inner values that share the same inner and outer keys. The list entries for entries 1 and 2 matching have the following general form: $\{\{\{\text{Measurement}_1\}, \{\text{Metadata}_1\}\}, \{\{\text{Measurement}_2\}, \{\text{Metadata}_2\}\}\}$,
MissingReplacement	Missing[]	MissingReplacement is an option for functions that handle missing data that indicates what value missing data should be globally assigned.

Examples (4)

Basic Examples (1)

We first load MathIOmica:

```
In[1]:= Needs["MathIOmica`"]
```

Let's consider the following two OmicsObject variables:

```
In[2]:= object1 = <|"FirstSample" → <|{"Symbol1", "RNA"} → {{0.937}, {1, 1}},
          {"Symbol2", "RNA"} → {{1.059}, {1, 1}}, {"Symbol3", "RNA"} → {{1.03}, {1, 1}},
          {"Symbol4", "RNA"} → {{1.268}, {1, 1}}, {"Symbol5", "RNA"} → Missing[]|>,
        "SecondSample" → <|{"Symbol1", "RNA"} → {{1.003}, {1, 2}}, {"Symbol2", "RNA"} → Missing[],
          {"Symbol3", "RNA"} → {{0.779}, {1, 2}}, {"Symbol4", "RNA"} → {{0.917}, {1, 2}},
          {"Symbol5", "RNA"} → {{0.921}, {1, 2}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.064}, {1, 3}},
          {"Symbol2", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{0.545}, {1, 3}},
          {"Symbol4", "RNA"} → Missing[], {"Symbol5", "RNA"} → {{0.87}, {1, 3}}|>|>;
      object2 = <|"FirstSample" → <|{"Symbol1", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{1.03}, {2, 1}},
          {"Symbol4", "RNA"} → {{1.268}, {2, 1}}, {"Symbol5", "RNA"} → Missing[],
          {"Symbol6", "RNA"} → {{1.1}, {2, 1}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.003}, {2, 3}},
          {"Symbol3", "RNA"} → {{0.779}, {2, 3}}, {"Symbol4", "RNA"} → {{0.917}, {2, 3}},
          {"Symbol5", "RNA"} → {{0.921}, {2, 3}}, {"Symbol6", "RNA"} → {{1.1}, {2, 3}}|>, "FourthSample" →
         <|{"Symbol1", "RNA"} → {{1.064}, {2, 4}}, {"Symbol3", "RNA"} → {{0.545}, {2, 4}}, {"Symbol4", "RNA"} →
           Missing[], {"Symbol5", "RNA"} → {{0.87}, {2, 4}}, {"Symbol6", "RNA"} → {{1.1}, {2, 4}}|>|>;
```

We now want to calculate the measurement differences for matched samples and matched symbols:

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```
In[3]:= OmicsObjectPairedMerge[object1, object2]

Out[3]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
          {Symbol4, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
          {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
        SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>, ThirdSample →
         <|{Symbol1, RNA} → {{0.061}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → {{-0.234}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol4, RNA} → Missing[],
          {Symbol5, RNA} → {{-0.051}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol6, RNA} → Missing[]|>,
        FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

Options (3)

FunctionForm (1)

```
In[1]:= Needs["MathIOmica`"]
```

FuncitonForm is a function used internally to perform OmicsObjectPairedMerge . It specifies the function used in combining paired values from the two OmicsObject inputs. We consider the following two OmicsObject variables:

```
In[2]:= object1 = <|"FirstSample" → <|{"Symbol1", "RNA"} → {{0.937}, {1, 1}},
          {"Symbol2", "RNA"} → {{1.059}, {1, 1}}, {"Symbol3", "RNA"} → {{1.03}, {1, 1}},
          {"Symbol4", "RNA"} → {{1.268}, {1, 1}}, {"Symbol5", "RNA"} → Missing[]|>,
        "SecondSample" → <|{"Symbol1", "RNA"} → {{1.003}, {1, 2}}, {"Symbol2", "RNA"} → Missing[],
          {"Symbol3", "RNA"} → {{0.779}, {1, 2}}, {"Symbol4", "RNA"} → {{0.917}, {1, 2}},
          {"Symbol5", "RNA"} → {{0.921}, {1, 2}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.064}, {1, 3}},
          {"Symbol2", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{0.545}, {1, 3}},
          {"Symbol4", "RNA"} → Missing[], {"Symbol5", "RNA"} → {{0.87}, {1, 3}}|>|>;
      object2 = <|"FirstSample" → <|{"Symbol1", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{1.03}, {2, 1}},
          {"Symbol4", "RNA"} → {{1.268}, {2, 1}}, {"Symbol5", "RNA"} → Missing[],
          {"Symbol6", "RNA"} → {{1.1}, {2, 1}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.003}, {2, 3}},
          {"Symbol3", "RNA"} → {{0.779}, {2, 3}}, {"Symbol4", "RNA"} → {{0.917}, {2, 3}},
          {"Symbol5", "RNA"} → {{0.921}, {2, 3}}, {"Symbol6", "RNA"} → {{1.1}, {2, 3}}|>, "FourthSample" →
         <|{"Symbol1", "RNA"} → {{1.064}, {2, 4}}, {"Symbol3", "RNA"} → {{0.545}, {2, 4}}, {"Symbol4", "RNA"} →
           Missing[], {"Symbol5", "RNA"} → {{0.87}, {2, 4}}, {"Symbol6", "RNA"} → {{1.1}, {2, 4}}|>|>;

In[3]:= OmicsObjectPairedMerge[object1, object2]

Out[3]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
          {Symbol4, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
          {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
        SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>, ThirdSample →
         <|{Symbol1, RNA} → {{0.061}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → {{-0.234}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol4, RNA} → Missing[],
          {Symbol5, RNA} → {{-0.051}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol6, RNA} → Missing[]|>,
        FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

Instead of the default, let us know list both values of the matched object labels and combine the metadata to explicitly identify measurement 1 and 2:

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```
In[4]:= OmicsObjectPairedMerge[object1, object2,
         FunctionForm → ({<|"Measurement 1" → #[[1, 1]], "Measurement 2" → #[[2, 1]]|>,
             Association["Metadata 1" -> #[[1, 2]], "Metadata 2" -> #[[2, 2]]]} &)]

Out[4]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} →
            {<|Measurement 1 → {1.03}, Measurement 2 → {1.03}|>, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
          {Symbol4, RNA} → {<|Measurement 1 → {1.268}, Measurement 2 → {1.268}|>,
            <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>}, {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
        SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>,
        ThirdSample → <|{Symbol1, RNA} → {<|Measurement 1 → {1.064}, Measurement 2 → {1.003}|>,
            <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol2, RNA} → Missing[], {Symbol3, RNA} →
            {<|Measurement 1 → {0.545}, Measurement 2 → {0.779}|>, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>},
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → {<|Measurement 1 → {0.87}, Measurement 2 → {0.921}|>,
            <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol6, RNA} → Missing[]|>,
        FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[],
          {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

To see the inputs explicitly, we set the function to a general function f:

```
In[5]:= OmicsObjectPairedMerge[object1, object2, FunctionForm → f]

Out[5]= <|FirstSample → <|{Symbol1, RNA} → Missing[],
          {Symbol2, RNA} → Missing[], {Symbol3, RNA} → f[{{{1.03}, {1, 1}}, {{1.03}, {2, 1}}}],
          {Symbol4, RNA} → f[{{{1.268}, {1, 1}}, {{1.268}, {2, 1}}}],
          {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
        SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>,
        ThirdSample → <|{Symbol1, RNA} → f[{{{1.064}, {1, 3}}, {{1.003}, {2, 3}}}], {Symbol2, RNA} → Missing[],
          {Symbol3, RNA} → f[{{{0.545}, {1, 3}}, {{0.779}, {2, 3}}}], {Symbol4, RNA} → Missing[],
          {Symbol5, RNA} → f[{{{0.87}, {1, 3}}, {{0.921}, {2, 3}}}], {Symbol6, RNA} → Missing[]|>,
        FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
          {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

MissingTest (1)

```
In[1]:= Needs["MathIOmica`"]
```

MissingTest is an option for functions that merge OmicsObject components that specifies the test function used to assign a Missing[] value. The function is applied to lists of inner values that share the same inner and outer keys. We consider here the following two objects:

```
In[2]:= object1 = <|"FirstSample" → <|{"Symbol1", "RNA"} → {{0.937}, {1, 1}},
            {"Symbol2", "RNA"} → {{1.059}, {1, 1}}, {"Symbol3", "RNA"} → {{1.03}, {1, 1}},
            {"Symbol4", "RNA"} → {{1.268}, {1, 1}}, {"Symbol5", "RNA"} → Missing[]|>,
          "SecondSample" → <|{"Symbol1", "RNA"} → {{1.003}, {1, 2}}, {"Symbol2", "RNA"} → Missing[],
            {"Symbol3", "RNA"} → {{0.779}, {1, 2}}, {"Symbol4", "RNA"} → {{0.917}, {1, 2}},
            {"Symbol5", "RNA"} → {{0.921}, {1, 2}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.064}, {1, 3}},
            {"Symbol2", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{0.545}, {1, 3}},
            {"Symbol4", "RNA"} → Missing[], {"Symbol5", "RNA"} → {{0.87}, {1, 3}}|>|>;
        object2 = <|"FirstSample" → <|{"Symbol1", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{1.03}, {2, 1}},
            {"Symbol4", "RNA"} → {{1.268}, {2, 1}}, {"Symbol5", "RNA"} → Missing[],
            {"Symbol6", "RNA"} → {{1.1}, {2, 1}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.003}, {2, 3}},
            {"Symbol3", "RNA"} → {{0.779}, {2, 3}}, {"Symbol4", "RNA"} → {{0.917}, {2, 3}},
            {"Symbol5", "RNA"} → {{0.921}, {2, 3}}, {"Symbol6", "RNA"} → {{1.1}, {2, 3}}|>, "FourthSample" →
          <|{"Symbol1", "RNA"} → {{1.064}, {2, 4}}, {"Symbol3", "RNA"} → {{0.545}, {2, 4}}, {"Symbol4", "RNA"} →
            Missing[], {"Symbol5", "RNA"} → {{0.87}, {2, 4}}, {"Symbol6", "RNA"} → {{1.1}, {2, 4}}|>|>;
```

The default MissingTest option value is a function that tests whether either of the

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matched entities have a Missing[] value, or only one of them has values:

```
In[3]:= OmicsObjectPairedMerge[object1, object2,
         MissingTest → (MemberQ[#, __Missing | {{__Missing}, __} | {__Missing, __}] || Length[#] < 2 &)]

Out[3]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
           {Symbol4, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
           {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
         SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} → Missing[],
           {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>, ThirdSample →
          <|{Symbol1, RNA} → {{0.061}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → {{-0.234}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol4, RNA} → Missing[],
           {Symbol5, RNA} → {{-0.051}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol6, RNA} → Missing[]|>,
         FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
           {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

For another example, let's set the `MissingTest` to a function that also tests for both values less than a constant, say 0.9.

```
In[4]:= missingTestFunction = (MemberQ[#, __Missing | {{__Missing}, __} | {__Missing, __}] ||
           Length[#] < 2 || ((#[[1, 1, 1]]) < 1 && (#[[2, 1, 1]] < 1))) &;

In[5]:= OmicsObjectPairedMerge[object1, object2, MissingTest → missingTestFunction]

Out[5]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
           {Symbol4, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
           {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
         SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
           {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>,
         ThirdSample → <|{Symbol1, RNA} → {{0.061}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>},
           {Symbol2, RNA} → Missing[], {Symbol3, RNA} → Missing[], {Symbol4, RNA} → Missing[],
           {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
         FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
           {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

MissingReplacement (1)

```
In[1]:= Needs["MathIOmica`"]
```

`MissingReplacement` is an option for functions that handle missing data that indicates what value missing data should be globally assigned. We consider here the following two objects:

```
In[2]:= object1 = <|"FirstSample" → <|{"Symbol1", "RNA"} → {{0.937}, {1, 1}},
           {"Symbol2", "RNA"} → {{1.059}, {1, 1}}, {"Symbol3", "RNA"} → {{1.03}, {1, 1}},
           {"Symbol4", "RNA"} → {{1.268}, {1, 1}}, {"Symbol5", "RNA"} → Missing[]|>,
         "SecondSample" → <|{"Symbol1", "RNA"} → {{1.003}, {1, 2}}, {"Symbol2", "RNA"} → Missing[],
           {"Symbol3", "RNA"} → {{0.779}, {1, 2}}, {"Symbol4", "RNA"} → {{0.917}, {1, 2}},
           {"Symbol5", "RNA"} → {{0.921}, {1, 2}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.064}, {1, 3}},
           {"Symbol2", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{0.545}, {1, 3}},
           {"Symbol4", "RNA"} → Missing[], {"Symbol5", "RNA"} → {{0.87}, {1, 3}}|>|>;
       object2 = <|"FirstSample" → <|{"Symbol1", "RNA"} → Missing[], {"Symbol3", "RNA"} → {{1.03}, {2, 1}},
           {"Symbol4", "RNA"} → {{1.268}, {2, 1}}, {"Symbol5", "RNA"} → Missing[],
           {"Symbol6", "RNA"} → {{1.1}, {2, 1}}|>, "ThirdSample" → <|{"Symbol1", "RNA"} → {{1.003}, {2, 3}},
           {"Symbol3", "RNA"} → {{0.779}, {2, 3}}, {"Symbol4", "RNA"} → {{0.917}, {2, 3}},
           {"Symbol5", "RNA"} → {{0.921}, {2, 3}}, {"Symbol6", "RNA"} → {{1.1}, {2, 3}}|>, "FourthSample" →
          <|{"Symbol1", "RNA"} → {{1.064}, {2, 4}}, {"Symbol3", "RNA"} → {{0.545}, {2, 4}}, {"Symbol4", "RNA"} →
            Missing[], {"Symbol5", "RNA"} → {{0.87}, {2, 4}}, {"Symbol6", "RNA"} → {{1.1}, {2, 4}}|>|>;
```

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The default is to replace missing values with Missing[]:

```
In[3]:= OmicsObjectPairedMerge[object1, object2, MissingReplacement → Missing[]]

Out[3]= <|FirstSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[],
    {Symbol3, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
    {Symbol4, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
    {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>,
  SecondSample → <|{Symbol1, RNA} → Missing[], {Symbol2, RNA} → Missing[], {Symbol3, RNA} → Missing[],
    {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[]|>, ThirdSample →
   <|{Symbol1, RNA} → {{0.061}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol2, RNA} → Missing[],
    {Symbol3, RNA} → {{-0.234}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol4, RNA} → Missing[],
    {Symbol5, RNA} → {{-0.051}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>}, {Symbol6, RNA} → Missing[]|>,
  FourthSample → <|{Symbol1, RNA} → Missing[], {Symbol3, RNA} → Missing[],
    {Symbol4, RNA} → Missing[], {Symbol5, RNA} → Missing[], {Symbol6, RNA} → Missing[]|>|>
```

For another example, we replace the values with a string:

```
In[4]:= OmicsObjectPairedMerge[object1, object2, MissingReplacement → "Data not Found"]

Out[4]= <|FirstSample → <|{Symbol1, RNA} → Data not Found, {Symbol2, RNA} → Data not Found,
    {Symbol3, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
    {Symbol4, RNA} → {{0.}, <|Metadata 1 → {1, 1}, Metadata 2 → {2, 1}|>},
    {Symbol5, RNA} → Data not Found, {Symbol6, RNA} → Data not Found|>,
  SecondSample → <|{Symbol1, RNA} → Data not Found, {Symbol2, RNA} → Data not Found,
    {Symbol3, RNA} → Data not Found, {Symbol4, RNA} → Data not Found, {Symbol5, RNA} → Data not Found|>,
  ThirdSample → <|{Symbol1, RNA} → {{0.061}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>},
    {Symbol2, RNA} → Data not Found, {Symbol3, RNA} → {{-0.234}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>},
    {Symbol4, RNA} → Data not Found, {Symbol5, RNA} → {{-0.051}, <|Metadata 1 → {1, 3}, Metadata 2 → {2, 3}|>},
    {Symbol6, RNA} → Data not Found|>,
  FourthSample → <|{Symbol1, RNA} → Data not Found, {Symbol3, RNA} → Data not Found,
    {Symbol4, RNA} → Data not Found, {Symbol5, RNA} → Data not Found, {Symbol6, RNA} → Data not Found|>|>
```

See Also

ConstantAssociator ▪ **DataImporter** ▪ **DataImporterDirect** ▪ **DataImporterDirectLabeled** ▪ **EnlargeInnerAssociation** ▪ **EnlargeOuterAssociation** ▪ **JoinNestedAssociations** ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **OmicsObjectMerge**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

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Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾

URL ▾

OmicsObjectUniqueMassConverter

`OmicsObjectUniqueMassConverter[omicsObject, massAccuracy]`
assigns a unique putative mass identification to each of *omicsObject*'s inner association keys, using the *massAccuracy* in parts per million.

Details

- `OmicsObjectUniqueMassConverter[omicsObject, massAccuracy]` assigns a unique putative mass identification to each of *omicsObject*'s inner association keys, using the *massAccuracy* in parts per million.
- If a unique mass identity match is found it is prepended to the front of the input identity. Otherwise the input identity is returned unchanged.
- The following options can be given:

MassMatcherOptions	{}	`MassMatcherOptions` is an option for MathIOmica functions that internally use MassMatcher, and provides a list of options to be passed to this internal MassMatcher function.

Examples (2)

Basic Examples (1)

First we need to load the MathIOmica package:

```
In[1]:= Needs["MathIOmica`"]
```

We consider the following example of an OmicsObject with metabolomics data:

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```
In[2]:= exampleOmicsObjectMetabolites = <|"8" → <|{200.0465`, 0.46338463`, "Meta"} →
          {{186943, 1, 142327}, {" [ C7 H9 Cl N4 O, db=0.00, overall=44.89, mfg=89.79 ]", ""}},
         {216.0412`, 0.4630277`, "Meta"} → {{9577920, 9465445, 8802456},
           {"Methoxsalen [ C12 H8 O4, db=53.88, overall=53.14, mfg=52.41, KEGG ID=C01864, CAS ID=298-81-7 ]",
            "298-81-7"}}, {150.0538`, 0.4622121`, "Meta"} →
          {{1, 131138, 133166}, {"1-Methylhypoxanthine [ C6 H6 N4 O, db=80.19, overall=77.83,
              mfg=82.46, KEGG ID=, CAS ID=1125-39-9 ]", "1125-39-9"}},
         {136.0382`, 0.46513885`, "Meta"} → {{133625, 133889, 145682}, {"Hypoxanthine [ C5 H4 N4
              O, db=94.36, overall=94.95, mfg=95.53, KEGG ID=C00262, CAS ID=68-94-0 ]",
            "68-94-0"}}, {192.0646`, 0.46539998`, "Meta"} → {{67369, 60605, 64663},
           {"Quinic acid [ C7 H12 O6, db=80.18, overall=81.10, mfg=82.01, KEGG ID=C00296, CAS ID=77-95-2 ]",
            "77-95-2"}}, {368.1161`, 0.46997148`, "Meta"} →
          {{53718, 49254, 72408}, {" [ C10 H24 O14, db=0.00, overall=45.84, mfg=91.69 ]", ""}},
         {466.9582`, 0.46816128`, "Meta"} → {{156680, 58129, 135681},
           {" [ C9 H20 Cl3 N3 O6 S3, db=0.00, overall=43.20, mfg=86.40 ]", ""}},
         {408.9988`, 0.46913895`, "Meta"} → {{244676, 201677, 213943},
           {" [ C14 H14 Cl3 N3 O5, db=0.00, overall=46.43, mfg=92.86 ]", ""}},
         {351.0404`, 0.47036007`, "Meta"} → {{256070, 232608, 241894},
           {" [ C13 H11 Cl2 N7 O, db=0.00, overall=44.47, mfg=88.94 ]", ""}},
         {293.0811`, 0.47077766`, "Meta"} → {{679912, 473539, 514175},
           {" [ C15 H16 Cl N O3, db=0.00, overall=46.76, mfg=93.52 ]", ""}},
         {278.0828`, 0.48142853`, "Meta"} → {{60750, 66349, 1}, {"Sulfadimidine [ C12 H14 N4 O2 S,
              db=77.19, overall=78.12, mfg=79.04, KEGG ID=, CAS ID=57-68-1 ]", "57-68-1"}}|>,
        "9" → <|{200.0465`, 0.46338463`, "Meta"} → {{151382, 159437, 145622},
           {" [ C7 H9 Cl N4 O, db=0.00, overall=44.89, mfg=89.79 ]", ""}},
         {216.0412`, 0.4630277`, "Meta"} → {{1.17`*^7, 1.16`*^7, 1.11`*^7},
           {"Methoxsalen [ C12 H8 O4, db=53.88, overall=53.14, mfg=52.41, KEGG ID=C01864, CAS ID=298-81-7 ]",
            "298-81-7"}}, {150.0538`, 0.4622121`, "Meta"} →
          {{126474, 117932, 126888}, {"1-Methylhypoxanthine [ C6 H6 N4 O, db=80.19,
              overall=77.83, mfg=82.46, KEGG ID=, CAS ID=1125-39-9 ]", "1125-39-9"}},
         {136.0382`, 0.46513885`, "Meta"} → {{169847, 127484, 145596}, {"Hypoxanthine [ C5 H4 N4
              O, db=94.36, overall=94.95, mfg=95.53, KEGG ID=C00262, CAS ID=68-94-0 ]",
            "68-94-0"}}, {192.0646`, 0.46539998`, "Meta"} → {{33170, 1, 39357},
           {"Quinic acid [ C7 H12 O6, db=80.18, overall=81.10, mfg=82.01, KEGG ID=C00296, CAS ID=77-95-2 ]",
            "77-95-2"}}, {368.1161`, 0.46997148`, "Meta"} →
          {{82246, 67519, 81785}, {" [ C10 H24 O14, db=0.00, overall=45.84, mfg=91.69 ]", ""}},
         {466.9582`, 0.46816128`, "Meta"} → {{26783, 191301, 142645},
           {" [ C9 H20 Cl3 N3 O6 S3, db=0.00, overall=43.20, mfg=86.40 ]", ""}},
         {408.9988`, 0.46913895`, "Meta"} → {{94484, 214406, 216930},
           {" [ C14 H14 Cl3 N3 O5, db=0.00, overall=46.43, mfg=92.86 ]", ""}},
         {351.0404`, 0.47036007`, "Meta"} → {{1, 232251, 244346},
           {" [ C13 H11 Cl2 N7 O, db=0.00, overall=44.47, mfg=88.94 ]", ""}},
         {293.0811`, 0.47077766`, "Meta"} → {{212466, 578496, 575496},
           {" [ C15 H16 Cl N O3, db=0.00, overall=46.76, mfg=93.52 ]", ""}},
         {278.0828`, 0.48142853`, "Meta"} → {{50542, 50832, 66481}, {"Sulfadimidine [ C12 H14 N4 O2 S,
              db=77.19, overall=78.12, mfg=79.04, KEGG ID=, CAS ID=57-68-1 ]", "57-68-1"}}|>|>;
```

We map putative unique identities across keys in this sample at 5 ppm:

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In[3]:=
```
OmicsObjectUniqueMassConverter[exampleOmicsObjectMetabolites, 5]
```

Out[3]=
```
<|8 → <|{cpd:C19444, 200.047, 0.463385, Meta} →
    {{186943, 1, 142327}, { [ C7 H9 Cl N4 O, db=0.00, overall=44.89, mfg=89.79 ], }},
   {216.041, 0.463028, Meta} → {{9577920, 9465445, 8802456},
     {Methoxsalen [ C12 H8 O4, db=53.88, overall=53.14, mfg=52.41, KEGG ID=C01864, CAS ID=298-81-7 ],
      298-81-7}}, {cpd:C08373, 150.054, 0.462212, Meta} →
    {{1, 131138, 133166}, {1-Methylhypoxanthine [ C6 H6 N4 O, db=80.19, overall=77.83,
        mfg=82.46, KEGG ID=, CAS ID=1125-39-9 ], 1125-39-9}},
   {cpd:C00262, 136.038, 0.465139, Meta} → {{133625, 133889, 145682},
     {Hypoxanthine [ C5 H4 N4 O, db=94.36, overall=94.95, mfg=95.53, KEGG ID=C00262, CAS ID=68-94-0 ],
      68-94-0}}, {192.065, 0.4654, Meta} → {{67369, 60605, 64663},
     {Quinic acid [ C7 H12 O6, db=80.18, overall=81.10, mfg=82.01, KEGG ID=C00296, CAS ID=77-95-2 ],
      77-95-2}}, {368.116, 0.469971, Meta} →
    {{53718, 49254, 72408}, { [ C10 H24 O14, db=0.00, overall=45.84, mfg=91.69 ], }},
   {466.958, 0.468161, Meta} → {{156680, 58129, 135681},
     { [ C9 H20 Cl3 N3 O6 S3, db=0.00, overall=43.20, mfg=86.40 ], }}, {408.999, 0.469139, Meta} →
    {{244676, 201677, 213943}, { [ C14 H14 Cl3 N3 O5, db=0.00, overall=46.43, mfg=92.86 ], }},
   {351.04, 0.47036, Meta} → {{256070, 232608, 241894},
     { [ C13 H11 Cl2 N7 O, db=0.00, overall=44.47, mfg=88.94 ], }}, {293.081, 0.470778, Meta} →
    {{679912, 473539, 514175}, { [ C15 H16 Cl N O3, db=0.00, overall=46.76, mfg=93.52 ], }},
   {cpd:C19530, 278.083, 0.481429, Meta} → {{60750, 66349, 1},
     {Sulfadimidine [ C12 H14 N4 O2 S, db=77.19, overall=78.12, mfg=79.04, KEGG ID=, CAS ID=57-68-1 ],
      57-68-1}}|>, 9 → <|{cpd:C19444, 200.047, 0.463385, Meta} →
    {{151382, 159437, 145622}, { [ C7 H9 Cl N4 O, db=0.00, overall=44.89, mfg=89.79 ], }},
   {216.041, 0.463028, Meta} → {{1.17×10^7, 1.16×10^7, 1.11×10^7},
     {Methoxsalen [ C12 H8 O4, db=53.88, overall=53.14, mfg=52.41, KEGG ID=C01864, CAS ID=298-81-7 ],
      298-81-7}}, {cpd:C08373, 150.054, 0.462212, Meta} →
    {{126474, 117932, 126888}, {1-Methylhypoxanthine [ C6 H6 N4 O, db=80.19,
        overall=77.83, mfg=82.46, KEGG ID=, CAS ID=1125-39-9 ], 1125-39-9}},
   {cpd:C00262, 136.038, 0.465139, Meta} → {{169847, 127484, 145596},
     {Hypoxanthine [ C5 H4 N4 O, db=94.36, overall=94.95, mfg=95.53, KEGG ID=C00262, CAS ID=68-94-0 ],
      68-94-0}}, {192.065, 0.4654, Meta} → {{33170, 1, 39357},
     {Quinic acid [ C7 H12 O6, db=80.18, overall=81.10, mfg=82.01, KEGG ID=C00296, CAS ID=77-95-2 ],
      77-95-2}}, {368.116, 0.469971, Meta} →
    {{82246, 67519, 81785}, { [ C10 H24 O14, db=0.00, overall=45.84, mfg=91.69 ], }},
   {466.958, 0.468161, Meta} → {{26783, 191301, 142645},
     { [ C9 H20 Cl3 N3 O6 S3, db=0.00, overall=43.20, mfg=86.40 ], }}, {408.999, 0.469139, Meta} →
    {{94484, 214406, 216930}, { [ C14 H14 Cl3 N3 O5, db=0.00, overall=46.43, mfg=92.86 ], }},
   {351.04, 0.47036, Meta} → {{1, 232251, 244346},
     { [ C13 H11 Cl2 N7 O, db=0.00, overall=44.47, mfg=88.94 ], }}, {293.081, 0.470778, Meta} →
    {{212466, 578496, 575496}, { [ C15 H16 Cl N O3, db=0.00, overall=46.76, mfg=93.52 ], }},
   {cpd:C19530, 278.083, 0.481429, Meta} → {{50542, 50832, 66481},
     {Sulfadimidine [ C12 H14 N4 O2 S, db=77.19, overall=78.12, mfg=79.04, KEGG ID=, CAS ID=57-68-1 ],
      57-68-1}}|>|>
```

Options (1)

MassMatcherOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

`MassMatcherOptions` is an option for MathIOmica functions that internally use MassMatcher, and provides a list of options to be passed to this internal MassMatcher function.

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```
In[2]:= exampleOmicsObjectMetabolites = <|"8" → <|{200.0465`, 0.46338463`, "Meta"} →
          {{186943, 1, 142327}, {" [ C7 H9 Cl N4 O, db=0.00, overall=44.89, mfg=89.79 ]", ""}},
         {216.0412`, 0.4630277`, "Meta"} → {{9577920, 9465445, 8802456},
           {"Methoxsalen [ C12 H8 O4, db=53.88, overall=53.14, mfg=52.41, KEGG ID=C01864, CAS ID=298-81-7 ]",
            "298-81-7"}}, {150.0538`, 0.4622121`, "Meta"} →
          {{1, 131138, 133166}, {"1-Methylhypoxanthine [ C6 H6 N4 O, db=80.19, overall=77.83,
              mfg=82.46, KEGG ID=, CAS ID=1125-39-9 ]", "1125-39-9"}},
         {136.0382`, 0.46513885`, "Meta"} → {{133625, 133889, 145682}, {"Hypoxanthine [ C5 H4 N4
              O, db=94.36, overall=94.95, mfg=95.53, KEGG ID=C00262, CAS ID=68-94-0 ]",
            "68-94-0"}}, {192.0646`, 0.46539998`, "Meta"} → {{67369, 60605, 64663},
           {"Quinic acid [ C7 H12 O6, db=80.18, overall=81.10, mfg=82.01, KEGG ID=C00296, CAS ID=77-95-2 ]",
            "77-95-2"}}, {368.1161`, 0.46997148`, "Meta"} →
          {{53718, 49254, 72408}, {" [ C10 H24 O14, db=0.00, overall=45.84, mfg=91.69 ]", ""}},
         {466.9582`, 0.46816128`, "Meta"} → {{156680, 58129, 135681},
           {" [ C9 H20 Cl3 N3 O6 S3, db=0.00, overall=43.20, mfg=86.40 ]", ""}},
         {408.9988`, 0.46913895`, "Meta"} → {{244676, 201677, 213943},
           {" [ C14 H14 Cl3 N3 O5, db=0.00, overall=46.43, mfg=92.86 ]", ""}},
         {351.0404`, 0.47036007`, "Meta"} → {{256070, 232608, 241894},
           {" [ C13 H11 Cl2 N7 O, db=0.00, overall=44.47, mfg=88.94 ]", ""}},
         {293.0811`, 0.47077766`, "Meta"} → {{679912, 473539, 514175},
           {" [ C15 H16 Cl N O3, db=0.00, overall=46.76, mfg=93.52 ]", ""}},
         {278.0828`, 0.48142853`, "Meta"} → {{60750, 66349, 1}, {"Sulfadimidine [ C12 H14 N4 O2 S,
              db=77.19, overall=78.12, mfg=79.04, KEGG ID=, CAS ID=57-68-1 ]", "57-68-1"}}|>,
        "9" → <|{200.0465`, 0.46338463`, "Meta"} → {{151382, 159437, 145622},
           {" [ C7 H9 Cl N4 O, db=0.00, overall=44.89, mfg=89.79 ]", ""}},
         {216.0412`, 0.4630277`, "Meta"} → {{1.17`*^7, 1.16`*^7, 1.11`*^7},
           {"Methoxsalen [ C12 H8 O4, db=53.88, overall=53.14, mfg=52.41, KEGG ID=C01864, CAS ID=298-81-7 ]",
            "298-81-7"}}, {150.0538`, 0.4622121`, "Meta"} →
          {{126474, 117932, 126888}, {"1-Methylhypoxanthine [ C6 H6 N4 O, db=80.19,
              overall=77.83, mfg=82.46, KEGG ID=, CAS ID=1125-39-9 ]", "1125-39-9"}},
         {136.0382`, 0.46513885`, "Meta"} → {{169847, 127484, 145596}, {"Hypoxanthine [ C5 H4 N4
              O, db=94.36, overall=94.95, mfg=95.53, KEGG ID=C00262, CAS ID=68-94-0 ]",
            "68-94-0"}}, {192.0646`, 0.46539998`, "Meta"} → {{33170, 1, 39357},
           {"Quinic acid [ C7 H12 O6, db=80.18, overall=81.10, mfg=82.01, KEGG ID=C00296, CAS ID=77-95-2 ]",
            "77-95-2"}}, {368.1161`, 0.46997148`, "Meta"} →
          {{82246, 67519, 81785}, {" [ C10 H24 O14, db=0.00, overall=45.84, mfg=91.69 ]", ""}},
         {466.9582`, 0.46816128`, "Meta"} → {{26783, 191301, 142645},
           {" [ C9 H20 Cl3 N3 O6 S3, db=0.00, overall=43.20, mfg=86.40 ]", ""}},
         {408.9988`, 0.46913895`, "Meta"} → {{94484, 214406, 216930},
           {" [ C14 H14 Cl3 N3 O5, db=0.00, overall=46.43, mfg=92.86 ]", ""}},
         {351.0404`, 0.47036007`, "Meta"} → {{1, 232251, 244346},
           {" [ C13 H11 Cl2 N7 O, db=0.00, overall=44.47, mfg=88.94 ]", ""}},
         {293.0811`, 0.47077766`, "Meta"} → {{212466, 578496, 575496},
           {" [ C15 H16 Cl N O3, db=0.00, overall=46.76, mfg=93.52 ]", ""}},
         {278.0828`, 0.48142853`, "Meta"} → {{50542, 50832, 66481}, {"Sulfadimidine [ C12 H14 N4 O2 S,
              db=77.19, overall=78.12, mfg=79.04, KEGG ID=, CAS ID=57-68-1 ]", "57-68-1"}}|>|>;
```

We map putative unique identities across keys in this sample at 5 ppm:

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```
In[3]:= OmicsObjectUniqueMassConverter[exampleOmicsObjectMetabolites,
         5, MassMatcherOptions → {MolecularSpecies → "cpd"}]
```

```
Out[3]= ⟨|8 → ⟨|{cpd:C19444, 200.047, 0.463385, Meta} →
        {{186943, 1, 142327}, { [ C7 H9 Cl N4 O, db=0.00, overall=44.89, mfg=89.79 ], }},
       {216.041, 0.463028, Meta} → {{9577920, 9465445, 8802456},
         {Methoxsalen [ C12 H8 O4, db=53.88, overall=53.14, mfg=52.41, KEGG ID=C01864, CAS ID=298-81-7 ],
          298-81-7}}, {cpd:C08373, 150.054, 0.462212, Meta} →
        {{1, 131138, 133166}, {1-Methylhypoxanthine [ C6 H6 N4 O, db=80.19, overall=77.83,
            mfg=82.46, KEGG ID=, CAS ID=1125-39-9 ], 1125-39-9}},
       {cpd:C00262, 136.038, 0.465139, Meta} → {{133625, 133889, 145682},
         {Hypoxanthine [ C5 H4 N4 O, db=94.36, overall=94.95, mfg=95.53, KEGG ID=C00262, CAS ID=68-94-0 ],
          68-94-0}}, {192.065, 0.4654, Meta} → {{67369, 60605, 64663},
         {Quinic acid [ C7 H12 O6, db=80.18, overall=81.10, mfg=82.01, KEGG ID=C00296, CAS ID=77-95-2 ],
          77-95-2}}, {368.116, 0.469971, Meta} →
        {{53718, 49254, 72408}, { [ C10 H24 O14, db=0.00, overall=45.84, mfg=91.69 ], }},
       {466.958, 0.468161, Meta} → {{156680, 58129, 135681},
         { [ C9 H20 Cl3 N3 O6 S3, db=0.00, overall=43.20, mfg=86.40 ], }}, {408.999, 0.469139, Meta} →
        {{244676, 201677, 213943}, { [ C14 H14 Cl3 N3 O5, db=0.00, overall=46.43, mfg=92.86 ], }},
       {351.04, 0.47036, Meta} → {{256070, 232608, 241894},
         { [ C13 H11 Cl2 N7 O, db=0.00, overall=44.47, mfg=88.94 ], }}, {293.081, 0.470778, Meta} →
        {{679912, 473539, 514175}, { [ C15 H16 Cl N O3, db=0.00, overall=46.76, mfg=93.52 ], }},
       {cpd:C19530, 278.083, 0.481429, Meta} → {{60750, 66349, 1},
         {Sulfadimidine [ C12 H14 N4 O2 S, db=77.19, overall=78.12, mfg=79.04, KEGG ID=, CAS ID=57-68-1 ],
          57-68-1}}|⟩, 9 → ⟨|{cpd:C19444, 200.047, 0.463385, Meta} →
        {{151382, 159437, 145622}, { [ C7 H9 Cl N4 O, db=0.00, overall=44.89, mfg=89.79 ], }},
       {216.041, 0.463028, Meta} → {{1.17×10^7, 1.16×10^7, 1.11×10^7},
         {Methoxsalen [ C12 H8 O4, db=53.88, overall=53.14, mfg=52.41, KEGG ID=C01864, CAS ID=298-81-7 ],
          298-81-7}}, {cpd:C08373, 150.054, 0.462212, Meta} →
        {{126474, 117932, 126888}, {1-Methylhypoxanthine [ C6 H6 N4 O, db=80.19,
            overall=77.83, mfg=82.46, KEGG ID=, CAS ID=1125-39-9 ], 1125-39-9}},
       {cpd:C00262, 136.038, 0.465139, Meta} → {{169847, 127484, 145596},
         {Hypoxanthine [ C5 H4 N4 O, db=94.36, overall=94.95, mfg=95.53, KEGG ID=C00262, CAS ID=68-94-0 ],
          68-94-0}}, {192.065, 0.4654, Meta} → {{33170, 1, 39357},
         {Quinic acid [ C7 H12 O6, db=80.18, overall=81.10, mfg=82.01, KEGG ID=C00296, CAS ID=77-95-2 ],
          77-95-2}}, {368.116, 0.469971, Meta} →
        {{82246, 67519, 81785}, { [ C10 H24 O14, db=0.00, overall=45.84, mfg=91.69 ], }},
       {466.958, 0.468161, Meta} → {{26783, 191301, 142645},
         { [ C9 H20 Cl3 N3 O6 S3, db=0.00, overall=43.20, mfg=86.40 ], }}, {408.999, 0.469139, Meta} →
        {{94484, 214406, 216930}, { [ C14 H14 Cl3 N3 O5, db=0.00, overall=46.43, mfg=92.86 ], }},
       {351.04, 0.47036, Meta} → {{1, 232251, 244346},
         { [ C13 H11 Cl2 N7 O, db=0.00, overall=44.47, mfg=88.94 ], }}, {293.081, 0.470778, Meta} →
        {{212466, 578496, 575496}, { [ C15 H16 Cl N O3, db=0.00, overall=46.76, mfg=93.52 ], }},
       {cpd:C19530, 278.083, 0.481429, Meta} → {{50542, 50832, 66481},
         {Sulfadimidine [ C12 H14 N4 O2 S, db=77.19, overall=78.12, mfg=79.04, KEGG ID=, CAS ID=57-68-1 ],
          57-68-1}}|⟩|⟩
```

See Also

GeneTranslation ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGDictionary** ▪ **KEGGPathwayVisual** ▪ **MassDictionary** ▪ **MassMatcher** ▪ **OBOGODictionary** ▪

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TimeSeriesClusters

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OversamplingRate

`OversamplingRate`
is an option for LombScargle to oversample a time series with zero–padding.

Details

- `OversamplingRate` takes values ≥ 1 by which to oversample the time series with zero-padding.

See Also

Autocorrelation ▪ **InverseAutocovariance** ▪ **LombScargle**

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QuantileEstimator

`QuantileEstimator[data, timepoints]`
obtains the quantile estimator following bootstrap for time series.

Details

- The `QuantileEstimator[data, timepoints]` function calculates the quantile value that can be used as a cutoff for classification of time series based on bootstrap simulations. It takes two inputs:

data	Association or list with series as values, from which to generate a distribution.
timepoints	Timepoints over which the time series run.

- The following options can be given:

AutocorrelationOptions	{}	Specific options when calculating autocorrelations for the time series.
InterpolationDeltaT	"Auto"	Time step used to grid the time window over which calculations will be performed. If set to "Auto" the step will correspond to dividing the span of the interval into a number of equal steps equal to the number of input time points.
InterpolationOptions	{}	Options list for the internal Interpolation function used to interpolate between data points that have Missing values or uneven spacing.
LombScargleOptions	{PairReturn → False, NormalizeIntensities → True}	Specific options when calculating LombScargle periodograms for the time series.
Method	"LombScargle"	Method of calculation. Choices include one of the following: {"LombScargle","Autocorrelation", "InterpolatedAutocorrelation","Spikes"}
QuantileValue	0.95	Which quantile to extract.

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- QuantileEstimator returns different output depending on the method :

Method	Output format
"Autocorrelation"	List of values corresponding to selected quantile of autocorrelations, with the ith lag quantile provided as the ith index, i.e. $\rho_c = \{\rho_{c1}, \rho_{c2,}, \ldots, \rho_{ci,}, \ldots, \rho_{ck}\}$ up to k lags, where 1≤ k ≤ n, and typically n=Floor[Length[timepoints]/2]. The method utilizes the Autocorrelation function internally.
"InterpolatedAutocorrelation"	List of values corresponding to selected quantile for autocorrelations, with the ith lag quantile provided as the ith index, i.e. $\rho_c = \{\rho_{c1}, \rho_{c2,}, \ldots, \rho_{ci,}, \ldots, \rho_{ck}\}$ up to k lags, where 1≤ k ≤ n, and typically n=(Length[timepoints]−1). The method utilizes an Interpolation followed by a CorrelationFunction implementation to compute autocorrelations, i.e. missing data or uneven sampling is handled by data interpolation.
"LombScargle"	Single value corresponding to selected quantile of maximum peak intensity of periodogram. The method utilizes the LombScargle function internally.
"Spikes"	Association with number, n, of data points as keys, and values corresponding to quantiles for maxima and minima of the series, in the form <|n → {Maximum Spike Quantile$_n$, Maximum Spike Quantile$_n$}|>. The keys are generated automatically so that so that Keys[output] ∈ {Possible lengths of numeric data}, i.e. all possible lengths of input series constructed by excluding Missing or other non−numeric values).

Examples (11)

Basic Examples (1)

Assuming we have a bootstrap distribution that has been analyzed as the rest of the data we can proceed directly to the application of the QuantileEstimator function. For the purpose of illustration we first create the datasets and analyze them including filters.

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Example for Spikes (1)

In[1]:=
```
Needs["MathIOmica`"]
```

As an example, let's assume we have a random series for which we would like to evaluate the maxima or minima (e.g. to use in a TimeSeriesClassification computation). We generate some data first for a series of varying lengths, 8 through 10:

In[2]:=
```
randomSeries =
  Join[RandomReal[{-1, 1}, {10^6, 8}], RandomReal[{-1, 1}, {10^6, 9}], RandomReal[{-1, 1}, {10^6, 10}]];
```

We can obtain an association of length to quantiles for maxima or minima:

In[3]:=
```
bootstrapSpikes = QuantileEstimator[randomSeries, {}, Method → "Spikes"]
```

Out[3]=
```
<|8 → {0.987316, -0.987306}, 9 → {0.988662, -0.988647}, 10 → {0.989824, -0.989733}|>
```

Extended Example To Create Bootstrap Dataset (1)

In[1]:=
```
Needs["MathIOmica`"]
```

Let's import the example transcriptome data to generate a set to sample. These are located at:

In[4]:=
```
exampleRNAFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "rnaExample"}
```

We can now get the data:

In[6]:=
```
exampleRNAData = Get[exampleRNAFile];
```

We can now perform a resampling of this set. For the example let's only create 20000 members for each set (actual application may need more, but this will suffice for illustrating the function usage).

In[7]:=
```
bootstrapSets = BootstrapGeneral[exampleRNAData, 20 000];
```

We can look at this example (please note that if you repeat the steps above you will most likely get a different dataset as this is a random selection process). We query again the first 5 elements in each dataset:

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In[8]:=
```
Query[All, 1 ;; 5]@bootstrapSets
```

Out[8]=
```
<|7 → <|1 → {{0}, {OK}}, 2 → {{1.42823}, {OK}},
    3 → {{0.120562}, {OK}}, 4 → {{0.0244774}, {OK}}, 5 → {{35.8455}, {OK}}|>,
  8 → <|1 → {{1.04973}, {OK}}, 2 → {{0.526297}, {OK}}, 3 → {{0}, {OK}}, 4 → {{8.49264}, {OK}},
    5 → {{0.00230458}, {OK}}|>, 9 → <|1 → {{0}, {OK}}, 2 → {{3.14157}, {OK}},
    3 → {{6.00749}, {OK}}, 4 → {{532.922}, {OK}}, 5 → {{0.0326532}, {OK}}|>,
  10 → <|1 → {{35.5092}, {OK}}, 2 → {{2.42909}, {OK}}, 3 → {{0.00791471}, {OK}},
    4 → {{14.241}, {OK}}, 5 → {{0.0226409}, {OK}}|>,
  11 → <|1 → {{16.1855}, {OK}}, 2 → {{0}, {OK}}, 3 → {{0}, {OK}}, 4 → {{0.0982475}, {OK}}, 5 → {{0}, {OK}}|>,
  12 → <|1 → {{0.136295}, {OK}}, 2 → {{3.44357}, {OK}}, 3 → {{0.520754}, {OK}},
    4 → {{6.90194}, {OK}}, 5 → {{2.97058}, {OK}}|>, 13 → <|1 → {{2.20956}, {OK}},
    2 → {{0.147191}, {OK}}, 3 → {{6.01576}, {OK}}, 4 → {{0}, {OK}}, 5 → {{97.5729}, {OK}}|>,
  14 → <|1 → {{0}, {OK}}, 2 → {{8.87452}, {OK}}, 3 → {{0}, {OK}}, 4 → {{0}, {OK}}, 5 → {{8.27738}, {OK}}|>,
  15 → <|1 → {{0.67933}, {OK}}, 2 → {{0}, {OK}},
    3 → {{11.2619}, {OK}}, 4 → {{23.4358}, {OK}}, 5 → {{0.100138}, {OK}}|>, 16 →
   <|1 → {{0}, {OK}}, 2 → {{2.80671}, {OK}}, 3 → {{0.00703911}, {OK}}, 4 → {{1.62344}, {OK}}, 5 → {{0}, {OK}}|>,
  17 → <|1 → {{17.1237}, {OK}}, 2 → {{0.0864652}, {OK}}, 3 → {{0}, {OK}}, 4 → {{0.0691603}, {OK}},
    5 → {{7.04913}, {OK}}|>, 18 → <|1 → {{2.80942}, {OK}}, 2 → {{9.15657}, {OK}},
    3 → {{0.00743612}, {OK}}, 4 → {{74.1373}, {OK}}, 5 → {{0}, {OK}}|>, 19 → <|1 → {{0.713172}, {OK}},
    2 → {{32.1935}, {OK}}, 3 → {{12.5973}, {OK}}, 4 → {{1.74249}, {OK}}, 5 → {{0.185677}, {OK}}|>,
  20 → <|1 → {{0}, {OK}}, 2 → {{1.88065}, {OK}}, 3 → {{0}, {OK}}, 4 → {{0}, {OK}}, 5 → {{0.00354656}, {OK}}|>,
  21 → <|1 → {{0}, {OK}}, 2 → {{15.6865}, {OK}}, 3 → {{11.0093}, {OK}}, 4 → {{1.84931}, {OK}}, 5 → {{0}, {OK}}|>|>
```

We do a data cleanup resembling a minimal analysis strategy. First, quantile normalization:

In[9]:=
```
bootstrapQNormed = QuantileNormalization[bootstrapSets];
```

We tag low values (<0.1) and filter the data:

In[11]:=
```
bootstrapQNormedTagged=LowValueTag[bootstrapQNormed, 0.1]
```

Out[11]=
```
<|7 → <|1 → {{Missing[]}, {OK}}, 2 → {{1.42823}, {OK}}, 3 → {{0.120562}, {OK}},
    4 → {{Missing[]}, {OK}}, ··· 19992 ···, 19997 → {{2.64426}, {OK}}, 19998 → {{Missing[]}, {OK}},
    19999 → {{Missing[]}, {OK}}, 20000 → {{2.2942}, {OK}}|>, ··· 13 ···, 21 → <| ··· 1 ··· |> |>
```

large output | show less | show more | show all | set size limit...

We next also tag noisy values (< 5) and replacement by a low default (1) :

In[12]:=
```
bootstrapQNormedTaggedFilter = LowValueTag[bootstrapQNormedTagged, 5, ValueReplacement → 1]
```

Out[12]=
```
<|7 → <|1 → {{Missing[]}, {OK}}, 2 → {{1}, {OK}}, 3 → {{1}, {OK}}, 4 → {{Missing[]}, {OK}},
    5 → {{35.8455}, {OK}}, ··· 19991 ···, 19997 → {{1}, {OK}}, 19998 → {{Missing[]}, {OK}},
    19999 → {{Missing[]}, {OK}}, 20000 → {{1}, {OK}}|>, ··· 13 ···, 21 → <| ··· 1 ··· |> |>
```

large output | show less | show more | show all | set size limit...

We filter series to have at least 3/4 of their timepoints and exclude data for which the reference point "8" is missing:

In[13]:=
```
bootstrapFiltered = FilterMissing[bootstrapQNormedTaggedFilter, 3/4, Reference → "8"];
```

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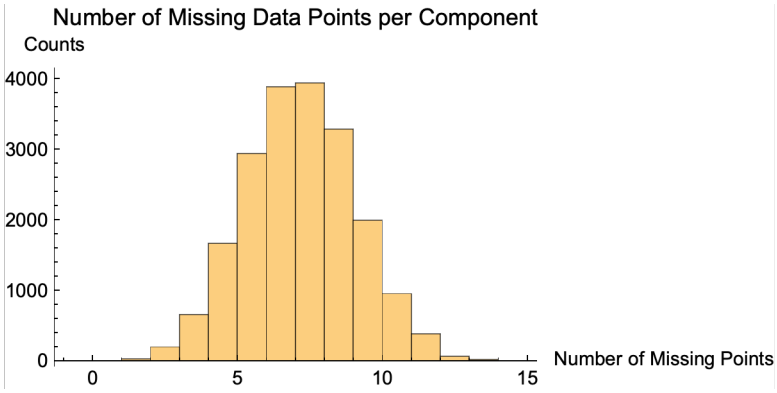
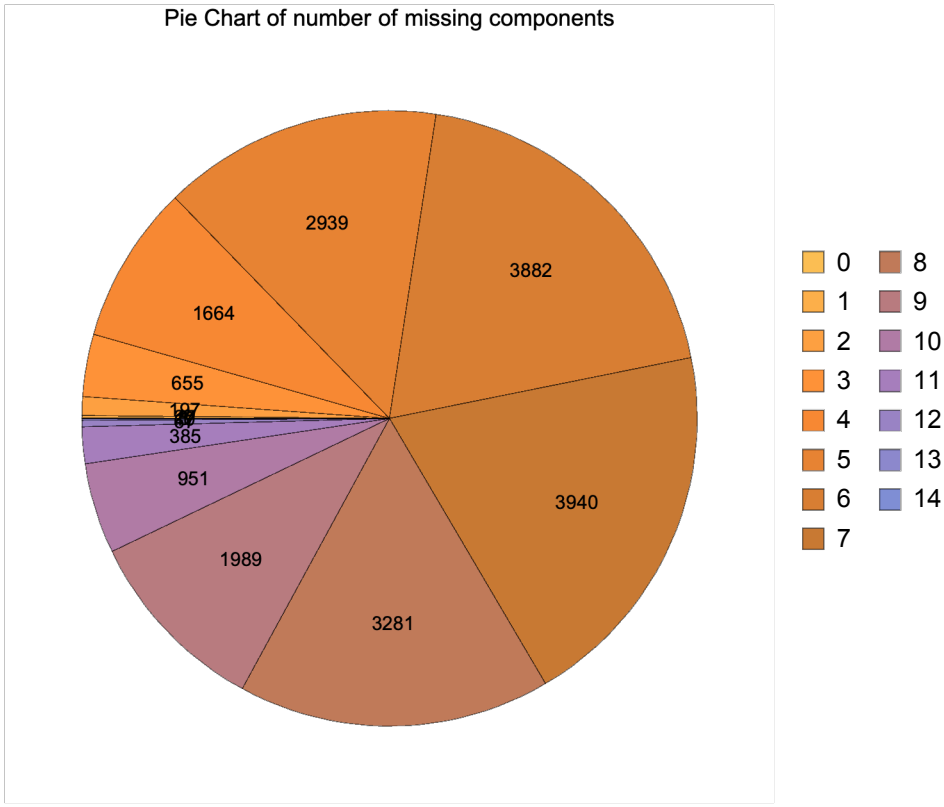



```
{Missing -> Counts: , <|0 → 3, 1 → 27, 2 → 197, 3 → 655, 4 → 1664, 5 → 2939, 6 → 3882,
  7 → 3940, 8 → 3281, 9 → 1989, 10 → 951, 11 → 385, 12 → 67, 13 → 19, 14 → 1|>}
```



We extract the time series across samples:

In[14]:=
```
bootstrapAllTimeSeries = CreateTimeSeries@bootstrapFiltered
```

Out[14]=
```
<|2 → {1, 1, 1, 1, Missing[], 1, 1, 8.87452, Missing[], 1, Missing[], 9.15657, 32.1935, 1, 15.6865},
 ··· 880 ···, 19 976 → {13.7713, 10.2886, 7.66842, 51.8244, 1, 1,
  13.9249, 10.5773, Missing[], 18.9217, 1, Missing[], 7.90121, 1, 19.3487}|>
```

large output | show less | show more | show all | set size limit...

We take the Log across samples :

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In[15]:=
```
bootstrapLogTransformed = SeriesApplier[Log, bootstrapAllTimeSeries]
```

Out[15]=
```
<|2 → {0, 0, 0, 0, Missing[], 0, 0, 2.18318, Missing[], 0, Missing[], 2.21447, 3.47176, 0, 2.7528},
 ··· 880 ···, 19976 → {2.62259, 2.33104, 2.03711, ··· 9 ···, 2.06702, 0, 2.96263}|>
```
large output | show less | show more | show all | set size limit...

We compare the datasets to the reference datapoint. Let's select the second point as a reference:

In[16]:=
```
bootstrapRatios = SeriesInternalCompare[bootstrapLogTransformed, ComparisonIndex → 2]
```

Out[16]=
```
<|2 → {0, 0, 0, 0, Missing[], 0, 0, 2.18318, Missing[], 0, Missing[], 2.21447, 3.47176, 0, 2.7528},
 48 → {··· 1 ···}, ··· 721 ···, 19891 → ··· 1 ···, 19976 → {0.29155, 0., ··· 11 ···, -2.33104, 0.631589}|>
```
large output | show less | show more | show all | set size limit...

We now normalize each time series as a vector:

In[17]:=
```
bootstrapNormed = SeriesApplier[Normalize, bootstrapRatios]
```

Out[17]=
```
<|2 → {0., 0., 0., 0., Missing[], 0., 0.,
   0.403318, Missing[], 0., Missing[], 0.409098, 0.641368, 0., 0.508548},
 ··· 723 ···, 19976 → {0.0577893, 0., ··· 11 ···, -0.462043, 0.12519}|>
```
large output | show less | show more | show all | set size limit...

Next we remove constant series:

In[18]:=
```
bootstrapFinal = ConstantSeriesClean[bootstrapNormed]
```

Out[18]=
```
<|2 → {0., 0., 0., 0., Missing[], 0., 0.,
   0.403318, Missing[], 0., Missing[], 0.409098, 0.641368, 0., 0.508548},
 ··· 723 ···, 19976 → {0.0577893, 0., ··· 11 ···, -0.462043, 0.12519}|>
```
large output | show less | show more | show all | set size limit...

In this example no series was removed.

Let's extract the time series information that that was encoded in the outer association keys when this OmicsObject was originally created. The samples were numbered as follows:

In[19]:=
```
bootstrapSamplesIndexes = TimeExtractor[bootstrapSets]
```

Out[19]=
```
{7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21}
```

The associated timepoints for each of the samples are actually given below as a sample→ day association:

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```
In[20]:= timeCorrespondence = <|7 → 186, 8 → 255, 9 → 289, 10 → 290, 11 → 292, 12 → 294,
           13 → 297, 14 → 301, 15 → 307, 16 → 311, 17 → 322, 18 → 329, 19 → 369, 20 → 380, 21 → 400|>;

In[21]:= bootstrapSamplesTimes = timeCorrespondence[#] & /@ bootstrapSamplesIndexes

Out[21]= {186, 255, 289, 290, 292, 294, 297, 301, 307, 311, 322, 329, 369, 380, 400}
```

Application of QuantileEstimator to Extended Example Data (1)

Now we perform a calculation of the LombScargle periodograms and extract the 0.95 quantile value:

```
In[22]:= bootstrapQ95 = QuantileEstimator[bootstrapFinal, bootstrapSamplesTimes]

Out[22]= 0.85979
```

Options (7)

```
In[1]:= Needs["MathIOmica`"]
```

N.B. The examples below utilize the data simulated in the main examples above. if you are evaluating the examples below, please evaluate the appropriate cells to create the data before proceeding.

AutocorrelationOptions (1)

AutocorrelationOptions allows us to pass options for the internal Autocorrelation function used. This assumes the Method option has been set for "Autocorrelation":

```
In[1]:= bootstrapAutocorrelationOpts = QuantileEstimator[bootstrapFinal, bootstrapSamplesTimes,
          Method → "Autocorrelation", AutocorrelationOptions → {UpperFrequencyFactor → 1} ]

Out[1]= {0.0662209, 0.813067, 0.251834, 0.562895, 0.402635, 0.480041, 0.284805}
```

InterpolationDeltaT (1)

InterpolationDeltaT allows us to explicitly set the time step for the interpolation used. This assumes the Method option has been set for "InterpolatedAutocorrelation". For example we can change set the time step to 25 in our example

```
In[1]:= bootstrapLombScargleOpts = QuantileEstimator[bootstrapFinal,
          bootstrapSamplesTimes, Method → "InterpolatedAutocorrelation", InterpolationDeltaT → 25]

Out[1]= {0.336419, 0.054624, 0.0104519, 0.0997317, 0.0842146, 0.0646496, 0.0503704, 0.0457236}
```

InterpolationOptions (1)

InterpolationOptions allows us to pass options for the internal Interpolation function used. This assumes the Method option has been set for "InterpolatedAutocorrelation". For example we can change the InterpolationOrder option:

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```
In[1]:= bootstrapLombScargleOpts = QuantileEstimator[bootstrapFinal, bootstrapSamplesTimes,
          Method → "InterpolatedAutocorrelation", InterpolationOptions → {InterpolationOrder → 3}]

Out[1]= {0.576709, 0.228183, 0.0798406, 0.0200007, 0.0365141, 0.10335, 0.0444726,
         0.0711313, 0.0786129, 0.0554864, 0.0473722, 0.0441157, 0.0383307, 0.0248386}
```

LombScargleOptions (1)

LombScargleOptions allows us to pass options for the internal LombScargle function used (which is the default Method option).

```
In[1]:= bootstrapLombScargleOpts = QuantileEstimator[bootstrapFinal,
          bootstrapSamplesTimes, LombScargleOptions → {NormalizeIntensities → False}]

Out[1]= 3.37476
```

Method (1)

We may choose different methods for the calculations (usually depending on the downstream application):

```
In[1]:= bootstrapAutocorrelation =
         QuantileEstimator[bootstrapFinal, bootstrapSamplesTimes, Method → "Autocorrelation"]

Out[1]= {0.0662209, 0.813067, 0.251834, 0.562895, 0.402635, 0.480041, 0.284805}

In[2]:= bootstrapInterpolatedAutocorrelation =
         QuantileEstimator[bootstrapFinal, bootstrapSamplesTimes, Method → "InterpolatedAutocorrelation"]

Out[2]= {0.576709, 0.228183, 0.0798406, 0.0200007, 0.0365141, 0.10335, 0.0444726,
         0.0711313, 0.0786129, 0.0554864, 0.0473722, 0.0441157, 0.0383307, 0.0248386}

In[3]:= bootstrapSpikes = QuantileEstimator[bootstrapFinal, bootstrapSamplesTimes, Method → "Spikes"]

Out[3]= <|12 → {0.822833, -0.426197}, 14 → {0.725296, -0.408614},
         13 → {0.800564, -0.411967}, 15 → {0.693243, -0.287086}|>
```

QuantileValue (1)

QuantileValue is an option to select which quantile to report. The default is the 0.95 quantile. We change this to 0.99 here:

```
In[1]:= bootstrapQ99 = QuantileEstimator[bootstrapFinal, bootstrapSamplesTimes, QuantileValue → .99]

Out[1]= 0.915253
```

See Also

Autocorrelation ▪ **BootstrapGeneral** ▪ **LombScargle** ▪ **OmicsObject**

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QuantileNormalization

QuantileNormalization[*data*]
performs quantile normalization of *data*.

Details

- QuantileNormalization[*data*] performs quantile normalization on input *data*. The data may be an association, an OmicsObject or a matrix (list of lists).
- The basic assumption of quantile normalization is that every sample data list has, approximately, an equivalent probability distribution over the values of the *M* variables. If the first sample data $\{x_{11}, x_{12}, \ldots, x_{1M}\}$ are sorted in order (increasing or decreasing), and the same is done for sample 2, $\{x_{21}, x_{22}, \ldots, x_{2M}\}$, through sample *N*, $\{x_{N1}, x_{N2}, \ldots, x_{NM}\}$ (essentially QuantileNormalization treats the samples as rows of a matrix). The variation between these sorted vectors would be negligible, since all of the columns are approximately identically distributed. An average over all the sorted vectors is then taken, and all sorted elements set equal to this average value. The average of all the ranked/sorted elements in all *N* samples are thus taken, and then all of these *M* element values that are set to be identically equal to said respective averages are then returned to their original positions prior to sorting. Quantile normalization is one possible procedure for standardizations of disparate data sets, along with other procedures such as applying an optimized Box-Cox transformation (ApplyBoxCoxTransform).
- Note that it is possible there may be equal values within the dataset. In such a scenario, the quantile normalization implementation considered here works by replacing the degenerate values with the mean over all the degenerate ranks. This behavior may be altered through the function's options. The position referencing is the same as in the function ApplierList.
- The following options can be given:

Averaging	Mean	With what value to replace the same–rank elements across samples. Default is to take the mean of same–rank elements.
ComponentIndex	Missing[]	Which component of a list to use in a multi–list data object (e.g. OmicsObject).
ListIndex	Missing[]	Which list of data values to use in a multi–list data object (e.g. OmicsObject).
Ties	Mean	How ties should be handled. Default is to replace ties with their mean.

Examples (8)

Basic Examples (4)

First we need to load the MathIOmica package.

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In[1]:=
```
Needs["MathIOmica`"]
```

Application to an OmicsObject (1)

Let's import the example transcriptome (RNA) data. These are located at:

In[1]:=
```
rnaExampleFile = FileNameJoin@{ConstantMathIOmicaExamplesDirectory, "rnaExample"}
```

Out[1]=
```
/Users/george/Library/Mathematica/Applications/MathIOmica/MathIOmicaData/ExampleData/rnaExample
```

We can now get the data:

In[2]:=
```
rnaExampleData = Get[rnaExampleFile];
```

Let' s query the first 3 genes across all datasets for this OmicsObject:

In[3]:=
```
rnaSubset = Query[All, 1 ;; 3]@rnaExampleData
```

Out[3]=
```
<|7 → <|{FAM138A, RNA} → {{0}, {OK}},
    {OR4F5, RNA} → {{0}, {OK}}, {LOC729737, RNA} → {{2.73998}, {OK}}|>,
 8 → <|{FAM138A, RNA} → {{0}, {OK}}, {OR4F5, RNA} → {{0}, {OK}},
    {LOC729737, RNA} → {{0.555218}, {OK}}|>,
```

We perform a QuantileNormalization of the subset as a simple example.

In[4]:=
```
QuantileNormalization[rnaSubset, ListIndex → 1, ComponentIndex → 1]
```

Out[4]=
```
<|7 → <|{FAM138A, RNA} → {{0.000297594}, {OK}},
    {OR4F5, RNA} → {{0.000297594}, {OK}}, {LOC729737, RNA} → {{2.48741}, {OK}}|>,
 8 → <|{FAM138A, RNA} → {{0.000297594}, {OK}}, {OR4F5, RNA} → {{0.000297594}, {OK}},
    {LOC729737, RNA} → {{2.48741}, {OK}}|>,
```

for the entire set we have

In[5]:=
```
quantileNormedRNAData = QuantileNormalization[rnaExampleData, ListIndex → 1, ComponentIndex → 1]
```

General: 9.85649`15.954589770191005*^-312 is too small to represent as a normalized machine number; precision may be lost.

General: 5.4191999999999999999999999999999999999`15.954589770191005*^-310 is too small to represent as a normalized machine number; precision may be lost.

General: 2.7255`15.954589770191005*^-310 is too small to represent as a normalized machine number; precision may be lost.

General: Further output of General::munfl will be suppressed during this calculation.

Out[5]=
```
<|7 → <|{FAM138A, RNA} → {{0.}, {OK}}, {OR4F5, RNA} → {{0.}, {OK}},
    {LOC729737, RNA} → {{2.2946}, {OK}}, ··· 25 262 ···, {LOC100507412, RNA} → {{0.}, {OK}},
    {RNA45S5, RNA} → {{0.}, {OK}}, {DUX4L, RNA} → {{0.}, {OK}}|>, ··· 13 ···, 21 → <|··· 1 ···|>|>
```

large output | show less | show more | show all | set size limit...

Let's plot the distribution of the sets with Keys "20" and "21" as an example to see that these look. Before normalization:

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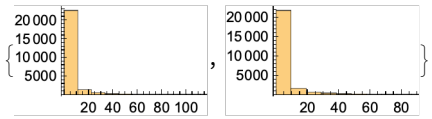
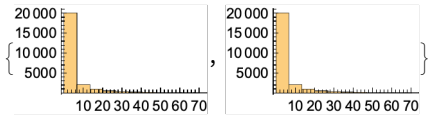
In[6]:=
```
Query[{Key["20"], Key["21"]} /* Values, All /* Values /* Chop /* Flatten /* Histogram, 1]@rnaExampleData
```

Out[6]=


After normalization

In[7]:=
```
Query[{Key["20"], Key["21"]} /* Values, All /* Values /* Flatten /* Histogram, 1]@quantileNormedRNAData
```

Out[7]=


As another example consider a simple OmicsObject

In[8]:=
```
omicsObjectMultiComponent = <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}},
      {"Measurement2"} → {{0.9, 1}, {13, "True"}}, {"Measurement3"} → {{0.5, 4}, {2, "False"}},
      {"Measurement4"} → {{0.2, 3}, {5, "True"}}, {"Measurement5"} → {{0.3, 2}, {11, "True"}}|>,
   "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
      {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
      {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
   "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
      {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
      {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → {{0.1, 1}, {12, "False"}}|>|>;
```

Let's perform quantile normalization of the second components in the first list for each measurement:

In[9]:=
```
QuantileNormalization[omicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 2]
```

Out[9]=
```
<|FirstSample → <|{Measurement1} → {{0.8, 1.83333}, {17., True}},
    {Measurement2} → {{0.9, 1.}, {13., True}}, {Measurement3} → {{0.5, 4.33333}, {2., False}},
    {Measurement4} → {{0.2, 3.66667}, {5., True}}, {Measurement5} → {{0.3, 1.83333}, {11., True}}|>,
  SecondSample → <|{Measurement1} → {{0.7, 1.33333}, {15., True}},
    {Measurement2} → {{0.7, 1.33333}, {12., True}}, {Measurement3} → {{0.3, 2.}, {11., False}},
    {Measurement4} → {{0.3, 4.}, {6., True}}, {Measurement5} → {{0.6, 4.}, {10., True}}|>,
  ThirdSample → <|{Measurement1} → {{0.9, 1.83333}, {16., True}},
    {Measurement2} → {{0.3, 3.66667}, {11., True}}, {Measurement3} → {{0.4, 4.33333}, {8., False}},
    {Measurement4} → {{0.3, 1.83333}, {7., True}}, {Measurement5} → {{0.1, 1.}, {12., False}}|>|>
```

Notice that the above example had ties

Application to Associations, Single List Values (1)

Let's consider the following association:

In[1]:=
```
dataAssociationExample = AssociationThread[Range[3] → {{1, 6, 3, 7}, {1, 2, 4, 5}, {6, 4, 5, 1}}]
```

Out[1]=
```
<|1 → {1, 6, 3, 7}, 2 → {1, 2, 4, 5}, 3 → {6, 4, 5, 1}|>
```

Let' s perform now a quantile normalization:

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In[2]:=
```
QuantileNormalization[dataAssociationExample]
```

Out[2]=
```
<|1 → {1., 5., 3., 6.}, 2 → {1., 3., 5., 6.}, 3 → {6., 3., 5., 1.}|>
```

Quantile normalization also works on lists of associations:

In[3]:=
```
listAssociations = {<|"Measurement1" → 1, "Measurement2" → 6,
    "Measurement3" → 7|>, <|"Measurement1" → 2, "Measurement2" → 1, "Measurement3" → 6|>,
   <|"Measurement1" → 2, "Measurement2" → 6, "Measurement3" → 1|>};
```

In[4]:=
```
QuantileNormalization[listAssociations]
```

Out[4]=
```
{<|Measurement1 → 1., Measurement2 → 3.33333, Measurement3 → 6.33333|>,
 <|Measurement1 → 3.33333, Measurement2 → 1., Measurement3 → 6.33333|>,
 <|Measurement1 → 3.33333, Measurement2 → 6.33333, Measurement3 → 1.|>}
```

Application to a List (1)

Let's perform quantile normalization of some random matrix.

In[1]:=
```
randData[n_] := RandomReal[{0, 1}, n];
```

In[2]:=
```
dataMatrix = RandomReal[{0, 1}, {3, 3}]
```

Out[2]=
```
{{0.581655, 0.924064, 0.546301}, {0.799408, 0.590655, 0.325999}, {0.293898, 0.897102, 0.338989}}
```

In[3]:=
```
QuantileNormalization[dataMatrix]
```

Out[3]=
```
{{0.503766, 0.873525, 0.388732}, {0.873525, 0.503766, 0.388732}, {0.388732, 0.873525, 0.503766}}
```

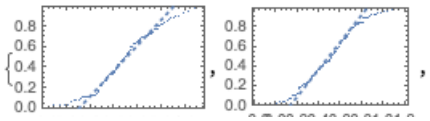
Let's see how this works for a larger dataset:

In[4]:=
```
dataMatrices = RandomReal[{0, 1}, {5, 100}];
```

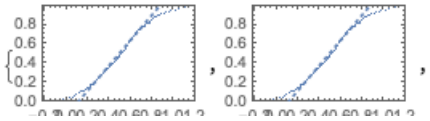
5 measurements each of 100 data points.

Here is a Q-Q plot of the various data without quantile normalization.

In[5]:=
```
QuantilePlot[#] & /@ dataMatrices
```

Out[5]=


In[6]:=
```
QuantilePlot[#] & /@ QuantileNormalization[dataMatrices]
```

Out[6]=


Options (4)

Averaging (1)

In[1]:=
```
Needs["MathIOmica`"]
```

Averaging is an option on what value to return for same-rank elements across samples. The

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function can be any function acting on a list and returning a single value, e.g. Mean, Median.

We consider the following example:

```
In[2]:= omicsObjectMultiComponent = <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}},
          {"Measurement2"} → {{0.9, 1}, {13, "True"}}, {"Measurement3"} → {{0.5, 4}, {2, "False"}},
          {"Measurement4"} → {{0.2, 3}, {5, "True"}}, {"Measurement5"} → {{0.3, 2}, {11, "True"}}|>,
        "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
          {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
          {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
        "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
          {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
          {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → {{0.1, 1}, {12, "False"}}|>|>;
```

The default Averaging option for QuantileNormalization is set to Mean:

```
In[3]:= QuantileNormalization[omicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 1, Averaging → Mean]

Out[3]= <|FirstSample → <|{Measurement1} → {{0.633333, 2.}, {17., True}},
          {Measurement2} → {{0.833333, 1.}, {13., True}}, {Measurement3} → {{0.466667, 4.}, {2., False}},
          {Measurement4} → {{0.2, 3.}, {5., True}}, {Measurement5} → {{0.3, 2.}, {11., True}}|>,
        SecondSample → <|{Measurement1} → {{0.733333, 1.}, {15., True}},
          {Measurement2} → {{0.733333, 1.}, {12., True}}, {Measurement3} → {{0.25, 2.}, {11., False}},
          {Measurement4} → {{0.25, 3.}, {6., True}}, {Measurement5} → {{0.466667, 3.}, {10., True}}|>,
        ThirdSample → <|{Measurement1} → {{0.833333, 2.}, {16., True}},
          {Measurement2} → {{0.383333, 5.}, {11., True}}, {Measurement3} → {{0.633333, 6.}, {8., False}},
          {Measurement4} → {{0.383333, 2.}, {7., True}}, {Measurement5} → {{0.2, 1.}, {12., False}}|>|>
```

We can instead use Median :

```
In[4]:= QuantileNormalization[omicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 1, Averaging → Median]

Out[4]= <|FirstSample → <|{Measurement1} → {{0.7, 2.}, {17., True}},
          {Measurement2} → {{0.9, 1.}, {13., True}}, {Measurement3} → {{0.5, 4.}, {2., False}},
          {Measurement4} → {{0.2, 3.}, {5., True}}, {Measurement5} → {{0.3, 2.}, {11., True}}|>,
        SecondSample → <|{Measurement1} → {{0.8, 1.}, {15., True}},
          {Measurement2} → {{0.8, 1.}, {12., True}}, {Measurement3} → {{0.25, 2.}, {11., False}},
          {Measurement4} → {{0.25, 3.}, {6., True}}, {Measurement5} → {{0.5, 3.}, {10., True}}|>,
        ThirdSample → <|{Measurement1} → {{0.9, 2.}, {16., True}}, {Measurement2} → {{0.4, 5.}, {11., True}},
          {Measurement3} → {{0.7, 6.}, {8., False}}, {Measurement4} → {{0.4, 2.}, {7., True}},
          {Measurement5} → {{0.2, 1.}, {12., False}}|>|>
```

Ties (1)

```
In[1]:= Needs["MathIOmica`"]
```

The Ties option is a choice for which function to use in reporting values of same rank elements within the same sample, i.e. in samples with ties. The function takes in a list of values and returns a single value. We consider the simple example

```
In[2]:= listAssociationsTies = {<|"Measurement1" → 1, "Measurement2" → 6, "Measurement3" → 3, "Measurement4" → 1|>, <|
          "Measurement1" → 2, "Measurement2" → 2, "Measurement3" → 2, "Measurement4" → 3|>,
        <|"Measurement1" → 2, "Measurement2" → 1, "Measurement3" → 1, "Measurement4" → 3|>};

In[3]:= QuantileNormalization[listAssociationsTies, ListIndex → 1, ComponentIndex → 1, Ties → Mean]

Out[3]= {<|Measurement1 → 1.33333, Measurement2 → 4., Measurement3 → 2.33333, Measurement4 → 1.33333|>,
         <|Measurement1 → 1.66667, Measurement2 → 1.66667, Measurement3 → 1.66667, Measurement4 → 4.|>,
         <|Measurement1 → 2.33333, Measurement2 → 1.33333, Measurement3 → 1.33333, Measurement4 → 4.|>}
```

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In[4]:=
```
QuantileNormalization[listAssociationsTies, ListIndex → 1, ComponentIndex → 1, Ties → Median]
```

Out[4]=
```
{<|Measurement1 → 1.33333, Measurement2 → 4., Measurement3 → 2.33333, Measurement4 → 1.33333|>,
 <|Measurement1 → 1.33333, Measurement2 → 1.33333, Measurement3 → 1.33333, Measurement4 → 4.|>,
 <|Measurement1 → 2.33333, Measurement2 → 1.33333, Measurement3 → 1.33333, Measurement4 → 4.|>}
```

ListIndex (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ListIndex allows us to choose from which list to select data that will be quantile normalized.

We consider the OmicsObject example:

In[2]:=
```
omicsObjectMultiComponent = <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}},
      {"Measurement2"} → {{0.9, 1}, {13, "True"}}, {"Measurement3"} → {{0.5, 4}, {2, "False"}},
      {"Measurement4"} → {{0.2, 3}, {5, "True"}}, {"Measurement5"} → {{0.3, 2}, {11, "True"}}|>,
   "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
      {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
      {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
   "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
      {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
      {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → {{0.1, 1}, {12, "False"}}|>|>;
```

Let's perform quantile normalization of the first lists first components:

In[3]:=
```
QuantileNormalization[omicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 1]
```

Out[3]=
```
<|FirstSample → <|{Measurement1} → {{0.633333, 2.}, {17., True}},
    {Measurement2} → {{0.833333, 1.}, {13., True}}, {Measurement3} → {{0.466667, 4.}, {2., False}},
    {Measurement4} → {{0.2, 3.}, {5., True}}, {Measurement5} → {{0.3, 2.}, {11., True}}|>,
  SecondSample → <|{Measurement1} → {{0.733333, 1.}, {15., True}},
    {Measurement2} → {{0.733333, 1.}, {12., True}}, {Measurement3} → {{0.25, 2.}, {11., False}},
    {Measurement4} → {{0.25, 3.}, {6., True}}, {Measurement5} → {{0.466667, 3.}, {10., True}}|>,
  ThirdSample → <|{Measurement1} → {{0.833333, 2.}, {16., True}},
    {Measurement2} → {{0.383333, 5.}, {11., True}}, {Measurement3} → {{0.633333, 6.}, {8., False}},
    {Measurement4} → {{0.383333, 2.}, {7., True}}, {Measurement5} → {{0.2, 1.}, {12., False}}|>|>
```

Let' s perform quantile normalization of the second lists first components:

In[4]:=
```
QuantileNormalization[omicsObjectMultiComponent, ListIndex → 2, ComponentIndex → 1]
```

Out[4]=
```
<|FirstSample → <|{Measurement1} → {{0.8, 2.}, {16., True}},
    {Measurement2} → {{0.9, 1.}, {12.3333, True}}, {Measurement3} → {{0.5, 4.}, {5., False}},
    {Measurement4} → {{0.2, 3.}, {7.66667, True}}, {Measurement5} → {{0.3, 2.}, {11., True}}|>,
  SecondSample → <|{Measurement1} → {{0.7, 1.}, {16., True}}, {Measurement2} → {{0.7, 1.}, {12.3333, True}},
    {Measurement3} → {{0.3, 2.}, {11., False}}, {Measurement4} → {{0.3, 3.}, {5., True}},
    {Measurement5} → {{0.6, 3.}, {7.66667, True}}|>,
  ThirdSample → <|{Measurement1} → {{0.9, 2.}, {16., True}}, {Measurement2} → {{0.3, 5.}, {11., True}},
    {Measurement3} → {{0.4, 6.}, {7.66667, False}}, {Measurement4} → {{0.3, 2.}, {5., True}},
    {Measurement5} → {{0.1, 1.}, {12.3333, False}}|>|>
```

ComponentIndex (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ComponentIndex allows us to choose from which component of a list to select data that will be quantile normalized.

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We consider the OmicsObject example:

```
In[2]:= omicsObjectMultiComponent = <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}},
          {"Measurement2"} → {{0.9, 1}, {13, "True"}}, {"Measurement3"} → {{0.5, 4}, {2, "False"}},
          {"Measurement4"} → {{0.2, 3}, {5, "True"}}, {"Measurement5"} → {{0.3, 2}, {11, "True"}}|>,
        "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
          {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
          {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
        "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
          {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
          {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → {{0.1, 1}, {12, "False"}}|>|>;
```

Let's perform quantile normalization of the first lists first components:

```
In[3]:= QuantileNormalization[omicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 1]

Out[3]= <|FirstSample → <|{Measurement1} → {{0.633333, 2.}, {17., True}},
          {Measurement2} → {{0.833333, 1.}, {13., True}}, {Measurement3} → {{0.466667, 4.}, {2., False}},
          {Measurement4} → {{0.2, 3.}, {5., True}}, {Measurement5} → {{0.3, 2.}, {11., True}}|>,
        SecondSample → <|{Measurement1} → {{0.733333, 1.}, {15., True}},
          {Measurement2} → {{0.733333, 1.}, {12., True}}, {Measurement3} → {{0.25, 2.}, {11., False}},
          {Measurement4} → {{0.25, 3.}, {6., True}}, {Measurement5} → {{0.466667, 3.}, {10., True}}|>,
        ThirdSample → <|{Measurement1} → {{0.833333, 2.}, {16., True}},
          {Measurement2} → {{0.383333, 5.}, {11., True}}, {Measurement3} → {{0.633333, 6.}, {8., False}},
          {Measurement4} → {{0.383333, 2.}, {7., True}}, {Measurement5} → {{0.2, 1.}, {12., False}}|>|>
```

Let' s perform quantile normalization of the first lists second components:

```
In[4]:= QuantileNormalization[omicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 2]

Out[4]= <|FirstSample → <|{Measurement1} → {{0.8, 1.83333}, {17., True}},
          {Measurement2} → {{0.9, 1.}, {13., True}}, {Measurement3} → {{0.5, 4.33333}, {2., False}},
          {Measurement4} → {{0.2, 3.66667}, {5., True}}, {Measurement5} → {{0.3, 1.83333}, {11., True}}|>,
        SecondSample → <|{Measurement1} → {{0.7, 1.33333}, {15., True}},
          {Measurement2} → {{0.7, 1.33333}, {12., True}}, {Measurement3} → {{0.3, 2.}, {11., False}},
          {Measurement4} → {{0.3, 4.}, {6., True}}, {Measurement5} → {{0.6, 4.}, {10., True}}|>,
        ThirdSample → <|{Measurement1} → {{0.9, 1.83333}, {16., True}},
          {Measurement2} → {{0.3, 3.66667}, {11., True}}, {Measurement3} → {{0.4, 4.33333}, {8., False}},
          {Measurement4} → {{0.3, 1.83333}, {7., True}}, {Measurement5} → {{0.1, 1.}, {12., False}}|>|>
```

See Also

ApplierList ▪ **BoxCoxTransform** ▪ **OmicsObject** ▪ **QuantileNormalization** ▪ **StandardizeExtended**

Tutorials

- MathIOmicaTutorial
- MathIOmica Dynamic Transcriptome

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- MathIOmica Guide

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- MathIOmicaGuide
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Returner

`Returner[originalAssociation, update]`
returns a modified *originalAssociation* updated at a specified position by the single association *update*, e.g. from Applier or ApplierList result.

Details

- `Returner[originalAssociation, update]` allows us to update an association with new information. Returner takes 2 inputs:

originalAssociation	Original association that will be updated.
update	Update of information.

- Typically a location will also be specified for the update if the association is an OmicsObject or has a nested structure.
- The following options can be given:

ListIndex	Missing[]	Selection of which list to use in the association or OmicsObject input values.
ComponentIndex	Missing[]	Selection of which component of a list to use in the association or OmicsObject input values.
HorizontalSelection	False	Horizontal selection across components for a single level association.

- Returner was implemented to be used in conjunction with Applier to facilitate new functions/modules acting on and returning an OmicsObject.

Examples (11)

Basic Examples (1)

First we need to load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

In the examples below we see how Returner works on a wide variety of structures.

Returner on an OmicsObject (1)

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Let' s suppose we have an OmicsObject,

```
In[38]:= omicsObjectExample = <|FirstSample → <|{A0AVT1} → {{0.937}, {17}}, {A0MZ66} → {{1.059}, {9}},
      {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[]|>,
    SecondSample → <|{A0AVT1} → {{1.003}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.779}, {11}},
      {A1L0T0} → {{0.917}, {4}}, {A0FGR8} → {{0.921}, {24}}|>, ThirdSample → <|{A0AVT1} → {{1.064}, {19}},
      {A0MZ66} → Missing[], {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {23}}|>|>;
```

and that we have calculated the rank of each member in this example:

```
In[39]:= rankUpdate = Applier[Ordering, omicsObjectExample, ListIndex → 1, ComponentIndex → 1]

Out[39]= <|FirstSample → <|{A0AVT1} → 1, {A0MZ66} → 3, {A1A4S6} → 2, {A1L0T0} → 4, {A0FGR8} → 5|>,
  SecondSample → <|{A0AVT1} → 3, {A0MZ66} → 4, {A1A4S6} → 5, {A1L0T0} → 1, {A0FGR8} → 2|>,
  ThirdSample → <|{A0AVT1} → 3, {A0MZ66} → 5, {A1A4S6} → 1, {A1L0T0} → 2, {A0FGR8} → 4|>|>
```

We can apply Returner to update/replace the information in the original association

```
In[40]:= Returner[omicsObjectExample, rankUpdate, ListIndex → 1, ComponentIndex → 1]

Out[40]= <|FirstSample → <|{A0AVT1} → {{1}, {17}}, {A0MZ66} → {{3}, {9}},
      {A1A4S6} → {{2}, {11}}, {A1L0T0} → {{4}, {4}}, {A0FGR8} → Missing[]|>,
  SecondSample → <|{A0AVT1} → {{3}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {{5}, {11}},
      {A1L0T0} → {{1}, {4}}, {A0FGR8} → {{2}, {24}}|>, ThirdSample → <|{A0AVT1} → {{3}, {19}},
      {A0MZ66} → Missing[], {A1A4S6} → {{1}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{4}, {23}}|>|>
```

Returner on General Associations (5)

Single Association, Lists of Values (1)

Consider a single association with multiple lists for its value:

```
In[1]:= associationExample = <|c1 → {{1, 3, 4}, {5, 2, 1}, {3, 4, 2}}|>

Out[1]= <|c1 → {{1, 3, 4}, {5, 2, 1}, {3, 4, 2}}|>
```

Let' s Standardize the first components:

```
In[2]:= updateSingleAssociationExample = Applier[Standardize, associationExample, ComponentIndex → 1]

Out[2]= <|c1 → {-1., 1., 0.}|>

In[3]:= Returner[associationExample, updateSingleAssociationExample, ComponentIndex → 1]

Out[3]= <|c1 → {{-1., 3, 4}, {1., 2, 1}, {0., 4, 2}}|>
```

Single Association, Nested Lists of Values (1)

Consider a single association with multilevel lists:

```
In[1]:= associationExampleLists = <|c1 → {{{3, 3, 1}, {1, 1, 1}}, {{1, 2, 2}, {3, 2, 3}}, {{0, 3, 2}, {1, 1, 1}}}|>

Out[1]= <|c1 → {{{3, 3, 1}, {1, 1, 1}}, {{1, 2, 2}, {3, 2, 3}}, {{0, 3, 2}, {1, 1, 1}}}|>
```

Let' s apply function an ordering to the entire association.

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```
In[2]:= updateAssociationExampleLists =
         Applier[Standardize, associationExampleLists, ListIndex → 1, ComponentIndex → 2]
Out[2]= <|c1 → {0.57735, -1.1547, 0.57735}|>
```

We can return this to the same position: to the first component list:

```
In[3]:= Returner[associationExampleLists, updateAssociationExampleLists, ListIndex → 1, ComponentIndex → 2]
Out[3]= <|c1 → {{{3, 0.57735, 1}, {1, 1, 1}}, {{1, -1.1547, 2}, {3, 2, 3}}, {{0, 0.57735, 2}, {1, 1, 1}}}|>
```

Single Level of Associations, Multi-Component Values (1)

Let's consider one level of associations with two lists with multiple components:

```
In[1]:= associationsMultiListExample =
         <|b11 → {{2, 2, 1}, {6, 3, 3}}, b12 → {{4, 25, 2}, {33, 22, 11}}, b13 → {{1, 33, 44}, {1, 4, 1}}|>
Out[1]= <|b11 → {{2, 2, 1}, {6, 3, 3}}, b12 → {{4, 25, 2}, {33, 22, 11}}, b13 → {{1, 33, 44}, {1, 4, 1}}|>
```

We need to set HorizontalSelection to True to be able to select across the Keys. Let's normalize across second components:

```
In[2]:= updateAsociationsMultiList = Applier[Standardize,
          associationsMultiListExample, ListIndex → 1, ComponentIndex → 2, HorizontalSelection → True]
Out[2]= <|b11 → -1.11847, b12 → 0.310685, b13 → 0.807781|>

In[3]:= Returner[associationsMultiListExample, updateAsociationsMultiList,
         ListIndex → 1, ComponentIndex → 2, HorizontalSelection → True]
Out[3]= <|b11 → {{2, -1.11847, 1}, {6, 3, 3}},
         b12 → {{4, 0.310685, 2}, {33, 22, 11}}, b13 → {{1, 0.807781, 44}, {1, 4, 1}}|>
```

Two Level Associations, Multi-Component Values (1)

Suppose we have a multi - component list for values:

```
In[1]:= nestedAssociationList = <|c1 → <|b11 → {a11, a12, a13}, b12 → {a21, a22, a23}, b13 → {a31, a32, a33}|>|>
Out[1]= <|c1 → <|b11 → {a11, a12, a13}, b12 → {a21, a22, a23}, b13 → {a31, a32, a33}|>|>
```

For example let's get the ordering across the first component:

```
In[2]:= updateNestedAssociationList = Applier[Ordering, nestedAssociationList, ComponentIndex → 1]
Out[2]= <|c1 → <|b11 → 1, b12 → 2, b13 → 3|>|>

In[3]:= Returner[nestedAssociationList, updateNestedAssociationList, ComponentIndex → 1]
Out[3]= <|c1 → <|b11 → {1, a12, a13}, b12 → {2, a22, a23}, b13 → {3, a32, a33}|>|>
```

Two Level Associations, Multi-List Values (1)

Suppose we have a multi - component list for values:

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```
In[1]:= nestedAssociationLists = <|c1 → <|b11 → {{a111, a112, a113}, {a121, a122, a123}},
          b12 → {{a211, a212, a213}, {a221, a222, a223}}, b13 → {{a311, a312, a313}, {a321, a322, a323}}|>|>

Out[1]= <|c1 → <|b11 → {{a111, a112, a113}, {a121, a122, a123}},
          b12 → {{a211, a212, a213}, {a221, a222, a223}}, b13 → {{a311, a312, a313}, {a321, a322, a323}}|>|>
```

For example let's get the ordering across the first list, first component, and keep track of the component that generated it:

```
In[2]:= updateNestedAssociationLists =
         Applier[Transpose@{Ordering[#], #} &, nestedAssociationLists, ListIndex → 1, ComponentIndex → 1]

Out[2]= <|c1 → <|b11 → {1, a111}, b12 → {2, a211}, b13 → {3, a311}|>|>

In[3]:= Returner[nestedAssociationLists, updateNestedAssociationLists, ListIndex → 1, ComponentIndex → 1]

Out[3]= <|c1 → <|b11 → {{{1, a111}, a112, a113}, {a121, a122, a123}},
          b12 → {{{2, a211}, a212, a213}, {a221, a222, a223}}, b13 → {{{3, a311}, a312, a313}, {a321, a322, a323}}|>|>
```

Options (3)

ListIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

ListIndex is an option that allows the selection of which list to choose from the inner values in the object considered. For example, let's look at an OmicsObject

```
In[2]:= omicsObjectExample = <|FirstSample → <|{A0AVT1} → {{0.937}, {17}}, {A0MZ66} → {{1.059}, {9}},
          {A1A4S6} → {{1.03}, {11}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[]|>,
         SecondSample → <|{A0AVT1} → {{1.003}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.779}, {11}},
          {A1L0T0} → {{0.917}, {4}}, {A0FGR8} → {{0.921}, {24}}|>, ThirdSample → <|{A0AVT1} → {{1.064}, {19}},
          {A0MZ66} → Missing[], {A1A4S6} → {{0.545}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {23}}|>|>;
```

We can calculate an ordering within each sample based on the first list, first component value.

```
In[3]:= updateOmicsObjectExample = Applier[Ordering, omicsObjectExample, ListIndex → 1, ComponentIndex → 1]

Out[3]= <|FirstSample → <|{A0AVT1} → 1, {A0MZ66} → 3, {A1A4S6} → 2, {A1L0T0} → 4, {A0FGR8} → 5|>,
         SecondSample → <|{A0AVT1} → 3, {A0MZ66} → 4, {A1A4S6} → 5, {A1L0T0} → 1, {A0FGR8} → 2|>,
         ThirdSample → <|{A0AVT1} → 3, {A0MZ66} → 5, {A1A4S6} → 1, {A1L0T0} → 2, {A0FGR8} → 4|>|>
```

We can obtain the original association structure by returning these values to the first list, first component value:

```
In[4]:= Returner[omicsObjectExample, updateOmicsObjectExample, ListIndex → 1, ComponentIndex → 1]

Out[4]= <|FirstSample → <|{A0AVT1} → {{1}, {17}}, {A0MZ66} → {{3}, {9}},
          {A1A4S6} → {{2}, {11}}, {A1L0T0} → {{4}, {4}}, {A0FGR8} → Missing[]|>,
         SecondSample → <|{A0AVT1} → {{3}, {17}}, {A0MZ66} → Missing[], {A1A4S6} → {{5}, {11}},
          {A1L0T0} → {{1}, {4}}, {A0FGR8} → {{2}, {24}}|>, ThirdSample → <|{A0AVT1} → {{3}, {19}},
          {A0MZ66} → Missing[], {A1A4S6} → {{1}, {5}}, {A1L0T0} → Missing[], {A0FGR8} → {{4}, {23}}|>|>
```

We could instead have returned these values to the second list, first component value.

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```
In[5]:= Returner[omicsObjectExample, updateOmicsObjectExample, ListIndex → 2, ComponentIndex → 1]

Out[5]= <|FirstSample → <|{A0AVT1} → {{0.937}, {1}}, {A0MZ66} → {{1.059}, {3}},
    {A1A4S6} → {{1.03}, {2}}, {A1L0T0} → {{1.268}, {4}}, {A0FGR8} → Missing[]|>,
  SecondSample → <|{A0AVT1} → {{1.003}, {3}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.779}, {5}},
    {A1L0T0} → {{0.917}, {1}}, {A0FGR8} → {{0.921}, {2}}|>,
  ThirdSample → <|{A0AVT1} → {{1.064}, {3}}, {A0MZ66} → Missing[], {A1A4S6} → {{0.545}, {1}},
    {A1L0T0} → Missing[], {A0FGR8} → {{0.87}, {4}}|>|>
```

ComponentIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

Let's consider a multi component OmicsObject:

```
In[2]:= omicsObjectMultiComponent =
  <|"FirstSample" → <|{"Measurement1"} → {{0.8, 2}, {17, "True"}}, {"Measurement2"} → Missing[],
      {"Measurement3"} → {{0.5, 4}, {2, "False"}}, {"Measurement4"} → {{0.2, 3}, {5, "True"}},
      {"Measurement5"} → Missing[]|>, "SecondSample" → <|{"Measurement1"} → {{0.7, 1}, {15, "True"}},
      {"Measurement2"} → {{0.7, 1}, {12, "True"}}, {"Measurement3"} → {{0.3, 2}, {11, "False"}},
      {"Measurement4"} → {{0.3, 3}, {6, "True"}}, {"Measurement5"} → {{0.6, 3}, {10, "True"}}|>,
    "ThirdSample" → <|{"Measurement1"} → {{0.9, 2}, {16, "True"}},
      {"Measurement2"} → {{0.3, 5}, {11, "True"}}, {"Measurement3"} → {{0.4, 6}, {8, "False"}},
      {"Measurement4"} → {{0.3, 2}, {7, "True"}}, {"Measurement5"} → Missing[]|>|>;
```

In this example we can obtain the rank within each sample for the first component of each measurement:

```
In[3]:= updateomicsObjectMultiComponent =
  Applier[Ordering, omicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 1]

Out[3]= <|FirstSample →
    <|{Measurement1} → 4, {Measurement2} → 3, {Measurement3} → 1, {Measurement4} → 2, {Measurement5} → 5|>,
  SecondSample → <|{Measurement1} → 3, {Measurement2} → 4, {Measurement3} → 5,
    {Measurement4} → 1, {Measurement5} → 2|>, ThirdSample →
    <|{Measurement1} → 2, {Measurement2} → 4, {Measurement3} → 3, {Measurement4} → 1, {Measurement5} → 5|>|>
```

We return this update to the original position of the values involved in the calculation, first list, first component:

```
In[4]:= Returner[omicsObjectMultiComponent, updateomicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 1]

Out[4]= <|FirstSample → <|{Measurement1} → {{4, 2}, {17, True}}, {Measurement2} → Missing[],
    {Measurement3} → {{1, 4}, {2, False}}, {Measurement4} → {{2, 3}, {5, True}}, {Measurement5} → Missing[]|>,
  SecondSample → <|{Measurement1} → {{3, 1}, {15, True}}, {Measurement2} → {{4, 1}, {12, True}},
    {Measurement3} → {{5, 2}, {11, False}}, {Measurement4} → {{1, 3}, {6, True}},
    {Measurement5} → {{2, 3}, {10, True}}|>,
  ThirdSample → <|{Measurement1} → {{2, 2}, {16, True}}, {Measurement2} → {{4, 5}, {11, True}},
    {Measurement3} → {{3, 6}, {8, False}}, {Measurement4} → {{1, 2}, {7, True}}, {Measurement5} → Missing[]|>|>
```

Or we can return to the first list, second component:

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```
In[5]:= Returner[omicsObjectMultiComponent, updateomicsObjectMultiComponent, ListIndex → 1, ComponentIndex → 2]

Out[5]= <|FirstSample → <|{Measurement1} → {{0.8, 4}, {17, True}},
    {Measurement2} → Missing[], {Measurement3} → {{0.5, 1}, {2, False}},
    {Measurement4} → {{0.2, 2}, {5, True}}, {Measurement5} → Missing[]|>,
  SecondSample → <|{Measurement1} → {{0.7, 3}, {15, True}}, {Measurement2} → {{0.7, 4}, {12, True}},
    {Measurement3} → {{0.3, 5}, {11, False}}, {Measurement4} → {{0.3, 1}, {6, True}},
    {Measurement5} → {{0.6, 2}, {10, True}}|>, ThirdSample → <|{Measurement1} → {{0.9, 2}, {16, True}},
    {Measurement2} → {{0.3, 4}, {11, True}}, {Measurement3} → {{0.4, 3}, {8, False}},
    {Measurement4} → {{0.3, 1}, {7, True}}, {Measurement5} → Missing[]|>|>
```

HorizontalSelection (1)

```
In[1]:= Needs["MathIOmica`"]
```

HorizontalSelection an option used typically when dealing with single-level associations. Depending on the choice we can select to act on components across Keys, or within the lists of the Keys:

```
In[2]:= associationExampleLists =
  <|{"Measurement1"} → {{1, 3, 2}, {0.1, 0.2, "a"}}, {"Measurement2"} → {{2, 3, 4}, {0.2, 0.1, "c"}},
   {"Measurement3"} → {{4, 2, 1}, {0.1, 0.3, "b"}}, {"Measurement4"} → {{3, 1, 5}, {0.3, 0.2, "d"}}|>;
```

We standardize the values of the second list, first components :

```
In[3]:= updateAssociationExampleLists = Applier[Standardize,
  associationExampleLists, ListIndex → 2, ComponentIndex → 1, HorizontalSelection → True]

Out[3]= <|{Measurement1} → -0.783349, {Measurement2} → 0.261116, {Measurement3} → -0.783349, {Measurement4} → 1.30558|>
```

To return the values we use Returner allows us to invoke the same HorizontalSelection option as well:

```
In[4]:= Returner[associationExampleLists, updateAssociationExampleLists,
  ListIndex → 2, ComponentIndex → 1, HorizontalSelection → True]

Out[4]= <|{Measurement1} → {{1, 3, 2}, {-0.783349, 0.2, a}}, {Measurement2} → {{2, 3, 4}, {0.261116, 0.1, c}},
  {Measurement3} → {{4, 2, 1}, {-0.783349, 0.3, b}}, {Measurement4} → {{3, 1, 5}, {1.30558, 0.2, d}}|>
```

Properties & Relations (1)

Applier acts as a complementary function that applies a function to the values of an input data with at the appropriate specified positions.

See Also

Applier ▪ **ApplierList** ▪ **MeasurementApplier** ▪ **OmicsObject** ▪ **Query**

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SampleKind

```
SampleKind
```
SampleKind is an option that allows to add a label for the kind of sample used.

Details

- The option is provided as a list.

See Also

DataImporterDirect ▪ **DataImporterDirectLabeled**

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SamplingFunction

```
SamplingFunction
```
SamplingFunction is an option for selecting a sampling strategy function.

Details

- SampingFunction options are used in BootstrapGeneral to select a bootstrap sampling strategy by selecting the sampling function for generating the simulated datasets.

See Also

BootstrapGeneral

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SelectionFunction

`SelectionFunction`
is an option for FilteringFunction to select which function will be used in filtering.

Details

- SelectionFunction is used in filtering applications, e.g. FilteringFunction , used to provide filtering based on a list value.

See Also

FilteringFunction

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SeriesApplier

SeriesApplier[*function*, *data*]
applies a given *function* to *data*, an association of lists, implementing masking for Missing values.

Details

- SeriesApplier[*function*, *data*] allows us to apply a *function* to an association of lists, *data* typically from time series data extracted from an OmicsObject. SeriesApplier takes two inputs:

function	Function that will be applied to each value, i.e. each list.
data	Association of lists of values.

- The following options can be given:

MissingMask	0	Value that is used to mask Missing data.

Examples (2)

Basic Examples (1)

First we load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

For a set of series measurements (e.g. created from an OmicsObject) we have:

In[2]:=
```
dataSeries = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
   {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {0.5, 4, 0.3, 2, 0.4, 6},
   {"Measurement4"} → {0.2, 3, Missing[], 3, 0.3, 2}, {"Measurement5"} → {Missing[], 0.6, 3, Missing[]}|>;
```

In[3]:=
```
SeriesApplier[Log, dataSeries]
```

Out[3]=
```
<|{Measurement1} → {-0.223144, Log[2], -0.356675, 0, -0.105361, Log[2]},
 {Measurement2} → {Missing[], -0.356675, 0, -1.20397, Log[5]},
 {Measurement3} → {-0.693147, Log[4], -1.20397, Log[2], -0.916291, Log[6]},
 {Measurement4} → {-1.60944, Log[3], Missing[], Log[3], -1.20397, Log[2]},
 {Measurement5} → {Missing[], -0.510826, Log[3], Missing[]}|>
```

Options (1)

MissingMask (1)

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```
In[1]:= Needs["MathIOmica`"]
```

`SeriesApplier` masks Missing values, by default setting them to 0 in the application of a function.

```
In[2]:= dataSeriesMissing = <|{"Measurement1"} → {1.1, 2.2, 3.3, Missing[]},
    {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {1, 4, Missing[], 2, 0.4, 6},
    {"Measurement4"} → {0.2, 3, 0.3, 3, 0.3, 2}, {"Measurement5"} → {Missing[], 4, 3.2, Missing[]}|>;
```

Let's standardize each series:

```
In[3]:= SeriesApplier[Standardize, dataSeriesMissing]

Out[3]= <|{Measurement1} → {-0.387298, 0.387298, 1.1619, Missing[]},
  {Measurement2} → {Missing[], -0.341769, -0.195296, -0.537065, 1.75767},
  {Measurement3} → {-0.528464, 0.756988, Missing[], -0.0999796, -0.785554, 1.61396},
  {Measurement4} → {-0.9281, 1.12349, -0.854829, 1.12349, -0.854829, 0.390779},
  {Measurement5} → {Missing[], 1.04565, 0.66541, Missing[]}|>
```

As the values produced by Standardize depend on the values calculated from the entire list (namely the mean and variance), setting the `MissingMask` to a value, e.g. 1 affects the entire computation:

```
In[4]:= SeriesApplier[Standardize, dataSeriesMissing, MissingMask → 1]

Out[4]= <|{Measurement1} → {-0.740656, 0.277746, 1.29615, Missing[]},
  {Measurement2} → {Missing[], -0.468204, -0.312136, -0.676295, 1.76877},
  {Measurement3} → {-0.644402, 0.73646, Missing[], -0.184115, -0.920575, 1.65703},
  {Measurement4} → {-0.9281, 1.12349, -0.854829, 1.12349, -0.854829, 0.390779},
  {Measurement5} → {Missing[], 1.10661, 0.58585, Missing[]}|>
```

See Also

ConstantSeriesClean ▪ **CreateTimeSeries** ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **SeriesCompare** ▪ **SeriesInternalCompare**

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SeriesCompare

SeriesCompare[$series_1$, $series_2$]
merges the values of two associations of series (lists) by pointwise operation (by default subtraction) on the values of each matching pair of keys.

Details

- SeriesCompare[$series_1$, $series_2$] takes as input two associations that have same size lists as values. SeriesCompare performs a pointwise operation (by default subtraction) on the values of each matching pair of keys in the associations and returns an association with the compared value list for each original intersecting key.
- The following options can be given:

CompareFunction	(If[MatchQ[Head[#1], Missing] || MatchQ[Head[#2], Missing], Missing[], #1 − #2] &)	The function is used by a Merge operation on the intersection of the two associations whose series are compared.

- If a value has a point that is Missing in either input series for a given key, then Missing[] will be the returned value for that data point.

Examples (3)

Basic Examples (1)

First we load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

We consider two sets of series measurements, (e.g. created from an OmicsObject):

In[2]:=
```
dataSeriesA = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
    {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {0.5, 4, 0.3, 2, 0.4, 6},
    {"Measurement4"} → {0.2, 3, 0.3`, 3, 0.3, 2}, {"Measurement5"} → {Missing[], 0.6, 3, Missing[]}|>;
dataSeriesB = <|{"Measurement2"} → {0.5, 1, 1.2, 0.3, 0.6, 1},
    {"Measurement2"} → {1.2, 0.7, 1, 0.3, Missing[]}, {"Measurement3"} → {0.2, 3.2, 0.1, 2.2, 0.3, 6.1},
    {"Measurement4"} → {Missing[], 3.1, 0.2, 3, 0.3, 2}, {"Measurement6"} → {2.1, 3.2, 1, Missing[]}|>;
```

The SeriesCompare function subtracts the two series when possible:

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In[3]:=
```
SeriesCompare[dataSeriesA, dataSeriesB]
```

Out[3]=
```
<|{Measurement2} → {Missing[], 0., 0, 0., Missing[]},
 {Measurement3} → {0.3, 0.8, 0.2, -0.2, 0.1, -0.1}, {Measurement4} → {Missing[], -0.1, 0.1, 0, 0., 0}|>
```

The input order does affect the output:

In[4]:=
```
SeriesCompare[dataSeriesB, dataSeriesA]
```

Out[4]=
```
<|{Measurement2} → {Missing[], 0., 0, 0., Missing[]},
 {Measurement3} → {-0.3, -0.8, -0.2, 0.2, -0.1, 0.1}, {Measurement4} → {Missing[], 0.1, -0.1, 0, 0., 0}|>
```

Options (1)

CompareFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

CompareFunction allows us to select the exact function used comparing the data series. We consider the example data series:

In[2]:=
```
dataSeriesA = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
   {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {0.5, 4, 0.3, 2, 0.4, 6},
   {"Measurement4"} → {0.2, 3, 0.3`, 3, 0.3, 2}, {"Measurement5"} → {Missing[], 0.6, 3, Missing[]}|>;
dataSeriesB = <|{"Measurement2"} → {0.5, 1, 1.2, 0.3, 0.6, 1},
   {"Measurement2"} → {1.2, 0.7, 1, 0.3, Missing[]}, {"Measurement3"} → {0.2, 3.2, 0.1, 2.2, 0.3, 6.1},
   {"Measurement4"} → {Missing[], 3.1, 0.2, 3, 0.3, 2}, {"Measurement6"} → {2.1, 3.2, 1, Missing[]}|>;
```

The default value for CompareFunction is subtraction implemented as :

In[3]:=
```
compareDefaultFunction = If[MatchQ[Head[#1], Missing] || MatchQ[Head[#2], Missing], Missing[], #1 - #2] &;
```

In[4]:=
```
SeriesCompare[dataSeriesA, dataSeriesB, CompareFunction → compareDefaultFunction]
```

Out[4]=
```
<|{Measurement2} → {Missing[], 0., 0, 0., Missing[]},
 {Measurement3} → {0.3, 0.8, 0.2, -0.2, 0.1, -0.1}, {Measurement4} → {Missing[], -0.1, 0.1, 0, 0., 0}|>
```

We could for example take logarithms before the subtraction:

In[5]:=
```
compareDefaultFunction2 =
  If[MatchQ[Head[#1], Missing] || MatchQ[Head[#2], Missing], Missing[], Log[#1] - Log[#2]] &;
```

In[6]:=
```
SeriesCompare[dataSeriesA, dataSeriesB, CompareFunction → compareDefaultFunction2]
```

Out[6]=
```
<|{Measurement2} → {Missing[], 0., 0, 0., Missing[]},
 {Measurement3} → {0.916291, 0.223144, 1.09861, -0.0953102, 0.287682, -0.0165293},
 {Measurement4} → {Missing[], -0.0327898, 0.405465, 0, 0., 0}|>
```

Properties & Relations (1)

SeriesCompare allows comparisons between different lists. SeriesInternalCompare allows comparisons to an internal individual list element for each individual list.

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See Also

CreateTimeSeries ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **SeriesApplier** ▪ **SeriesInternalCompare**

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SeriesInternalCompare

`SeriesInternalCompare[associationOfLists]`
compares each value in each list of *associationOfLists* to an internal reference value in the list, if the reference point itself is not Missing.

Details

- `SeriesInternalCompare[associationOfLists]` takes in an association *associationOfLists* that has series values (i.e. lists) and performs for each value a comparison of the data (typically the difference) to an internal reference point. The default operation compares the distance of each data point in a given list to the first value in the same list.
- If the comparison value in a given list is Missing, the corresponding key is removed from the output.
- The following options can be given:

CompareFunction	(If[MatchQ[Head[#2], Missing], Missing[], (#1 – #2)] &)	The function is used by a Query operation on non–missing input data. Namely: `Query[All, CompareFunction[#, #[[ComparisonIndex]]] &]@`
ComparisonIndex	1	List position of list value that will be used as a reference data point.

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DeleteRule	{Head, Missing}	`DeleteRule` allows the customization of how to select values for the reference data point for which its key should be deleted. The `DeleteRule` value takes the structure
		`deleteRuleOptionValue = .`
		`{MatchQ first argument,`
		`MatchQ second argument}`
		The MatchQ function referred to here is implemented by SeriesInternalCompare internally, and uses the `deleteRuleOptionValue` as:
		`MatchQ[`
		`deleteRuleOptionValue[[1]][`
		`reference`
		`comparison value],`
		`deleteRuleOptionValue[[2]]]`
		The default removes the corresponding key if the value used for reference in the comparison is actually Missing, i.e. the comparison reference point has Head that matches Missing.

Examples (5)

Basic Examples (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

We consider the following set of series measurements:

```
In[2]:= dataSeries = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
    {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {0.5, 4, 0.3, 2, 0.4, 6},
    {"Measurement4"} → {0.2, 3, Missing[], 3, 0.3, 2}, {"Measurement5"} → {Missing[], 0.6, 3, Missing[]}|>;

In[3]:= SeriesInternalCompare[dataSeries]

Out[3]= <|{Measurement1} → {0., 1.2, -0.1, 0.2, 0.1, 1.2},
  {Measurement3} → {0., 3.5, -0.2, 1.5, -0.1, 5.5}, {Measurement4} → {0., 2.8, Missing[], 2.8, 0.1, 1.8}|>
```

We notice that key/value combinations, for which the first component that is used in the comparison was Missing, have been removed.

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Options (3)

CompareFunction (1)

```
In[1]:= Needs["MathIOmica`"]
```

CompareFunction allows us to select the exact function used comparing to the reference value in each data series. We consider our example data series:

```
In[2]:= dataSeries = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
    {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {0.5, 4, 0.3, 2, 0.4, 6},
    {"Measurement4"} → {0.2, 3, Missing[], 3, 0.3, 2}, {"Measurement5"} → {Missing[], 0.6, 3, Missing[]}|>;
```

The default value for CompareFunction is subtraction implemented as:

```
In[3]:= compareInternalDefault = (If[MatchQ[Head[#2], Missing], Missing[], (#1 - #2)] &);
```

The two function inputs are #1: the entire list, #2 the comparison value in the list as specified by the ComparisonIndex value. The function is used by a Query operation on non-missing input data. Namely:

```
In[1]:= Query[All,CompareFunctionValue[#,#[[ComparisonIndexValue]]]&]

Out[0]= Query[All, CompareFunctionValue[#1, #1[[ComparisonIndexValue]]] &]
```

The default compares the difference to the first value in each series:

```
In[4]:= SeriesInternalCompare[dataSeries, CompareFunction → compareInternalDefault]

Out[4]= <|{Measurement1} → {0., 1.2, -0.1, 0.2, 0.1, 1.2}, {Measurement3} → {0., 3.5, -0.2, 1.5, -0.1, 5.5},
  {Measurement4} → {0., 2.8, -0.2 + Missing[], 2.8, 0.1, 1.8}|>
```

We could for example take the ratio of values instead:

```
In[5]:= compareInternalExample = ((#1 / #2) &);

In[6]:= SeriesInternalCompare[dataSeries, CompareFunction → compareInternalExample]

Out[6]= <|{Measurement1} → {1., 2.5, 0.875, 1.25, 1.125, 2.5},
  {Measurement3} → {1., 8., 0.6, 4., 0.8, 12.}, {Measurement4} → {1., 15., 5. Missing[], 15., 1.5, 10.}|>
```

ComparisonIndex (1)

```
In[1]:= Needs["MathIOmica`"]
```

ComparisonIndex allows us to select which value of the list to use for comparison. For example, consider the following series:

```
In[2]:= dataSeries = <|{"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2},
    {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5}, {"Measurement3"} → {0.5, 4, 0.3, 2, 0.4, 6},
    {"Measurement4"} → {0.2, 3, Missing[], 3, 0.3, 2}, {"Measurement5"} → {Missing[], 0.6, 3, Missing[]}|>;
```

We can compare values to the second component of a list:

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```
In[3]:= SeriesInternalCompare[dataSeries, ComparisonIndex → 2]

Out[3]= <| {Measurement1} → {-1.2, 0, -1.3, -1, -1.1, 0},
  {Measurement2} → {Missing[], 0., 0.3, -0.4, 4.3}, {Measurement3} → {-3.5, 0, -3.7, -2, -3.6, 2},
  {Measurement4} → {-2.8, 0, Missing[], 0, -2.7, -1}, {Measurement5} → {Missing[], 0., 2.4, Missing[]} |>
```

Negative values can be used to select from the end. For example comparing to the last component:

```
In[4]:= SeriesInternalCompare[dataSeries, ComparisonIndex → -1]

Out[4]= <| {Measurement1} → {-1.2, 0, -1.3, -1, -1.1, 0}, {Measurement2} → {Missing[], -4.3, -4, -4.7, 0},
  {Measurement3} → {-5.5, -2, -5.7, -4, -5.6, 0}, {Measurement4} → {-1.8, 1, Missing[], 1, -1.7, 0} |>
```

DeleteRule (1)

```
In[1]:= Needs["MathIOmica`"]
```

DeleteRule allows the customization of how to select values that will be removed for the comparison index value. The option value takes the structure deleteRuleOptionValue={MatchQ first argument, MatchQ second argument}. The MatchQ function referred to is implemented by SeriesInternalCompare internally, and uses the deleteRuleOptionValue as: MatchQ[deleteRuleOptionValue[[1]][comparison value], deleteRuleOptionValue[[2]]]. The default removes the corresponding key if the value used for reference in the comparison is actually Missing, i.e. the comparison reference point has Head that matches Missing. For example, the default value matches the Head of the value to Missing:

```
In[2]:= defaultDeleteRule = {Head, Missing};
```

Consider the following series:

```
In[3]:= dataSeriesExample =
   <| {"Measurement1"} → {0.8, 2, 0.7, 1, 0.9, 2}, {"Measurement2"} → {Missing[], 0.7, 1, 0.3, 5},
    {"Measurement3"} → {a, b, c, d, e, f}, {"Measurement4"} → {"SomeString", 3, Missing[], 3, 0.3, 2},
    {"Measurement5"} → {Missing[], 0.6, 3, Missing[]} |>;

In[4]:= SeriesInternalCompare[dataSeriesExample, DeleteRule → defaultDeleteRule]

Out[4]= <| {Measurement1} → {0., 1.2, -0.1, 0.2, 0.1, 1.2}, {Measurement3} → {0, -a + b, -a + c, -a + d, -a + e, -a + f},
  {Measurement4} → {0, 3 - SomeString, Missing[], 3 - SomeString, 0.3 - SomeString, 2 - SomeString} |>
```

We can change this to remove everything for example that matches Head String or Missing:

```
In[5]:= exampleDeleteRule = {Head, Missing | String};

In[6]:= SeriesInternalCompare[dataSeriesExample, DeleteRule → exampleDeleteRule]

Out[6]= <| {Measurement1} → {0., 1.2, -0.1, 0.2, 0.1, 1.2}, {Measurement3} → {0, -a + b, -a + c, -a + d, -a + e, -a + f} |>
```

We can extend this to remove only specific value, say 0.8:

```
In[7]:= exampleDeleteRule2 = {# &, 0.8};
```

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```
In[8]:= SeriesInternalCompare[dataSeriesExample, DeleteRule → exampleDeleteRule2]
Out[8]= ⟨|{Measurement2} → Missing[], {Measurement3} → {0, -a + b, -a + c, -a + d, -a + e, -a + f},
  {Measurement4} → {0, 3 - SomeString, Missing[], 3 - SomeString, 0.3 - SomeString, 2 - SomeString},
  {Measurement5} → Missing[]|⟩
```

We notice above that if the comparison is Missing the entire key is marked in this case as missing. This behavior can be adjusted by modifying the CompareFunction option, for example to just carry out simple subtraction:

```
In[9]:= SeriesInternalCompare[dataSeriesExample, DeleteRule → exampleDeleteRule2, CompareFunction → ((#1 - #2) &)]
Out[9]= ⟨|{Measurement2} → {0, 0.7 - Missing[], 1 - Missing[], 0.3 - Missing[], 5 - Missing[]},
  {Measurement3} → {0, -a + b, -a + c, -a + d, -a + e, -a + f},
  {Measurement4} → {0, 3 - SomeString, -SomeString + Missing[], 3 - SomeString, 0.3 - SomeString, 2 - SomeString},
  {Measurement5} → {0, 0.6 - Missing[], 3 - Missing[], 0}|⟩
```

Properties & Relations (1)

SeriesInternalCompare allows comparisons to an internal individual list element for each individual list. SeriesCompare allows comparisons between different lists.

See Also

ConstantSeriesClean ▪ **CreateTimeSeries** ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **SeriesApplier** ▪ **SeriesCompare**

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StandardizeExtended

StandardizeExtended[*inputList*, *subtract*, *divide*]
allows standardization of data that may ignore Missing or text values with specified transformations.

Details

- StandardizeExtended[*inputList*, *subtract*, *divide*] can perform data standardization on datasets that may include Missing values or other string values. The Missing/String values are ignored, and StandardizeExtended performs operations only on Real values. StandardizeExtended takes as inputs:

inputList	Data that will be standardized.
subtract	Function of all data used for subtraction from each data point (e.g. Mean).
divide	Function of all data used for division of each data point (e.g. StandardDeviation).

Examples (2)

Basic Examples (1)

First we load the MathIOmica package:

```
In[1]:= Needs["MathIOmica`"]
```

Let's consider some data:

```
In[2]:= dataExample = {3, 34, 11, Missing[], 32, 22, 11, 12, 33, 23, Missing[], "NA"};

In[3]:= StandardizeExtended[dataExample, Mean, MedianDeviation]

Out[3]= {-1.55556, 1.26263, -0.828283, Missing[], 1.08081,
         0.171717, -0.828283, -0.737374, 1.17172, 0.262626, Missing[], NA}
```

Properties & Relations (1)

The inbuilt Standardize function can also handle Missing values (Version Mathematica 10.4+) and may be used to the same effect. StandardizeExtended can also ignore String variables in the data.

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See Also

Applier ▪ **ApplyBoxCoxTransform** ▪ **OmicsObject** ▪ **Returner** ▪ **QuantileNormalization** ▪ **Query**

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TimeExtractor

TimeExtractor[*omicsObject*]
extracts a list of sorted times from an OmicsObject's outer keys.

Details

- TimeExtractor[*omicsObject*] is a function that takes as input an OmicsObject that has been created so that its outer keys are strings of numbers corresponding to time points for a time series, and constructs a list of the times (i.e. keys) in the OmicsObject.
- TimeExtractor has same functionality as Sort[ToExpression@Keys@dataIn].

Examples (1)

Basic Examples (1)

First we load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

For an OmicsObject that was created from a series we have:

```
In[2]:= omicsObject1 = <|"7" → <|{"A0AVT1"} → {{0.937`}, {17}}, {"A0FGR8"} → {{1.073`}, {24}},
          {"A0MZ66"} → {{1.059`}, {9}}, {"A1A4S6"} → {{1.03`}, {11}}, {"A1L0T0"} → {{1.268`}, {4}}|>,
        "9" → <|{"A0AVT1"} → {{1.003`}, {17}}, {"A0FGR8"} → {{0.921`}, {24}}, {"A0MZ66"} → {{1.479`}, {9}},
          {"A1A4S6"} → {{0.779`}, {11}}, {"A1L0T0"} → {{0.917`}, {4}}|>,
        "10" → <|{"A0AVT1"} → {{0.966`}, {17}}, {"A0FGR8"} → {{1.007`}, {24}}, {"A0MZ66"} → {{1.455`}, {9}},
          {"A1A4S6"} → {{0.951`}, {11}}, {"A1L0T0"} → {{1.058`}, {4}}|>,
        "11" → <|{"A0AVT1"} → {{0.982`}, {17}}, {"A0FGR8"} → {{0.913`}, {24}}, {"A0MZ66"} → {{1.689`}, {9}},
          {"A1A4S6"} → {{0.78`}, {11}}, {"A1L0T0"} → {{1.091`}, {4}}|>,
        "14" → <|{"A0AVT1"} → {{1.024`}, {17}}, {"A0FGR8"} → {{0.937`}, {24}}, {"A0MZ66"} → {{1.312`}, {9}},
          {"A1A4S6"} → {{0.818`}, {11}}, {"A1L0T0"} → {{0.936`}, {4}}|>|>;
```

We create the corresponding time series lists:

```
In[3]:= TimeExtractor[omicsObject1]
Out[3]= {7, 9, 10, 11, 14}
```

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See Also

ConstantSeriesClean ▪ **CreateTimeSeries** ▪ **OmicsObject** ▪ **OmicsObjectCreator** ▪ **SeriesApplier** ▪ **SeriesCompare** ▪ **SeriesInternalCompare** ▪ **TimeSeriesClassification**

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TimeSeriesClassification

TimeSeriesClassification[*data*, *setTimes*]
identifies classes of temporal behavior in time series datasets that run over a specified set of time points.

Details

- TimeSeriesClassification[*data*, *setTimes*] takes a *data* association (or list of lists) of values corresponding to intensities collected over time and classifies the values into classes (groups) that show distinct similar temporal patterns. TimeSeriesClassification takes as inputs:

data	Association with series as values, or a list of series, where the series contain information regarding time intensities/observations. Each series may include Missing data points and may be entered as list of N signal intensities corresponding one–to–one to the N *setTimes* with Missing inserted appropriately if the data is absent, $\{X_1 = X(t_1), X_2 = X(t_2), \ldots, X_N = X(t_N)\}$. Alternatively, each series data may be a list of pairs of values $\{\{t_1,X_1\},\{t_2,X_2\},\ldots,\{t_N,X_N\}\}$ for only existing measurements.
setTimes	A global complete set of all possible N times during which all data series could have been collected in the window of the experiment, including times for which no values were reported or are missing, $\{t_1, t_2, \ldots, t_N\}$.

- The default output for TimeSeriesClassification is an Association with outer keys being the classification classes, inner keys being the class members, and each class member value being a list of {{computed classification vector}, {input data list}}. The general output structure is for M output classes of each having m_i members:

- <|Class$_1$ → <|Member$_{11}$ → {{classification vector$_{11}$}, {input data vector$_{11}$}},
  Member$_{12}$ → {{classification vector$_{12}$}, {input data vector$_{12}$}}, ...,
  Member$_{1\,m_1}$ → {{classification vector$_{1\,m_1}$}, {input data vector$_{1\,m_1}$}}|>,
  Class$_2$ → <|Member$_{21}$ -> {{classification vector$_{21}$}, {input data vector$_{21}$}},
  Member$_{22}$ -> {{classification vector$_{22}$}, {input data vector$_{22}$}}, ...,
  Member$_{2\,m_2}$ → {{classification vector$_{2\,m_2}$}, {input data vector$_{2\,m_2}$}}|>, ...,
  Class$_M$ → <|Member$_{M1}$ -> {{classification vector$_{M1}$}, {input data vector$_{M1}$}},
  Member$_{M2}$ -> {{classification vector$_{M2}$}, {input data vector$_{M2}$}}, ...,
  Member$_{Mm_M}$ → {{classification vector$_{Mm_M}$}, {input data vector$_{Mm_M}$}}|>|>

- The following options can be given:

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AutocorrelationCutoffs	{0}	Cutoffs, for "Autocorrelation" and "InterpolatedAutocorrelation" methods, for different lags that will be used to filter out data series for which the lags are not within cutoffs. The list length corresponds to cuttofs at different lags, with the ith lag cutoff provided as the ith index, i.e. $\rho_c = \{\rho_{c1}, \rho_{c2,}, \ldots, \rho_{ci,}, \ldots, \rho_{ck}\}$ up to k, where 1≤ k ≤ n, and typically n=Floor[Length[setTimes]/2]. The classification will only consider lags up to the length of the list provided. The cutoffs are user–provided and typically calculated through simulation.
AutocorrelationLogic	False	Option to return the autocorrelation logic list for each signal, with the default set to False. If set to True, a logic vector is returned indicating whether or not at a particular lag the autocorrelation for a signal is above or below the AutocorrelationCutoffs.
AutocorrelationOptions	{UpperFrequencyFactor → 1}	Options that are used by the internal Autocorrelation function in the case that the Method –> "Autocorrelation" is set.
InterpolationDeltaT	"Auto"	Time step used to grid the time window over which calculations will be performed. If set to "Auto" the step will correspond to dividing the span of the interval into a number of equal steps equal to the number of input time points.
InterpolationOptions	{}	Options list for the internal Interpolation function used to interpolate between data points that have Missing values or uneven spacing.
LombScargleCutoff	0	Cutoff value for "LombScargle" method, for filtering the highest intensity observed in the power spectrum. The cutoff is user–provided and typically calculated through simulation.

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LombScargleOptions	{PairReturn → False, NormalizeIntensities → True}	Options that are used by the internal LombScargle function if the case that the Method → "LombScargle" is set.
Method	"LombScargle"	Selection of which algorithm to use in the classification scheme.
ReturnAllSpikes	False	Option whether each signal may maintain unique membership to each spike class, or be allowed to belong to multiple classes. Used in "Autocorrelation" and "InterpolatedAutocorrelation" methods. If set to False, first spike maxima are classified, and only signals found not to belong to spike maxima are then considered for membership in the spike minima class.
ReturnData	True	If set to True will return input keys to data associations in the classification. If set to False will only return the keys of the input data in the classification.
ReturnModels	False	Whether to return the models as well as the classification information for the input data. The data is returned as an association with the key "TimeSeriesClasses" for classification groups and one of the following: (i) "Models" for model–based methods, (ii) "LombScargle" for periodograms in the "LombScargle" method, (iii) "Autocorrelations" for autocorrelation based methods.

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SpikeCutoffs	<|1 → {.99, –99}, 2 → {.99, –99}|>	Association with number, n, of data points as keys, and values corresponding to cutoffs, in the form <|n → {Maximum Spike Cutoff$_n$, Minimum Spike Cutoff$_n$}|> used to call spike maxima and minima for a time series with this number of datapoints. The values are provided by the user depending on data approach based on simulation. The default values are only place–holders and should be replaced by real values. The association must have corresponding keys for all lengths of input datasets, so that Keys[OptionValue[, i.e. all SpikeCutoffs]] ∈ {Possible lengths of numeric data}. possible lengths of series constructed by excluding Missing or other non–numeric values).

- For each series, the data has to be in the order that the set times appear. In general the data are list of time series signal values, e.g. $\{X_1 = X(t_1), X_2 = X(t_2), \ldots, X_N = X(t_N)\}$ over a list of ordered sampling times, where $t_1 < t_2 < \ldots < t_N$. Note that $\{t_1, t_2, \ldots, t_N\}$ is necessarily a subset of the input *setTimes*, since any time point during which data was collected is necessarily a possible time point during which it could have been collected.

- Multiple Methods can be used, depending on the algorithm of choice, statistics, and computational resources. The methods are discussed further below, and briefly include:

"LombScargle"	Classification based on periodograms (power spectra) generated by a Lomb–Scargle computation as implemented internally by the LombScargle function. The data is classified into classes of major (highest intensity) frequencies and spikes (maxima or minima in real signal intensity), depending on cutoffs typically provided by simulation and passed to the function by the LombScargleCutoffs and SpikeCutoffs option values. The returned {computed classification vector} for this method is the intensity list of the periodogram for each signal.

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"Autocorrelation"	Classification based on autocorrelations generated by a Lomb–Scargle approach using an inverser Fourier transform of spectral intensities, as implemented through the Autocorrelation function. The data is classified into autocorrelations at different lags and spikes (maxima or minima) classes, depending on cutoffs typically provided by simulation. The returned {computed classification vector} for this method is the autocorrelation list for each signal.
"InterpolatedAutocorrelation"	Classification based on autocorrelations generated directly in time, with Missing data handled through interpolation. The data is classified into autocorrelations at different lags and spikes (maxima or minima) classes depending on cutoffs typically provided by simulation. The returned {computed classification vector} for this method is the autocorrelation list for each signal.
"TimeSeriesModelAggregate"	Classification based on model fitting of time series through TimeSeriesModelFit and all available models therein. The data is classified into aggregate model classes. The returned {computed classification vector} for this method is the actual input signal.
"TimeSeriesModelDetailed"	Classification based on model fitting of time series through TimeSeriesModelFit and all available models therein. The data is classified into model classes based on individual model degree parameters. The returned {computed classification vector} for this method is the "BestFitParameters" for the model fit. If this list is empty an integer list is returned {token integer} – this is used in subsequent clustering applications.

Background

General

- For sets of time series measurement, (e.g. gene expression levels, protein intensities, compound concentrations, temperature) we would like to identify groups of entities whose temporal behavior is similar. If we can classify temporal signals that show similar behavior into classes, then we can also look for associations for the members of each class. The behavior of a given signal can be considered in terms of time or frequency (if we can Fourier transform the signal). The structure of the signal can then be described through autocorrelations, or equivalently its power spectrum (periodogram). Additionally, a signal can also be modeled with a time series model that has certain structure, e.g. autoregressive (AR), moving-average (MA), autoregressive moving-average ARMA etc. (see also TimeSeriesModelFit).

- A complication that may arise in real experimental data is that the time series measurements may not be evenly spaced. The same uneven spacing can also result from regular time sampling that for various reasons has led to missing data. Many methods exist to handle unevenly sampled time series, including Lomb-Scargle transformations and interpolation methods.

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- The TimeSeriesClassification Methods are described in more detail below:

Method: "LombScargle"

- The "LombScargle" method relies on transformation of a time signal (may include missing data or be unevenly sampled) to a periodogram/power spectrum. The maximum intensity across all frequencies is then used to filter signals based on whether they display a dominant frequency signal, typically using a cutoff that is user-supplied based on simulations. If a frequency is found that is so judged to be significant, the signals are selected and separated into classes based on what the dominant frequency was.

- Specifically, for a given signal X_j, with length N, we have N time measurements, namely $X_j = \{X_j(t_1), X_j(t_2), \ldots, X_j(t_N)\}$ and can calculate the signal's periodogram. The method uses the LombScargle function periodogram to provide n = Floor[M / 2] frequencies, $f_j = \{f_{j1}, f_{j2}, \ldots, f_{jk}, \ldots, f_{jn}\}$, and corresponding n intensities, $I_j = \{I_{j1}, I_{j2}, \ldots, I_{jn}\}$. The default is for I_j to be calculated as a normalized vector. The maximum intensity of this vector, $I_{j\,k_{max}}$ = Max[I_j] corresponds to a dominant frequency $f_{j\,k_{max}}$, and occurs at some index k_{max}. For each signal X_j we can then compare $I_{j\,k_{max}}$ to a cutoff intensity I_{cutoff} to see if $I_{j\,k_{max}} > I_{cutoff}$. If so, the signal is placed in class $f_{k_{max}}$. A maximum of n classes is thus possible, and possible classes are labeled=$\{f_1, f_2, \ldots, f_k, \ldots, f_n\}$. The exact frequency list will depend on n, and hence the length of the input set times M, and is determined automatically by the LombScargle function.

- Signals that do not show a maximum intensity in frequency space above the cutoff intensity, i.e. signals j for which $I_{j\,k} \leq I_{cutoff}$ for all k, are checked for sudden signal spikes at any time point, and if so classified as spike maxima or minima. For each signal not showing a maximum periodogram intensity, $\tilde{X}_j$, we can calculate the real signal maximum, $\max_j = \text{Max}[\tilde{X}_j]$, and minimum, $\min_j = \text{Min}[\tilde{X}_j]$, from signal intensities across all time points. We can compare these values against cutoffs {Maximum Spike Cutoff$_n$, Maximum Spike Cutoff$_n$} provided by the user: These cutoffs are dependent on the length of a time series, n, and typically would correspond to the 99th quantile of distributions of maxima and minima of randomly generated signals. These cutoff values are provided by the SpikeCutoffs option value for each length n involved in the computation as part of an association for different lengths
  <| ..., n → {Maximum Spike Cutoff$_n$, Maximum Spike Cutoff$_n$}, ... length i → {Maximum Spike Cutoff$_i$, Maximum Spike Cutoff$_i$}, ...|>. If a signal of length n, $\tilde{X}_j$ has $\max_j >$ Maximum Spike Cutoff$_n$ it is classified in the "SpikeMax" class, or otherwise if a signal $\tilde{X}_j$ has $\min_j <$ Maximum Spike Cutoff$_n$ it is classified in the "SpikeMin" class. Signals for which the maximum signal intensity is not above the cutoffs are not reported.

- The default output for this method is an Association with outer keys being the classification classes C, where $C \in \{f_1, f_2, \ldots, f_k, \ldots, f_n,$ SpikeMax, SpikeMin$\}$, inner keys being the class members, signals X_j, and each class member value being a list of {{periodogram intensity list for signal X_j}, {input data list for X_j}}.

Method: "Autocorrelation"

- The "Autocorrelation" method of classification successively identifies time series from the dataset that have autocorrelations at particular time lags. Specifically, for a given signal X_j, with length N, we have N time measurements, namely $X_j = \{X_j(t_1), X_j(t_2), \ldots, X_j(t_N)\}$ and can calculate the signal's autocorrelations. The method uses the Autocorrelation function, based on a Lomb-Scargle approach, to obtain a list of autocorrelations from lag 0 to lag n, $\rho_j = \{\rho_{j0}, \rho_{j1}, \ldots, \rho_{jk}, \ldots, \rho_{jn}\}$, where typically n = Floor[N / 2]. The autocorrelations are then compared against a list of cutoffs, provided by the user through the AutocorrelationCutoffs option, in the form $\rho_c = \{\rho_{c1}, \rho_{c2}, \ldots, \rho_{ck}\}$, i.e. for lags 1 to a chosen lag k,where $1 \leq k \leq n$. If $\rho_{ji} \geq \rho_{ci}$ for any i, then the signal is placed in a class corresponding to the lowest lag for which this is true, i.e. in class "Lag l" where l = Min[{i : $\rho_{ji} \geq \rho_{ci}$} and i ∈ {1, ..., k}. This results in a unique classification for each signal into "Lag" classes, or not - we note that this behavior may be changed bye setting the ReturnUniqueAutocorrelation option to False. We note that autocorrelations at time lag τ_2 partially depend on those at τ_1, those at τ_3 partially depend on those at τ_2, and so on. The choice to classify uniquely ensures that any identified autocorrelation at a particular (higher) lag cannot possibly arise due to dependence on autocorrelations at prior (lower) lags.

- The signals that do not show autocorrelation at any lag compared to the autocorrelation cutoff list are subsequently checked for sudden signal spikes at any time point, and if so classified as spike maxima or minima. For each signal not showing autocorrelation, $\tilde{X}_j$, we can calculate the real signal maximum, $\max_j = \text{Max}[\tilde{X}_j]$, and minimum, $\min_j = \text{Min}[\tilde{X}_j]$, from signal intensities across all time points. We can compare these values against cutoffs {Maximum Spike Cutoff$_n$, Maximum Spike Cutoff$_n$} provided by the user: These cutoff values are provided by the SpikeCutoffs option value for each length n involved in the computation as part of an association for different lengths
  <| ..., n → {Maximum Spike Cutoff$_n$, Maximum Spike Cutoff$_n$}, ... length i → {Maximum Spike Cutoff$_i$, Maximum Spike Cutoff$_i$}, ...|>. If a signal of length n, $\tilde{X}_j$ has $\max_j >$ Maximum Spike Cutoff$_n$ it is classified in the "SpikeMax" class, or otherwise if a signal $\tilde{X}_j$ has $\min_j <$ Maximum Spike Cutoff$_n$ it is classified in the "SpikeMin" class. Signals for which the maximum signal intensity is not above the cutoffs are not reported.

- Classification, then, identifies which signals contain significant autocorrelation compared to the AutocorrelationCutoffs list, and of those signals that do not contain significant autocorrelation, which contain significant positive or negative spikes, compared to values provided in the SpikeCutoffs associations.. Three groups of classes are reported: 1) Significant autocorrelations at various lags, 2) No autocorrelations, but positive spikes present, 3) No autocorrelations, but negative spikes present.

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- The default output for this method is an Association with outer keys being the classification classes C, where $C \in \{\text{lag1}, \ldots \text{lag2}, \ldots, \text{lag}_n, \text{SpikeMax}, \text{SpikeMin}\}$, inner keys being the class members, signals X_j, and each class member value being a list of $\{\{\text{autocorrelation list for signal } X_j\}, \{\text{input data list for } X_j\}\}$.

Method: "InterpolatedAutocorrelation"

- The "InterpolatedAutocorrelation" method is similar in classification approach to the "Autocorrelation" "Autocorrelation " method but differs in the computation of the autocorrelations. It uses Interpolation for each signal to handle missing data or uneven sampling, followed by computation of the autocorrelations using CorrelationFunction.

- Specifically, for a given signal X_j, with length N, we have N time measurements, namely $X_j = \{X_j(t_1), X_j(t_2), \ldots, X_j(t_N)\}$ and can calculate the signal's autocorrelations. The "InterpolatedAutocorrelation" method uses the ListInterpolation function to create an interpolation over each signal data. The interpolated data is then sampled over an evenly spaced grid: For an input set times provided $\{t_1, \ldots, t_N\}$ the data is sampled at intervals $\frac{t_N - t_1}{N-1}$, or at a user specified interval $\triangle_t = (\text{InterpolationDeltaT value})$. The autocorrelation list of any given signal is then computed using CorrelationFunction to obtain a list of autocorrelations from lag 0 to lag n, $\rho_j = \{\rho_{j0}, \rho_{j1}, \ldots, \rho_{jk}, \ldots, \rho_{jn}\}$, where $n = N - 1$. The classification the proceeds as with the "Autocorrelation" method above, as repeated here:

- The autocorrelations for each signal are compared against a list of cutoffs, provided by the user through the AutocorrelationCutoffs option, in the form $\rho_c = \{\rho_{c1}, \rho_{c2,}, \ldots, \rho_{ck}\}$, i.e. for lags 1 to a chosen lag k,where $1 \leq k \leq n$. If $\rho_{ji} \geq \rho_{ci}$ for any i, then the signal is placed in a class corresponding to the lowest lag for which this is true, i.e. in class "Lag l" where $l = \text{Min}[\{i : \rho_{ji} \geq \rho_{ci}\}$ and $i \in \{1, \ldots, k\}$. This results in a unique classification for each signal into "Lag" classes, or not - we note that this behavior may be changed bye setting the ReturnUniqueAutocorrelation option to False. We note that autocorrelations at time lag τ_2 partially depend on those at τ_1, those at τ_3 partially depend on those at τ_2, and so on. The choice to classify uniquely ensures that any identified autocorrelation at a particular (higher) lag cannot possibly arise due to dependence on autocorrelations at prior (lower) lags.

- The signals that do not show autocorrelation at any lag compared to the autocorrelation cutoff list are subsequently checked for sudden signal spikes at any time point, and if so classified as spike maxima or minima. For each signal not showing autocorrelation, $\tilde{X}_j$, we can calculate the real signal maximum, $\max_j = \text{Max}[\tilde{X}_j]$, and minimum, $\min_j = \text{Min}[\tilde{X}_j]$, from signal intensities across all time points. We can compare these values against cutoffs $\{\text{Maximum Spike Cutoff}_n, \text{Maximum Spike Cutoff}_n\}$ provided by the user: These cutoff values are provided by the SpikeCutoffs option value for each length n involved in the computation as part of an association for different lengths $\langle| \ldots, n \to \{\text{Maximum Spike Cutoff}_n, \text{Maximum Spike Cutoff}_n\}, \ldots \text{length } i \to \{\text{Maximum Spike Cutoff}_i, \text{Maximum Spike Cutoff}_i\}, \ldots |\rangle$. If a signal of length n, $\tilde{X}_j$ has $\max_j > \text{Maximum Spike Cutoff}_n$ it is classified in the "SpikeMax" class, or otherwise if a signal $\tilde{X}_j$ has $\min_j < \text{Maximum Spike Cutoff}_n$ it is classified in the "SpikeMin" class. Signals for which the maximum signal intensity is not above the cutoffs are not reported.

- Classification, then, identifies which signals contain significant autocorrelation compared to the AutocorrelationCutoffs list, and of those signals that do not contain significant autocorrelation, which contain significant positive or negative spikes, compared to values provided in the SpikeCutoffs associations.. Three groups of classes are reported: 1) Significant autocorrelations at various lags, 2) No autocorrelations, but positive spikes present, 3) No autocorrelations, but negative spikes present.

- The default output for this method is an Association with outer keys being the classification classes C, where $C \in \{\text{lag1}, \ldots \text{lag2}, \ldots, \text{lag}_n, \text{SpikeMax}, \text{SpikeMin}\}$, inner keys being the class members, signals X_j, and each class member value being a list of $\{\{\text{autocorrelation list for signal } X_j\}, \{\text{input data list for } X_j\}\}$.

Method: "TimeSeriesModelAggregate"

- The "TimeSeriesModelAggregate" method is a classification approach that separates signals into classes based on a best temporal model fit. The method does not use any cutoffs in its approach.

- Specifically, for a given signal X_j, with length N, we have N time measurements, namely $X_j = \{X_j(t_1), X_j(t_2), \ldots, X_j(t_N)\}$. For all non-missing data, we can fit the signal/time series to a model, utilizing TimeSeriesModelFit. The signals are classified by best fit model family (on aggregate), with classes labeled as "Model family". This classification does not take into account other specific parameters of the model (e.g. order). We note that model fitting may be time consuming and the classification may take a while to compute depending on the number of signals, and/or time points per signal.

- The default output for this method is an Association with outer keys being the classification classes C, where $C \in \{\text{ModelFamily}_1, \ldots, \text{ModelFamily}_2, \ldots\}$, inner keys being the class members, signals X_j, and each class member value being a list of $\{\{\text{input data list for } X_j\}, \{\text{input data list for } X_j\}\}$ (the reason for this form is that this vector may subsequently be used in clustering algorithms).

Method: "TimeSeriesModelDetailed"

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- The "TimeSeriesModelDetailed" method is a classification approach that separates signals into classes based on a best temporal model fit. Compared to the "TimeSeriesModelAggregate" method it offers a refinement in classifying the signals not only by model family, but also by parameters of the model. The method does not use any cutoffs in its approach.

- Specifically, for a given signal X_j, with length N, we have N time measurements, namely $X_j = \{X_j(t_1), X_j(t_2), \ldots, X_j(t_N)\}$. For all non-missing data, we can fit the signal/time series to a model, utilizing TimeSeriesModelFit. The signals are classified by best fit model process form, with classes named after the specific best fit Time Series Processes. We note that model fitting may be time consuming and the classification may take a while to compute depending on the number of signals, and/or time points per signal.

- The default output for this method is an Association with outer keys being the classification classes C, where $C \in \{\text{ModelFamily}_1[\text{parameter set } A], \text{ModelFamily}_1[\text{parameter set } B], \ldots, \text{ModelFamily}_n[\text{parameter set } M]\}$, inner keys being the class members, signals X_j, and each class member value being a list of `{{BestFitParameters}, {input data list for Xj}}`. If the BestFitParameter list for any signal is empty a token counter integer is returned instead (the reason for this form is that this vector may subsequently be used in clustering algorithms).

Examples (18)

Basic Examples (1)

First we need to load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

We create the following data for our example:

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
```

Let's see what the first ten data points look like:

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In[3]:=
```
classificationExample1[[1 ;; 10]]
```

Out[3]=
```
<| SpikePositive_1 → {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
    0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
    -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732},
  SpikePositive_2 → {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829,
    0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
    -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543},
  SpikePositive_3 → {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993,
    -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
    0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977},
  SpikePositive_4 → {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033, -0.0772898,
    0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
    0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859},
  SpikePositive_5 → {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663, 0.0676522,
    0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
    0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368},
  SpikePositive_6 → {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416, 0.0326082,
    -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
    0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102},
  SpikePositive_7 → {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442, -0.00304927,
    0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
    0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004},
  SpikePositive_8 → {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677,
    -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
    -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763},
  SpikePositive_9 → {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483,
    -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062},
  SpikePositive_10 → {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367,
    -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457} |>
```

The data is a mixture of spikes, linear signals and sinusoids with background noise. We can generate a set of data that have this kind of noisy signals:

In[4]:=
```
backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
```

The time point list for the series is:

In[5]:=
```
timePointsExample = Range[20];
```

We can use the background to determine our data cutoffs for the "LombScargle" default method. We work with the QuantileEstimator function to generate a value for the LombScargleCutoff, by default using the 0.95th quantile:

In[6]:=
```
bootstrapQ95 = QuantileEstimator[backgroundExample, timePointsExample]
```

Out[6]=
```
0.890567
```

We can work again with the QuantileEstimator function to also generate a value for the SpikeCutoffs:

In[7]:=
```
bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"]
```

Out[7]=
```
<| 20 → {0.42185, -0.421758} |>
```

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Let's perform the classification:

In[8]:=
```
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes]
```

```
Method → "LombScargle"
```

Out[8]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
      0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
      -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
      0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
      0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
      0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
      0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
      0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
      0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
      0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
      0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
      -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
      0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
      0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
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      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
      0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
      0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
      -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
      0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
      0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
      0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
      0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
   SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
      0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
      -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
      0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
   SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
      0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
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      -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
   SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
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      -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
  SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
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      -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
  SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
      0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
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  SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
      0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
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      0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
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      0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
      0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
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      0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
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      -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
      -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
  SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
      0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
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      -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
      0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
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      -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
  SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
      0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
      -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
      0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
      0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
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      -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
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  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
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      -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
      0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
      -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
      -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
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      0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
      -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
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  SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
      0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
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  SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
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  SpikeNegative_13 → {{0.173083, 0.379193, 0.338228, 0.384591, 0.344256, 0.301779, 0.172933,
    0.337034, 0.332955, 0.316239}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
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    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{0.369536, 0.475376, 0.186202, 0.236301, 0.19825, 0.237895, 0.260777,
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    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
    0.315364, 0.382839, 0.290684}, {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309,
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  SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
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  SpikeNegative_17 → {{0.197001, 0.246358, 0.358498, 0.402863, 0.27067, 0.34906, 0.104226,
    0.386107, 0.331869, 0.380125}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
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  SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
    0.16152, 0.319203, 0.158339}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
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  SpikeNegative_19 → {{0.392542, 0.277194, 0.303304, 0.316005, 0.451557, 0.178107, 0.336152,
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    -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{0.373567, 0.348518, 0.182641, 0.399653, 0.340024, 0.197691, 0.337761,
    0.284486, 0.34594, 0.276612}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
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  LinearPositive_3 → {{0.983778, 0.169007, 0.0312598, 0.00266983, 0.0014985,
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  LinearPositive_4 → {{0.984544, 0.162861, 0.0316916, 0.00219377, 0.00149925, 0.011724,
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  LinearPositive_6 → {{0.982932, 0.171949, 0.0327492, 0.00164224, 0.002379, 0.0113266,
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  LinearPositive_7 → {{0.98472, 0.163134, 0.0312689, 0.00212913, 0.0016404, 0.0102459,
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  LinearPositive_8 → {{0.98371, 0.168572, 0.0284284, 0.00170281, 0.00185745, 0.010751,
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LinearPositive_9 → {{0.98365, 0.168058, 0.033981, 0.00241806, 0.00210287, 0.0115589,
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LinearPositive_10 → {{0.983876, 0.167373, 0.0315427, 0.00211686, 0.00191546, 0.0115056,
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LinearPositive_11 → {{0.985278, 0.159772, 0.0170525, 0.00324467, 0.00218142, 0.0151391,
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LinearPositive_12 → {{0.985678, 0.154732, 0.0287579, 0.00132291, 0.00382878, 0.0177303,
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LinearPositive_13 → {{0.980798, 0.186414, 0.0294262, 0.00278288, 0.00330631, 0.0108519,
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LinearPositive_14 → {{0.981111, 0.181783, 0.0375471, 0.00148453, 0.000312388,
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LinearPositive_15 → {{0.984521, 0.158493, 0.0449595, 0.00110501, 0.00265532, 0.0107268,
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LinearPositive_16 → {{0.979313, 0.188576, 0.0419809, 0.00521628, 0.000903989,
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LinearPositive_17 → {{0.983915, 0.163837, 0.0268448, 0.00291022, 0.00438077, 0.0123819,
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LinearNegative_2 → {{0.983975, 0.157281, 0.0272884, 0.00492376, 0.00030144, 0.0209059,
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LinearNegative_3 → {{0.981452, 0.174458, 0.0229664, 0.001764, 0.000281227, 0.0288508,
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  Sinusoidal3_28 → {{0.00292996, 0.0773356, 0.991977, 0.0880559, 0.0367946, 0.0176203,
    0.00875596, 0.00325153, 0.0220462, 0.00118298}, {0.187562, -0.10053, -0.297144, -0.250552,
    0.00476677, 0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453,
    0.301104, 0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{0.00262506, 0.0711674, 0.99281, 0.0827274, 0.0380578, 0.0177335, 0.00874852,
    0.00232562, 0.0238141, 0.000654616}, {0.189755, -0.100643, -0.295957, -0.251445,
    -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
    0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
  Sinusoidal3_30 → {{0.00427552, 0.071229, 0.992804, 0.0839262, 0.0365748, 0.018534, 0.00877504,
    0.00265531, 0.0209496, 0.000906179}, {0.186539, -0.100579, -0.301622, -0.251977,
    0.00452805, 0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
    0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
    0.0294955, 0.00418398, 0.028168, 0.00135728}, {-0.0952089, -0.252202, 0.25704, 0.097318,
    -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
    0.00565905, 0.0259503, 0.00224675}, {-0.101498, -0.25529, 0.251653, 0.0972642,
    -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
    0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395,
    0.00472652, 0.0285215, 0.00169662}, {-0.0918789, -0.259087, 0.253065, 0.103093,
    -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
    0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735,
    0.00386219, 0.0290145, 0.00118185}, {-0.0939856, -0.25429, 0.25073, 0.100441,
    -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
    0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
    0.00582096, 0.0271664, 0.00231721}, {-0.0916775, -0.260977, 0.251061, 0.104141,
    -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
    0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
    0.00436252, 0.0286975, 0.00143738}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
    -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
```

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```
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868,
    0.00399143, 0.0293851, 0.00124852}, {-0.102994, -0.260616, 0.250831, 0.0989794,
    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
    0.00452946, 0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
    0.00512062, 0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
    -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
    0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
    -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
    -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
    0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
    0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
    -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
    0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
    0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
    -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
  Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
    0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
    0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
    -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
    0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
    0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
    -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
    -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

If we want the classes produced, we can query the keys:

```
In[9]:= Query[Keys]@classification1
Out[9]= {SpikeMax, SpikeMin, f1, f3, f5, f6}
```

For the members in each class we have:

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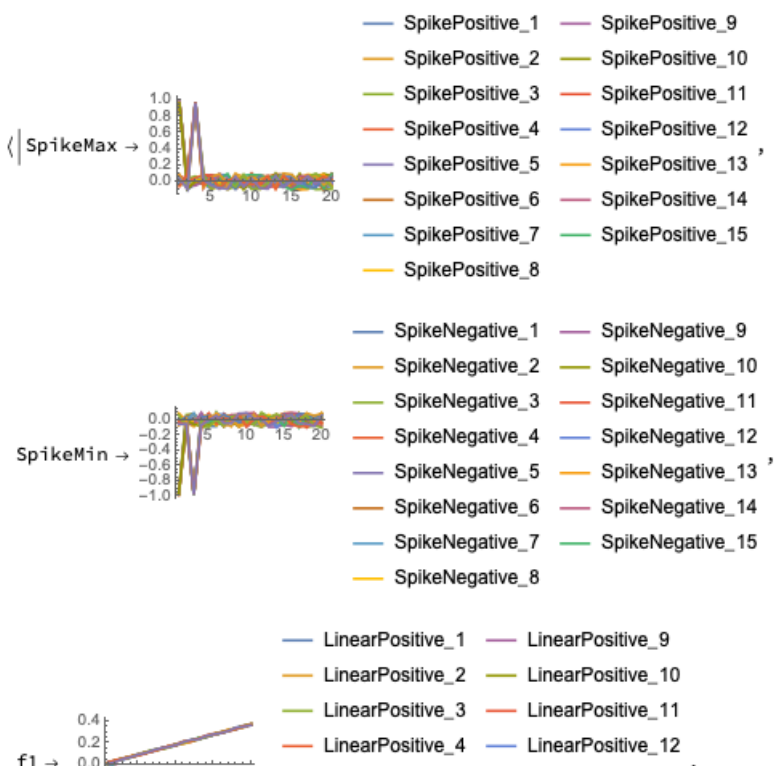
```
In[10]:= Query[All, Length]@classification1
Out[10]= ⟨|SpikeMax → 20, SpikeMin → 20, f1 → 40, f3 → 10, f5 → 10, f6 → 10|⟩
```

Specific membership labels to each class can also be obtained:

```
In[11]:= Query[All, Keys]@classification1
Out[11]= ⟨|SpikeMax → {SpikePositive_1, SpikePositive_2, SpikePositive_3, SpikePositive_4, SpikePositive_5,
    SpikePositive_6, SpikePositive_7, SpikePositive_8, SpikePositive_9, SpikePositive_10,
    SpikePositive_11, SpikePositive_12, SpikePositive_13, SpikePositive_14, SpikePositive_15,
    SpikePositive_16, SpikePositive_17, SpikePositive_18, SpikePositive_19, SpikePositive_20},
  SpikeMin → {SpikeNegative_1, SpikeNegative_2, SpikeNegative_3, SpikeNegative_4, SpikeNegative_5,
    SpikeNegative_6, SpikeNegative_7, SpikeNegative_8, SpikeNegative_9, SpikeNegative_10,
    SpikeNegative_11, SpikeNegative_12, SpikeNegative_13, SpikeNegative_14, SpikeNegative_15,
    SpikeNegative_16, SpikeNegative_17, SpikeNegative_18, SpikeNegative_19, SpikeNegative_20},
  f1 → {LinearPositive_1, LinearPositive_2, LinearPositive_3, LinearPositive_4, LinearPositive_5,
    LinearPositive_6, LinearPositive_7, LinearPositive_8, LinearPositive_9, LinearPositive_10,
    LinearPositive_11, LinearPositive_12, LinearPositive_13, LinearPositive_14, LinearPositive_15,
    LinearPositive_16, LinearPositive_17, LinearPositive_18, LinearPositive_19, LinearPositive_20,
    LinearNegative_1, LinearNegative_2, LinearNegative_3, LinearNegative_4, LinearNegative_5,
    LinearNegative_6, LinearNegative_7, LinearNegative_8, LinearNegative_9, LinearNegative_10,
    LinearNegative_11, LinearNegative_12, LinearNegative_13, LinearNegative_14, LinearNegative_15,
    LinearNegative_16, LinearNegative_17, LinearNegative_18, LinearNegative_19, LinearNegative_20},
  f3 → {Sinusoidal3_21, Sinusoidal3_22, Sinusoidal3_23, Sinusoidal3_24, Sinusoidal3_25,
    Sinusoidal3_26, Sinusoidal3_27, Sinusoidal3_28, Sinusoidal3_29, Sinusoidal3_30},
  f5 → {Sinusoidal2_11, Sinusoidal2_12, Sinusoidal2_13, Sinusoidal2_14, Sinusoidal2_15,
    Sinusoidal2_16, Sinusoidal2_17, Sinusoidal2_18, Sinusoidal2_19, Sinusoidal2_20},
  f6 → {Sinusoidal1_1, Sinusoidal1_2, Sinusoidal1_3, Sinusoidal1_4, Sinusoidal1_5,
    Sinusoidal1_6, Sinusoidal1_7, Sinusoidal1_8, Sinusoidal1_9, Sinusoidal1_10}|⟩
```

We can plot all the signals in each set:

```
In[12]:= Query[All, ListLinePlot[#[[All, 2]], PlotRange → Full] &]@classification1
```



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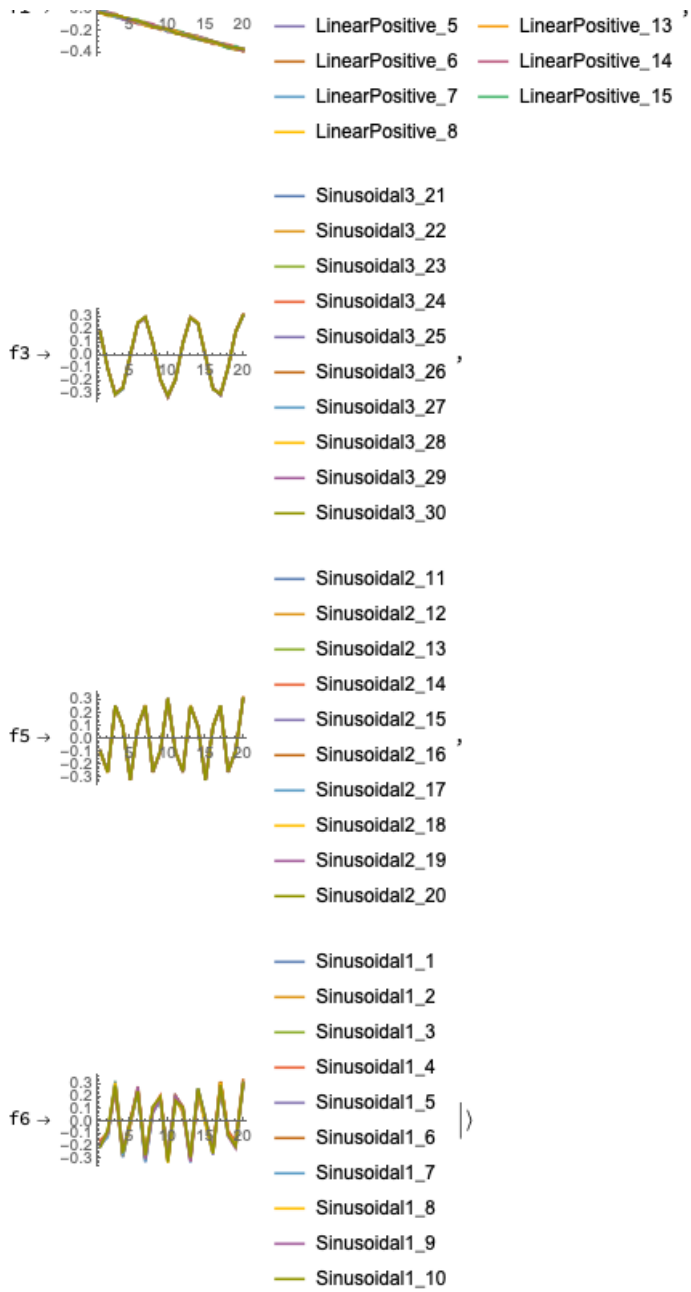
Out[12]=



The actual value of the possible frequencies can also be obtained if necessary using any of the signals and looking at its LombScargle transformation. In the example considered we have:

In[13]:=
```
frequenciesPossible = LombScargle[classificationExample1[[1]], timePointsExample, FrequenciesOnly → True]
```

Out[13]=
```
<|f1 → 0.0554017, f2 → 0.110803, f3 → 0.166205, f4 → 0.221607, f5 → 0.277008,
 f6 → 0.33241, f7 → 0.387812, f8 → 0.443213, f9 → 0.498615, f10 → 0.554017|>
```

The data could also have been provided in the form of a list, instead of an association. The returned classification would then use original position index as a reference to return in the

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classification

In[14]:=
```
classification1List = TimeSeriesClassification[Values@classificationExample1,
  timePointsExample, LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes]
  Method → "LombScargle"
```

Out[14]=
```
<|SpikeMax →
  <|1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463, 0.41637, 0.423696},
     {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682, -0.0371416,
      0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411, -0.00869189,
      -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765, 0.112284, 0.503656, 0.118252},
     {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829, 0.017722,
      -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463, 0.387482, 0.47078, 0.408939},
     {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993, -0.0955887,
      -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843, 0.0402401,
      -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251, 0.168013, 0.698351, 0.179431},
     {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033, -0.0772898, 0.0399612,
      -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539, 0.0509389,
      0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585, 0.200919, 0.656615, 0.247551},
     {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663, 0.0676522, 0.0605738,
      0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931, 0.0796911,
      -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831, 0.273102, 0.555147, 0.282891},
     {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416, 0.0326082, -0.0159531,
      0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387, 0.0872339,
      -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206, 0.331779, 0.403391, 0.350929},
     {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442, -0.00304927,
      0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295, 0.338817, 0.410956, 0.340837},
     {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677, -0.0238371,
      -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
      -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947, 0.276317, 0.441555, 0.279417},
     {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483, -0.0385902,
      -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
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f5 → <|91 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193, 0.0294955,
    0.00418398, 0.028168, 0.00135728}, {-0.0952089, -0.252202, 0.25704, 0.097318,
    -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  92 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648, 0.00565905,
    0.0259503, 0.00224675}, {-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067,
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    0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  93 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395, 0.00472652,
    0.0285215, 0.00169662}, {-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667,
    0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963, 0.254435,
    0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  94 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
    0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  95 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735, 0.00386219,
    0.0290145, 0.00118185}, {-0.0939856, -0.25429, 0.25073, 0.100441, -0.313599,
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    0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  96 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366, 0.00582096,
    0.0271664, 0.00231721}, {-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132,
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    0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  97 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
    0.00436252, 0.0286975, 0.00143738}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
    -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
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```
    98 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868, 0.00399143,
       0.0293851, 0.00124852}, {-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724,
       0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
       0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
    99 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723, 0.00452946,
       0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977,
       0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469, 0.251806,
       0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
    100 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217, 0.00512062,
       0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484,
       0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815,
       0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
  f6 → <|81 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408, 0.101662,
       0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184, -0.0168796,
       0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701, -0.331998,
       0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
    82 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
       0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
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       -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
    83 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873, 0.00950723,
       0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161, 0.00567862,
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       0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
    84 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885, 0.109754,
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    85 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056, 0.120877, 0.0081269,
       0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517, -0.0163677,
       0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444, -0.303865,
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    86 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302, 0.00951716,
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    87 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
       0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
       -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
       -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
    88 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165, 0.0100832,
       0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322,
       0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394, -0.280218,
       0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
    89 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453, 0.00677996,
       0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817,
       0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813, -0.323289,
       0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
    90 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157, 0.0859493,
       0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
       0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
       -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

The data could also have been provided in the form of pairs of times with values:

In[15]:=
```
Query[All, Transpose[{timePointsExample, #}] &]@classificationExample1
```

Out[15]=
```
<|SpikePositive_1 → {{1, 0.970569}, {2, -0.0988615}, {3, -0.0240026}, {4, -0.0115612}, ··· 13 ···,
   {18, -0.015177}, {19, -0.0708976}, {20, -0.0557732}}, ··· 108 ···, Sinusoidal3_30 → {··· 1 ···}|>
```

large output | show less | show more | show all | set size limit...

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In[16]:=
```
classification1Pairs =
 TimeSeriesClassification[Query[All, Transpose[{timePointsExample, #}] &]@classificationExample1,
  timePointsExample, LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes]
```

```
Method → "LombScargle"
```

Out[16]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
      0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
      -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
      0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
      0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
      0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
      0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
      0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
      0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
      0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
      0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
      -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
      0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
      0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
      0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
      0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
      0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
      -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
      0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
      0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
      0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
      0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
   SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
      0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
      -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
      0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
   SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
      0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
      0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
      -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
   SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
      0.156306, 0.49338, 0.197723}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
      0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
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    -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
  SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
    0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
    -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
    -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
  SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
    0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
    0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
    0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
  SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
    0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
    -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
    0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
    0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
    -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
    0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
    -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
    0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
    0.469391, 0.294777, 0.463012, 0.279525}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
    -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
    -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
  SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
    0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
    -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
    -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
    0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
    0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
    -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
  SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
    0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
    -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
    0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
    0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
    0.341117, 0.381366, 0.325221}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
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    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
    0.214233, 0.523873, 0.243986}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
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    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
    0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
    -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
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  SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
    0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
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  SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
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   SpikeNegative_14 → {{0.369536, 0.475376, 0.186202, 0.236301, 0.19825, 0.237895, 0.260777,
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   SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
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   SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
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   SpikeNegative_17 → {{0.197001, 0.246358, 0.358498, 0.402863, 0.27067, 0.34906, 0.104226,
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   SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
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   SpikeNegative_19 → {{0.392542, 0.277194, 0.303304, 0.316005, 0.451557, 0.178107, 0.336152,
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   SpikeNegative_20 → {{0.373567, 0.348518, 0.182641, 0.399653, 0.340024, 0.197691, 0.337761,
      0.284486, 0.34594, 0.276612}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
      0.057722, -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007,
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   LinearPositive_3 → {{0.983778, 0.169007, 0.0312598, 0.00266983, 0.0014985,
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   LinearPositive_4 → {{0.984544, 0.162861, 0.0316916, 0.00219377, 0.00149925, 0.011724,
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   LinearPositive_5 → {{0.983951, 0.167274, 0.0329686, 0.00225602, 0.00179127, 0.0107481,
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      0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
   LinearPositive_6 → {{0.982932, 0.171949, 0.0327492, 0.00164224, 0.002379, 0.0113266,
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      0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
   LinearPositive_7 → {{0.98472, 0.163134, 0.0312689, 0.00212913, 0.0016404, 0.0102459,
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   LinearPositive_8 → {{0.98371, 0.168572, 0.0284284, 0.00170281, 0.00185745, 0.010751,
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    0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}},
LinearPositive_9 → {{0.98365, 0.168058, 0.033981, 0.00241806, 0.00210287, 0.0115589,
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LinearPositive_10 → {{0.983876, 0.167373, 0.0315427, 0.00211686, 0.00191546, 0.0115056,
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LinearPositive_11 → {{0.985278, 0.159772, 0.0170525, 0.00324467, 0.00218142, 0.0151391,
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LinearPositive_12 → {{0.985678, 0.154732, 0.0287579, 0.00132291, 0.00382878, 0.0177303,
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LinearPositive_13 → {{0.980798, 0.186414, 0.0294262, 0.00278288, 0.00330631, 0.0108519,
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    0.241086, 0.263228, 0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}},
LinearPositive_14 → {{0.981111, 0.181783, 0.0375471, 0.00148453, 0.000312388,
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LinearPositive_15 → {{0.984521, 0.158493, 0.0449595, 0.00110501, 0.00265532, 0.0107268,
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    0.250473, 0.25777, 0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}},
LinearPositive_16 → {{0.979313, 0.188576, 0.0419809, 0.00521628, 0.000903989,
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LinearPositive_17 → {{0.983915, 0.163837, 0.0268448, 0.00291022, 0.00438077, 0.0123819,
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LinearPositive_18 → {{0.983959, 0.16518, 0.0329124, 0.00150854, 0.000803325, 0.0135443,
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LinearPositive_19 → {{0.987202, 0.147191, 0.027074, 0.00249316, 0.000777253,
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    0.216792, 0.223063, 0.241101, 0.270774, 0.282283, 0.293887, 0.315058, 0.334039, 0.359611, 0.369743}},
LinearPositive_20 → {{0.983551, 0.167679, 0.0393618, 0.00233188, 0.0011172, 0.0161293,
    0.0224214, 0.0278122, 0.0194605, 0.0322579}, {0.00952752, 0.0286979, 0.0547226,
    0.0709501, 0.0958101, 0.109505, 0.135844, 0.152431, 0.165158, 0.182651, 0.210505,
    0.231304, 0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
LinearNegative_1 → {{0.984203, 0.159785, 0.0568416, 0.00506241, 0.000881747, 0.023661,
    0.00860998, 0.0262898, 0.0191746, 0.0293783}, {-0.0218046, -0.0446169, -0.0612231, -0.0738948,
    -0.109733, -0.115191, -0.124469, -0.148293, -0.159758, -0.176361, -0.217843, -0.224298,
    -0.23172, -0.273794, -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733}},
LinearNegative_2 → {{0.983975, 0.157281, 0.0272884, 0.00492376, 0.00030144, 0.0209059,
    0.0314594, 0.044367, 0.0195659, 0.0500937}, {-0.0137543, -0.0552134, -0.0387902, -0.0787876,
    -0.0972777, -0.0993326, -0.131634, -0.158204, -0.178021, -0.176063, -0.209858, -0.230763,
    -0.248781, -0.268592, -0.290148, -0.294015, -0.319548, -0.339092, -0.343638, -0.357122}},
LinearNegative_3 → {{0.981452, 0.174458, 0.0229664, 0.001764, 0.000281227, 0.0288508,
    0.0279993, 0.0404567, 0.0193861, 0.0464356}, {-0.0283384, -0.0528281, -0.0527884, -0.0740599,
    -0.0921776, -0.0948819, -0.146225, -0.165182, -0.160057, -0.18686, -0.220224, -0.211812,
    -0.237918, -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
LinearNegative_4 → {{0.97237, 0.220138, 0.0433705, 0.00935025, 0.000670999, 0.00240098,
    0.0233417, 0.0327997, 0.0336189, 0.0361833}, {-0.0158873, -0.0248133, -0.0382326, -0.0881019,
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    -0.243003, -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844}},
LinearNegative_5 → {{0.977089, 0.200269, 0.0364024, 0.00199978, 0.00231623, 0.00860671,
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    0.0111157, 0.0372061, 0.025344, 0.04037}, {-0.0201624, -0.0405386, -0.0436406, -0.0738225,
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  LinearNegative_7 → {{0.974629, 0.205946, 0.0323035, 0.00710776, 0.0022957, 0.0115893,
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    -0.23516, -0.248536, -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923}},
  LinearNegative_8 → {{0.982135, 0.172786, 0.0318874, 0.00532189, 0.00125899, 0.00528407,
    0.0345412, 0.03715, 0.00888127, 0.0427758}, {-0.0170306, -0.0378539, -0.0394845, -0.0767312,
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    -0.238911, -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
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  LinearNegative_11 → {{0.984307, 0.167887, 0.0231976, 0.00646005, 0.000895278, 0.0137762,
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  LinearNegative_13 → {{0.98451, 0.16303, 0.0227595, 0.00132012, 0.00348595, 0.0126863,
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  LinearNegative_16 → {{0.979857, 0.186118, 0.0444944, 0.00475256, 0.00394217, 0.0176745,
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  LinearNegative_18 → {{0.981857, 0.181794, 0.0372624, 0.00157464, 0.00102441, 0.00691753,
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  LinearNegative_19 → {{0.986834, 0.144628, 0.035256, 0.00310318, 0.000702006, 0.0165652,
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  LinearNegative_20 → {{0.985534, 0.158105, 0.0328843, 0.00243514, 0.000101469, 0.0195265,
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f3 → <|Sinusoidal3_21 → {{0.003093, 0.067983, 0.992591, 0.0880879, 0.0381938, 0.0201564,
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f5 → <|Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
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  Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
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  Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
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    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
    0.00452946, 0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
    0.00512062, 0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
    -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
    0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
    -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
    -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
    0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
    0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
    -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
    0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
    0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
    -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
  Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
    0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
    0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
    -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
    0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
    0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
    -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
    -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

The classification can also handle missing data. We consider the previous example, with say up to 2 data points removed/set to Missing[].

```
In[17]:= classificationExample2 =
  Query[All, Nest[ReplacePart[#, RandomInteger[{1, 20}] → Missing[]] &, #, RandomInteger[{1, 2}]] &] @
   classificationExample1

Out[17]= <|SpikePositive_1 → {Missing[], -0.0988615, -0.0240026, -0.0115612, -0.0977222,
    0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, Missing[], -0.0110224, -0.055411,
    -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732},
  SpikePositive_2 → {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829,
    0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
```

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```
  -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, Missing[], 0.0905543},
SpikePositive_3 → {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993,
  -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
  0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, Missing[], Missing[]},
SpikePositive_4 → {0.958583, Missing[], Missing[], 0.0838796, 0.0778033, -0.0772898,
  0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
  0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859},
SpikePositive_5 → {0.966833, Missing[], -0.0101601, Missing[], 0.0804663, 0.0676522,
  0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
  0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368},
SpikePositive_6 → {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416, 0.0326082,
  Missing[], 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
  0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102},
SpikePositive_7 → {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442, Missing[],
  0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
  0.0872978, 0.0241062, Missing[], -0.0831706, -0.07202, 0.0810017, -0.0303004},
SpikePositive_8 → {0.973714, -0.0655433, 0.00410752, Missing[], -0.0178775, -0.0116677,
  -0.0238371, -0.0535769, Missing[], 0.0754105, -0.0540901, -0.0502273, -0.0192342,
  -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763},
SpikePositive_9 → {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483,
  -0.0385902, -0.0121923, -0.0467585, Missing[], 0.0208798, -0.0177267, Missing[],
  -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062},
SpikePositive_10 → {0.961551, -0.0906575, 0.00581915, Missing[], 0.0455119, 0.0618367,
  -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
  -0.0322946, -0.0461255, Missing[], -0.0517594, -0.00829841, 0.0959418, 0.0674457},
SpikePositive_11 → {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068, 0.0325846,
  -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
  0.0377134, 0.0259428, Missing[], Missing[], 0.0104191, -0.0990718, 0.101205},
SpikePositive_12 → {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803, 0.0850629,
  0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
  0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, Missing[], -0.00749826},
SpikePositive_13 → {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903, -0.0475178,
  -0.0708036, 0.0962073, -0.0355342, 0.0473543, Missing[], -0.045626, 0.0398952,
  0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773},
SpikePositive_14 → {Missing[], Missing[], 0.968597, -0.0798072, 0.0669311, 0.0642856,
  -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
  -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114},
SpikePositive_15 → {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922, 0.0322486,
  0.0966403, Missing[], 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
  -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378},
SpikePositive_16 → {-0.0123015, 0.0180774, Missing[], 0.0737459, -0.0312647, Missing[],
  -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381, -0.0588352,
  -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908},
SpikePositive_17 → {0.0894556, Missing[], 0.955206, -0.0721055, 0.0609444, 0.09185,
  -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
  0.101663, 0.086855, 0.000889116, Missing[], 0.0723495, -0.0396682, 0.0309544},
SpikePositive_18 → {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144, -0.0566396,
  0.00932272, -0.0627836, 0.0853683, -0.0927231, Missing[], -0.0206424, 0.0179427,
  0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999},
SpikePositive_19 → {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727, -0.0813174,
  0.0169025, 0.03397, -0.00559207, Missing[], -0.0310815, Missing[], -0.0924997,
  0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065},
SpikePositive_20 → {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833, -0.0790448,
  -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909,
  -0.0700673, 0.0119244, -0.0203333, Missing[], -0.0174003, 0.010671, 0.051381},
SpikeNegative_1 → {Missing[], 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627,
  0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467, -0.0370811,
  0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511},
SpikeNegative_2 → {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113, -0.0217826,
  -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501, -0.0295528,
  0.0389368, 0.0814642, Missing[], 0.080829, -0.0461636, -0.00536829, -0.053342},
SpikeNegative_3 → {-0.953174, Missing[], 0.081267, -0.0893468, -0.0891095, 0.102466,
  -0.0311731, 0.0363503, -0.043063, 0.0536749, Missing[], -0.0930647, -0.0384319,
  -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636},
SpikeNegative_4 → {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556, -0.0455452,
  Missing[], 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
```

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  0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411},
SpikeNegative_5 → {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968, 0.0456577,
  -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, Missing[],
  -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712},
SpikeNegative_6 → {-0.980123, 0.0414029, 0.0844458, -0.0197615, Missing[], -0.058058,
  0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
  0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539},
SpikeNegative_7 → {Missing[], 0.00651176, 0.0927783, -0.0613428, -0.0810109, 0.0874465,
  -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
  -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901},
SpikeNegative_8 → {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887, Missing[],
  0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
  -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666},
SpikeNegative_9 → {-0.964652, -0.0492164, -0.044027, Missing[], -0.0799416, 0.0325626,
  -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
  -0.0901265, -0.0600632, -0.0839437, Missing[], -0.00450166, -0.0244654, 0.0251653},
SpikeNegative_10 → {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025, Missing[],
  -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, Missing[],
  -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664},
SpikeNegative_11 → {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755, Missing[],
  -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052, 0.0300314,
  0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954},
SpikeNegative_12 → {0.0228997, -0.0356184, -0.973634, Missing[], 0.0107571, Missing[],
  0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
  -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734},
SpikeNegative_13 → {Missing[], -0.00831708, -0.964283, -0.0122152, -0.0196036, 0.0881039,
  0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, Missing[], -0.028162,
  0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681},
SpikeNegative_14 → {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594, Missing[],
  0.00336549, Missing[], 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
  0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977},
SpikeNegative_15 → {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309, 0.000455216,
  Missing[], 0.0349969, 0.0713349, Missing[], -0.0365053, -0.00194281, 0.0312967,
  0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439},
SpikeNegative_16 → {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464, 0.0166785,
  0.0680268, Missing[], -0.0297585, -0.00701137, 0.0550893, -0.0727101, 0.0309736,
  -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422},
SpikeNegative_17 → {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312, 0.0616787,
  -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667, 0.022695,
  0.0217809, 0.00120993, 0.0625404, -0.0147936, Missing[], 0.0565877, 0.0859092},
SpikeNegative_18 → {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604, 0.0000556895,
  -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971, 0.099183, 0.0322089,
  0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, Missing[]},
SpikeNegative_19 → {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693, 0.0216656,
  0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, Missing[], 0.0105588,
  Missing[], 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696},
SpikeNegative_20 → {-0.0543654, -0.0510581, -0.970055, -0.0636564, Missing[], Missing[],
  -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007, -0.0175827,
  0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}, LinearPositive_1 →
 {0.018415, 0.0377122, 0.0574444, 0.0761646, 0.0918826, 0.112863, 0.131264, 0.149525, Missing[], 0.18659,
  0.205188, 0.223266, 0.241367, 0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, Missing[]},
LinearPositive_2 → {0.0183904, 0.0374466, 0.0550304, 0.0738563, 0.0928923, 0.110677,
  0.130133, Missing[], 0.167272, 0.186766, 0.206807, 0.224025, 0.242161, 0.261728,
  0.280689, Missing[], 0.316418, 0.335012, 0.355339, 0.375155}, LinearPositive_3 →
 {Missing[], 0.0388961, 0.055949, 0.0753517, 0.0937248, 0.112155, 0.1288, 0.150982, 0.166685, 0.187482,
  0.204397, 0.22244, 0.241027, 0.262217, Missing[], 0.299561, 0.317724, 0.336804, 0.355812, 0.372089},
LinearPositive_4 → {0.0188591, 0.0384796, 0.0552706, 0.0761382, 0.0941127, 0.11255,
  0.131257, 0.150426, 0.166514, 0.185049, 0.206061, 0.222052, 0.24344, 0.261751,
  Missing[], Missing[], 0.316607, 0.33422, 0.355535, 0.374989}, LinearPositive_5 →
 {0.0196474, 0.0375735, 0.0561861, 0.0745382, 0.094777, 0.113054, 0.132423, Missing[], 0.169563, 0.188068,
  0.205612, 0.225889, 0.242492, 0.261976, 0.279334, Missing[], 0.316353, 0.33459, 0.353954, 0.372244},
LinearPositive_6 → {0.0186014, 0.0381755, 0.0550572, 0.074646, 0.0932816, 0.113886,
  0.132134, 0.149767, 0.168659, 0.185415, 0.205262, 0.222624, 0.242621, 0.260049,
  Missing[], 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}, LinearPositive_7 →
 {0.0186204, Missing[], 0.0569047, 0.0757329, 0.092018, 0.111558, 0.130244, 0.148133, 0.167451, 0.186409,
  0.204805, 0.22423, 0.241912, Missing[], 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923},
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LinearPositive_8 → {0.0170019, 0.0382694, 0.0569482, 0.0754625, 0.0914347, 0.110031,
  0.132014, 0.15073, 0.169121, Missing[], 0.205265, Missing[], 0.242529, 0.260421,
  0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}, LinearPositive_9 →
 {0.0185501, 0.0388643, 0.0547098, 0.0747468, 0.0938687, 0.113558, 0.129413, 0.148929, 0.168743, 0.186495,
  0.204247, 0.225298, 0.241691, 0.261072, Missing[], 0.298507, 0.318632, 0.337602, Missing[], 0.372608},
LinearPositive_10 → {0.0174864, 0.0370712, 0.0572236, 0.0748823, 0.0926627, 0.111129,
  Missing[], 0.148771, 0.168913, 0.186275, 0.206359, 0.223211, 0.241838, 0.260952,
  0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}, LinearPositive_11 →
 {Missing[], 0.0406398, 0.0607801, 0.0781742, 0.0921015, 0.112119, 0.128868, 0.151429, 0.171509, 0.192449,
  0.211181, 0.216208, 0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, Missing[]},
LinearPositive_12 → {0.0219335, 0.0431422, 0.0502095, 0.0696589, 0.0884956, 0.116468,
  0.123447, 0.151797, 0.168869, 0.179094, 0.204522, 0.228042, 0.240546, 0.269187,
  0.279387, 0.302162, 0.315899, 0.330232, Missing[], 0.381055}, LinearPositive_13 →
 {0.022617, 0.0284408, 0.0607512, Missing[], 0.0880775, 0.119613, 0.134238, 0.152698, 0.169261, 0.181713,
  0.197855, 0.217149, 0.241086, 0.263228, 0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015},
LinearPositive_14 → {0.0276601, 0.0348994, 0.0578995, 0.0764811, 0.0865063, 0.115217,
  0.136395, 0.15157, 0.16455, 0.180615, 0.213666, 0.215142, 0.243638, 0.254281,
  0.280739, Missing[], 0.313921, 0.336645, 0.361637, 0.373861}, LinearPositive_15 →
 {0.0152129, 0.0390101, 0.0602871, 0.0702062, Missing[], 0.118718, 0.136185, 0.146481, 0.161128, 0.179922,
  0.215359, 0.218444, 0.250473, 0.25777, 0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849},
LinearPositive_16 → {0.0164478, 0.0360481, 0.048135, Missing[], 0.101186, 0.114916,
  0.129433, 0.153936, 0.164281, 0.192697, Missing[], 0.223277, 0.236402, 0.257694,
  0.277977, 0.296096, 0.311924, 0.344353, 0.357433, 0.375096}, LinearPositive_17 →
 {0.0153802, 0.0408047, 0.0548321, 0.0765604, 0.0991872, 0.117741, 0.128177, 0.147496, 0.159869, 0.189666,
  0.195939, 0.215447, 0.240506, 0.262803, 0.283339, Missing[], 0.3159, Missing[], 0.349837, 0.380979},
LinearPositive_18 → {0.0115844, 0.0455792, 0.0534286, 0.068487, 0.0918771, 0.107837,
  0.137609, 0.144956, 0.162508, Missing[], 0.206224, 0.229689, 0.232407, 0.261637,
  0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}, LinearPositive_19 →
 {0.0205961, 0.045526, 0.0569898, 0.0724948, Missing[], 0.105806, 0.12769, 0.145665, 0.170669, 0.180276,
  0.216792, 0.223063, 0.241101, 0.270774, 0.282283, 0.293887, 0.315058, 0.334039, 0.359611, 0.369743},
LinearPositive_20 → {0.00952752, 0.0286979, 0.0547226, 0.0709501, 0.0958101, 0.109505,
  0.135844, Missing[], 0.165158, 0.182651, 0.210505, 0.231304, 0.235391,
  0.267585, 0.28298, 0.294497, 0.314251, 0.344366, Missing[], 0.366536},
LinearNegative_1 → {-0.0218046, -0.0446169, -0.0612231, -0.0738948, -0.109733, -0.115191,
  Missing[], -0.148293, -0.159758, -0.176361, -0.217843, -0.224298, -0.23172,
  -0.273794, -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733},
LinearNegative_2 → {-0.0137543, -0.0552134, -0.0387902, -0.0787876, -0.0972777, -0.0993326,
  -0.131634, Missing[], -0.178021, -0.176063, -0.209858, -0.230763, -0.248781,
  -0.268592, -0.290148, -0.294015, Missing[], -0.339092, -0.343638, -0.357122},
LinearNegative_3 → {-0.0283384, -0.0528281, -0.0527884, -0.0740599, -0.0921776, -0.0948819,
  -0.146225, -0.165182, -0.160057, Missing[], -0.220224, -0.211812, -0.237918,
  -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769},
LinearNegative_4 → {-0.0158873, -0.0248133, -0.0382326, -0.0881019, -0.0887054, -0.128386,
  -0.128859, -0.161147, -0.159022, Missing[], -0.200777, -0.210411, -0.243003,
  -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844},
LinearNegative_5 → {-0.0201624, -0.0405386, -0.0436406, Missing[], -0.0817467, -0.105404,
  -0.114359, -0.154377, -0.169473, -0.174198, -0.212011, -0.225376, Missing[],
  -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219},
LinearNegative_6 → {-0.0267223, -0.0446999, -0.0523138, -0.0699606, -0.0987645, -0.126896,
  -0.126614, -0.165572, -0.172297, -0.184872, -0.208135, -0.237294, -0.243037,
  -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, Missing[], -0.381481},
LinearNegative_7 → {-0.00172329, -0.032268, -0.068173, Missing[], -0.0881686, -0.107137,
  -0.140409, -0.14992, -0.182962, -0.175511, -0.200764, -0.226349, -0.23516,
  -0.248536, -0.268245, -0.303398, Missing[], -0.349618, -0.352678, -0.371923},
LinearNegative_8 → {Missing[], -0.0378539, -0.0394845, -0.0767312, -0.0942537, -0.105065,
  -0.146528, Missing[], -0.186411, -0.174071, -0.194782, -0.232787, -0.238911,
  -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678},
LinearNegative_9 → {-0.0287969, -0.0189698, -0.0530075, -0.0828922, -0.0936032, -0.115414,
  -0.114422, -0.130851, -0.167598, -0.173937, Missing[], -0.23569, -0.258977,
  -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269},
LinearNegative_10 → {-0.00155633, -0.0271325, -0.0625737, -0.0744387, -0.0901925,
  -0.0932579, -0.138846, -0.15092, -0.157289, -0.198281, Missing[], -0.206968,
  -0.259028, -0.273261, -0.270544, -0.29133, -0.328913, Missing[], -0.335503, -0.37816},
LinearNegative_11 → {-0.0105542, -0.0364589, -0.0515525, -0.0708746, -0.0862196, -0.118392,
  -0.123851, -0.151596, -0.176372, -0.191037, -0.213033, -0.221631, -0.235518,
  -0.271564, Missing[], -0.293001, -0.310129, -0.328328, -0.364455, -0.366174},
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LinearNegative_12 → {-0.0105234, -0.0459122, -0.0631169, -0.0780043, -0.0883748, -0.108962,
  -0.137461, Missing[], -0.163604, -0.184293, -0.210166, Missing[], -0.245066,
  -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709},
LinearNegative_13 → {-0.01186, -0.0431645, Missing[], -0.0756374, -0.0887624, -0.1144,
  -0.121973, -0.156462, -0.165726, -0.190329, -0.20958, -0.216046, -0.244405,
  -0.264186, Missing[], -0.307757, -0.312755, -0.331563, -0.35751, -0.373596},
LinearNegative_14 → {-0.0187992, -0.0431131, -0.0473458, Missing[], -0.0879629, -0.116006,
  -0.12521, -0.152395, -0.170415, -0.184268, -0.196593, -0.22289, -0.23237,
  -0.26046, -0.276864, -0.301954, Missing[], -0.336453, -0.361973, -0.377956},
LinearNegative_15 → {-0.0162872, -0.0293132, Missing[], -0.0807767, -0.0935334, -0.121112,
  -0.124004, Missing[], -0.165828, -0.191582, -0.205406, -0.219926, -0.248657,
  -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295},
LinearNegative_16 → {-0.0225164, -0.0461677, -0.0473716, -0.067817, -0.0986701, -0.119505,
  -0.130459, -0.1556, -0.169469, -0.1814, -0.198572, -0.221935, -0.24543,
  -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, Missing[], -0.371628},
LinearNegative_17 → {Missing[], -0.0309644, -0.0613334, -0.0794837, -0.0865967, -0.117058,
  -0.128048, -0.153332, Missing[], -0.192254, -0.208455, -0.223898, -0.240133,
  -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276},
LinearNegative_18 → {-0.0251341, -0.0366273, -0.0488411, -0.0708482, -0.0895021, -0.108048,
  -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921, Missing[],
  -0.254831, -0.285694, Missing[], -0.326762, -0.328866, -0.362472, -0.367752},
LinearNegative_19 → {-0.0210969, -0.0344615, -0.0471464, -0.078958, -0.100694, -0.103899,
  -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276, -0.241033,
  -0.263307, -0.281329, Missing[], -0.315673, -0.329753, -0.355337, -0.38137},
LinearNegative_20 → {-0.024006, -0.0432239, -0.0496914, -0.0682004, Missing[], -0.103335,
  -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471, -0.23997,
  -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106},
Sinusoidal1_1 → {-0.20264, -0.107877, 0.278896, -0.289184, -0.0168796, Missing[],
  -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701, -0.331998,
  0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146},
Sinusoidal1_2 → {-0.153886, -0.0875347, 0.297854, -0.276583, Missing[], 0.260377,
  -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307, -0.288819,
  0.270239, 0.0126278, Missing[], 0.317945, -0.0686757, -0.20361, 0.297505},
Sinusoidal1_3 → {-0.187066, -0.0732084, 0.32812, Missing[], 0.00567862, 0.253731,
  -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439, -0.297199,
  0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, Missing[]},
Sinusoidal1_4 → {-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004, 0.261223,
  -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987, -0.322486, Missing[],
  0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, Missing[]}, Sinusoidal1_5 →
 {-0.20104, -0.101657, 0.31364, -0.234517, -0.0163677, 0.270631, -0.291058, Missing[], 0.181012, -0.326971,
  0.209134, 0.118444, -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537},
Sinusoidal1_6 → {-0.17526, -0.106684, 0.304186, -0.27676, -0.0299081, 0.264665,
  -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573, -0.282169,
  0.247232, 0.00318229, -0.241778, Missing[], -0.0967336, -0.164922, 0.339059},
Sinusoidal1_7 → {-0.179672, -0.126709, 0.328842, -0.280026, -0.0129078, 0.249841,
  -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949, -0.27099,
  0.269353, Missing[], -0.238668, 0.285517, -0.11389, Missing[], 0.31436},
Sinusoidal1_8 → {-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322, 0.285866,
  -0.282711, 0.113113, Missing[], -0.332705, 0.191007, 0.0780394, -0.280218,
  0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, Missing[], 0.305921},
Sinusoidal1_9 → {-0.179756, -0.0938318, Missing[], -0.224439, -0.0137817, 0.286427,
  -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813, -0.323289,
  0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, Missing[], 0.309654},
Sinusoidal1_10 → {-0.203834, -0.0722574, 0.294696, -0.254799, 0.00423677, 0.247448,
  -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167, Missing[],
  0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941},
Sinusoidal2_11 → {-0.0952089, Missing[], 0.25704, 0.097318, -0.313852, 0.0940832,
  0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865, 0.258725,
  0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, Missing[], 0.313889},
Sinusoidal2_12 → {-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067, 0.0980672,
  0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668, 0.262301,
  Missing[], -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903},
Sinusoidal2_13 → {-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667, 0.104182,
  0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963, 0.254435,
  0.0947659, -0.322671, Missing[], 0.251173, -0.252867, -0.092285, 0.311489},
Sinusoidal2_14 → {-0.0971308, -0.259618, 0.249762, 0.0996953, -0.311793, 0.0980176,
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  0.26024, Missing[], -0.100238, 0.318125, -0.100697, -0.257698, 0.256122,
  0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, Missing[]},
Sinusoidal2_15 → {Missing[], -0.25429, 0.25073, 0.100441, -0.313599, 0.0944084,
  0.258905, -0.254543, Missing[], 0.315559, -0.0966098, -0.259627, 0.255722,
  0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476},
Sinusoidal2_16 → {-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132, 0.0966092,
  0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, Missing[], 0.256443,
  0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152},
Sinusoidal2_17 → {-0.0991608, -0.252958, 0.255513, 0.0985052, -0.309591, 0.0946333,
  0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, Missing[], 0.259191,
  0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317},
Sinusoidal2_18 → {-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724, 0.0944222,
  Missing[], -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843, 0.258552,
  0.0991506, -0.312675, 0.10202, Missing[], -0.252332, -0.102226, 0.317809},
Sinusoidal2_19 → {-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977, 0.0989163,
  0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469, Missing[],
  0.101187, -0.319249, 0.100504, 0.251478, -0.255713, Missing[], 0.309885},
Sinusoidal2_20 → {-0.0946325, -0.259177, 0.259154, Missing[], -0.320484, 0.101942,
  0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815,
  0.0941545, -0.321907, 0.0941883, Missing[], -0.253272, -0.0958086, 0.313467},
Sinusoidal3_21 → {0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461, 0.254971,
  0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096, 0.29637,
  0.252844, -0.00335276, -0.262031, -0.296035, Missing[], 0.188443, Missing[]},
Sinusoidal3_22 → {0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846, 0.258728,
  0.299815, 0.101596, -0.183948, -0.320966, -0.180033, Missing[], 0.303756,
  0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941},
Sinusoidal3_23 → {0.18264, -0.0994704, -0.295137, -0.250857, 0.00157044, Missing[],
  0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036, 0.298633,
  0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813},
Sinusoidal3_24 → {0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361, 0.252171,
  Missing[], 0.101024, -0.190512, -0.312491, -0.18742, 0.100939, 0.304721,
  0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758},
Sinusoidal3_25 → {0.191347, -0.0982886, -0.29771, -0.261082, 0.00611569, 0.249936,
  0.298887, 0.101714, -0.1867, Missing[], -0.191881, 0.0933799, 0.302028,
  0.251166, -0.00172715, -0.251226, Missing[], -0.0943973, 0.181288, 0.31225},
Sinusoidal3_26 → {0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724, 0.255415,
  0.302354, 0.0997498, -0.183287, -0.320935, Missing[], 0.0968444, 0.296927,
  0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366},
Sinusoidal3_27 → {0.185809, -0.10192, -0.303748, -0.261172, 0.000202029, 0.258446,
  0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227, 0.302676,
  0.24961, -0.00174468, Missing[], -0.305591, -0.0963953, 0.182678, 0.311459},
Sinusoidal3_28 → {0.187562, -0.10053, -0.297144, -0.250552, 0.00476677, 0.261432,
  0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453, 0.301104,
  0.258413, Missing[], -0.255345, -0.298729, -0.095819, 0.181572, 0.323712},
Sinusoidal3_29 → {0.189755, -0.100643, -0.295957, -0.251445, -0.0055221, 0.252696,
  0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546, 0.296096,
  Missing[], -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756},
Sinusoidal3_30 → {0.186539, -0.100579, -0.301622, -0.251977, 0.00452805, Missing[],
  0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063, 0.296225,
  0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}|>
```

We also need additional spike cutoffs for the varying data sizes, i.e. for lengths 18,19 in addition to 20:

```
In[18]:= backgroundExample18 = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 18}];
         backgroundExample19 = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 19}];
         backgroundExample20 = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];

In[19]:= bootstrapQ95Spikes2 = Join @@ (QuantileEstimator[#, {}, Method → "Spikes", QuantileValue → .95] & /@
             {backgroundExample18, backgroundExample19, backgroundExample20})

Out[19]= <|18 → {0.445046, -0.445395}, 19 → {0.433436, -0.433543}, 20 → {0.421925, -0.422305}|>
```

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In[20]:=
```
classification2 = TimeSeriesClassification[classificationExample2,
  timePointsExample, LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes2]
```

```
Method → "LombScargle"
```

Out[20]=
```
<|SpikeMax →
  <|SpikePositive_2 → {{0.401489, 0.316586, 0.248799, 0.316863, 0.240431, 0.39388, 0.320934, 0.112859,
      0.48304, 0.119434}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829,
      0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, Missing[], 0.0905543}},
   SpikePositive_3 → {{0.207159, 0.459406, 0.19139, 0.3335, 0.161743, 0.279164, 0.290908,
      0.349599, 0.388726, 0.368958}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, Missing[], Missing[]}},
   SpikePositive_4 → {{0.329782, 0.164606, 0.174127, 0.369893, 0.136642, 0.250382, 0.0545938,
      0.146927, 0.751816, 0.160782}, {0.958583, Missing[], Missing[], 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.29172, 0.113905, 0.393634, 0.217466, 0.26927, 0.146723, 0.268111,
      0.174384, 0.673926, 0.221769}, {0.966833, Missing[], -0.0101601, Missing[], 0.0804663,
      0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
      0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.0781576, 0.218877, 0.358336, 0.157303, 0.16193, 0.343204, 0.418271,
      0.237367, 0.596099, 0.249393}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, Missing[], 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.0946384, 0.110029, 0.238915, 0.332807, 0.362353, 0.420714, 0.421401,
      0.305239, 0.359865, 0.320225}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
      Missing[], 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, Missing[], -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.322425, 0.378019, 0.129279, 0.260167, 0.188947, 0.409724, 0.276574,
      0.285411, 0.473016, 0.288916}, {0.973714, -0.0655433, 0.00410752, Missing[], -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, Missing[], 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{0.191105, 0.275682, 0.32701, 0.255944, 0.180156, 0.439177, 0.388446,
      0.313011, 0.377773, 0.313249}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
      0.0935483, -0.0385902, -0.0121923, -0.0467585, Missing[], 0.0208798, -0.0177267, Missing[],
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{0.269094, 0.107892, 0.339723, 0.229668, 0.261779, 0.526297, 0.223798,
      0.306505, 0.410917, 0.29898}, {0.961551, -0.0906575, 0.00581915, Missing[], 0.0455119,
      0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
      -0.0322946, -0.0461255, Missing[], -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{0.269238, 0.304908, 0.453771, 0.275775, 0.31034, 0.254392, 0.317248,
      0.287148, 0.343133, 0.301189}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
      0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
      -0.036531, 0.0377134, 0.0259428, Missing[], Missing[], 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{0.281881, 0.232178, 0.265124, 0.184305, 0.388704, 0.39217, 0.253012,
      0.23097, 0.541798, 0.215829}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, Missing[], -0.00749826}},
   SpikePositive_13 → {{0.209017, 0.412364, 0.26908, 0.246868, 0.419405, 0.241436, 0.524973,
      0.236218, 0.167974, 0.243138}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
      -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, Missing[], -0.045626, 0.0398952,
      0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
   SpikePositive_14 → {{0.420556, 0.184865, 0.172076, 0.295361, 0.276236, 0.170829, 0.34837,
      0.225062, 0.57875, 0.24424}, {Missing[], Missing[], 0.968597, -0.0798072, 0.0669311,
      0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
      -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
   SpikePositive_15 → {{0.228594, 0.324869, 0.194898, 0.376639, 0.412698, 0.33014, 0.355593,
      0.143594, 0.45131, 0.179735}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
      0.0322486, 0.0966403, Missing[], 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
      -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
   SpikePositive_17 → {{0.206836, 0.160373, 0.286362, 0.208243, 0.279088, 0.513246, 0.280994,
      0.345995, 0.372696, 0.356717}, {0.0894556, Missing[], 0.955206, -0.0721055, 0.0609444,
      0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
      0.101663, 0.086855, 0.000889116, Missing[], 0.0723495, -0.0396682, 0.0309544}},
```

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```
    SpikePositive_18 → {{0.208992, 0.245658, 0.273181, 0.395548, 0.450731, 0.392578, 0.324435,
        0.195396, 0.348608, 0.206514}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
        -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, Missing[], -0.0206424, 0.0179427,
        0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
    SpikePositive_19 → {{0.229345, 0.221674, 0.334832, 0.328915, 0.316585, 0.238101, 0.162855,
        0.47798, 0.211976, 0.47024}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
        -0.0813174, 0.0169025, 0.03397, -0.00559207, Missing[], -0.0310815, Missing[], -0.0924997,
        0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
    SpikePositive_20 → {{0.254928, 0.266356, 0.380803, 0.329529, 0.27411, 0.207859, 0.449543,
        0.301562, 0.351766, 0.274511}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
        -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
        0.0759909, -0.0700673, 0.0119244, -0.0203333, Missing[], -0.0174003, 0.010671, 0.051381}}|>,
  SpikeMin → <|SpikeNegative_2 → {{0.201027, 0.2533, 0.378679, 0.167108, 0.270137, 0.248185,
        0.200695, 0.252156, 0.635982, 0.284958}, {-0.969717, -0.0281117, -0.0848724, 0.0813594,
        -0.068113, -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
        -0.0295528, 0.0389368, 0.0814642, Missing[], 0.080829, -0.0461636, -0.00536829, -0.053342}},
    SpikeNegative_3 → {{0.306816, 0.219838, 0.212828, 0.217635, 0.539877, 0.304605, 0.251366,
        0.170127, 0.502528, 0.189633}, {-0.953174, Missing[], 0.081267, -0.0893468, -0.0891095,
        0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, Missing[], -0.0930647, -0.0384319,
        -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
    SpikeNegative_4 → {{0.287947, 0.202993, 0.335656, 0.135444, 0.273031, 0.432871, 0.330138,
        0.289344, 0.457079, 0.285159}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
        -0.0455452, Missing[], 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
        0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
    SpikeNegative_5 → {{0.184512, 0.139601, 0.439058, 0.28352, 0.351701, 0.281463, 0.235172,
        0.196901, 0.572454, 0.220492}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
        0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, Missing[],
        -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
    SpikeNegative_6 → {{0.24003, 0.198029, 0.242104, 0.426336, 0.214492, 0.342892, 0.33318,
        0.318328, 0.439298, 0.306411}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, Missing[],
        -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
        0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
    SpikeNegative_8 → {{0.381282, 0.157767, 0.269371, 0.366372, 0.278413, 0.179056, 0.362667,
        0.323836, 0.407057, 0.333583}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
        Missing[], 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
        -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
    SpikeNegative_9 → {{0.289209, 0.095184, 0.166566, 0.251417, 0.196926, 0.530524, 0.174432,
        0.321159, 0.504724, 0.328317}, {-0.964652, -0.0492164, -0.044027, Missing[], -0.0799416,
        0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
        -0.0901265, -0.0600632, -0.0839437, Missing[], -0.00450166, -0.0244654, 0.0251653}},
    SpikeNegative_10 → {{0.160615, 0.159723, 0.323455, 0.219262, 0.268763, 0.437439, 0.319328,
        0.227699, 0.547887, 0.280017}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
        Missing[], -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, Missing[],
        -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
    SpikeNegative_11 → {{0.372753, 0.224186, 0.332747, 0.219099, 0.324108, 0.55278, 0.296587,
        0.141442, 0.332394, 0.151673}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
        Missing[], -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052, 0.0300314,
        0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
    SpikeNegative_12 → {{0.199221, 0.412546, 0.434554, 0.269585, 0.224221, 0.450773, 0.217203,
        0.288445, 0.228841, 0.303951}, {0.0228997, -0.0356184, -0.973634, Missing[], 0.0107571,
        Missing[], 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
        -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
    SpikeNegative_13 → {{0.187249, 0.364868, 0.281771, 0.316867, 0.286018, 0.257369, 0.172911,
        0.381015, 0.437267, 0.371067}, {Missing[], -0.00831708, -0.964283, -0.0122152,
        -0.0196036, 0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, Missing[],
        -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
    SpikeNegative_14 → {{0.390724, 0.411363, 0.210825, 0.277571, 0.202907, 0.285812, 0.367755,
        0.257123, 0.404216, 0.262712}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594,
        Missing[], 0.00336549, Missing[], 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
        0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
    SpikeNegative_15 → {{0.234039, 0.289061, 0.308041, 0.36043, 0.481004, 0.256839, 0.166486,
        0.313316, 0.362503, 0.286787}, {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309,
        0.000455216, Missing[], 0.0349969, 0.0713349, Missing[], -0.0365053, -0.00194281,
        0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
    SpikeNegative_16 → {{0.130678, 0.323917, 0.306476, 0.305053, 0.213762, 0.367849, 0.337956,
        0.393596, 0.274868, 0.406601}, {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464,
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    0.0166785, 0.0680268, Missing[], -0.0297585, -0.00701137, 0.0550893, -0.0727101,
    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{0.191958, 0.199784, 0.293147, 0.37627, 0.344335, 0.473294, 0.123909,
    0.334196, 0.334792, 0.337675}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
    0.0616787, -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667,
    0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, Missing[], 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{0.529548, 0.380227, 0.302828, 0.300729, 0.341568, 0.14826, 0.294503,
    0.19491, 0.309629, 0.183365}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
    0.0000556895, -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971, 0.099183,
    0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, Missing[]}},
  SpikeNegative_19 → {{0.273146, 0.322495, 0.231244, 0.361588, 0.429349, 0.21201, 0.242226,
    0.394452, 0.158082, 0.410639}, {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693,
    0.0216656, 0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, Missing[], 0.0105588,
    Missing[], 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{0.449705, 0.316565, 0.119238, 0.32488, 0.334773, 0.261797, 0.365547,
    0.274258, 0.342813, 0.266108}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, Missing[],
    Missing[], -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007,
    -0.0175827, 0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}}|>,
f1 → <|LinearPositive_1 → {{0.958924, 0.256678, 0.0884449, 0.0596168, 0.0209536, 0.0183356,
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    0.0761646, 0.0918826, 0.112863, 0.131264, 0.149525, Missing[], 0.18659, 0.205188, 0.223266,
    0.241367, 0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, Missing[]}},
  LinearPositive_2 → {{0.971049, 0.19319, 0.0774574, 0.0270439, 0.00987197, 0.0761467,
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    0.0928923, 0.110677, 0.130133, Missing[], 0.167272, 0.186766, 0.206807, 0.224025,
    0.242161, 0.261728, 0.280689, Missing[], 0.316418, 0.335012, 0.355339, 0.375155}},
  LinearPositive_3 → {{0.942566, 0.280325, 0.156647, 0.0312733, 0.0150294,
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    0.204397, 0.22244, 0.241027, 0.262217, Missing[], 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}},
  LinearPositive_4 → {{0.956192, 0.191505, 0.195225, 0.0505162, 0.0333387, 0.0618551, 0.0385685,
    0.0241856, 0.0213065, 0.0299147}, {0.0188591, 0.0384796, 0.0552706, 0.0761382,
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    0.24344, 0.261751, Missing[], Missing[], 0.316607, 0.33422, 0.355535, 0.374989}},
  LinearPositive_5 → {{0.97031, 0.197271, 0.0796741, 0.0289259, 0.00990001, 0.0746017,
    0.0592053, 0.035772, 0.0179451, 0.0403458}, {0.0196474, 0.0375735, 0.0561861, 0.0745382,
    0.094777, 0.113054, 0.132423, Missing[], 0.169563, 0.188068, 0.205612, 0.225889,
    0.242492, 0.261976, 0.279334, Missing[], 0.316353, 0.33459, 0.353954, 0.372244}},
  LinearPositive_6 → {{0.972358, 0.195838, 0.0906833, 0.00995542, 0.0232414, 0.0238343,
    0.00400059, 0.045004, 0.0499162, 0.0469434}, {0.0186014, 0.0381755, 0.0550572, 0.074646,
    0.0932816, 0.113886, 0.132134, 0.149767, 0.168659, 0.185415, 0.205262, 0.222624,
    0.242621, 0.260049, Missing[], 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
  LinearPositive_7 → {{0.932087, 0.204566, 0.0204162, 0.0340388, 0.059403, 0.0498602,
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    0.241912, Missing[], 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
  LinearPositive_8 → {{0.974338, 0.211696, 0.0208036, 0.00646526, 0.00603914, 0.0112957,
    0.0239217, 0.0432135, 0.0158752, 0.0502048}, {0.0170019, 0.0382694, 0.0569482, 0.0754625,
    0.0914347, 0.110031, 0.132014, 0.15073, 0.169121, Missing[], 0.205265, Missing[],
    0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}},
  LinearPositive_9 → {{0.912567, 0.132338, 0.0629325, 0.064955, 0.116364, 0.0793909, 0.0634597,
    0.159123, 0.250838, 0.171514}, {0.0185501, 0.0388643, 0.0547098, 0.0747468,
    0.0938687, 0.113558, 0.129413, 0.148929, 0.168743, 0.186495, 0.204247, 0.225298,
    0.241691, 0.261072, Missing[], 0.298507, 0.318632, 0.337602, Missing[], 0.372608}},
  LinearPositive_10 → {{0.967527, 0.232111, 0.052193, 0.000745118, 0.00814914, 0.00342978,
    0.0461045, 0.0463868, 0.00797956, 0.0535925}, {0.0174864, 0.0370712, 0.0572236,
    0.0748823, 0.0926627, 0.111129, Missing[], 0.148771, 0.168913, 0.186275, 0.206359,
    0.223211, 0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
  LinearPositive_11 → {{0.95939, 0.242183, 0.0884774, 0.0762599, 0.0531554, 0.0337044,
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    0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, Missing[]}},
  LinearPositive_12 → {{0.955728, 0.130125, 0.0161685, 0.0166533, 0.042065, 0.0902977,
    0.0888795, 0.124962, 0.133347, 0.133767}, {0.0219335, 0.0431422, 0.0502095, 0.0696589,
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LinearPositive_13 → {{0.977866, 0.121146, 0.0301648, 0.0404631, 0.0133151, 0.00272022,
    0.0423373, 0.0951044, 0.0757395, 0.0989706}, {0.022617, 0.0284408, 0.0607512, Missing[],
    0.0880775, 0.119613, 0.134238, 0.152698, 0.169261, 0.181713, 0.197855, 0.217149,
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LinearPositive_14 → {{0.977537, 0.156912, 0.0971447, 0.0269981, 0.0166191,
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LinearPositive_15 → {{0.979814, 0.132482, 0.100215, 0.0274201, 0.00894523, 0.053936,
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LinearPositive_16 → {{0.971769, 0.116962, 0.0467276, 0.0421332, 0.0171045,
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LinearPositive_17 → {{0.97585, 0.0482084, 0.032869, 0.0167111, 0.0250197, 0.0917911,
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    0.240506, 0.262803, 0.283339, Missing[], 0.3159, Missing[], 0.349837, 0.380979}},
LinearPositive_18 → {{0.982766, 0.171053, 0.0318087, 0.00259854, 0.00156821, 0.0124847,
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    0.232407, 0.261637, 0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}},
LinearPositive_19 → {{0.984211, 0.116586, 0.0712958, 0.0348496, 0.0117674,
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LinearPositive_20 → {{0.94448, 0.196049, 0.0215665, 0.0398381, 0.028797, 0.113644, 0.106781,
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LinearNegative_1 → {{0.965033, 0.232181, 0.084373, 0.0000776734, 0.0123562, 0.0108952,
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LinearNegative_2 → {{0.97341, 0.129473, 0.0368972, 0.0157177, 0.0370657, 0.00780627, 0.0551865,
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LinearNegative_3 → {{0.979884, 0.182122, 0.0215849, 0.00295037, 0.000814355, 0.0276174,
    0.0345045, 0.0398335, 0.0226924, 0.0461297}, {-0.0283384, -0.0528281, -0.0527884, -0.0740599,
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LinearNegative_4 → {{0.972548, 0.217432, 0.0457049, 0.00824967, 0.000256393, 0.00349695,
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LinearNegative_5 → {{0.967087, 0.177069, 0.0419436, 0.0197786, 0.0416481, 0.000869468,
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    Missing[], -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}},
LinearNegative_6 → {{0.948927, 0.158631, 0.0312903, 0.0331402, 0.0448984, 0.0828057,
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    -0.0987645, -0.126896, -0.126614, -0.165572, -0.172297, -0.184872, -0.208135, -0.237294,
    -0.243037, -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, Missing[], -0.381481}},
LinearNegative_7 → {{0.936507, 0.0640128, 0.00394309, 0.022139, 0.0618691, 0.0244874,
    0.0191825, 0.216109, 0.154912, 0.207013}, {-0.00172329, -0.032268, -0.068173, Missing[],
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    -0.23516, -0.248536, -0.268245, -0.303398, Missing[], -0.349618, -0.352678, -0.371923}},
LinearNegative_8 → {{0.931258, 0.33298, 0.110322, 0.0356421, 0.0861804, 0.010297, 0.00562524,
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    -0.238911, -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
LinearNegative_9 → {{0.99156, 0.109504, 0.0365536, 0.00761587, 0.00279355, 0.00498051,
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    -0.0936032, -0.115414, -0.114422, -0.130851, -0.167598, -0.173937, Missing[], -0.23569,
    -0.258977, -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
  LinearNegative_10 → {{0.990609, 0.0919168, 0.00143729, 0.00816255, 0.0521766, 0.0757424,
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  LinearNegative_11 → {{0.973161, 0.199187, 0.0803896, 0.0091538, 0.0198705, 0.0236705,
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  LinearNegative_12 → {{0.958067, 0.277387, 0.0183978, 0.00356121, 0.00162316, 0.0259922,
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  LinearNegative_13 → {{0.98466, 0.121876, 0.0102215, 0.0448545, 0.0818218, 0.0164974,
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  LinearNegative_14 → {{0.953128, 0.0556755, 0.00391605, 0.02916, 0.0624531, 0.0152097,
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  LinearNegative_15 → {{0.985914, 0.135818, 0.00072227, 0.043864, 0.0376762, 0.0457941, 0.061562,
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  LinearNegative_16 → {{0.949498, 0.159585, 0.0230732, 0.0176032, 0.0501018, 0.0964765,
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  LinearNegative_17 → {{0.943491, 0.312959, 0.0740163, 0.054634, 0.0256701, 0.00668292, 0.0160457,
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    -0.240133, -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}},
  LinearNegative_18 → {{0.959355, 0.238995, 0.07069, 0.0231668, 0.0155546, 0.0767033, 0.100662,
    0.014317, 0.0124554, 0.0191679}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
    -0.0895021, -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921,
    Missing[], -0.254831, -0.285694, Missing[], -0.326762, -0.328866, -0.362472, -0.367752}},
  LinearNegative_19 → {{0.98212, 0.121275, 0.082056, 0.0312473, 0.00686255, 0.0584051, 0.0789979,
    0.0359578, 0.0056077, 0.044722}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
    -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
    -0.241033, -0.263307, -0.281329, Missing[], -0.315673, -0.329753, -0.355337, -0.38137}},
  LinearNegative_20 → {{0.98188, 0.128205, 0.079467, 0.0330693, 0.0126232, 0.073092, 0.0638245,
    0.0315392, 0.00785516, 0.0378776}, {-0.024006, -0.0432239, -0.0496914, -0.0682004,
    Missing[], -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
    -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}}|>,
f3 → <|Sinusoidal3_21 → {{0.0146384, 0.108557, 0.990622, 0.0714609, 0.0295762, 0.0167215,
    0.0123958, 0.0100773, 0.00479885, 0.0113594}, {0.18867, -0.0972321, -0.306583, -0.251354,
    -0.00388461, 0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096,
    0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, Missing[], 0.188443, Missing[]}},
  Sinusoidal3_22 → {{0.00496229, 0.0699684, 0.990201, 0.109326, 0.0284318, 0.0368765, 0.0045959,
    0.00785367, 0.0188286, 0.0049219}, {0.181513, -0.0928691, -0.305475, -0.251164,
    0.00419846, 0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, Missing[],
    0.303756, 0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
  Sinusoidal3_23 → {{0.00398326, 0.0454171, 0.991858, 0.0486794, 0.066171, 0.0659138, 0.0171141,
    0.00307867, 0.0520456, 0.00599141}, {0.18264, -0.0994704, -0.295137, -0.250857,
    0.00157044, Missing[], 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036,
    0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
  Sinusoidal3_24 → {{0.00606681, 0.0827236, 0.979887, 0.12688, 0.11769, 0.0130258, 0.0105975,
    0.038691, 0.0201748, 0.0283914}, {0.183018, -0.0977985, -0.296248, -0.251125,
    -0.00333361, 0.252171, Missing[], 0.101024, -0.190512, -0.312491, -0.18742, 0.100939,
    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
  Sinusoidal3_25 → {{0.0147918, 0.0306279, 0.971009, 0.127842, 0.0512332, 0.0983062, 0.0595818,
    0.115496, 0.00136141, 0.102276}, {0.191347, -0.0982886, -0.29771, -0.261082,
    0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, Missing[], -0.191881, 0.0933799,
    0.302028, 0.251166, -0.00172715, -0.251226, Missing[], -0.0943973, 0.181288, 0.31225}},
```

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```
  Sinusoidal3_26 → {{0.0137289, 0.0637027, 0.988988, 0.121869, 0.0308108, 0.0338255, 0.0099234,
      0.0101093, 0.021097, 0.00806647}, {0.185284, -0.0936261, -0.306395, -0.25385,
      0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, Missing[], 0.0968444,
      0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{0.00314556, 0.111029, 0.981165, 0.0952101, 0.100192, 0.0496168, 0.00748381,
      0.00440921, 0.0573094, 0.00722437}, {0.185809, -0.10192, -0.303748, -0.261172,
      0.000202029, 0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227,
      0.302676, 0.24961, -0.00174468, Missing[], -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.00331654, 0.0796994, 0.991246, 0.0937241, 0.0360166, 0.0197206,
      0.00858685, 0.00337592, 0.0226139, 0.00117631}, {0.187562, -0.10053, -0.297144, -0.250552,
      0.00476677, 0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453,
      0.301104, 0.258413, Missing[], -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{0.0249177, 0.0310922, 0.989613, 0.0767119, 0.10636, 0.0194987, 0.00537129,
      0.0275011, 0.0188455, 0.0190104}, {0.189755, -0.100643, -0.295957, -0.251445, -0.0055221,
      0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546, 0.296096,
      Missing[], -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
  Sinusoidal3_30 → {{0.00303092, 0.0408345, 0.991871, 0.0482278, 0.0644053, 0.0697725,
      0.0187521, 0.00342482, 0.0526244, 0.00635495}, {0.186539, -0.100579, -0.301622, -0.251977,
      0.00452805, Missing[], 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
      0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|Sinusoidal2_11 → {{0.0233309, 0.0291947, 0.0475496, 0.102873, 0.9291, 0.348232, 0.0338303,
      0.00723328, 0.00193263, 0.0082003}, {-0.0952089, Missing[], 0.25704, 0.097318,
      -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
      0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, Missing[], 0.313889}},
  Sinusoidal2_12 → {{0.00858769, 0.00716117, 0.0256561, 0.133611, 0.919997, 0.365852,
      0.0180025, 0.015086, 0.0223099, 0.00854783}, {-0.101498, -0.25529, 0.251653, 0.0972642,
      -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
      0.262301, Missing[], -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{0.0108451, 0.0177926, 0.0174256, 0.0718749, 0.941402, 0.325256, 0.0369548,
      0.0148421, 0.020233, 0.0084607}, {-0.0918789, -0.259087, 0.253065, 0.103093,
      -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
      0.254435, 0.0947659, -0.322671, Missing[], 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_15 → {{0.00480532, 0.00313337, 0.0417568, 0.0614637, 0.901797, 0.41346,
      0.0767057, 0.00258268, 0.066092, 0.000359656}, {Missing[], -0.25429, 0.25073, 0.100441,
      -0.313599, 0.0944084, 0.258905, -0.254543, Missing[], 0.315559, -0.0966098, -0.259627,
      0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{0.0171343, 0.0542338, 0.00603775, 0.235702, 0.91115, 0.319822, 0.0794124,
      0.0158717, 0.043722, 0.0149572}, {-0.0916775, -0.260977, 0.251061, 0.104141,
      -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, Missing[],
      0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{0.0163557, 0.0566152, 0.0067179, 0.228934, 0.921114, 0.296861, 0.0703243,
      0.0145747, 0.0462716, 0.0139656}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
      -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, Missing[],
      0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.00163134, 0.170531, 0.114791, 0.0191856, 0.895901, 0.368987, 0.0598101,
      0.0151582, 0.121436, 0.00520511}, {-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724,
      0.0944222, Missing[], -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
      0.258552, 0.0991506, -0.312675, 0.10202, Missing[], -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{0.0379966, 0.00257647, 0.070253, 0.0985216, 0.918452, 0.349725, 0.12424,
      0.0205762, 0.0418162, 0.0209512}, {-0.0979953, -0.254783, 0.260889, 0.100358,
      -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
      Missing[], 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, Missing[], 0.309885}},
  Sinusoidal2_20 → {{0.0235815, 0.0372427, 0.0578103, 0.0691755, 0.910715, 0.381742, 0.0131144,
      0.00512015, 0.120136, 0.0130165}, {-0.0946325, -0.259177, 0.259154, Missing[], -0.320484,
      0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815,
      0.0941545, -0.321907, 0.0941883, Missing[], -0.253272, -0.0958086, 0.313467}}|>,
f6 → <|Sinusoidal1_1 → {{0.015177, 0.0171693, 0.0654794, 0.0422104, 0.044205, 0.992207,
      0.0667561, 0.00785256, 0.0487241, 0.00925138}, {-0.20264, -0.107877, 0.278896, -0.289184,
      -0.0168796, Missing[], -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
      -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{0.00810858, 0.0106603, 0.0543911, 0.0844513, 0.101721, 0.978257, 0.136463,
      0.00260984, 0.0609552, 0.0072149}, {-0.153886, -0.0875347, 0.297854, -0.276583,
      Missing[], 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
      -0.288819, 0.270239, 0.0126278, Missing[], 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{0.0182074, 0.0433855, 0.0780744, 0.0930064, 0.0700417, 0.967112, 0.202372,
      0.0304402, 0.00806878, 0.0297077}, {-0.187066, -0.0732084, 0.32812, Missing[], 0.00567862,
```

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```
    0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439, -0.297199,
    0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, Missing[]}},
Sinusoidal1_4 → {{0.0197633, 0.0110429, 0.0610554, 0.0728547, 0.0242443, 0.983168, 0.136087,
    0.0391107, 0.0468223, 0.0316742}, {-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004,
    0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987, -0.322486,
    Missing[], 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, Missing[]}},
Sinusoidal1_5 → {{0.00152104, 0.025619, 0.0118255, 0.0409131, 0.119631, 0.980744, 0.14499,
    0.00209986, 0.0181909, 0.000366341}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, Missing[], 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
Sinusoidal1_6 → {{0.0242002, 0.0567059, 0.0514547, 0.0490252, 0.0498147, 0.985479, 0.0922941,
    0.00149858, 0.094591, 0.00549097}, {-0.17526, -0.106684, 0.304186, -0.27676, -0.0299081,
    0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573, -0.282169,
    0.247232, 0.00318229, -0.241778, Missing[], -0.0967336, -0.164922, 0.339059}},
Sinusoidal1_7 → {{0.00265614, 0.0114682, 0.0157748, 0.0206755, 0.0871281, 0.977082, 0.18873,
    0.0266401, 0.0145671, 0.0190702}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, Missing[], -0.238668, 0.285517, -0.11389, Missing[], 0.31436}},
Sinusoidal1_8 → {{0.0220708, 0.0165329, 0.00331846, 0.0692529, 0.0782482, 0.977633, 0.165597,
    0.0554427, 0.00114806, 0.0452331}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, Missing[], -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, Missing[], 0.305921}},
Sinusoidal1_9 → {{0.00254906, 0.0012681, 0.0000592768, 0.020206, 0.0367533, 0.96803, 0.244845,
    0.0240221, 0.00554271, 0.0243887}, {-0.179756, -0.0938318, Missing[], -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, Missing[], 0.309654}},
Sinusoidal1_10 → {{0.0167623, 0.0578473, 0.0198611, 0.0664621, 0.187587, 0.975844, 0.0503686,
    0.0282644, 0.0150374, 0.0232248}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    Missing[], 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

If we want the classes produced, we can query the keys:

```
In[21]:= Query[Keys]@classification2
Out[21]= {SpikeMax, SpikeMin, f1, f3, f5, f6}
```

For the members in each class we have:

```
In[22]:= Query[All, Length]@classification2
Out[22]= <|SpikeMax → 18, SpikeMin → 18, f1 → 40, f3 → 10, f5 → 9, f6 → 10|>
```

Specific membership labels to each class can also be obtained:

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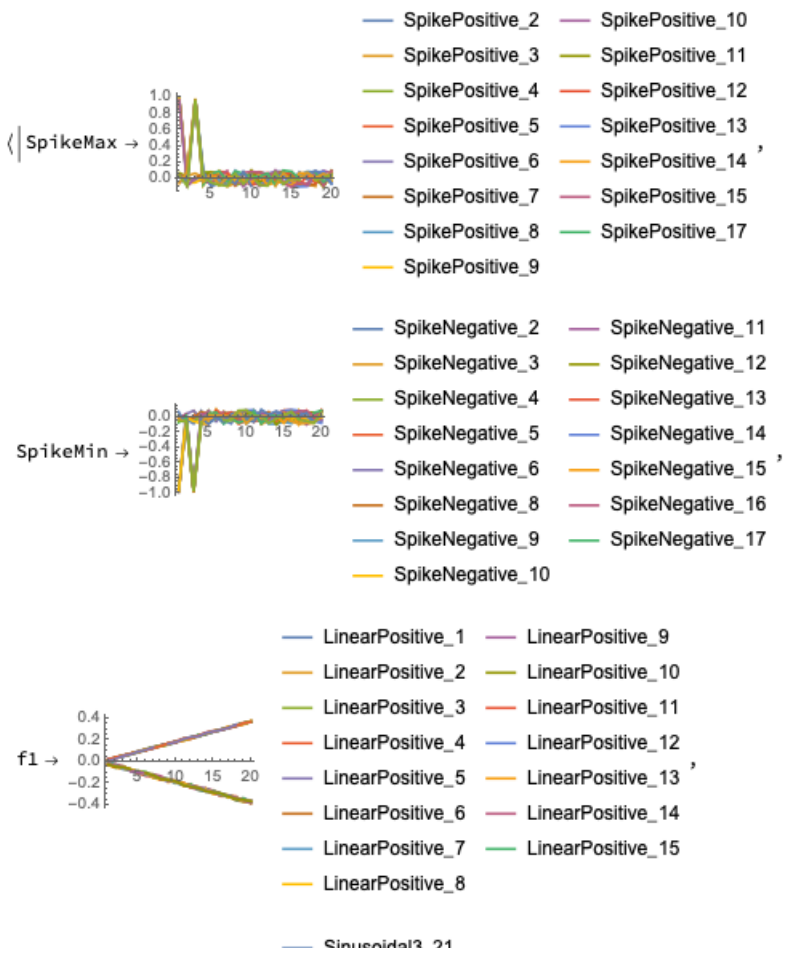
In[23]:=
```
Query[All, Keys]@classification2
```

Out[23]=
```
<|SpikeMax → {SpikePositive_2, SpikePositive_3, SpikePositive_4,
   SpikePositive_5, SpikePositive_6, SpikePositive_7, SpikePositive_8, SpikePositive_9,
   SpikePositive_10, SpikePositive_11, SpikePositive_12, SpikePositive_13, SpikePositive_14,
   SpikePositive_15, SpikePositive_17, SpikePositive_18, SpikePositive_19, SpikePositive_20},
 SpikeMin → {SpikeNegative_2, SpikeNegative_3, SpikeNegative_4, SpikeNegative_5,
   SpikeNegative_6, SpikeNegative_8, SpikeNegative_9, SpikeNegative_10, SpikeNegative_11,
   SpikeNegative_12, SpikeNegative_13, SpikeNegative_14, SpikeNegative_15, SpikeNegative_16,
   SpikeNegative_17, SpikeNegative_18, SpikeNegative_19, SpikeNegative_20},
 f1 → {LinearPositive_1, LinearPositive_2, LinearPositive_3, LinearPositive_4, LinearPositive_5,
   LinearPositive_6, LinearPositive_7, LinearPositive_8, LinearPositive_9, LinearPositive_10,
   LinearPositive_11, LinearPositive_12, LinearPositive_13, LinearPositive_14, LinearPositive_15,
   LinearPositive_16, LinearPositive_17, LinearPositive_18, LinearPositive_19, LinearPositive_20,
   LinearNegative_1, LinearNegative_2, LinearNegative_3, LinearNegative_4, LinearNegative_5,
   LinearNegative_6, LinearNegative_7, LinearNegative_8, LinearNegative_9, LinearNegative_10,
   LinearNegative_11, LinearNegative_12, LinearNegative_13, LinearNegative_14, LinearNegative_15,
   LinearNegative_16, LinearNegative_17, LinearNegative_18, LinearNegative_19, LinearNegative_20},
 f3 → {Sinusoidal3_21, Sinusoidal3_22, Sinusoidal3_23, Sinusoidal3_24, Sinusoidal3_25,
   Sinusoidal3_26, Sinusoidal3_27, Sinusoidal3_28, Sinusoidal3_29, Sinusoidal3_30},
 f5 → {Sinusoidal2_11, Sinusoidal2_12, Sinusoidal2_13, Sinusoidal2_15, Sinusoidal2_16,
   Sinusoidal2_17, Sinusoidal2_18, Sinusoidal2_19, Sinusoidal2_20},
 f6 → {Sinusoidal1_1, Sinusoidal1_2, Sinusoidal1_3, Sinusoidal1_4, Sinusoidal1_5,
   Sinusoidal1_6, Sinusoidal1_7, Sinusoidal1_8, Sinusoidal1_9, Sinusoidal1_10}|>
```

We can plot all the signals in each set:

In[24]:=
```
Query[All, ListLinePlot[#[[All, 2]], PlotRange → Full] &]@classification2
```



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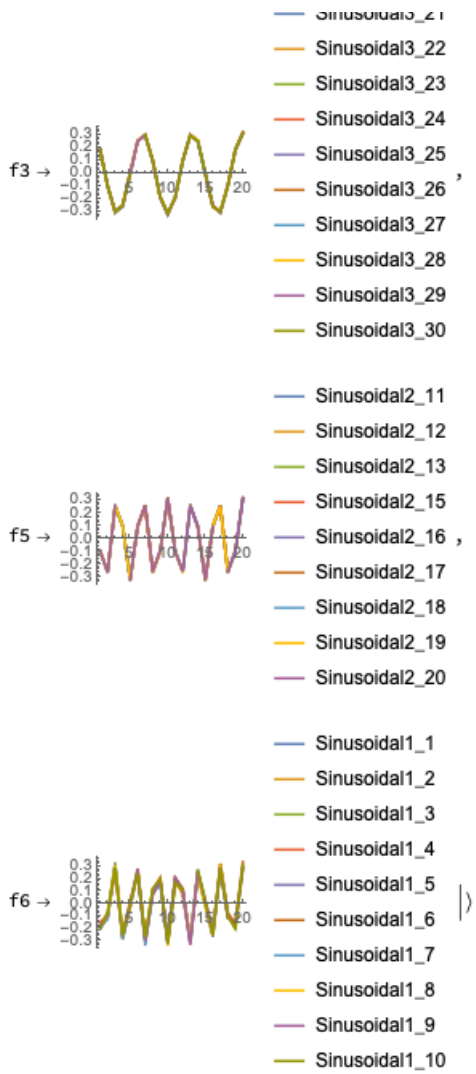
Out[24]=



Options (17)

AutocorrelationCutoffs (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The AutocorrelationCutoffs are used for Methods "Autocorrelation" and "InterpolatedAutocorrelation", providing cutoffs at different lags (sequentially as a list) that will be used to filter out data series for which the autocorrelation at a given lag is lower than the cutoff. For example, we can provide cutoffs for different lags (we use the same main example, and background noise example for 20 timepoints):

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```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
          Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["Sinusoidal2_" <> ToString[i] →
             5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
            {i, 21, 30}]]];
        backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
        timePointsExample = Range[20];
```

We can use the background to determine our data cutoffs for the "Autocorrelation" method. We work with the QuantileEstimator function to generate a value for the AutocorrelationCutoffs, by default using the 0.95th quantile. (N.B. the following computaiton may be time consuming depending on number of samples in the background simulation):

```
In[3]:= bootstrapQ95Autocorrelation =
         QuantileEstimator[backgroundExample, timePointsExample , Method → "Autocorrelation"]

Out[3]= {0.104569, 0.750865, 0.330876, 0.582844, 0.384145, 0.476242, 0.361702, 0.407732, 0.30536}
```

We can work again with the QuantileEstimator function to also generate a value for the SpikeCutoffs:

```
In[4]:= bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"]

Out[4]= <|20 → {0.42185, -0.421758}|>
```

Let's perform the classification, including the entire cutoff list:

```
In[5]:= classificationAutocorrelation1 = TimeSeriesClassification[classificationExample1,
          timePointsExample, AutocorrelationCutoffs → bootstrapQ95Autocorrelation,
          SpikeCutoffs → bootstrapQ95Spikes, Method → "Autocorrelation"]

          Method → "Autocorrelation"

Out[5]= <|SpikeMax →
          <|SpikePositive_1 → {{1., -0.452395, 0.219937, -0.141456, -0.040982, 0.0671421, -0.0204863, -0.0225783,
              0.00336149, 0.0248339}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
              0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
              -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
           SpikePositive_2 → {{1., -0.33332, 0.178978, -0.043203, 0.0330959, 0.0187841, 0.0643953,
              -0.167683, -0.0783794, -0.134626}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
              0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
              -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
           SpikePositive_3 → {{1., -0.150943, 0.25591, -0.077747, 0.03904, -0.112386, -0.130446,
              -0.111423, -0.0923815, 0.0100807}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
              -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
              0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
           SpikePositive_4 → {{1., -0.329658, 0.231525, 0.0162836, 0.164488, -0.166715, 0.0989705,
              -0.163788, -0.0754534, 0.0143191}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
```

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```
    -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
    0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
SpikePositive_5 → {{1., -0.354501, 0.199318, -0.099174, 0.199, -0.0363005, 0.158313,
    -0.0231566, 0.0362299, -0.135361}, {0.966833, -0.0172757, -0.0101601, 0.0449156,
    0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
    -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
SpikePositive_6 → {{1., -0.466257, 0.137607, -0.192065, -0.0315355, -0.0729004, -0.0550543,
    -0.104833, 0.0601693, -0.0827568}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
    0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
    0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
SpikePositive_7 → {{1., -0.389552, 0.144053, -0.0395178, 0.0603777, -0.112134, -0.0357364,
    -0.00620881, -0.073946, -0.0864452}, {0.973634, -0.0197451, 0.00381691, 0.0632199,
    0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
    0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
SpikePositive_8 → {{1., -0.394532, 0.210425, -0.0366925, 0.0213409, -0.067476, 0.000171715,
    -0.0864154, -0.128194, 0.0081353}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
    -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
    -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
SpikePositive_9 → {{1., -0.400547, 0.143122, -0.118456, -0.00900312, 0.125105, 0.0177367,
    -0.061955, -0.00116964, -0.150973}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
    0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
SpikePositive_10 → {{1., -0.486387, 0.214384, -0.107572, 0.107945, 0.0130167, 0.0145573,
    0.0233586, -0.0802024, -0.127062}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
    0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
SpikePositive_11 → {{1., -0.338874, 0.300856, -0.187073, -0.0720043, -0.0204714, -0.0156668,
    0.0397913, -0.0000121023, -0.147044}, {0.0696283, 0.0251021, 0.968196, 0.0511374,
    0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
    -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
SpikePositive_12 → {{1., -0.490403, 0.230471, -0.02836, 0.158686, -0.26022, 0.158602,
    -0.177464, 0.0371373, -0.0785755}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
    0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
SpikePositive_13 → {{1., -0.380553, -0.0954718, -0.150478, -0.0658297, 0.106079, -0.0357483,
    -0.0423526, 0.134218, -0.0648447}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
    -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
    0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
SpikePositive_14 → {{1., -0.526563, 0.402071, -0.0816825, 0.0766719, -0.117882, 0.0465972,
    -0.195255, 0.0724303, -0.107586}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
    0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
SpikePositive_15 → {{1., -0.498776, 0.12023, -0.0909257, 0.179612, -0.241152, 0.0697987,
    0.00693521, 0.0904771, -0.0399131}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
    0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
    -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
SpikePositive_16 → {{1., -0.252346, -0.0181276, -0.202654, 0.0588694, -0.165692, 0.058152,
    -0.0733224, 0.0688338, 0.00969476}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
    -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
    -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
SpikePositive_17 → {{1., -0.868718, 0.44914, -0.120491, -0.0616033, -0.0228913, 0.14139,
    -0.0932499, -0.0473214, 0.036701}, {0.0894556, -0.0939456, 0.955206, -0.0721055,
    0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
    -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
SpikePositive_18 → {{1., -0.362902, -0.122098, -0.129486, 0.0562719, -0.0830183, 0.122331,
    -0.122383, -0.180395, -0.0773557}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
    -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
    0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
SpikePositive_19 → {{1., -0.42077, 0.0763867, -0.227391, 0.0475263, 0.0245878, -0.0251915,
    -0.0584293, -0.118635, 0.0240546}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
    -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
SpikePositive_20 → {{1., -0.507801, 0.163243, -0.238989, -0.0407895, 0.101176, -0.0803686,
    0.0171814, 0.00408016, -0.268402}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
    -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
    0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
```

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```
SpikeMin → <|SpikeNegative_1 → {{1., -0.423906, 0.0870199, -0.0546103, 0.153795, 0.0753404,
      -0.11792, -0.102237, 0.144444, -0.0974828}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
      -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
      -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
  SpikeNegative_2 → {{1., -0.254883, 0.246154, -0.281797, 0.168139, -0.0510077, 0.0696523,
      0.044741, -0.0493091, -0.173802}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
      -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
      -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_3 → {{1., -0.52844, 0.0128591, 0.0401754, 0.156405, -0.25313, 0.0143667,
      -0.105044, 0.0118936, -0.135968}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
      0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
      -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
  SpikeNegative_4 → {{1., -0.261291, 0.197729, -0.0669671, -0.0489197, 0.019136, -0.0777287,
      -0.0858975, 0.0311934, -0.0488232}, {-0.978499, -0.0375369, -0.0308657, -0.0197828,
      0.087556, -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659,
      -0.0303762, 0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{1., -0.275359, 0.08563, -0.0927664, 0.179004, -0.137792, 0.112485,
      -0.0158152, -0.046442, -0.180954}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
      0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
      -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{1., -0.398833, 0.0778628, -0.044104, 0.0333735, 0.0658697, -0.0029231,
      -0.0938463, -0.0655049, -0.0116685}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
      -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
      0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{1., -0.42086, -0.00214872, 0.0208358, 0.127917, -0.202863, 0.0631005,
      -0.00894861, 0.0102268, 0.000991105}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
      0.0874465, -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
      -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{1., -0.167986, 0.132625, -0.161643, 0.0190856, 0.0689723, -0.0356912,
      -0.0774932, -0.0382031, -0.110421}, {-0.971714, -0.0689738, -0.0116232, 0.0693961,
      0.0405887, -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389,
      0.06932, -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{1., -0.280681, 0.131522, -0.27773, 0.125519, -0.158639, 0.0827061,
      -0.0794961, -0.159761, -0.0325458}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
      0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
      -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{1., -0.351869, 0.262355, -0.0376404, 0.155982, -0.124093, 0.105999,
      -0.0645218, 0.0405128, 0.0335434}, {-0.972673, -0.00291876, -0.0540171, -0.0812638,
      -0.0617025, 0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018,
      -0.0213425, -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
  SpikeNegative_11 → {{1., -0.413539, 0.0679203, 0.00410847, 0.0261914, -0.0181218, 0.0852791,
      -0.0436318, -0.0440867, -0.13617}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
      -0.0488362, -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052,
      0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{1., -0.395846, 0.0894882, -0.237998, -0.0446471, -0.0524744, 0.0771359,
      -0.0422126, -0.134419, 0.0146231}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
      0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
      -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{1., -0.343983, 0.00454468, -0.205612, 0.0119525, -0.102592, 0.103107,
      0.0746079, -0.0154823, -0.032091}, {0.089408, -0.00831708, -0.964283, -0.0122152,
      -0.0196036, 0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
      -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{1., -0.332802, 0.244793, -0.20513, 0.0810854, -0.132165, -0.0116365,
      -0.109746, -0.0688768, -0.10264}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594,
      0.0528555, 0.00336549, 0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
      0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{1., -0.409677, 0.104665, -0.110113, 0.152765, -0.103758, -0.130233,
      -0.0168568, 0.0773673, -0.0765506}, {-0.00121514, -0.0078406, -0.978821, -0.0221297,
      -0.026309, 0.000455216, -0.0829657, 0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281,
      0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{1., -0.458875, 0.142195, -0.117197, -0.0328704, -0.0724729, 0.062644,
      0.0215451, -0.0873599, 0.0313895}, {-0.00639921, 0.0369683, -0.976295, 0.0340422,
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      0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{1., -0.28948, 0.0899977, -0.14795, 0.137414, -0.00541154, 0.0773486,
      0.045355, -0.117622, -0.0110899}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
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      0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{1., -0.219411, 0.0906106, -0.0586132, 0.117458, -0.0973521, -0.064392,
      -0.0844588, 0.106035, -0.112353}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
      0.0000556895, -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971, 0.099183,
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  SpikeNegative_19 → {{1., -0.25374, 0.0112197, -0.122395, -0.0226519, -0.0591994, -0.111793,
      0.0410923, 0.02981, -0.137959}, {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693,
      0.0216656, 0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588,
      -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{1., -0.223368, 0.0633665, -0.177509, 0.103343, 0.0332846, -0.0776252,
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      0.057722, -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007,
      -0.0175827, 0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}}|>,
Lag1 → <|LinearPositive_1 → {{1., 0.812153, 0.688835, 0.540544, 0.408977, 0.277736,
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     {0.018415, 0.0377122, 0.0574444, 0.0761646, 0.0918826, 0.112863, 0.131264, 0.149525, 0.166786, 0.18659,
      0.205188, 0.223266, 0.241367, 0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, 0.373425}},
  LinearPositive_2 → {{1., 0.812426, 0.690113, 0.540471, 0.410253, 0.280388, 0.156519,
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      0.0928923, 0.110677, 0.130133, 0.148914, 0.167272, 0.186766, 0.206807, 0.224025, 0.242161,
      0.261728, 0.280689, 0.29779, 0.316418, 0.335012, 0.355339, 0.375155}}, LinearPositive_3 →
    {{1., 0.815438, 0.691427, 0.540957, 0.409589, 0.278307, 0.155771, 0.0411641, -0.0628612, -0.153798},
     {0.0204364, 0.0388961, 0.055949, 0.0753517, 0.0937248, 0.112155, 0.1288, 0.150982, 0.166685, 0.187482,
      0.204397, 0.22244, 0.241027, 0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}},
  LinearPositive_4 → {{1., 0.811366, 0.688737, 0.538759, 0.409453, 0.280276, 0.156679,
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      0.0941127, 0.11255, 0.131257, 0.150426, 0.166514, 0.185049, 0.206061, 0.222052,
      0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}},
  LinearPositive_5 → {{1., 0.813098, 0.689554, 0.539503, 0.407967, 0.278017, 0.155904,
      0.0442389, -0.0605631, -0.152923}, {0.0196474, 0.0375735, 0.0561861, 0.0745382,
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      0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
  LinearPositive_6 → {{1., 0.812702, 0.691452, 0.540319, 0.407464, 0.275268, 0.153852,
      0.0444982, -0.0610502, -0.151125}, {0.0186014, 0.0381755, 0.0550572, 0.074646,
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      0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
  LinearPositive_7 → {{1., 0.812932, 0.68944, 0.541059, 0.410632, 0.279722, 0.156421,
      0.0440386, -0.0617287, -0.154271}, {0.0186204, 0.0363314, 0.0569047, 0.0757329,
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      0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
  LinearPositive_8 → {{1., 0.811593, 0.690699, 0.541512, 0.410794, 0.279002, 0.153279,
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      0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}},
  LinearPositive_9 → {{1., 0.814527, 0.692284, 0.539635, 0.407699, 0.277329, 0.156518,
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      0.241691, 0.261072, 0.279055, 0.298507, 0.318632, 0.337602, 0.353993, 0.372608}},
  LinearPositive_10 → {{1., 0.812617, 0.690354, 0.540412, 0.408665, 0.278245, 0.15546,
      0.0437986, -0.0619469, -0.152171}, {0.0174864, 0.0370712, 0.0572236, 0.0748823,
      0.0926627, 0.111129, 0.130239, 0.148771, 0.168913, 0.186275, 0.206359, 0.223211,
      0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
  LinearPositive_11 → {{1., 0.804492, 0.685812, 0.542844, 0.417517, 0.287434, 0.157954,
      0.0358356, -0.0694331, -0.151321}, {0.013623, 0.0406398, 0.0607801, 0.0781742,
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  LinearPositive_12 → {{1., 0.812692, 0.699529, 0.549384, 0.416283, 0.279929, 0.163007,
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  LinearPositive_13 → {{1., 0.811422, 0.68853, 0.541446, 0.403324, 0.270859, 0.150227,
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      0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}}, LinearPositive_14 →
    {{1., 0.813574, 0.682615, 0.535016, 0.406904, 0.26943, 0.14607, 0.0454285, -0.0585137, -0.144055},
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  {0.0276601, 0.0348994, 0.0578995, 0.0764811, 0.0865063, 0.115217, 0.136395, 0.15157, 0.16455, 0.180615,
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LinearPositive_15 → {{1., 0.809318, 0.686477, 0.535556, 0.404368, 0.274978, 0.157388,
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   0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}}, LinearPositive_16 →
 {{1., 0.810881, 0.682948, 0.521149, 0.393493, 0.270986, 0.153462, 0.0425078, -0.0520434, -0.143292},
  {0.0164478, 0.0360481, 0.048135, 0.0712245, 0.101186, 0.114916, 0.129433, 0.153936, 0.164281, 0.192697,
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LinearPositive_17 → {{1., 0.806478, 0.69134, 0.537476, 0.410291, 0.278818, 0.158116,
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   0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
LinearPositive_18 → {{1., 0.808358, 0.691342, 0.539614, 0.409352, 0.280974, 0.150255,
   0.0423746, -0.0533218, -0.151273}, {0.0115844, 0.0455792, 0.0534286, 0.068487, 0.0918771,
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   0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}}, LinearPositive_19 →
 {{1., 0.81667, 0.69756, 0.549924, 0.42015, 0.288918, 0.160474, 0.039693, -0.0722049, -0.157988},
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LinearPositive_20 → {{1., 0.811999, 0.686267, 0.532886, 0.404237, 0.279336, 0.155285,
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   0.0958101, 0.109505, 0.135844, 0.152431, 0.165158, 0.182651, 0.210505, 0.231304,
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LinearNegative_1 → {{1., 0.816083, 0.69022, 0.532722, 0.391788, 0.275312, 0.170471, 0.0446087,
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LinearNegative_2 → {{1., 0.821326, 0.717404, 0.546117, 0.420827, 0.293304, 0.153503,
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LinearNegative_3 → {{1., 0.7994, 0.689563, 0.54124, 0.413475, 0.28062, 0.146429, 0.0329069,
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   -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
LinearNegative_4 → {{1., 0.810147, 0.673108, 0.506627, 0.392328, 0.257163, 0.143303,
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LinearNegative_5 → {{1., 0.824394, 0.693531, 0.533655, 0.410999, 0.263856, 0.139629,
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LinearNegative_6 → {{1., 0.798686, 0.686017, 0.542515, 0.404526, 0.253837, 0.145439,
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LinearNegative_7 → {{1., 0.794993, 0.672705, 0.521019, 0.397866, 0.258824, 0.137151,
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   -0.23516, -0.248536, -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923}},
LinearNegative_8 → {{1., 0.809117, 0.687749, 0.52855, 0.409176, 0.285162, 0.144781, 0.0442807,
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LinearNegative_9 → {{1., 0.822069, 0.699828, 0.550014, 0.43437, 0.295909, 0.177084, 0.052593,
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LinearNegative_10 → {{1., 0.793864, 0.690767, 0.539565, 0.408436, 0.282279, 0.155187,
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LinearNegative_11 → {{1., 0.808637, 0.681433, 0.538256, 0.411633, 0.281455, 0.159477,
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LinearNegative_12 → {{1., 0.81097, 0.694207, 0.546444, 0.416182, 0.277742, 0.152118,
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LinearNegative_13 → {{1., 0.805711, 0.688968, 0.545194, 0.415927, 0.275731, 0.160197,
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LinearNegative_14 → {{1., 0.813584, 0.690966, 0.53621, 0.402116, 0.265448, 0.150454,
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LinearNegative_15 → {{1., 0.80731, 0.678574, 0.536884, 0.408767, 0.281237, 0.169746,
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    -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
LinearNegative_16 → {{1., 0.816224, 0.694855, 0.53266, 0.392939, 0.271184, 0.156789,
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    -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}},
LinearNegative_17 → {{1., 0.808181, 0.680533, 0.535776, 0.40837, 0.273865, 0.154831,
    0.0431743, -0.0575939, -0.147855}, {-0.0130003, -0.0309644, -0.0613334, -0.0794837,
    -0.0865967, -0.117058, -0.128048, -0.153332, -0.167054, -0.192254, -0.208455, -0.223898,
    -0.240133, -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}},
LinearNegative_18 → {{1., 0.819864, 0.693802, 0.543666, 0.404933, 0.275224, 0.145932,
    0.0398621, -0.0573997, -0.157583}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
    -0.0895021, -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921,
    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
LinearNegative_19 → {{1., 0.80655, 0.684193, 0.531796, 0.408803, 0.289272, 0.161874,
    0.0485676, -0.0588794, -0.150081}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
    -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
    -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
LinearNegative_20 → {{1., 0.826495, 0.708181, 0.552333, 0.416142, 0.286253, 0.158391,
    0.0329808, -0.0709138, -0.160329}, {-0.024006, -0.0432239, -0.0496914, -0.0682004,
    -0.0867373, -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
    -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}},
Sinusoidal3_21 → {{1., 0.247123, -0.557445, -0.939795, -0.653303, 0.0229178, 0.617163,
    0.727312, 0.357869, -0.205849}, {0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461,
    0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096, 0.29637,
    0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
Sinusoidal3_22 → {{1., 0.25169, -0.557413, -0.944049, -0.656755, 0.0183542, 0.61891,
    0.732724, 0.361424, -0.20497}, {0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846,
    0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523, 0.303756,
    0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{1., 0.251844, -0.557571, -0.947176, -0.65663, 0.0177201, 0.617109,
    0.73334, 0.36597, -0.200787}, {0.18264, -0.0994704, -0.295137, -0.250857, 0.00157044,
    0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036, 0.298633,
    0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{1., 0.25092, -0.558801, -0.94624, -0.654133, 0.0216276, 0.621752, 0.731812,
    0.356685, -0.208697}, {0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361,
    0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939, 0.304721,
    0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
Sinusoidal3_25 → {{1., 0.248531, -0.559984, -0.948885, -0.651591, 0.0192409, 0.621271,
    0.733629, 0.360855, -0.207618}, {0.191347, -0.0982886, -0.29771, -0.261082, 0.00611569,
    0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799, 0.302028,
    0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
Sinusoidal3_26 → {{1., 0.250536, -0.560428, -0.945524, -0.654639, 0.0206229, 0.618008,
    0.729843, 0.360449, -0.204321}, {0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724,
    0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444, 0.296927,
    0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
Sinusoidal3_27 → {{1., 0.25091, -0.557951, -0.945799, -0.653107, 0.0190659, 0.616088,
    0.729145, 0.361895, -0.203958}, {0.185809, -0.10192, -0.303748, -0.261172, 0.000202029,
    0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227, 0.302676,
    0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
```

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```
    Sinusoidal3_28 → {{1., 0.250094, -0.554849, -0.945719, -0.657297, 0.0161014, 0.61427,
       0.731466, 0.368519, -0.19556}, {0.187562, -0.10053, -0.297144, -0.250552, 0.00476677,
       0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453, 0.301104,
       0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
    Sinusoidal3_29 → {{1., 0.24794, -0.557153, -0.947197, -0.653095, 0.0208478, 0.622396,
       0.732075, 0.361144, -0.208204}, {0.189755, -0.100643, -0.295957, -0.251445, -0.0055221,
       0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546, 0.296096,
       0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
    Sinusoidal3_30 → {{1., 0.250844, -0.557432, -0.945813, -0.655932, 0.0188606, 0.618245,
       0.729494, 0.359139, -0.206123}, {0.186539, -0.100579, -0.301622, -0.251977, 0.00452805,
       0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063, 0.296225,
       0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
  Lag3 → <|Sinusoidal1_1 → {{1., -1.62035, 0.360419, 1.21497, -1.21821, -0.141878, 1.2192,
       -0.78073, -0.461427, 1.00856}, {-0.20264, -0.107877, 0.278896, -0.289184, -0.0168796,
       0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701, -0.331998,
       0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
    Sinusoidal1_2 → {{1., -1.66532, 0.355438, 1.22652, -1.2175, -0.172353, 1.22186, -0.77432,
       -0.462836, 1.00478}, {-0.153886, -0.0875347, 0.297854, -0.276583, 0.004457,
       0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307, -0.288819,
       0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
    Sinusoidal1_3 → {{1., -1.64445, 0.326285, 1.20792, -1.19633, -0.166442, 1.18651, -0.75412,
       -0.488243, 1.0025}, {-0.187066, -0.0732084, 0.32812, -0.266161, 0.00567862,
       0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439, -0.297199,
       0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
    Sinusoidal1_4 → {{1., -1.64431, 0.377649, 1.22081, -1.23917, -0.150641, 1.23362, -0.812858,
       -0.479352, 1.02686}, {-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004,
       0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987, -0.322486,
       0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
    Sinusoidal1_5 → {{1., -1.63326, 0.350694, 1.19562, -1.24989, -0.119703, 1.19466, -0.824007,
       -0.44053, 1.03035}, {-0.20104, -0.101657, 0.31364, -0.234517, -0.0163677,
       0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444, -0.303865,
       0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
    Sinusoidal1_6 → {{1., -1.61745, 0.362188, 1.18112, -1.19845, -0.108432, 1.16148, -0.801294,
       -0.406369, 1.00513}, {-0.17526, -0.106684, 0.304186, -0.27676, -0.0299081,
       0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573, -0.282169,
       0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
    Sinusoidal1_7 → {{1., -1.62603, 0.364189, 1.15957, -1.20495, -0.116659, 1.18331, -0.778645,
       -0.412438, 0.991653}, {-0.179672, -0.126709, 0.328842, -0.280026, -0.0129078,
       0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949, -0.27099,
       0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
    Sinusoidal1_8 → {{1., -1.63516, 0.349888, 1.18931, -1.23013, -0.107577, 1.16798, -0.826875,
       -0.408475, 1.00889}, {-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322,
       0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394, -0.280218,
       0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
    Sinusoidal1_9 → {{1., -1.63545, 0.3389, 1.19087, -1.23845, -0.122747, 1.21239, -0.803972,
       -0.441409, 1.00971}, {-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817,
       0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813, -0.323289,
       0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
    Sinusoidal1_10 → {{1., -1.62154, 0.318378, 1.205, -1.20671, -0.172296, 1.21745, -0.763933,
       -0.495003, 1.01357}, {-0.203834, -0.0722574, 0.294696, -0.254799, 0.00423677,
       0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167, -0.291561,
       0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}},
    Sinusoidal2_11 → {{1., -1.17252, -0.601542, 1.19408, 0.25188, -1.13858, 0.0704528, 0.976677,
       -0.291154, -0.781135}, {-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852,
       0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865, 0.258725,
       0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
    Sinusoidal2_12 → {{1., -1.16785, -0.598321, 1.19453, 0.248915, -1.13786, 0.0682078, 0.978793,
       -0.291032, -0.776961}, {-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067,
       0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668, 0.262301,
       0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
    Sinusoidal2_13 → {{1., -1.17536, -0.59477, 1.20107, 0.24206, -1.14339, 0.0770172, 0.974134,
       -0.300202, -0.775021}, {-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667,
       0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963, 0.254435,
       0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
    Sinusoidal2_14 → {{1., -1.1688, -0.593543, 1.19507, 0.242189, -1.14297, 0.0748801, 0.976008,
       -0.300757, -0.77767}, {-0.0971308, -0.259618, 0.249762, 0.0996953, -0.311793,
```

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    0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698, 0.256122,
    0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
 Sinusoidal2_15 → {{1., -1.17333, -0.597548, 1.19893, 0.246055, -1.14361, 0.077823, 0.976081,
    -0.300583, -0.777469}, {-0.0939856, -0.25429, 0.25073, 0.100441, -0.313599,
    0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627, 0.255722,
    0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
 Sinusoidal2_16 → {{1., -1.17552, -0.594542, 1.19905, 0.240051, -1.13983, 0.0800883, 0.973032,
    -0.306018, -0.774319}, {-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132,
    0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968, 0.256443,
    0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
 Sinusoidal2_17 → {{1., -1.16939, -0.601413, 1.1928, 0.254696, -1.14293, 0.0645867, 0.979436,
    -0.29009, -0.783073}, {-0.0991608, -0.252958, 0.255513, 0.0985052, -0.309591,
    0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
 Sinusoidal2_18 → {{1., -1.16579, -0.598353, 1.19062, 0.252474, -1.13536, 0.0710946, 0.973451,
    -0.292364, -0.776772}, {-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724,
    0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
 Sinusoidal2_19 → {{1., -1.17252, -0.600788, 1.19475, 0.249722, -1.13835, 0.070574, 0.977201,
    -0.28997, -0.779946}, {-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977,
    0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469, 0.251806,
    0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
 Sinusoidal2_20 → {{1., -1.17271, -0.596923, 1.19503, 0.249005, -1.13678, 0.0667731, 0.972508,
    -0.289316, -0.780821}, {-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484,
    0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815,
    0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>|>
```

```
In[6]:= Query[Keys]@classificationAutocorrelation1
Out[6]= {SpikeMax, SpikeMin, Lag1, Lag3}

In[7]:= Query[All, Length]@classificationAutocorrelation1
Out[7]= <|SpikeMax → 20, SpikeMin → 20, Lag1 → 50, Lag3 → 20|>
```

We can limit the possible set of cutoff lists to exclude higher autocorrelations, by truncating the AutocorrelationCutoffs list to be the same length as the lag cutoffs required. For example if we want only lag 1 and lag 2 classes as a possibility, we provide a list of length 2 for AutocorrelationCutoffs:

```
In[8]:= classificationAutocorrelation2 = TimeSeriesClassification[classificationExample1,
          timePointsExample, AutocorrelationCutoffs → bootstrapQ95Autocorrelation[[1 ;; 2]],
          SpikeCutoffs → bootstrapQ95Spikes, Method → "Autocorrelation"]

          Method → "Autocorrelation"

Out[8]= <|SpikeMax →
          <|SpikePositive_1 → {{1., -0.452395, 0.219937, -0.141456, -0.040982, 0.0671421, -0.0204863, -0.0225783,
              0.00336149, 0.0248339}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
              0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
              -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
           SpikePositive_2 → {{1., -0.33332, 0.178978, -0.043203, 0.0330959, 0.0187841, 0.0643953,
              -0.167683, -0.0783794, -0.134626}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
              0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
              -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
           SpikePositive_3 → {{1., -0.150943, 0.25591, -0.077747, 0.03904, -0.112386, -0.130446,
              -0.111423, -0.0923815, 0.0100807}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
              -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
              0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
           SpikePositive_4 → {{1., -0.329658, 0.231525, 0.0162836, 0.164488, -0.166715, 0.0989705,
              -0.163788, -0.0754534, 0.0143191}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
              -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
              0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
```

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```
    SpikePositive_5 → {{1., -0.354501, 0.199318, -0.099174, 0.199, -0.0363005, 0.158313,
       -0.0231566, 0.0362299, -0.135361}, {0.966833, -0.0172757, -0.0101601, 0.0449156,
       0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
       -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
    SpikePositive_6 → {{1., -0.466257, 0.137607, -0.192065, -0.0315355, -0.0729004, -0.0550543,
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       0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
    SpikePositive_7 → {{1., -0.389552, 0.144053, -0.0395178, 0.0603777, -0.112134, -0.0357364,
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       0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
    SpikePositive_8 → {{1., -0.394532, 0.210425, -0.0366925, 0.0213409, -0.067476, 0.000171715,
       -0.0864154, -0.128194, 0.0081353}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
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       -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
    SpikePositive_9 → {{1., -0.400547, 0.143122, -0.118456, -0.00900312, 0.125105, 0.0177367,
       -0.061955, -0.00116964, -0.150973}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
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       -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
    SpikePositive_10 → {{1., -0.486387, 0.214384, -0.107572, 0.107945, 0.0130167, 0.0145573,
       0.0233586, -0.0802024, -0.127062}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
       0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
       -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
    SpikePositive_11 → {{1., -0.338874, 0.300856, -0.187073, -0.0720043, -0.0204714, -0.0156668,
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       -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
    SpikePositive_12 → {{1., -0.490403, 0.230471, -0.02836, 0.158686, -0.26022, 0.158602,
       -0.177464, 0.0371373, -0.0785755}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
       0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
       0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
    SpikePositive_13 → {{1., -0.380553, -0.0954718, -0.150478, -0.0658297, 0.106079, -0.0357483,
       -0.0423526, 0.134218, -0.0648447}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
       -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
       0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
    SpikePositive_14 → {{1., -0.526563, 0.402071, -0.0816825, 0.0766719, -0.117882, 0.0465972,
       -0.195255, 0.0724303, -0.107586}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
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       -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
    SpikePositive_15 → {{1., -0.498776, 0.12023, -0.0909257, 0.179612, -0.241152, 0.0697987,
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    SpikePositive_16 → {{1., -0.252346, -0.0181276, -0.202654, 0.0588694, -0.165692, 0.058152,
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       -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
    SpikePositive_17 → {{1., -0.868718, 0.44914, -0.120491, -0.0616033, -0.0228913, 0.14139,
       -0.0932499, -0.0473214, 0.036701}, {0.0894556, -0.0939456, 0.955206, -0.0721055,
       0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
       -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
    SpikePositive_18 → {{1., -0.362902, -0.122098, -0.129486, 0.0562719, -0.0830183, 0.122331,
       -0.122383, -0.180395, -0.0773557}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
       -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
       0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
    SpikePositive_19 → {{1., -0.42077, 0.0763867, -0.227391, 0.0475263, 0.0245878, -0.0251915,
       -0.0584293, -0.118635, 0.0240546}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
       -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
       0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
    SpikePositive_20 → {{1., -0.507801, 0.163243, -0.238989, -0.0407895, 0.101176, -0.0803686,
       0.0171814, 0.00408016, -0.268402}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
       -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
       0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
  SpikeMin → <|SpikeNegative_1 → {{1., -0.423906, 0.0870199, -0.0546103, 0.153795, 0.0753404,
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    -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
SpikeNegative_2 → {{1., -0.254883, 0.246154, -0.281797, 0.168139, -0.0510077, 0.0696523,
    0.044741, -0.0493091, -0.173802}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
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    -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
SpikeNegative_3 → {{1., -0.52844, 0.0128591, 0.0401754, 0.156405, -0.25313, 0.0143667,
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    -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
SpikeNegative_4 → {{1., -0.261291, 0.197729, -0.0669671, -0.0489197, 0.019136, -0.0777287,
    -0.0858975, 0.0311934, -0.0488232}, {-0.978499, -0.0375369, -0.0308657, -0.0197828,
    0.087556, -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659,
    -0.0303762, 0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
SpikeNegative_5 → {{1., -0.275359, 0.08563, -0.0927664, 0.179004, -0.137792, 0.112485,
    -0.0158152, -0.046442, -0.180954}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
    0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
SpikeNegative_6 → {{1., -0.398833, 0.0778628, -0.044104, 0.0333735, 0.0658697, -0.0029231,
    -0.0938463, -0.0655049, -0.0116685}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
    -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
SpikeNegative_7 → {{1., -0.42086, -0.00214872, 0.0208358, 0.127917, -0.202863, 0.0631005,
    -0.00894861, 0.0102268, 0.000991105}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
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    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
SpikeNegative_8 → {{1., -0.167986, 0.132625, -0.161643, 0.0190856, 0.0689723, -0.0356912,
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    0.06932, -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
SpikeNegative_9 → {{1., -0.280681, 0.131522, -0.27773, 0.125519, -0.158639, 0.0827061,
    -0.0794961, -0.159761, -0.0325458}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
SpikeNegative_10 → {{1., -0.351869, 0.262355, -0.0376404, 0.155982, -0.124093, 0.105999,
    -0.0645218, 0.0405128, 0.0335434}, {-0.972673, -0.00291876, -0.0540171, -0.0812638,
    -0.0617025, 0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018,
    -0.0213425, -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
SpikeNegative_11 → {{1., -0.413539, 0.0679203, 0.00410847, 0.0261914, -0.0181218, 0.0852791,
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    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
SpikeNegative_12 → {{1., -0.395846, 0.0894882, -0.237998, -0.0446471, -0.0524744, 0.0771359,
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    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
SpikeNegative_13 → {{1., -0.343983, 0.00454468, -0.205612, 0.0119525, -0.102592, 0.103107,
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    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
SpikeNegative_14 → {{1., -0.332802, 0.244793, -0.20513, 0.0810854, -0.132165, -0.0116365,
    -0.109746, -0.0688768, -0.10264}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594,
    0.0528555, 0.00336549, 0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
SpikeNegative_15 → {{1., -0.409677, 0.104665, -0.110113, 0.152765, -0.103758, -0.130233,
    -0.0168568, 0.0773673, -0.0765506}, {-0.00121514, -0.0078406, -0.978821, -0.0221297,
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    0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
SpikeNegative_16 → {{1., -0.458875, 0.142195, -0.117197, -0.0328704, -0.0724729, 0.062644,
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    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
SpikeNegative_17 → {{1., -0.28948, 0.0899977, -0.14795, 0.137414, -0.00541154, 0.0773486,
    0.045355, -0.117622, -0.0110899}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
    0.0616787, -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667,
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    SpikeNegative_18 → {{1., -0.219411, 0.0906106, -0.0586132, 0.117458, -0.0973521, -0.064392,
       -0.0844588, 0.106035, -0.112353}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
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       0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
    SpikeNegative_19 → {{1., -0.25374, 0.0112197, -0.122395, -0.0226519, -0.0591994, -0.111793,
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       -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
    SpikeNegative_20 → {{1., -0.223368, 0.0633665, -0.177509, 0.103343, 0.0332846, -0.0776252,
       -0.201757, -0.0689057, -0.1005}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
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  Lag1 → <|LinearPositive_1 → {{1., 0.812153, 0.688835, 0.540544, 0.408977, 0.277736,
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    LinearPositive_2 → {{1., 0.812426, 0.690113, 0.540471, 0.410253, 0.280388, 0.156519,
       0.0439961, -0.0614494, -0.153365}, {0.0183904, 0.0374466, 0.0550304, 0.0738563,
       0.0928923, 0.110677, 0.130133, 0.148914, 0.167272, 0.186766, 0.206807, 0.224025, 0.242161,
       0.261728, 0.280689, 0.29779, 0.316418, 0.335012, 0.355339, 0.375155}}, LinearPositive_3 →
     {{1., 0.815438, 0.691427, 0.540957, 0.409589, 0.278307, 0.155771, 0.0411641, -0.0628612, -0.153798},
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    LinearPositive_4 → {{1., 0.811366, 0.688737, 0.538759, 0.409453, 0.280276, 0.156679,
       0.0447032, -0.061104, -0.152171}, {0.0188591, 0.0384796, 0.0552706, 0.0761382,
       0.0941127, 0.11255, 0.131257, 0.150426, 0.166514, 0.185049, 0.206061, 0.222052,
       0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}},
    LinearPositive_5 → {{1., 0.813098, 0.689554, 0.539503, 0.407967, 0.278017, 0.155904,
       0.0442389, -0.0605631, -0.152923}, {0.0196474, 0.0375735, 0.0561861, 0.0745382,
       0.094777, 0.113054, 0.132423, 0.150372, 0.169563, 0.188068, 0.205612, 0.225889,
       0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
    LinearPositive_6 → {{1., 0.812702, 0.691452, 0.540319, 0.407464, 0.275268, 0.153852,
       0.0444982, -0.0610502, -0.151125}, {0.0186014, 0.0381755, 0.0550572, 0.074646,
       0.0932816, 0.113886, 0.132134, 0.149767, 0.168659, 0.185415, 0.205262, 0.222624,
       0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
    LinearPositive_7 → {{1., 0.812932, 0.68944, 0.541059, 0.410632, 0.279722, 0.156421,
       0.0440386, -0.0617287, -0.154271}, {0.0186204, 0.0363314, 0.0569047, 0.0757329,
       0.092018, 0.111558, 0.130244, 0.148133, 0.167451, 0.186409, 0.204805, 0.22423,
       0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
    LinearPositive_8 → {{1., 0.811593, 0.690699, 0.541512, 0.410794, 0.279002, 0.153279,
       0.0423887, -0.0616868, -0.152772}, {0.0170019, 0.0382694, 0.0569482, 0.0754625,
       0.0914347, 0.110031, 0.132014, 0.15073, 0.169121, 0.188274, 0.205265, 0.223358,
       0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}},
    LinearPositive_9 → {{1., 0.814527, 0.692284, 0.539635, 0.407699, 0.277329, 0.156518,
       0.0441157, -0.0614669, -0.153495}, {0.0185501, 0.0388643, 0.0547098, 0.0747468,
       0.0938687, 0.113558, 0.129413, 0.148929, 0.168743, 0.186495, 0.204247, 0.225298,
       0.241691, 0.261072, 0.279055, 0.298507, 0.318632, 0.337602, 0.353993, 0.372608}},
    LinearPositive_10 → {{1., 0.812617, 0.690354, 0.540412, 0.408665, 0.278245, 0.15546,
       0.0437986, -0.0619469, -0.152171}, {0.0174864, 0.0370712, 0.0572236, 0.0748823,
       0.0926627, 0.111129, 0.130239, 0.148771, 0.168913, 0.186275, 0.206359, 0.223211,
       0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
    LinearPositive_11 → {{1., 0.804492, 0.685812, 0.542844, 0.417517, 0.287434, 0.157954,
       0.0358356, -0.0694331, -0.151321}, {0.013623, 0.0406398, 0.0607801, 0.0781742,
       0.0921015, 0.112119, 0.128868, 0.151429, 0.171509, 0.192449, 0.211181, 0.216208,
       0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, 0.373621}},
    LinearPositive_12 → {{1., 0.812692, 0.699529, 0.549384, 0.416283, 0.279929, 0.163007,
       0.0403969, -0.0666296, -0.155679}, {0.0219335, 0.0431422, 0.0502095, 0.0696589,
       0.0884956, 0.116468, 0.123447, 0.151797, 0.168869, 0.179094, 0.204522, 0.228042,
       0.240546, 0.269187, 0.279387, 0.302162, 0.315899, 0.330232, 0.349931, 0.381055}},
    LinearPositive_13 → {{1., 0.811422, 0.68853, 0.541446, 0.403324, 0.270859, 0.150227,
       0.0393064, -0.0633769, -0.14861}, {0.022617, 0.0284408, 0.0607512, 0.0795972, 0.0880775,
       0.119613, 0.134238, 0.152698, 0.169261, 0.181713, 0.197855, 0.217149, 0.241086, 0.263228,
       0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}}, LinearPositive_14 →
     {{1., 0.813574, 0.682615, 0.535016, 0.406904, 0.26943, 0.14607, 0.0454285, -0.0585137, -0.144055},
      {0.0276601, 0.0348994, 0.0578995, 0.0764811, 0.0865063, 0.115217, 0.136395, 0.15157, 0.16455, 0.180615,
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LinearPositive_15 → {{1., 0.809318, 0.686477, 0.535556, 0.404368, 0.274978, 0.157388,
    0.054953, -0.0565598, -0.149852}, {0.0152129, 0.0390101, 0.0602871, 0.0702062, 0.091338,
    0.118718, 0.136185, 0.146481, 0.161128, 0.179922, 0.215359, 0.218444, 0.250473, 0.25777,
    0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}}, LinearPositive_16 →
 {{1., 0.810881, 0.682948, 0.521149, 0.393493, 0.270986, 0.153462, 0.0425078, -0.0520434, -0.143292},
  {0.0164478, 0.0360481, 0.048135, 0.0712245, 0.101186, 0.114916, 0.129433, 0.153936, 0.164281, 0.192697,
    0.203977, 0.223277, 0.236402, 0.257694, 0.277977, 0.296096, 0.311924, 0.344353, 0.357433, 0.375096}},
LinearPositive_17 → {{1., 0.806478, 0.69134, 0.537476, 0.410291, 0.278818, 0.158116,
    0.0430172, -0.0619995, -0.156113}, {0.0153802, 0.0408047, 0.0548321, 0.0765604,
    0.0991872, 0.117741, 0.128177, 0.147496, 0.159869, 0.189666, 0.195939, 0.215447,
    0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
LinearPositive_18 → {{1., 0.808358, 0.691342, 0.539614, 0.409352, 0.280974, 0.150255,
    0.0423746, -0.0533218, -0.151273}, {0.0115844, 0.0455792, 0.0534286, 0.068487, 0.0918771,
    0.107837, 0.137609, 0.144956, 0.162508, 0.185864, 0.206224, 0.229689, 0.232407, 0.261637,
    0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}}, LinearPositive_19 →
 {{1., 0.81667, 0.69756, 0.549924, 0.42015, 0.288918, 0.160474, 0.039693, -0.0722049, -0.157988},
  {0.0205961, 0.045526, 0.0569898, 0.0724948, 0.0867427, 0.105806, 0.12769, 0.145665, 0.170669, 0.180276,
    0.216792, 0.223063, 0.241101, 0.270774, 0.282283, 0.293887, 0.315058, 0.334039, 0.359611, 0.369743}},
LinearPositive_20 → {{1., 0.811999, 0.686267, 0.532886, 0.404237, 0.279336, 0.155285,
    0.0427134, -0.0540973, -0.146741}, {0.00952752, 0.0286979, 0.0547226, 0.0709501,
    0.0958101, 0.109505, 0.135844, 0.152431, 0.165158, 0.182651, 0.210505, 0.231304,
    0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
LinearNegative_1 → {{1., 0.816083, 0.69022, 0.532722, 0.391788, 0.275312, 0.170471, 0.0446087,
    -0.0611309, -0.147816}, {-0.0218046, -0.0446169, -0.0612231, -0.0738948, -0.109733,
    -0.115191, -0.124469, -0.148293, -0.159758, -0.176361, -0.217843, -0.224298, -0.23172,
    -0.273794, -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733}},
LinearNegative_2 → {{1., 0.821326, 0.717404, 0.546117, 0.420827, 0.293304, 0.153503,
    0.0344508, -0.0759091, -0.162306}, {-0.0137543, -0.0552134, -0.0387902, -0.0787876,
    -0.0972777, -0.0993326, -0.131634, -0.158204, -0.178021, -0.176063, -0.209858, -0.230763,
    -0.248781, -0.268592, -0.290148, -0.294015, -0.319548, -0.339092, -0.343638, -0.357122}},
LinearNegative_3 → {{1., 0.7994, 0.689563, 0.54124, 0.413475, 0.28062, 0.146429, 0.0329069,
    -0.0628257, -0.140667}, {-0.0283384, -0.0528281, -0.0527884, -0.0740599, -0.0921776,
    -0.0948819, -0.146225, -0.165182, -0.160057, -0.18686, -0.220224, -0.211812, -0.237918,
    -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
LinearNegative_4 → {{1., 0.810147, 0.673108, 0.506627, 0.392328, 0.257163, 0.143303,
    0.0398545, -0.0536507, -0.139413}, {-0.0158873, -0.0248133, -0.0382326, -0.0881019,
    -0.0887054, -0.128386, -0.128859, -0.161147, -0.159022, -0.205319, -0.200777, -0.210411,
    -0.243003, -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844}},
LinearNegative_5 → {{1., 0.824394, 0.693531, 0.533655, 0.410999, 0.263856, 0.139629,
    0.0341737, -0.0617561, -0.143612}, {-0.0201624, -0.0405386, -0.0436406, -0.0738225,
    -0.0817467, -0.105404, -0.114359, -0.154377, -0.169473, -0.174198, -0.212011, -0.225376,
    -0.230144, -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}},
LinearNegative_6 → {{1., 0.798686, 0.686017, 0.542515, 0.404526, 0.253837, 0.145439,
    0.0446877, -0.0469226, -0.140381}, {-0.0267223, -0.0446999, -0.0523138, -0.0699606,
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    -0.243037, -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481}},
LinearNegative_7 → {{1., 0.794993, 0.672705, 0.521019, 0.397866, 0.258824, 0.137151,
    0.0450355, -0.0533671, -0.127923}, {-0.00172329, -0.032268, -0.068173, -0.0857129,
    -0.0881686, -0.107137, -0.140409, -0.14992, -0.182962, -0.175511, -0.200764, -0.226349,
    -0.23516, -0.248536, -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923}},
LinearNegative_8 → {{1., 0.809117, 0.687749, 0.52855, 0.409176, 0.285162, 0.144781, 0.0442807,
    -0.062147, -0.15603}, {-0.0170306, -0.0378539, -0.0394845, -0.0767312, -0.0942537,
    -0.105065, -0.146528, -0.134698, -0.186411, -0.174071, -0.194782, -0.232787, -0.238911,
    -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
LinearNegative_9 → {{1., 0.822069, 0.699828, 0.550014, 0.43437, 0.295909, 0.177084, 0.052593,
    -0.079476, -0.184474}, {-0.0287969, -0.0189698, -0.0530075, -0.0828922, -0.0936032,
    -0.115414, -0.114422, -0.130851, -0.167598, -0.173937, -0.198609, -0.23569, -0.258977,
    -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
LinearNegative_10 → {{1., 0.793864, 0.690767, 0.539565, 0.408436, 0.282279, 0.155187,
    0.0459489, -0.0651142, -0.167602}, {-0.00155633, -0.0271325, -0.0625737, -0.0744387,
    -0.0901925, -0.0932579, -0.138846, -0.15092, -0.157289, -0.198281, -0.189392, -0.206968,
    -0.259028, -0.273261, -0.270544, -0.29133, -0.328913, -0.352948, -0.335503, -0.37816}},
LinearNegative_11 → {{1., 0.808637, 0.681433, 0.538256, 0.411633, 0.281455, 0.159477,
    0.0340981, -0.069137, -0.147822}, {-0.0105542, -0.0364589, -0.0515525, -0.0708746,
    -0.0862196, -0.118392, -0.123851, -0.151596, -0.176372, -0.191037, -0.213033, -0.221631,
    -0.235518, -0.271564, -0.288178, -0.293001, -0.310129, -0.328328, -0.364455, -0.366174}},
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LinearNegative_12 → {{1., 0.81097, 0.694207, 0.546444, 0.416182, 0.277742, 0.152118,
   0.0468388, -0.0635984, -0.155436}, {-0.0105234, -0.0459122, -0.0631169, -0.0780043,
   -0.0883748, -0.108962, -0.137461, -0.144887, -0.163604, -0.184293, -0.210166, -0.217602,
   -0.245066, -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
LinearNegative_13 → {{1., 0.805711, 0.688968, 0.545194, 0.415927, 0.275731, 0.160197,
   0.0399382, -0.0660995, -0.150625}, {-0.01186, -0.0431645, -0.0590873, -0.0756374,
   -0.0887624, -0.1144, -0.121973, -0.156462, -0.165726, -0.190329, -0.20958, -0.216046,
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LinearNegative_14 → {{1., 0.813584, 0.690966, 0.53621, 0.402116, 0.265448, 0.150454,
   0.0360438, -0.0604747, -0.145439}, {-0.0187992, -0.0431131, -0.0473458, -0.070655,
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   -0.23237, -0.26046, -0.276864, -0.301954, -0.319987, -0.336453, -0.361973, -0.377956}},
LinearNegative_15 → {{1., 0.80731, 0.678574, 0.536884, 0.408767, 0.281237, 0.169746,
   0.0496114, -0.0649204, -0.157199}, {-0.0162872, -0.0293132, -0.0552218, -0.0807767,
   -0.0935334, -0.121112, -0.124004, -0.147926, -0.165828, -0.191582, -0.205406, -0.219926,
   -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
LinearNegative_16 → {{1., 0.816224, 0.694855, 0.53266, 0.392939, 0.271184, 0.156789,
   0.0435767, -0.0608658, -0.149563}, {-0.0225164, -0.0461677, -0.0473716, -0.067817,
   -0.0986701, -0.119505, -0.130459, -0.1556, -0.169469, -0.1814, -0.198572, -0.221935,
   -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}},
LinearNegative_17 → {{1., 0.808181, 0.680533, 0.535776, 0.40837, 0.273865, 0.154831,
   0.0431743, -0.0575939, -0.147855}, {-0.0130003, -0.0309644, -0.0613334, -0.0794837,
   -0.0865967, -0.117058, -0.128048, -0.153332, -0.167054, -0.192254, -0.208455, -0.223898,
   -0.240133, -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}},
LinearNegative_18 → {{1., 0.819864, 0.693802, 0.543666, 0.404933, 0.275224, 0.145932,
   0.0398621, -0.0573997, -0.157583}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
   -0.0895021, -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921,
   -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
LinearNegative_19 → {{1., 0.80655, 0.684193, 0.531796, 0.408803, 0.289272, 0.161874,
   0.0485676, -0.0588794, -0.150081}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
   -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
   -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
LinearNegative_20 → {{1., 0.826495, 0.708181, 0.552333, 0.416142, 0.286253, 0.158391,
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   -0.0867373, -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
   -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}},
Sinusoidal3_21 → {{1., 0.247123, -0.557445, -0.939795, -0.653303, 0.0229178, 0.617163,
   0.727312, 0.357869, -0.205849}, {0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461,
   0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096, 0.29637,
   0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
Sinusoidal3_22 → {{1., 0.25169, -0.557413, -0.944049, -0.656755, 0.0183542, 0.61891,
   0.732724, 0.361424, -0.20497}, {0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846,
   0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523, 0.303756,
   0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{1., 0.251844, -0.557571, -0.947176, -0.65663, 0.0177201, 0.617109,
   0.73334, 0.36597, -0.200787}, {0.18264, -0.0994704, -0.295137, -0.250857, 0.00157044,
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   0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{1., 0.25092, -0.558801, -0.94624, -0.654133, 0.0216276, 0.621752, 0.731812,
   0.356685, -0.208697}, {0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361,
   0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939, 0.304721,
   0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
Sinusoidal3_25 → {{1., 0.248531, -0.559984, -0.948885, -0.651591, 0.0192409, 0.621271,
   0.733629, 0.360855, -0.207618}, {0.191347, -0.0982886, -0.29771, -0.261082, 0.00611569,
   0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799, 0.302028,
   0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
Sinusoidal3_26 → {{1., 0.250536, -0.560428, -0.945524, -0.654639, 0.0206229, 0.618008,
   0.729843, 0.360449, -0.204321}, {0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724,
   0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444, 0.296927,
   0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
Sinusoidal3_27 → {{1., 0.25091, -0.557951, -0.945799, -0.653107, 0.0190659, 0.616088,
   0.729145, 0.361895, -0.203958}, {0.185809, -0.10192, -0.303748, -0.261172, 0.000202029,
   0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227, 0.302676,
   0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
Sinusoidal3_28 → {{1., 0.250094, -0.554849, -0.945719, -0.657297, 0.0161014, 0.61427,
   0.731466, 0.368519, -0.19556}, {0.187562, -0.10053, -0.297144, -0.250552, 0.00476677,
```

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```
    0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453, 0.301104,
    0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
Sinusoidal3_29 → {{1., 0.24794, -0.557153, -0.947197, -0.653095, 0.0208478, 0.622396,
    0.732075, 0.361144, -0.208204}, {0.189755, -0.100643, -0.295957, -0.251445, -0.0055221,
    0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546, 0.296096,
    0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
Sinusoidal3_30 → {{1., 0.250844, -0.557432, -0.945813, -0.655932, 0.0188606, 0.618245,
    0.729494, 0.359139, -0.206123}, {0.186539, -0.100579, -0.301622, -0.251977, 0.00452805,
    0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063, 0.296225,
    0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>|>
```

This means Lag3 is not reported in this case, as it was excluded as a possible class:

```
In[9]:= Query[All, Length]@classificationAutocorrelation2
Out[9]= <|SpikeMax → 20, SpikeMin → 20, Lag1 → 50|>
```

AutocorrelationLogic (1)

```
In[1]:= Needs["MathIOmica`"]
```

AutocorrelationLogic is an option used for any Method that employs classification into autocorrelation classes, i.e. "Autocorrelation" and "InterpolatedAutocorrelation" method. The default value for AutocorrelationLogic is False, which returns the classification. If set to True, for each signal a logical list is returned that has checked the signal's autocorrelation list to see if each of this is higher (True) or lower (False) compared against all autocorrelation cutoffs (i.e. from the AutocorrelationCutoffs option value).

We consider the example data:

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
 backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
 timePointsExample = Range[20];
```

We can evaluate the appropriate cutoffs to be used with this method using QuantileEstimation for autocorrelations and spikes:

```
In[3]:= bootstrapQ95Autocorrelation =
  QuantileEstimator[backgroundExample, timePointsExample , Method → "Autocorrelation"]
Out[3]= {0.104569, 0.750865, 0.330876, 0.582844, 0.384145, 0.476242, 0.361702, 0.407732, 0.30536}

In[4]:= bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

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Let's perform the classification returning unique autocorrelations:

In[5]:=
```
classificationAutocorrelation1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, AutocorrelationCutoffs → bootstrapQ95Autocorrelation,
  SpikeCutoffs → bootstrapQ95Spikes, Method → "Autocorrelation"]
```

```
Method → "Autocorrelation"
```

Out[5]=
```
<| SpikeMax →
  <| SpikePositive_1 → {{1., -0.452395, 0.219937, -0.141456, -0.040982, 0.0671421, -0.0204863, -0.0225783,
      0.00336149, 0.0248339}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
      0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{1., -0.33332, 0.178978, -0.043203, 0.0330959, 0.0187841, 0.0643953,
      -0.167683, -0.0783794, -0.134626}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{1., -0.150943, 0.25591, -0.077747, 0.03904, -0.112386, -0.130446,
      -0.111423, -0.0923815, 0.0100807}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{1., -0.329658, 0.231525, 0.0162836, 0.164488, -0.166715, 0.0989705,
      -0.163788, -0.0754534, 0.0143191}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{1., -0.354501, 0.199318, -0.099174, 0.199, -0.0363005, 0.158313,
      -0.0231566, 0.0362299, -0.135361}, {0.966833, -0.0172757, -0.0101601, 0.0449156,
      0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
      -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{1., -0.466257, 0.137607, -0.192065, -0.0315355, -0.0729004, -0.0550543,
      -0.104833, 0.0601693, -0.0827568}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{1., -0.389552, 0.144053, -0.0395178, 0.0603777, -0.112134, -0.0357364,
      -0.00620881, -0.073946, -0.0864452}, {0.973634, -0.0197451, 0.00381691, 0.0632199,
      0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
      0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{1., -0.394532, 0.210425, -0.0366925, 0.0213409, -0.067476, 0.000171715,
      -0.0864154, -0.128194, 0.0081353}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{1., -0.400547, 0.143122, -0.118456, -0.00900312, 0.125105, 0.0177367,
      -0.061955, -0.00116964, -0.150973}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
      0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{1., -0.486387, 0.214384, -0.107572, 0.107945, 0.0130167, 0.0145573,
      0.0233586, -0.0802024, -0.127062}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
      0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
      -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{1., -0.338874, 0.300856, -0.187073, -0.0720043, -0.0204714, -0.0156668,
      0.0397913, -0.0000121023, -0.147044}, {0.0696283, 0.0251021, 0.968196, 0.0511374,
      0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
      -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{1., -0.490403, 0.230471, -0.02836, 0.158686, -0.26022, 0.158602,
      -0.177464, 0.0371373, -0.0785755}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
   SpikePositive_13 → {{1., -0.380553, -0.0954718, -0.150478, -0.0658297, 0.106079, -0.0357483,
      -0.0423526, 0.134218, -0.0648447}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
      -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
      0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
   SpikePositive_14 → {{1., -0.526563, 0.402071, -0.0816825, 0.0766719, -0.117882, 0.0465972,
      -0.195255, 0.0724303, -0.107586}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
      0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
      -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
```

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```
    SpikePositive_15 → {{1., -0.498776, 0.12023, -0.0909257, 0.179612, -0.241152, 0.0697987,
       0.00693521, 0.0904771, -0.0399131}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
       0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
       -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
    SpikePositive_16 → {{1., -0.252346, -0.0181276, -0.202654, 0.0588694, -0.165692, 0.058152,
       -0.0733224, 0.0688338, 0.00969476}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
       -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
       -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
    SpikePositive_17 → {{1., -0.868718, 0.44914, -0.120491, -0.0616033, -0.0228913, 0.14139,
       -0.0932499, -0.0473214, 0.036701}, {0.0894556, -0.0939456, 0.955206, -0.0721055,
       0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
       -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
    SpikePositive_18 → {{1., -0.362902, -0.122098, -0.129486, 0.0562719, -0.0830183, 0.122331,
       -0.122383, -0.180395, -0.0773557}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
       -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
       0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
    SpikePositive_19 → {{1., -0.42077, 0.0763867, -0.227391, 0.0475263, 0.0245878, -0.0251915,
       -0.0584293, -0.118635, 0.0240546}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
       -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
       0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
    SpikePositive_20 → {{1., -0.507801, 0.163243, -0.238989, -0.0407895, 0.101176, -0.0803686,
       0.0171814, 0.00408016, -0.268402}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
       -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
       0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
  SpikeMin → <|SpikeNegative_1 → {{1., -0.423906, 0.0870199, -0.0546103, 0.153795, 0.0753404,
       -0.11792, -0.102237, 0.144444, -0.0974828}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
       -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
       -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
    SpikeNegative_2 → {{1., -0.254883, 0.246154, -0.281797, 0.168139, -0.0510077, 0.0696523,
       0.044741, -0.0493091, -0.173802}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
       -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
       -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
    SpikeNegative_3 → {{1., -0.52844, 0.0128591, 0.0401754, 0.156405, -0.25313, 0.0143667,
       -0.105044, 0.0118936, -0.135968}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
       0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
       -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
    SpikeNegative_4 → {{1., -0.261291, 0.197729, -0.0669671, -0.0489197, 0.019136, -0.0777287,
       -0.0858975, 0.0311934, -0.0488232}, {-0.978499, -0.0375369, -0.0308657, -0.0197828,
       0.087556, -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659,
       -0.0303762, 0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
    SpikeNegative_5 → {{1., -0.275359, 0.08563, -0.0927664, 0.179004, -0.137792, 0.112485,
       -0.0158152, -0.046442, -0.180954}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
       0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
       -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
    SpikeNegative_6 → {{1., -0.398833, 0.0778628, -0.044104, 0.0333735, 0.0658697, -0.0029231,
       -0.0938463, -0.0655049, -0.0116685}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
       -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
       0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
    SpikeNegative_7 → {{1., -0.42086, -0.00214872, 0.0208358, 0.127917, -0.202863, 0.0631005,
       -0.00894861, 0.0102268, 0.000991105}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
       0.0874465, -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
       -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
    SpikeNegative_8 → {{1., -0.167986, 0.132625, -0.161643, 0.0190856, 0.0689723, -0.0356912,
       -0.0774932, -0.0382031, -0.110421}, {-0.971714, -0.0689738, -0.0116232, 0.0693961,
       0.0405887, -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389,
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    SpikeNegative_16 → {{1., -0.458875, 0.142195, -0.117197, -0.0328704, -0.0724729, 0.062644,
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    SpikeNegative_18 → {{1., -0.219411, 0.0906106, -0.0586132, 0.117458, -0.0973521, -0.064392,
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    SpikeNegative_20 → {{1., -0.223368, 0.0633665, -0.177509, 0.103343, 0.0332846, -0.0776252,
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  Lag1 → <|LinearPositive_1 → {{1., 0.812153, 0.688835, 0.540544, 0.408977, 0.277736,
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    LinearPositive_6 → {{1., 0.812702, 0.691452, 0.540319, 0.407464, 0.275268, 0.153852,
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    LinearPositive_7 → {{1., 0.812932, 0.68944, 0.541059, 0.410632, 0.279722, 0.156421,
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LinearPositive_9 → {{1., 0.814527, 0.692284, 0.539635, 0.407699, 0.277329, 0.156518,
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LinearPositive_10 → {{1., 0.812617, 0.690354, 0.540412, 0.408665, 0.278245, 0.15546,
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LinearPositive_17 → {{1., 0.806478, 0.69134, 0.537476, 0.410291, 0.278818, 0.158116,
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LinearPositive_18 → {{1., 0.808358, 0.691342, 0.539614, 0.409352, 0.280974, 0.150255,
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LinearPositive_20 → {{1., 0.811999, 0.686267, 0.532886, 0.404237, 0.279336, 0.155285,
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LinearNegative_1 → {{1., 0.816083, 0.69022, 0.532722, 0.391788, 0.275312, 0.170471, 0.0446087,
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LinearNegative_3 → {{1., 0.7994, 0.689563, 0.54124, 0.413475, 0.28062, 0.146429, 0.0329069,
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LinearNegative_4 → {{1., 0.810147, 0.673108, 0.506627, 0.392328, 0.257163, 0.143303,
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LinearNegative_5 → {{1., 0.824394, 0.693531, 0.533655, 0.410999, 0.263856, 0.139629,
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LinearNegative_6 → {{1., 0.798686, 0.686017, 0.542515, 0.404526, 0.253837, 0.145439,
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LinearNegative_7 → {{1., 0.794993, 0.672705, 0.521019, 0.397866, 0.258824, 0.137151,
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LinearNegative_8 → {{1., 0.809117, 0.687749, 0.52855, 0.409176, 0.285162, 0.144781, 0.0442807,
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LinearNegative_9 → {{1., 0.822069, 0.699828, 0.550014, 0.43437, 0.295909, 0.177084, 0.052593,
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    -0.115414, -0.114422, -0.130851, -0.167598, -0.173937, -0.198609, -0.23569, -0.258977,
    -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
LinearNegative_10 → {{1., 0.793864, 0.690767, 0.539565, 0.408436, 0.282279, 0.155187,
    0.0459489, -0.0651142, -0.167602}, {-0.00155633, -0.0271325, -0.0625737, -0.0744387,
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LinearNegative_11 → {{1., 0.808637, 0.681433, 0.538256, 0.411633, 0.281455, 0.159477,
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LinearNegative_12 → {{1., 0.81097, 0.694207, 0.546444, 0.416182, 0.277742, 0.152118,
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    -0.245066, -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
LinearNegative_13 → {{1., 0.805711, 0.688968, 0.545194, 0.415927, 0.275731, 0.160197,
    0.0399382, -0.0660995, -0.150625}, {-0.01186, -0.0431645, -0.0590873, -0.0756374,
    -0.0887624, -0.1144, -0.121973, -0.156462, -0.165726, -0.190329, -0.20958, -0.216046,
    -0.244405, -0.264186, -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596}},
LinearNegative_14 → {{1., 0.813584, 0.690966, 0.53621, 0.402116, 0.265448, 0.150454,
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LinearNegative_15 → {{1., 0.80731, 0.678574, 0.536884, 0.408767, 0.281237, 0.169746,
    0.0496114, -0.0649204, -0.157199}, {-0.0162872, -0.0293132, -0.0552218, -0.0807767,
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    -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
LinearNegative_16 → {{1., 0.816224, 0.694855, 0.53266, 0.392939, 0.271184, 0.156789,
    0.0435767, -0.0608658, -0.149563}, {-0.0225164, -0.0461677, -0.0473716, -0.067817,
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LinearNegative_17 → {{1., 0.808181, 0.680533, 0.535776, 0.40837, 0.273865, 0.154831,
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LinearNegative_18 → {{1., 0.819864, 0.693802, 0.543666, 0.404933, 0.275224, 0.145932,
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    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
LinearNegative_19 → {{1., 0.80655, 0.684193, 0.531796, 0.408803, 0.289272, 0.161874,
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    -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
LinearNegative_20 → {{1., 0.826495, 0.708181, 0.552333, 0.416142, 0.286253, 0.158391,
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    -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}},
Sinusoidal3_21 → {{1., 0.247123, -0.557445, -0.939795, -0.653303, 0.0229178, 0.617163,
    0.727312, 0.357869, -0.205849}, {0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461,
    0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096, 0.29637,
    0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
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    Sinusoidal3_22 → {{1., 0.25169, -0.557413, -0.944049, -0.656755, 0.0183542, 0.61891,
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        0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
    Sinusoidal3_23 → {{1., 0.251844, -0.557571, -0.947176, -0.65663, 0.0177201, 0.617109,
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        0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
    Sinusoidal3_24 → {{1., 0.25092, -0.558801, -0.94624, -0.654133, 0.0216276, 0.621752, 0.731812,
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    Sinusoidal3_25 → {{1., 0.248531, -0.559984, -0.948885, -0.651591, 0.0192409, 0.621271,
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    Sinusoidal3_26 → {{1., 0.250536, -0.560428, -0.945524, -0.654639, 0.0206229, 0.618008,
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        0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
    Sinusoidal3_27 → {{1., 0.25091, -0.557951, -0.945799, -0.653107, 0.0190659, 0.616088,
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    Sinusoidal3_28 → {{1., 0.250094, -0.554849, -0.945719, -0.657297, 0.0161014, 0.61427,
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        0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
    Sinusoidal3_29 → {{1., 0.24794, -0.557153, -0.947197, -0.653095, 0.0208478, 0.622396,
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    Sinusoidal3_30 → {{1., 0.250844, -0.557432, -0.945813, -0.655932, 0.0188606, 0.618245,
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  Lag3 → <|Sinusoidal1_1 → {{1., -1.62035, 0.360419, 1.21497, -1.21821, -0.141878, 1.2192,
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    Sinusoidal1_2 → {{1., -1.66532, 0.355438, 1.22652, -1.2175, -0.172353, 1.22186, -0.77432,
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    Sinusoidal1_6 → {{1., -1.61745, 0.362188, 1.18112, -1.19845, -0.108432, 1.16148, -0.801294,
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    Sinusoidal1_7 → {{1., -1.62603, 0.364189, 1.15957, -1.20495, -0.116659, 1.18331, -0.778645,
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    Sinusoidal1_8 → {{1., -1.63516, 0.349888, 1.18931, -1.23013, -0.107577, 1.16798, -0.826875,
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Sinusoidal2_11 → {{1., -1.17252, -0.601542, 1.19408, 0.25188, -1.13858, 0.0704528, 0.976677,
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Sinusoidal2_13 → {{1., -1.17536, -0.59477, 1.20107, 0.24206, -1.14339, 0.0770172, 0.974134,
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Sinusoidal2_19 → {{1., -1.17252, -0.600788, 1.19475, 0.249722, -1.13835, 0.070574, 0.977201,
    -0.28997, -0.779946}, {-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977,
    0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469, 0.251806,
    0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
Sinusoidal2_20 → {{1., -1.17271, -0.596923, 1.19503, 0.249005, -1.13678, 0.0667731, 0.972508,
    -0.289316, -0.780821}, {-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484,
    0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815,
    0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>|>
```

Now we can check each signal if it had multi-class membership for autocorrelations in each signal:

```
In[6]:= classificationAutocorrelationMembership = TimeSeriesClassification[
          classificationExample1, timePointsExample, AutocorrelationCutoffs → bootstrapQ95Autocorrelation,
          SpikeCutoffs → bootstrapQ95Spikes, Method → "Autocorrelation", AutocorrelationLogic → True]

        Method → "Autocorrelation"

Out[6]= <|SpikePositive_1 → {False, False, False, False, False, False, False, False, False},
         SpikePositive_2 → {False, False, False, False, False, False, False, False, False},
         SpikePositive_3 → {False, False, False, False, False, False, False, False, False},
         SpikePositive_4 → {False, False, False, False, False, False, False, False, False},
```

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```
SpikePositive_5 → {False, False, False, False, False, False, False, False, False},
SpikePositive_6 → {False, False, False, False, False, False, False, False, False},
SpikePositive_7 → {False, False, False, False, False, False, False, False, False},
SpikePositive_8 → {False, False, False, False, False, False, False, False, False},
SpikePositive_9 → {False, False, False, False, False, False, False, False, False},
SpikePositive_10 → {False, False, False, False, False, False, False, False, False},
SpikePositive_11 → {False, False, False, False, False, False, False, False, False},
SpikePositive_12 → {False, False, False, False, False, False, False, False, False},
SpikePositive_13 → {False, False, False, False, False, False, False, False, False},
SpikePositive_14 → {False, False, False, False, False, False, False, False, False},
SpikePositive_15 → {False, False, False, False, False, False, False, False, False},
SpikePositive_16 → {False, False, False, False, False, False, False, False, False},
SpikePositive_17 → {False, False, False, False, False, False, False, False, False},
SpikePositive_18 → {False, False, False, False, False, False, False, False, False},
SpikePositive_19 → {False, False, False, False, False, False, False, False, False},
SpikePositive_20 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_1 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_2 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_3 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_4 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_5 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_6 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_7 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_8 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_9 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_10 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_11 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_12 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_13 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_14 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_15 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_16 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_17 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_18 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_19 → {False, False, False, False, False, False, False, False, False},
SpikeNegative_20 → {False, False, False, False, False, False, False, False, False},
LinearPositive_1 → {True, False, True, False, False, False, False, False, False},
LinearPositive_2 → {True, False, True, False, False, False, False, False, False},
LinearPositive_3 → {True, False, True, False, False, False, False, False, False},
LinearPositive_4 → {True, False, True, False, False, False, False, False, False},
LinearPositive_5 → {True, False, True, False, False, False, False, False, False},
LinearPositive_6 → {True, False, True, False, False, False, False, False, False},
LinearPositive_7 → {True, False, True, False, False, False, False, False, False},
LinearPositive_8 → {True, False, True, False, False, False, False, False, False},
LinearPositive_9 → {True, False, True, False, False, False, False, False, False},
LinearPositive_10 → {True, False, True, False, False, False, False, False, False},
LinearPositive_11 → {True, False, True, False, False, False, False, False, False},
LinearPositive_12 → {True, False, True, False, False, False, False, False, False},
LinearPositive_13 → {True, False, True, False, False, False, False, False, False},
LinearPositive_14 → {True, False, True, False, False, False, False, False, False},
LinearPositive_15 → {True, False, True, False, False, False, False, False, False},
LinearPositive_16 → {True, False, True, False, False, False, False, False, False},
LinearPositive_17 → {True, False, True, False, False, False, False, False, False},
LinearPositive_18 → {True, False, True, False, False, False, False, False, False},
LinearPositive_19 → {True, False, True, False, False, False, False, False, False},
LinearPositive_20 → {True, False, True, False, False, False, False, False, False},
LinearNegative_1 → {True, False, True, False, False, False, False, False, False},
LinearNegative_2 → {True, False, True, False, False, False, False, False, False},
LinearNegative_3 → {True, False, True, False, False, False, False, False, False},
LinearNegative_4 → {True, False, True, False, False, False, False, False, False},
LinearNegative_5 → {True, False, True, False, False, False, False, False, False},
LinearNegative_6 → {True, False, True, False, False, False, False, False, False},
LinearNegative_7 → {True, False, True, False, False, False, False, False, False},
LinearNegative_8 → {True, False, True, False, False, False, False, False, False},
LinearNegative_9 → {True, False, True, False, False, False, False, False, False},
LinearNegative_10 → {True, False, True, False, False, False, False, False, False},
```

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```
LinearNegative_11 → {True, False, True, False, False, False, False, False, False},
LinearNegative_12 → {True, False, True, False, False, False, False, False, False},
LinearNegative_13 → {True, False, True, False, False, False, False, False, False},
LinearNegative_14 → {True, False, True, False, False, False, False, False, False},
LinearNegative_15 → {True, False, True, False, False, False, False, False, False},
LinearNegative_16 → {True, False, True, False, False, False, False, False, False},
LinearNegative_17 → {True, False, True, False, False, False, False, False, False},
LinearNegative_18 → {True, False, True, False, False, False, False, False, False},
LinearNegative_19 → {True, False, True, False, False, False, False, False, False},
LinearNegative_20 → {True, False, True, False, False, False, False, False, False},
Sinusoidal1_1 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_2 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_3 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_4 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_5 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_6 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_7 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_8 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_9 → {False, False, True, False, False, True, False, False, True},
Sinusoidal1_10 → {False, False, True, False, False, True, False, False, True},
Sinusoidal2_11 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_12 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_13 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_14 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_15 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_16 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_17 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_18 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_19 → {False, False, True, False, False, False, True, False, False},
Sinusoidal2_20 → {False, False, True, False, False, False, True, False, False},
Sinusoidal3_21 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_22 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_23 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_24 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_25 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_26 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_27 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_28 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_29 → {True, False, False, False, False, True, True, False, False},
Sinusoidal3_30 → {True, False, False, False, False, True, True, False, False}|>
```

AutocorrelationOptions (1)

```
In[1]:= Needs["MathIOmica`"]
```

AutocorrelationOptions are passed to the internal Autocorrelation function when using Method "Autocorrelation".

For example, we can provide cutoffs for different lags (we use the same main example, and background noise example for 20 timepoints):

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```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
          Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["Sinusoidal2_" <> ToString[i] →
             5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
            {i, 21, 30}]]];
        backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
        timePointsExample = Range[20];
```

We can use the background to determine our data cutoffs for the "Autocorrelation" method. We work with the QuantileEstimator function to generate a value for the AutocorrelationCutoffs, by default using the 0.95th quantile. (N.B. the following computaiton may be time consuming depending on number of samples in the background simulation):

```
In[3]:= bootstrapQ95Autocorrelation =
         QuantileEstimator[backgroundExample, timePointsExample , Method → "Autocorrelation"]

Out[3]= {0.104569, 0.750865, 0.330876, 0.582844, 0.384145, 0.476242, 0.361702, 0.407732, 0.30536}
```

We can work again with the QuantileEstimator function to also generate a value for the SpikeCutoffs:

```
In[4]:= bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"]

Out[4]= <|20 → {0.42185, -0.421758}|>
```

Let's perform the classification,

```
In[5]:= classificationAutocorrelation1 = TimeSeriesClassification[classificationExample1,
          timePointsExample, AutocorrelationCutoffs → bootstrapQ95Autocorrelation,
          SpikeCutoffs → bootstrapQ95Spikes, Method → "Autocorrelation"]

          Method → "Autocorrelation"

Out[5]= <|SpikeMax →
          <|SpikePositive_1 → {{1., -0.452395, 0.219937, -0.141456, -0.040982, 0.0671421, -0.0204863, -0.0225783,
              0.00336149, 0.0248339}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
              0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
              -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
           SpikePositive_2 → {{1., -0.33332, 0.178978, -0.043203, 0.0330959, 0.0187841, 0.0643953,
              -0.167683, -0.0783794, -0.134626}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
              0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
              -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
           SpikePositive_3 → {{1., -0.150943, 0.25591, -0.077747, 0.03904, -0.112386, -0.130446,
              -0.111423, -0.0923815, 0.0100807}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
              -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
              0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
           SpikePositive_4 → {{1., -0.329658, 0.231525, 0.0162836, 0.164488, -0.166715, 0.0989705,
              -0.163788, -0.0754534, 0.0143191}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
```

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```
    -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
    0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
SpikePositive_5 → {{1., -0.354501, 0.199318, -0.099174, 0.199, -0.0363005, 0.158313,
    -0.0231566, 0.0362299, -0.135361}, {0.966833, -0.0172757, -0.0101601, 0.0449156,
    0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
    -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
SpikePositive_6 → {{1., -0.466257, 0.137607, -0.192065, -0.0315355, -0.0729004, -0.0550543,
    -0.104833, 0.0601693, -0.0827568}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
    0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
    0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
SpikePositive_7 → {{1., -0.389552, 0.144053, -0.0395178, 0.0603777, -0.112134, -0.0357364,
    -0.00620881, -0.073946, -0.0864452}, {0.973634, -0.0197451, 0.00381691, 0.0632199,
    0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
    0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
SpikePositive_8 → {{1., -0.394532, 0.210425, -0.0366925, 0.0213409, -0.067476, 0.000171715,
    -0.0864154, -0.128194, 0.0081353}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
    -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
    -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
SpikePositive_9 → {{1., -0.400547, 0.143122, -0.118456, -0.00900312, 0.125105, 0.0177367,
    -0.061955, -0.00116964, -0.150973}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
    0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
SpikePositive_10 → {{1., -0.486387, 0.214384, -0.107572, 0.107945, 0.0130167, 0.0145573,
    0.0233586, -0.0802024, -0.127062}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
    0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
SpikePositive_11 → {{1., -0.338874, 0.300856, -0.187073, -0.0720043, -0.0204714, -0.0156668,
    0.0397913, -0.0000121023, -0.147044}, {0.0696283, 0.0251021, 0.968196, 0.0511374,
    0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
    -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
SpikePositive_12 → {{1., -0.490403, 0.230471, -0.02836, 0.158686, -0.26022, 0.158602,
    -0.177464, 0.0371373, -0.0785755}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
    0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
SpikePositive_13 → {{1., -0.380553, -0.0954718, -0.150478, -0.0658297, 0.106079, -0.0357483,
    -0.0423526, 0.134218, -0.0648447}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
    -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
    0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
SpikePositive_14 → {{1., -0.526563, 0.402071, -0.0816825, 0.0766719, -0.117882, 0.0465972,
    -0.195255, 0.0724303, -0.107586}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
    0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
SpikePositive_15 → {{1., -0.498776, 0.12023, -0.0909257, 0.179612, -0.241152, 0.0697987,
    0.00693521, 0.0904771, -0.0399131}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
    0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
    -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
SpikePositive_16 → {{1., -0.252346, -0.0181276, -0.202654, 0.0588694, -0.165692, 0.058152,
    -0.0733224, 0.0688338, 0.00969476}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
    -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
    -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
SpikePositive_17 → {{1., -0.868718, 0.44914, -0.120491, -0.0616033, -0.0228913, 0.14139,
    -0.0932499, -0.0473214, 0.036701}, {0.0894556, -0.0939456, 0.955206, -0.0721055,
    0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
    -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
SpikePositive_18 → {{1., -0.362902, -0.122098, -0.129486, 0.0562719, -0.0830183, 0.122331,
    -0.122383, -0.180395, -0.0773557}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
    -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
    0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
SpikePositive_19 → {{1., -0.42077, 0.0763867, -0.227391, 0.0475263, 0.0245878, -0.0251915,
    -0.0584293, -0.118635, 0.0240546}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
    -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
SpikePositive_20 → {{1., -0.507801, 0.163243, -0.238989, -0.0407895, 0.101176, -0.0803686,
    0.0171814, 0.00408016, -0.268402}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
    -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
    0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
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SpikeMin → <|SpikeNegative_1 → {{1., -0.423906, 0.0870199, -0.0546103, 0.153795, 0.0753404,
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  SpikeNegative_2 → {{1., -0.254883, 0.246154, -0.281797, 0.168139, -0.0510077, 0.0696523,
      0.044741, -0.0493091, -0.173802}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
      -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
      -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_3 → {{1., -0.52844, 0.0128591, 0.0401754, 0.156405, -0.25313, 0.0143667,
      -0.105044, 0.0118936, -0.135968}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
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      -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
  SpikeNegative_4 → {{1., -0.261291, 0.197729, -0.0669671, -0.0489197, 0.019136, -0.0777287,
      -0.0858975, 0.0311934, -0.0488232}, {-0.978499, -0.0375369, -0.0308657, -0.0197828,
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      -0.0303762, 0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{1., -0.275359, 0.08563, -0.0927664, 0.179004, -0.137792, 0.112485,
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  SpikeNegative_6 → {{1., -0.398833, 0.0778628, -0.044104, 0.0333735, 0.0658697, -0.0029231,
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  SpikeNegative_7 → {{1., -0.42086, -0.00214872, 0.0208358, 0.127917, -0.202863, 0.0631005,
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      -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{1., -0.167986, 0.132625, -0.161643, 0.0190856, 0.0689723, -0.0356912,
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  SpikeNegative_9 → {{1., -0.280681, 0.131522, -0.27773, 0.125519, -0.158639, 0.0827061,
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  SpikeNegative_10 → {{1., -0.351869, 0.262355, -0.0376404, 0.155982, -0.124093, 0.105999,
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  SpikeNegative_11 → {{1., -0.413539, 0.0679203, 0.00410847, 0.0261914, -0.0181218, 0.0852791,
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      0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{1., -0.395846, 0.0894882, -0.237998, -0.0446471, -0.0524744, 0.0771359,
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      -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{1., -0.343983, 0.00454468, -0.205612, 0.0119525, -0.102592, 0.103107,
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      0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{1., -0.409677, 0.104665, -0.110113, 0.152765, -0.103758, -0.130233,
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  SpikeNegative_16 → {{1., -0.458875, 0.142195, -0.117197, -0.0328704, -0.0724729, 0.062644,
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  SpikeNegative_17 → {{1., -0.28948, 0.0899977, -0.14795, 0.137414, -0.00541154, 0.0773486,
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  SpikeNegative_19 → {{1., -0.25374, 0.0112197, -0.122395, -0.0226519, -0.0591994, -0.111793,
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  SpikeNegative_20 → {{1., -0.223368, 0.0633665, -0.177509, 0.103343, 0.0332846, -0.0776252,
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Lag1 → <|LinearPositive_1 → {{1., 0.812153, 0.688835, 0.540544, 0.408977, 0.277736,
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  LinearPositive_2 → {{1., 0.812426, 0.690113, 0.540471, 0.410253, 0.280388, 0.156519,
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  LinearPositive_4 → {{1., 0.811366, 0.688737, 0.538759, 0.409453, 0.280276, 0.156679,
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      0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}},
  LinearPositive_5 → {{1., 0.813098, 0.689554, 0.539503, 0.407967, 0.278017, 0.155904,
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  LinearPositive_6 → {{1., 0.812702, 0.691452, 0.540319, 0.407464, 0.275268, 0.153852,
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  LinearPositive_7 → {{1., 0.812932, 0.68944, 0.541059, 0.410632, 0.279722, 0.156421,
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      0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
  LinearPositive_8 → {{1., 0.811593, 0.690699, 0.541512, 0.410794, 0.279002, 0.153279,
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  LinearPositive_9 → {{1., 0.814527, 0.692284, 0.539635, 0.407699, 0.277329, 0.156518,
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  LinearPositive_10 → {{1., 0.812617, 0.690354, 0.540412, 0.408665, 0.278245, 0.15546,
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  LinearPositive_11 → {{1., 0.804492, 0.685812, 0.542844, 0.417517, 0.287434, 0.157954,
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  LinearPositive_12 → {{1., 0.812692, 0.699529, 0.549384, 0.416283, 0.279929, 0.163007,
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  LinearPositive_13 → {{1., 0.811422, 0.68853, 0.541446, 0.403324, 0.270859, 0.150227,
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      0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}}, LinearPositive_14 →
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LinearPositive_15 → {{1., 0.809318, 0.686477, 0.535556, 0.404368, 0.274978, 0.157388,
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   0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}}, LinearPositive_16 →
 {{1., 0.810881, 0.682948, 0.521149, 0.393493, 0.270986, 0.153462, 0.0425078, -0.0520434, -0.143292},
  {0.0164478, 0.0360481, 0.048135, 0.0712245, 0.101186, 0.114916, 0.129433, 0.153936, 0.164281, 0.192697,
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LinearPositive_17 → {{1., 0.806478, 0.69134, 0.537476, 0.410291, 0.278818, 0.158116,
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   0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
LinearPositive_18 → {{1., 0.808358, 0.691342, 0.539614, 0.409352, 0.280974, 0.150255,
   0.0423746, -0.0533218, -0.151273}, {0.0115844, 0.0455792, 0.0534286, 0.068487, 0.0918771,
   0.107837, 0.137609, 0.144956, 0.162508, 0.185864, 0.206224, 0.229689, 0.232407, 0.261637,
   0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}}, LinearPositive_19 →
 {{1., 0.81667, 0.69756, 0.549924, 0.42015, 0.288918, 0.160474, 0.039693, -0.0722049, -0.157988},
  {0.0205961, 0.045526, 0.0569898, 0.0724948, 0.0867427, 0.105806, 0.12769, 0.145665, 0.170669, 0.180276,
   0.216792, 0.223063, 0.241101, 0.270774, 0.282283, 0.293887, 0.315058, 0.334039, 0.359611, 0.369743}},
LinearPositive_20 → {{1., 0.811999, 0.686267, 0.532886, 0.404237, 0.279336, 0.155285,
   0.0427134, -0.0540973, -0.146741}, {0.00952752, 0.0286979, 0.0547226, 0.0709501,
   0.0958101, 0.109505, 0.135844, 0.152431, 0.165158, 0.182651, 0.210505, 0.231304,
   0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
LinearNegative_1 → {{1., 0.816083, 0.69022, 0.532722, 0.391788, 0.275312, 0.170471, 0.0446087,
   -0.0611309, -0.147816}, {-0.0218046, -0.0446169, -0.0612231, -0.0738948, -0.109733,
   -0.115191, -0.124469, -0.148293, -0.159758, -0.176361, -0.217843, -0.224298, -0.23172,
   -0.273794, -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733}},
LinearNegative_2 → {{1., 0.821326, 0.717404, 0.546117, 0.420827, 0.293304, 0.153503,
   0.0344508, -0.0759091, -0.162306}, {-0.0137543, -0.0552134, -0.0387902, -0.0787876,
   -0.0972777, -0.0993326, -0.131634, -0.158204, -0.178021, -0.176063, -0.209858, -0.230763,
   -0.248781, -0.268592, -0.290148, -0.294015, -0.319548, -0.339092, -0.343638, -0.357122}},
LinearNegative_3 → {{1., 0.7994, 0.689563, 0.54124, 0.413475, 0.28062, 0.146429, 0.0329069,
   -0.0628257, -0.140667}, {-0.0283384, -0.0528281, -0.0527884, -0.0740599, -0.0921776,
   -0.0948819, -0.146225, -0.165182, -0.160057, -0.18686, -0.220224, -0.211812, -0.237918,
   -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
LinearNegative_4 → {{1., 0.810147, 0.673108, 0.506627, 0.392328, 0.257163, 0.143303,
   0.0398545, -0.0536507, -0.139413}, {-0.0158873, -0.0248133, -0.0382326, -0.0881019,
   -0.0887054, -0.128386, -0.128859, -0.161147, -0.159022, -0.205319, -0.200777, -0.210411,
   -0.243003, -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844}},
LinearNegative_5 → {{1., 0.824394, 0.693531, 0.533655, 0.410999, 0.263856, 0.139629,
   0.0341737, -0.0617561, -0.143612}, {-0.0201624, -0.0405386, -0.0436406, -0.0738225,
   -0.0817467, -0.105404, -0.114359, -0.154377, -0.169473, -0.174198, -0.212011, -0.225376,
   -0.230144, -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}},
LinearNegative_6 → {{1., 0.798686, 0.686017, 0.542515, 0.404526, 0.253837, 0.145439,
   0.0446877, -0.0469226, -0.140381}, {-0.0267223, -0.0446999, -0.0523138, -0.0699606,
   -0.0987645, -0.126896, -0.126614, -0.165572, -0.172297, -0.184872, -0.208135, -0.237294,
   -0.243037, -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481}},
LinearNegative_7 → {{1., 0.794993, 0.672705, 0.521019, 0.397866, 0.258824, 0.137151,
   0.0450355, -0.0533671, -0.127923}, {-0.00172329, -0.032268, -0.068173, -0.0857129,
   -0.0881686, -0.107137, -0.140409, -0.14992, -0.182962, -0.175511, -0.200764, -0.226349,
   -0.23516, -0.248536, -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923}},
LinearNegative_8 → {{1., 0.809117, 0.687749, 0.52855, 0.409176, 0.285162, 0.144781, 0.0442807,
   -0.062147, -0.15603}, {-0.0170306, -0.0378539, -0.0394845, -0.0767312, -0.0942537,
   -0.105065, -0.146528, -0.134698, -0.186411, -0.174071, -0.194782, -0.232787, -0.238911,
   -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
LinearNegative_9 → {{1., 0.822069, 0.699828, 0.550014, 0.43437, 0.295909, 0.177084, 0.052593,
   -0.079476, -0.184474}, {-0.0287969, -0.0189698, -0.0530075, -0.0828922, -0.0936032,
   -0.115414, -0.114422, -0.130851, -0.167598, -0.173937, -0.198609, -0.23569, -0.258977,
   -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
LinearNegative_10 → {{1., 0.793864, 0.690767, 0.539565, 0.408436, 0.282279, 0.155187,
   0.0459489, -0.0651142, -0.167602}, {-0.00155633, -0.0271325, -0.0625737, -0.0744387,
   -0.0901925, -0.0932579, -0.138846, -0.15092, -0.157289, -0.198281, -0.189392, -0.206968,
   -0.259028, -0.273261, -0.270544, -0.29133, -0.328913, -0.352948, -0.335503, -0.37816}},
LinearNegative_11 → {{1., 0.808637, 0.681433, 0.538256, 0.411633, 0.281455, 0.159477,
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    -0.0862196, -0.118392, -0.123851, -0.151596, -0.176372, -0.191037, -0.213033, -0.221631,
    -0.235518, -0.271564, -0.288178, -0.293001, -0.310129, -0.328328, -0.364455, -0.366174}},
LinearNegative_12 → {{1., 0.81097, 0.694207, 0.546444, 0.416182, 0.277742, 0.152118,
    0.0468388, -0.0635984, -0.155436}, {-0.0105234, -0.0459122, -0.0631169, -0.0780043,
    -0.0883748, -0.108962, -0.137461, -0.144887, -0.163604, -0.184293, -0.210166, -0.217602,
    -0.245066, -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
LinearNegative_13 → {{1., 0.805711, 0.688968, 0.545194, 0.415927, 0.275731, 0.160197,
    0.0399382, -0.0660995, -0.150625}, {-0.01186, -0.0431645, -0.0590873, -0.0756374,
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    -0.244405, -0.264186, -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596}},
LinearNegative_14 → {{1., 0.813584, 0.690966, 0.53621, 0.402116, 0.265448, 0.150454,
    0.0360438, -0.0604747, -0.145439}, {-0.0187992, -0.0431131, -0.0473458, -0.070655,
    -0.0879629, -0.116006, -0.12521, -0.152395, -0.170415, -0.184268, -0.196593, -0.22289,
    -0.23237, -0.26046, -0.276864, -0.301954, -0.319987, -0.336453, -0.361973, -0.377956}},
LinearNegative_15 → {{1., 0.80731, 0.678574, 0.536884, 0.408767, 0.281237, 0.169746,
    0.0496114, -0.0649204, -0.157199}, {-0.0162872, -0.0293132, -0.0552218, -0.0807767,
    -0.0935334, -0.121112, -0.124004, -0.147926, -0.165828, -0.191582, -0.205406, -0.219926,
    -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
LinearNegative_16 → {{1., 0.816224, 0.694855, 0.53266, 0.392939, 0.271184, 0.156789,
    0.0435767, -0.0608658, -0.149563}, {-0.0225164, -0.0461677, -0.0473716, -0.067817,
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    -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}},
LinearNegative_17 → {{1., 0.808181, 0.680533, 0.535776, 0.40837, 0.273865, 0.154831,
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    -0.240133, -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}},
LinearNegative_18 → {{1., 0.819864, 0.693802, 0.543666, 0.404933, 0.275224, 0.145932,
    0.0398621, -0.0573997, -0.157583}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
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    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
LinearNegative_19 → {{1., 0.80655, 0.684193, 0.531796, 0.408803, 0.289272, 0.161874,
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    -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
LinearNegative_20 → {{1., 0.826495, 0.708181, 0.552333, 0.416142, 0.286253, 0.158391,
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    -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}},
Sinusoidal3_21 → {{1., 0.247123, -0.557445, -0.939795, -0.653303, 0.0229178, 0.617163,
    0.727312, 0.357869, -0.205849}, {0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461,
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    0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
Sinusoidal3_22 → {{1., 0.25169, -0.557413, -0.944049, -0.656755, 0.0183542, 0.61891,
    0.732724, 0.361424, -0.20497}, {0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846,
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    0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{1., 0.251844, -0.557571, -0.947176, -0.65663, 0.0177201, 0.617109,
    0.73334, 0.36597, -0.200787}, {0.18264, -0.0994704, -0.295137, -0.250857, 0.00157044,
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    0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{1., 0.25092, -0.558801, -0.94624, -0.654133, 0.0216276, 0.621752, 0.731812,
    0.356685, -0.208697}, {0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361,
    0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939, 0.304721,
    0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
Sinusoidal3_25 → {{1., 0.248531, -0.559984, -0.948885, -0.651591, 0.0192409, 0.621271,
    0.733629, 0.360855, -0.207618}, {0.191347, -0.0982886, -0.29771, -0.261082, 0.00611569,
    0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799, 0.302028,
    0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
Sinusoidal3_26 → {{1., 0.250536, -0.560428, -0.945524, -0.654639, 0.0206229, 0.618008,
    0.729843, 0.360449, -0.204321}, {0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724,
    0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444, 0.296927,
    0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
Sinusoidal3_27 → {{1., 0.25091, -0.557951, -0.945799, -0.653107, 0.0190659, 0.616088,
    0.729145, 0.361895, -0.203958}, {0.185809, -0.10192, -0.303748, -0.261172, 0.000202029,
    0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227, 0.302676,
    0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
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    Sinusoidal3_28 → {{1., 0.250094, -0.554849, -0.945719, -0.657297, 0.0161014, 0.61427,
       0.731466, 0.368519, -0.19556}, {0.187562, -0.10053, -0.297144, -0.250552, 0.00476677,
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       0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
    Sinusoidal3_29 → {{1., 0.24794, -0.557153, -0.947197, -0.653095, 0.0208478, 0.622396,
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       0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
    Sinusoidal3_30 → {{1., 0.250844, -0.557432, -0.945813, -0.655932, 0.0188606, 0.618245,
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       0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
  Lag3 → <|Sinusoidal1_1 → {{1., -1.62035, 0.360419, 1.21497, -1.21821, -0.141878, 1.2192,
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    Sinusoidal1_2 → {{1., -1.66532, 0.355438, 1.22652, -1.2175, -0.172353, 1.22186, -0.77432,
       -0.462836, 1.00478}, {-0.153886, -0.0875347, 0.297854, -0.276583, 0.004457,
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       0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
    Sinusoidal1_3 → {{1., -1.64445, 0.326285, 1.20792, -1.19633, -0.166442, 1.18651, -0.75412,
       -0.488243, 1.0025}, {-0.187066, -0.0732084, 0.32812, -0.266161, 0.00567862,
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       0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
    Sinusoidal1_4 → {{1., -1.64431, 0.377649, 1.22081, -1.23917, -0.150641, 1.23362, -0.812858,
       -0.479352, 1.02686}, {-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004,
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    Sinusoidal1_5 → {{1., -1.63326, 0.350694, 1.19562, -1.24989, -0.119703, 1.19466, -0.824007,
       -0.44053, 1.03035}, {-0.20104, -0.101657, 0.31364, -0.234517, -0.0163677,
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       0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
    Sinusoidal1_6 → {{1., -1.61745, 0.362188, 1.18112, -1.19845, -0.108432, 1.16148, -0.801294,
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    Sinusoidal1_7 → {{1., -1.62603, 0.364189, 1.15957, -1.20495, -0.116659, 1.18331, -0.778645,
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       0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
    Sinusoidal1_8 → {{1., -1.63516, 0.349888, 1.18931, -1.23013, -0.107577, 1.16798, -0.826875,
       -0.408475, 1.00889}, {-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322,
       0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394, -0.280218,
       0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
    Sinusoidal1_9 → {{1., -1.63545, 0.3389, 1.19087, -1.23845, -0.122747, 1.21239, -0.803972,
       -0.441409, 1.00971}, {-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817,
       0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813, -0.323289,
       0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
    Sinusoidal1_10 → {{1., -1.62154, 0.318378, 1.205, -1.20671, -0.172296, 1.21745, -0.763933,
       -0.495003, 1.01357}, {-0.203834, -0.0722574, 0.294696, -0.254799, 0.00423677,
       0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167, -0.291561,
       0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}},
    Sinusoidal2_11 → {{1., -1.17252, -0.601542, 1.19408, 0.25188, -1.13858, 0.0704528, 0.976677,
       -0.291154, -0.781135}, {-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852,
       0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865, 0.258725,
       0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
    Sinusoidal2_12 → {{1., -1.16785, -0.598321, 1.19453, 0.248915, -1.13786, 0.0682078, 0.978793,
       -0.291032, -0.776961}, {-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067,
       0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668, 0.262301,
       0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
    Sinusoidal2_13 → {{1., -1.17536, -0.59477, 1.20107, 0.24206, -1.14339, 0.0770172, 0.974134,
       -0.300202, -0.775021}, {-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667,
       0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963, 0.254435,
       0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
    Sinusoidal2_14 → {{1., -1.1688, -0.593543, 1.19507, 0.242189, -1.14297, 0.0748801, 0.976008,
       -0.300757, -0.77767}, {-0.0971308, -0.259618, 0.249762, 0.0996953, -0.311793,
```

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```
    0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698, 0.256122,
    0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{1., -1.17333, -0.597548, 1.19893, 0.246055, -1.14361, 0.077823, 0.976081,
    -0.300583, -0.777469}, {-0.0939856, -0.25429, 0.25073, 0.100441, -0.313599,
    0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627, 0.255722,
    0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{1., -1.17552, -0.594542, 1.19905, 0.240051, -1.13983, 0.0800883, 0.973032,
    -0.306018, -0.774319}, {-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132,
    0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968, 0.256443,
    0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{1., -1.16939, -0.601413, 1.1928, 0.254696, -1.14293, 0.0645867, 0.979436,
    -0.29009, -0.783073}, {-0.0991608, -0.252958, 0.255513, 0.0985052, -0.309591,
    0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{1., -1.16579, -0.598353, 1.19062, 0.252474, -1.13536, 0.0710946, 0.973451,
    -0.292364, -0.776772}, {-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724,
    0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{1., -1.17252, -0.600788, 1.19475, 0.249722, -1.13835, 0.070574, 0.977201,
    -0.28997, -0.779946}, {-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977,
    0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469, 0.251806,
    0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{1., -1.17271, -0.596923, 1.19503, 0.249005, -1.13678, 0.0667731, 0.972508,
    -0.289316, -0.780821}, {-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484,
    0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815,
    0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>|>
```

In[6]:=
```
classificationAutocorrelationOptions = TimeSeriesClassification[classificationExample1, timePointsExample,
  AutocorrelationCutoffs → bootstrapQ95Autocorrelation, SpikeCutoffs → bootstrapQ95Spikes,
  Method → "Autocorrelation", AutocorrelationOptions → {UpperFrequencyFactor → 1.2}]
```

Method → "Autocorrelation"

Out[6]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{1., -0.448107, 0.19515, -0.137, 0.103207, -0.246581, 0.247634, -0.128763, 0.0275437,
    -0.0035198, -0.0277137, 0.0617355}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
    0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
    -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
  SpikePositive_2 → {{1., -0.30327, 0.138845, -0.0743606, 0.152, -0.16335, 0.186196, -0.064872,
    0.00531876, -0.170837, -0.0570867, -0.0957013}, {0.973207, 0.00872172, -0.00191539, 0.0695064,
    -0.00641562, 0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666,
    -0.00648697, -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
  SpikePositive_3 → {{1., -0.176305, 0.270832, -0.0671965, 0.109717, -0.123197, 0.0284556,
    -0.190265, -0.0767183, -0.0725411, -0.102876, 0.0696515}, {0.95896, 0.0348607, 0.0657694, 0.0097693,
    -0.0146057, -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763,
    -0.00816843, 0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
  SpikePositive_4 → {{1., -0.312125, 0.176887, -0.0318752, 0.210911, -0.0301327, -0.023496,
    -0.0303044, 0.0153235, -0.18077, -0.0101789, 0.0122639}, {0.958583, 0.00400217, 0.0429904, 0.0838796,
    0.0778033, -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858,
    0.0195539, 0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
  SpikePositive_5 → {{1., -0.351889, 0.192532, -0.131518, 0.16019, -0.0121721, 0.11486, 0.00271922,
    0.116568, -0.0567199, 0.0385502, -0.161062}, {0.966833, -0.0172757, -0.0101601, 0.0449156,
    0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
    -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
  SpikePositive_6 → {{1., -0.441135, 0.133391, -0.195775, 0.0766342, -0.244021, 0.13668, -0.190095,
    0.00461704, -0.0659338, 0.0541197, -0.0859265}, {0.971085, -0.0737213, -0.0183259, -0.0280164,
    -0.0370416, 0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791,
    0.0886387, 0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
  SpikePositive_7 → {{1., -0.358035, 0.116234, -0.104562, 0.166076, -0.126896, 0.0419643, -0.135121,
    0.0332885, -0.0182779, -0.113458, -0.0238333}, {0.973634, -0.0197451, 0.00381691, 0.0632199,
    0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
    0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
  SpikePositive_8 → {{1., -0.376226, 0.163173, -0.0690058, 0.156717, -0.163026, 0.0825951, -0.0929165,
    -0.00352011, -0.0945384, -0.120808, 0.063724}, {0.973714, -0.0655433, 0.00410752, 0.0489941,
    -0.0178775, -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
    -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
```

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```
    SpikePositive_9 → {{1., -0.373416, 0.128741, -0.146909, 0.115486, -0.216379, 0.306518, -0.107934,
       0.0394555, -0.0551497, -0.0289673, -0.118127}, {0.979998, -0.049438, -0.0488434, 0.00681623,
       -0.062095, 0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267,
       -0.0503857, -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
    SpikePositive_10 → {{1., -0.476256, 0.183467, -0.135193, 0.152855, -0.106371, 0.170156, -0.0850368,
       0.0410825, 0.0373664, -0.185864, 0.00673478}, {0.961551, -0.0906575, 0.00581915, 0.00875268,
       0.0455119, 0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431,
       0.101266, -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
    SpikePositive_11 → {{1., -0.372984, 0.292046, -0.119777, 0.0540391, -0.264483, 0.163302,
       -0.131727, 0.0554959, 0.0632212, -0.111434, -0.0452364}, {0.0696283, 0.0251021, 0.968196, 0.0511374,
       0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
       -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
    SpikePositive_12 → {{1., -0.458072, 0.152802, -0.0690342, 0.206054, -0.0691842, -0.0732783,
       -0.0292297, 0.0632443, -0.187954, 0.10919, -0.130912}, {0.0427773, -0.0204301, 0.972226, -0.00645026,
       0.0200803, 0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808,
       0.00471403, 0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
    SpikePositive_13 → {{1., -0.286904, -0.0747798, -0.24193, 0.0625534, -0.240194, 0.279719,
       -0.151261, 0.0385969, -0.0204341, 0.143357, -0.122741}, {-0.0343175, -0.0155132, 0.955818, 0.0636753,
       -0.0900903, -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626,
       0.0398952, 0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
    SpikePositive_14 → {{1., -0.548317, 0.313362, -0.0569758, 0.192789, -0.192288, 0.120036,
       -0.136653, 0.0199805, -0.162301, 0.123901, -0.167445}, {0.0757209, -0.0202174, 0.968597, -0.0798072,
       0.0669311, 0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164,
       -0.0464562, -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
    SpikePositive_15 → {{1., -0.454112, 0.0909021, -0.158657, 0.172598, -0.0366675, -0.0680768,
       -0.0846226, 0.0960095, 0.0132684, 0.0465065, -0.0157031}, {0.0367157, 0.00909492, 0.955211,
       -0.0373177, -0.0545922, 0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346,
       0.0584456, -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
    SpikePositive_16 → {{1., -0.196369, 0.0305693, -0.234033, 0.0165035, -0.0755592, -0.0474139, -0.0508272,
       0.0351423, -0.0605961, 0.0925574, -0.0195714}, {-0.0123015, 0.0180774, 0.974876, 0.0737459,
       -0.0312647, -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
       -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
    SpikePositive_17 → {{1., -0.835796, 0.285861, -0.0710775, 0.174847, -0.330151, 0.212893,
       -0.0501907, 0.072194, -0.0967869, -0.0320239, 0.0578855}, {0.0894556, -0.0939456, 0.955206,
       -0.0721055, 0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
       -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
    SpikePositive_18 → {{1., -0.257696, -0.106149, -0.23202, 0.0669667, -0.0742076, 0.0179041,
       0.0196077, 0.041985, -0.203832, -0.106406, -0.0759572}, {-0.0361007, -0.0216285, 0.964135, 0.085142,
       -0.0857144, -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
       0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
    SpikePositive_19 → {{1., -0.398995, 0.11227, -0.240966, 0.0413117, -0.120189, 0.154574, -0.0878654,
       -0.0235225, -0.0449991, -0.134318, 0.0816079}, {-0.0584325, 0.0880122, 0.972312, -0.0409534,
       0.0540727, -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323,
       -0.0924997, 0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
    SpikePositive_20 → {{1., -0.495849, 0.169411, -0.226031, 0.0651043, -0.270583, 0.315341,
       -0.202372, 0.034281, 0.0621377, -0.141543, -0.124834}, {0.0411315, -0.0931735, 0.964126, 0.020519,
       -0.0485833, -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
       0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
  SpikeMin → <|SpikeNegative_1 → {{1., -0.378572, 0.0749814, -0.156765, 0.198588, -0.0756428,
       0.259553, -0.214618, -0.0419981, -0.00700381, 0.102523, -0.0994454},
      {-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627, 0.0839417,
       -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467, -0.0370811,
       0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
    SpikeNegative_2 → {{1., -0.308758, 0.310856, -0.216374, 0.0244407, -0.0137386, 0.0817184,
       -0.0339345, 0.0671982, 0.0564136, -0.169523, -0.0475348}, {-0.969717, -0.0281117, -0.0848724,
       0.0813594, -0.068113, -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293,
       -0.0520501, -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
    SpikeNegative_3 → {{1., -0.427974, -0.0531574, -0.114033, 0.24553, -0.0508005, -0.085664,
       -0.12713, 0.0381449, -0.117304, 0.045997, -0.170561}, {-0.953174, 0.0687073, 0.081267, -0.0893468,
       -0.0891095, 0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647,
       -0.0384319, -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
    SpikeNegative_4 → {{1., -0.251995, 0.182501, -0.0765892, 0.112993, -0.226428, 0.184602, -0.165594,
       -0.0269214, -0.0418235, 0.0222962, -0.0519491}, {-0.978499, -0.0375369, -0.0308657, -0.0197828,
       0.087556, -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659,
       -0.0303762, 0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
    SpikeNegative_5 → {{1., -0.242387, 0.102218, -0.15381, 0.13204, 0.0118847, -0.0165521, -0.0151858,
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    -0.0851968, 0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457,
    0.0411812, -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{1., -0.344318, 0.0529629, -0.126714, 0.157787, -0.155295, 0.219351,
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  SpikeNegative_7 → {{1., -0.329439, -0.0432519, -0.119053, 0.208082, -0.0494009, -0.0661466, -0.0690331,
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    0.0537136, -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{1., -0.165632, 0.181288, -0.159786, 0.0462298, -0.133135, 0.201592, -0.107226,
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    0.0405887, -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389,
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  SpikeNegative_9 → {{1., -0.291364, 0.194493, -0.237561, -0.00620369, -0.0164464, -0.0550088,
    -0.0000434217, 0.00594841, -0.0892194, -0.175671, 0.0556107}, {-0.964652, -0.0492164, -0.044027,
    0.0970846, -0.0799416, 0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659,
    -0.0888441, -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{1., -0.354094, 0.22041, -0.0590442, 0.179462, -0.0402384, 0.0180424, -0.0210457,
    0.0553431, -0.0618828, 0.0621794, 0.00905573}, {-0.972673, -0.00291876, -0.0540171, -0.0812638,
    -0.0617025, 0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018,
    -0.0213425, -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
  SpikeNegative_11 → {{1., -0.337596, 0.0121178, -0.088666, 0.180238, -0.15997, 0.136099, -0.0469544,
    0.0759579, -0.0746132, -0.0598542, -0.0940299}, {-0.03227, 0.0360081, -0.974536, -0.0562723,
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    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{1., -0.371443, 0.113549, -0.219835, 0.00310758, -0.195098, 0.0807429,
    -0.023683, 0.0441132, -0.0804844, -0.123699, 0.0605891}, {0.0228997, -0.0356184, -0.973634,
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    0.029504, -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{1., -0.2949, 0.0415667, -0.235597, 0.0254648, -0.135246, 0.0248431,
    -0.0190933, 0.128025, 0.0270883, -0.0582158, 0.0158311}, {0.089408, -0.00831708, -0.964283,
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    -0.0365538, -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{1., -0.359153, 0.260644, -0.16505, 0.0688376, -0.116282, 0.0397623,
    -0.12509, -0.0106567, -0.0824438, -0.0979009, -0.0296165}, {-0.0381839, 0.0217806, -0.963264,
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  SpikeNegative_15 → {{1., -0.380266, 0.109455, -0.178188, 0.151347, -0.0535533, 0.0633343, -0.21195,
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    -0.026309, 0.000455216, -0.0829657, 0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281,
    0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{1., -0.4277, 0.117569, -0.143211, 0.102771, -0.211973, 0.083273, -0.0593111,
    0.0900384, -0.0360747, -0.0816342, 0.057343}, {-0.00639921, 0.0369683, -0.976295, 0.0340422,
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    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{1., -0.271487, 0.125631, -0.184915, 0.0838418, -0.0117988, 0.0898273,
    0.00375451, 0.0644186, 0.0156567, -0.174835, 0.0852403}, {-0.0701592, 0.0172702, -0.96504, -0.0844552,
    0.0472312, 0.0616787, -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667,
    0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{1., -0.181916, 0.102843, -0.125026, 0.144893, -0.0588845, 0.0543265,
    -0.168339, -0.00966562, -0.0306539, 0.0903792, -0.135541}, {0.0700203, -0.100452, -0.962503,
    -0.0223616, -0.0879604, 0.0000556895, -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971,
    0.099183, 0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
  SpikeNegative_19 → {{1., -0.203174, 0.0452477, -0.186078, 0.0732826, -0.177607, 0.0894062,
    -0.196745, 0.0291774, 0.0575484, -0.0378827, -0.113797}, {-0.023199, -0.0672119, -0.973318,
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    0.0105588, -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{1., -0.200871, 0.118472, -0.208293, 0.0615977, -0.0609034, 0.171594, -0.14394,
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    -0.0810007, -0.0175827, 0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}}|>,
Lag1 → <|LinearPositive_1 → {{1., 0.832165, 0.737304, 0.603614, 0.506978, 0.376341,
    0.287584, 0.170278, 0.0843088, -0.00771653, -0.0904942, -0.163454},
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    0.205188, 0.223266, 0.241367, 0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, 0.373425}},
LinearPositive_2 → {{1., 0.831703, 0.738775, 0.603777, 0.507206, 0.377587, 0.290233, 0.172056,
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LinearPositive_3 → {{1., 0.835271, 0.740587, 0.605539, 0.507056, 0.377435, 0.287925,
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    0.204397, 0.22244, 0.241027, 0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}},
LinearPositive_4 → {{1., 0.830571, 0.737641, 0.601934, 0.505707, 0.376853, 0.289998, 0.172257,
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    0.222052, 0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}},
LinearPositive_5 → {{1., 0.832843, 0.738492, 0.603471, 0.505816, 0.375406, 0.287901, 0.171027,
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    0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
LinearPositive_6 → {{1., 0.831488, 0.740002, 0.60452, 0.506391, 0.37456, 0.284903, 0.168979,
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    0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
LinearPositive_7 → {{1., 0.832829, 0.738128, 0.604062, 0.507712, 0.378189, 0.289458, 0.171892,
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LinearPositive_8 → {{1., 0.830476, 0.738927, 0.604238, 0.508496, 0.377509, 0.289272, 0.168688,
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    0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}},
LinearPositive_9 → {{1., 0.833398, 0.741435, 0.604846, 0.505684, 0.37511, 0.287031, 0.171626,
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LinearPositive_10 → {{1., 0.831924, 0.738943, 0.604125, 0.506695, 0.376022, 0.287934,
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LinearPositive_11 → {{1., 0.823852, 0.732056, 0.601429, 0.511365, 0.384302, 0.297253,
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    0.216208, 0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, 0.373621}},
LinearPositive_12 → {{1., 0.829893, 0.745036, 0.613267, 0.515151, 0.383054, 0.288696,
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    0.240546, 0.269187, 0.279387, 0.302162, 0.315899, 0.330232, 0.349931, 0.381055}},
LinearPositive_13 → {{1., 0.832234, 0.735882, 0.605139, 0.506245, 0.370346, 0.280795,
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    0.241086, 0.263228, 0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}},
LinearPositive_14 → {{1., 0.834882, 0.73393, 0.597537, 0.501713, 0.376363, 0.277181,
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   {0.0276601, 0.0348994, 0.0578995, 0.0764811, 0.0865063, 0.115217, 0.136395, 0.15157, 0.16455, 0.180615,
    0.213666, 0.215142, 0.243638, 0.254281, 0.280739, 0.299298, 0.313921, 0.336645, 0.361637, 0.373861}},
LinearPositive_15 → {{1., 0.828186, 0.735692, 0.59894, 0.501888, 0.372039, 0.283647, 0.172277,
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    0.250473, 0.25777, 0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}},
LinearPositive_16 → {{1., 0.829856, 0.735741, 0.589906, 0.488065, 0.360802, 0.281792,
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LinearPositive_17 → {{1., 0.822893, 0.739018, 0.600545, 0.50594, 0.375338, 0.289894, 0.171647,
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    0.0765604, 0.0991872, 0.117741, 0.128177, 0.147496, 0.159869, 0.189666, 0.195939,
    0.215447, 0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
LinearPositive_18 → {{1., 0.825739, 0.739048, 0.602352, 0.507562, 0.374165, 0.293272,
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    0.164693, 0.0810205, -0.00431074, -0.0841038, -0.162696}, {0.0115844, 0.0455792, 0.0534286,
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    0.232407, 0.261637, 0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}},
LinearPositive_19 → {{1., 0.835069, 0.745051, 0.612695, 0.516098, 0.388636, 0.29719,
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LinearPositive_20 → {{1., 0.831792, 0.736577, 0.598173, 0.499575, 0.37205, 0.289457, 0.17087,
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    0.231304, 0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
LinearNegative_1 → {{1., 0.83719, 0.739381, 0.604169, 0.494219, 0.361473, 0.283183, 0.185222,
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LinearNegative_2 → {{1., 0.829461, 0.767243, 0.615865, 0.514221, 0.385724, 0.304069, 0.172351,
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    -0.248781, -0.268592, -0.290148, -0.294015, -0.319548, -0.339092, -0.343638, -0.357122}},
LinearNegative_3 → {{1., 0.815032, 0.734558, 0.600452, 0.509977, 0.377932, 0.291328, 0.163398,
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    -0.237918, -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
LinearNegative_4 → {{1., 0.829256, 0.731172, 0.575195, 0.476762, 0.361192, 0.266288, 0.157162,
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    -0.243003, -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844}},
LinearNegative_5 → {{1., 0.842646, 0.748382, 0.60178, 0.500648, 0.381665, 0.27033, 0.158453,
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    -0.230144, -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}},
LinearNegative_6 → {{1., 0.81763, 0.729298, 0.602152, 0.508859, 0.368736, 0.263636, 0.156693,
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LinearNegative_7 → {{1., 0.81259, 0.722858, 0.580771, 0.490702, 0.363984, 0.267705, 0.152222,
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LinearNegative_8 → {{1., 0.824138, 0.740414, 0.591637, 0.499434, 0.374508, 0.297429, 0.161081,
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LinearNegative_9 → {{1., 0.839454, 0.750303, 0.612054, 0.519281, 0.4047, 0.302112, 0.194963,
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LinearNegative_10 → {{1., 0.807521, 0.734326, 0.598406, 0.509809, 0.368318, 0.297468, 0.165497,
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LinearNegative_11 → {{1., 0.830986, 0.72962, 0.599235, 0.505198, 0.38074, 0.289829, 0.176566,
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    -0.235518, -0.271564, -0.288178, -0.293001, -0.310129, -0.328328, -0.364455, -0.366174}},
LinearNegative_12 → {{1., 0.828247, 0.741448, 0.607429, 0.513849, 0.382612, 0.287038, 0.167987,
    0.0839585, -0.00447479, -0.0965002, -0.165182}, {-0.0105234, -0.0459122, -0.0631169, -0.0780043,
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    -0.245066, -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
LinearNegative_13 → {{1., 0.824885, 0.734317, 0.605062, 0.512476, 0.382771, 0.284238, 0.175112,
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LinearNegative_14 → {{1., 0.83284, 0.740112, 0.603071, 0.501544, 0.369385, 0.27489, 0.164737,
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  Sinusoidal3_26 → {{1., 0.437669, -0.245066, -0.788608, -0.88414, -0.57365, 0.000620753,
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  Sinusoidal3_27 → {{1., 0.436832, -0.242083, -0.787947, -0.883353, -0.5724, -0.000610968,
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  Sinusoidal3_28 → {{1., 0.434852, -0.239399, -0.785986, -0.883365, -0.577437, -0.00247087,
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  Sinusoidal3_29 → {{1., 0.432849, -0.241347, -0.788321, -0.883222, -0.572714, 0.00169048,
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  Sinusoidal3_30 → {{1., 0.436835, -0.241993, -0.787199, -0.884213, -0.57526, -0.000792777,
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Lag3 → <|Sinusoidal1_1 → {{1., -1.13596, -0.528291, 0.888744, 0.702229, -1.36619, 0.133247,
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    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>,
Lag4 → <|Sinusoidal2_11 → {{1., -0.680106, -1.06595, 0.288917, 1.10516, -0.0236389, -0.956492,
    -0.28344, 0.837326, 0.424768, -0.58074, -0.577766}, {-0.0952089, -0.252202, 0.25704, 0.097318,
    -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{1., -0.676698, -1.06291, 0.291233, 1.10455, -0.025792, -0.956588, -0.284587,
    0.836888, 0.428066, -0.582526, -0.571677}, {-0.101498, -0.25529, 0.251653, 0.0972642,
    -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
    0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{1., -0.682672, -1.06371, 0.29729, 1.10734, -0.0336773, -0.960122, -0.279161,
    0.840127, 0.416383, -0.584556, -0.571068}, {-0.0918789, -0.259087, 0.253065, 0.103093,
    -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{1., -0.67812, -1.0598, 0.29465, 1.10281, -0.0321286, -0.961201, -0.279692,
    0.838932, 0.420375, -0.58906, -0.570753}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{1., -0.680605, -1.06526, 0.294895, 1.10645, -0.0286809, -0.962226, -0.277509,
    0.840732, 0.418887, -0.587251, -0.57214}, {-0.0939856, -0.25429, 0.25073, 0.100441,
    -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
    0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{1., -0.68303, -1.06304, 0.296513, 1.10519, -0.0351794, -0.956985, -0.27577,
    0.840171, 0.413609, -0.589863, -0.568031}, {-0.0916775, -0.260977, 0.251061, 0.104141,
    -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
    0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{1., -0.677819, -1.06459, 0.287945, 1.10474, -0.0201893, -0.96178, -0.287565,
    0.835205, 0.430551, -0.584366, -0.576436}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
    -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
```

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```
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{1., -0.675432, -1.06131, 0.288762, 1.10238, -0.0219162, -0.954852, -0.281505,
    0.83498, 0.423006, -0.581237, -0.573025}, {-0.102994, -0.260616, 0.250831, 0.0989794,
    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{1., -0.680113, -1.06568, 0.28986, 1.10523, -0.0259042, -0.955863, -0.283714,
    0.838021, 0.425032, -0.579062, -0.577411}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{1., -0.681323, -1.06167, 0.290936, 1.10571, -0.0280148, -0.95218, -0.287545,
    0.834333, 0.421727, -0.576558, -0.579726}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
    -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>|>
```

```
In[7]:= Query[All, Length]@classificationAutocorrelationOptions
Out[7]= <|SpikeMax → 20, SpikeMin → 20, Lag1 → 50, Lag3 → 10, Lag4 → 10|>
```

InterpolationDeltaT (1)

```
In[1]:= Needs["MathIOmica`"]
```

InterpolationDeltaT allows us to explicitly set the time step for the interpolation used. This assumes the Method option has been set for "InterpolatedAutocorrelation".

For example, we can provide cutoffs for different lags (we use the same main example, and background noise example for 20 timepoints):

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
 backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
 timePointsExample = Range[20];
```

We can use the background to determine our data cutoffs for the "InterpolatedAutocorrelation" method. We work with the QuantileEstimator function to generate a value for the AutocorrelationCutoffs, by default using the 0.95th quantile. (N.B. the following computaiton may be time consuming depending on number of samples in the background simulation). In our example we will use InterpolationDeltaT→ 2, so this must be used in the quantile estimations as well:

```
In[3]:= bootstrapQ95InterpolatedAutocorrelationDeltaT2 = QuantileEstimator[backgroundExample,
   timePointsExample , Method → "InterpolatedAutocorrelation", InterpolationDeltaT → 2]
Out[3]= {0.367041, 0.354262, 0.348226, 0.338135, 0.32526, 0.291474, 0.249861, 0.201187, 0.142794}
```

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We can work again with the QuantileEstimator function to also generate a value for the SpikeCutoffs:

```
In[4]:= bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"]
Out[4]= <|20 → {0.42185, -0.421758}|>
```

Let's perform the classification, setting the InterpolationDeltaT to 2:

```
In[5]:= classificationInterpolatedAutocorrelationDeltaT = TimeSeriesClassification[classificationExample1,
  timePointsExample, AutocorrelationCutoffs → bootstrapQ95InterpolatedAutocorrelationDeltaT2,
  SpikeCutoffs → bootstrapQ95Spikes, Method → "InterpolatedAutocorrelation", InterpolationDeltaT → 2]
```

Method → "InterpolatedAutocorrelation"

```
Out[5]= <|SpikeMax →
  <|SpikePositive_1 → {{1., 0.00410902, -0.0870523, -0.0342394, -0.0156175, -0.025083, -0.074007, -0.0484823,
      -0.0916302, -0.127997}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
      0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{1., -0.0161829, -0.0370334, -0.022535, -0.0837819, 0.0185967, -0.0740317,
      -0.137188, -0.106721, -0.0411227}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{1., 0.0937336, -0.0181049, -0.108545, -0.079746, 0.0544699, -0.0331148,
      -0.129622, -0.124931, -0.15414}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{1., 0.0419235, 0.0381467, 0.0142504, -0.0515556, -0.130312, -0.0575156,
      -0.0194415, -0.15389, -0.181606}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{1., 0.0204049, 0.0888548, 0.0539044, -0.0391513, -0.0878807, -0.121269,
      -0.127843, -0.135391, -0.151629}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
      0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
      0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{1., -0.0527878, -0.0810995, -0.0936634, -0.0141846, 0.0204539, 0.0320604,
      -0.161713, -0.0318565, -0.117209}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{1., -0.0340483, -0.00200042, -0.042967, -0.0994171, 0.0115602, -0.0332613,
      -0.0647428, -0.198903, -0.0362205}, {0.973634, -0.0197451, 0.00381691, 0.0632199,
      0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
      0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{1., 0.0168409, -0.0205142, -0.047613, -0.0968282, -0.121036, -0.101734,
      -0.108596, -0.00768252, -0.0128373}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{1., -0.030172, -0.049422, -0.0364252, -0.0627082, 0.00679192, -0.0791254,
      -0.126166, -0.0214671, -0.101307}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
      0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{1., 0.00499094, 0.0209404, -0.0182719, -0.121846, -0.159969, 0.0301172,
      -0.120893, -0.140272, 0.00520325}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
      0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
      -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{1., 0.0644065, -0.0976295, -0.0370324, -0.075139, -0.0805995, -0.0212728,
      -0.0747864, -0.181519, 0.0035717}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
      0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
      0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{1., -0.149654, 0.0123306, 0.00372967, -0.0480748, -0.101192, -0.0140265,
      -0.0853756, -0.133597, 0.0158605}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
```

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```
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
    SpikePositive_13 → {{1., -0.185142, -0.0917431, -0.0618227, 0.0597219, 0.0231785, -0.130899,
      -0.145579, 0.0340128, -0.00172783}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
      -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
      0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
    SpikePositive_14 → {{1., 0.0160122, -0.0293784, -0.055754, -0.00480707, -0.125004, -0.179339,
      -0.0300836, -0.0953402, 0.00369356}, {0.0757209, -0.0202174, 0.968597, -0.0798072,
      0.0669311, 0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164,
      -0.0464562, -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
    SpikePositive_15 → {{1., -0.121795, 0.0699542, -0.00264422, -0.00198093, 0.00312771, -0.162774,
      -0.127618, -0.169147, 0.0128775}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
      0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
      -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
    SpikePositive_16 → {{1., -0.175467, -0.0249048, -0.0145199, 0.0195989, -0.120716, 0.00849912,
      -0.137274, -0.0656731, 0.0104567}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
      -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
      -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
    SpikePositive_17 → {{1., -0.0151768, -0.09117, 0.0382957, -0.0507115, -0.178628, 0.00854639,
      -0.0559961, -0.160687, 0.00552753}, {0.0894556, -0.0939456, 0.955206, -0.0721055,
      0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
      -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
    SpikePositive_18 → {{1., -0.255853, -0.00175953, 0.0610855, -0.137393, -0.0195575, -0.102007,
      -0.00626728, -0.0459179, 0.00766957}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
      -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
      0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
    SpikePositive_19 → {{1., -0.110425, -0.00553436, -0.0391654, -0.0810071, -0.15365, -0.0849102,
      -0.000902989, -0.0305533, 0.00614854}, {-0.0584325, 0.0880122, 0.972312, -0.0409534,
      0.0540727, -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323,
      -0.0924997, 0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
    SpikePositive_20 → {{1., -0.0890285, -0.0865333, -0.0961887, -0.121304, 0.0257782, -0.0570337,
      -0.00313745, -0.0768446, 0.00429182}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
      -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
      0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
  SpikeMin → <|SpikeNegative_1 → {{1., -0.101744, 0.0438062, -0.160357, 0.0142096, -0.0286236,
      -0.0416032, -0.0763343, -0.0491543, -0.100199}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
      -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
      -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
    SpikeNegative_2 → {{1., 0.0895658, 0.0422544, 0.00989784, -0.118547, -0.027519, -0.0533989,
      -0.172756, -0.176767, -0.0927297}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
      -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
      -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
    SpikeNegative_3 → {{1., -0.161397, 0.0279888, -0.0453001, -0.0475332, -0.0343681, -0.0722216,
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      -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
    SpikeNegative_4 → {{1., 0.0368973, -0.0850944, -0.0925464, -0.00430084, -0.135344, -0.0174178,
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      -0.0303762, 0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
    SpikeNegative_5 → {{1., -0.0497702, 0.0570587, 0.0350493, -0.106695, -0.000952622, -0.127232,
      -0.0795974, -0.157, -0.0708604}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
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      -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
    SpikeNegative_6 → {{1., -0.0715958, -0.0208192, -0.0428877, -0.0582989, -0.0664149, -0.0412187,
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      -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
      0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
    SpikeNegative_7 → {{1., -0.129348, 0.0421249, 0.0138537, -0.0196273, -0.0410833, -0.130338,
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    SpikeNegative_8 → {{1., 0.0312729, -0.0317954, -0.0578051, -0.0791657, -0.100503, -0.124564,
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      0.06932, -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
    SpikeNegative_9 → {{1., -0.0041917, 0.00730401, 0.0243157, -0.142822, -0.0753031, -0.020826,
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  SpikeNegative_10 → {{1., 0.0561481, 0.0433998, 0.0287897, 0.0205456, -0.135019, -0.0576998,
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  SpikeNegative_11 → {{1., -0.14533, -0.0111378, 0.0292942, -0.0764784, -0.0765193, -0.0151034,
    -0.146135, -0.0628998, 0.00430969}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
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    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{1., -0.0943721, -0.0680213, 0.0403258, -0.091261, -0.0511237, -0.0183944,
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  SpikeNegative_13 → {{1., -0.210299, -0.0421202, 0.052353, -0.0728334, -0.019462, -0.152028,
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    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{1., -0.0125454, -0.0129208, -0.075111, -0.112869, 0.0310825, -0.145504,
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    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{1., -0.156699, 0.0481614, -0.138248, -0.0216867, -0.106084, -0.0125703,
    -0.000875418, -0.130169, 0.0181705}, {-0.00121514, -0.0078406, -0.978821, -0.0221297,
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    0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{1., -0.0883184, -0.0527533, 0.0349908, -0.0662344, -0.0437328, -0.096258,
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    0.0583464, 0.0166785, 0.0680268, 0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101,
    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{1., -0.105001, 0.0518312, 0.0484384, -0.116041, -0.0936974, -0.0802334,
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    0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{1., -0.124903, 0.0245441, -0.110707, 0.0251984, -0.114783, -0.102646,
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    0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
  SpikeNegative_19 → {{1., -0.102323, -0.026114, -0.0998426, -0.0529457, -0.0685194, -0.135343,
    0.00982041, -0.0269417, 0.00220889}, {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693,
    0.0216656, 0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588,
    -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{1., -0.0908484, 0.00860196, -0.131651, -0.0782976, 0.00974228, -0.129907,
    -0.0612688, -0.0287008, 0.00232944}, {-0.0543654, -0.0510581, -0.970055, -0.0636564,
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    -0.0810007, -0.0175827, 0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}}|>,
Lag1 → <|LinearPositive_1 → {{1., 0.698956, 0.412364, 0.146444, -0.0770518,
    -0.257126, -0.373513, -0.422617, -0.38124, -0.246216},
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    0.205188, 0.223266, 0.241367, 0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, 0.373425}},
  LinearPositive_2 → {{1., 0.699891, 0.413234, 0.148678, -0.0780676, -0.260488, -0.375522,
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    0.110677, 0.130133, 0.148914, 0.167272, 0.186766, 0.206807, 0.224025, 0.242161,
    0.261728, 0.280689, 0.29779, 0.316418, 0.335012, 0.355339, 0.375155}}, LinearPositive_3 →
   {{1., 0.700646, 0.411791, 0.148849, -0.0788867, -0.258405, -0.376018, -0.420902, -0.382238, -0.244836},
   {0.0204364, 0.0388961, 0.055949, 0.0753517, 0.0937248, 0.112155, 0.1288, 0.150982, 0.166685, 0.187482,
    0.204397, 0.22244, 0.241027, 0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}},
  LinearPositive_4 → {{1., 0.699912, 0.412975, 0.149003, -0.0780986, -0.260631, -0.375614,
    -0.42103, -0.381062, -0.245454}, {0.0188591, 0.0384796, 0.0552706, 0.0761382,
    0.0941127, 0.11255, 0.131257, 0.150426, 0.166514, 0.185049, 0.206061, 0.222052,
    0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}},
  LinearPositive_5 → {{1., 0.699012, 0.409909, 0.147461, -0.0777493, -0.254354, -0.373743,
    -0.421018, -0.38327, -0.246247}, {0.0196474, 0.0375735, 0.0561861, 0.0745382,
    0.094777, 0.113054, 0.132423, 0.150372, 0.169563, 0.188068, 0.205612, 0.225889,
    0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
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LinearPositive_6 → {{1., 0.702317, 0.409629, 0.146671, -0.0781576, -0.255419, -0.37451,
   -0.422494, -0.384575, -0.24346}, {0.0186014, 0.0381755, 0.0550572, 0.074646,
   0.0932816, 0.113886, 0.132134, 0.149767, 0.168659, 0.185415, 0.205262, 0.222624,
   0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
LinearPositive_7 → {{1., 0.699843, 0.413686, 0.147529, -0.0789497, -0.257681, -0.375962,
   -0.422455, -0.380461, -0.24555}, {0.0186204, 0.0363314, 0.0569047, 0.0757329,
   0.092018, 0.111558, 0.130244, 0.148133, 0.167451, 0.186409, 0.204805, 0.22423,
   0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
LinearPositive_8 → {{1., 0.699729, 0.413908, 0.145757, -0.0788936, -0.255386, -0.37538,
   -0.423949, -0.380244, -0.245541}, {0.0170019, 0.0382694, 0.0569482, 0.0754625,
   0.0914347, 0.110031, 0.132014, 0.15073, 0.169121, 0.188274, 0.205265, 0.223358,
   0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}},
LinearPositive_9 → {{1., 0.701365, 0.409562, 0.148288, -0.0792438, -0.254797, -0.375691,
   -0.420883, -0.384347, -0.244252}, {0.0185501, 0.0388643, 0.0547098, 0.0747468,
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   0.241691, 0.261072, 0.279055, 0.298507, 0.318632, 0.337602, 0.353993, 0.372608}},
LinearPositive_10 → {{1., 0.699034, 0.411326, 0.148169, -0.0780022, -0.256703, -0.37461,
   -0.42094, -0.382114, -0.24616}, {0.0174864, 0.0370712, 0.0572236, 0.0748823,
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   0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
LinearPositive_11 → {{1., 0.691706, 0.42131, 0.144066, -0.0772766, -0.259843, -0.372966,
   -0.426236, -0.371003, -0.249758}, {0.013623, 0.0406398, 0.0607801, 0.0781742,
   0.0921015, 0.112119, 0.128868, 0.151429, 0.171509, 0.192449, 0.211181, 0.216208,
   0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, 0.373621}},
LinearPositive_12 → {{1., 0.712985, 0.419487, 0.148913, -0.0876302, -0.265606, -0.388139,
   -0.426315, -0.379494, -0.234201}, {0.0219335, 0.0431422, 0.0502095, 0.0696589,
   0.0884956, 0.116468, 0.123447, 0.151797, 0.168869, 0.179094, 0.204522, 0.228042,
   0.240546, 0.269187, 0.279387, 0.302162, 0.315899, 0.330232, 0.349931, 0.381055}},
LinearPositive_13 → {{1., 0.713968, 0.41629, 0.135655, -0.0850199, -0.250161, -0.382346,
   -0.435835, -0.380987, -0.231563}, {0.022617, 0.0284408, 0.0607512, 0.0795972, 0.0880775,
   0.119613, 0.134238, 0.152698, 0.169261, 0.181713, 0.197855, 0.217149, 0.241086, 0.263228,
   0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}}, LinearPositive_14 →
 {{1., 0.699048, 0.421186, 0.144637, -0.0743318, -0.273686, -0.373155, -0.426828, -0.373656, -0.243214},
  {0.0276601, 0.0348994, 0.0578995, 0.0764811, 0.0865063, 0.115217, 0.136395, 0.15157, 0.16455, 0.180615,
   0.213666, 0.215142, 0.243638, 0.254281, 0.280739, 0.299298, 0.313921, 0.336645, 0.361637, 0.373861}},
LinearPositive_15 → {{1., 0.689553, 0.416711, 0.154817, -0.0712844, -0.278647, -0.371692,
   -0.414268, -0.373615, -0.251574}, {0.0152129, 0.0390101, 0.0602871, 0.0702062, 0.091338,
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   0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}}, LinearPositive_16 →
 {{1., 0.689357, 0.396543, 0.148461, -0.0689227, -0.248777, -0.361273, -0.412373, -0.390673, -0.252341},
  {0.0164478, 0.0360481, 0.048135, 0.0712245, 0.101186, 0.114916, 0.129433, 0.153936, 0.164281, 0.192697,
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LinearPositive_17 → {{1., 0.699246, 0.408729, 0.148228, -0.0789643, -0.255037, -0.375143,
   -0.419389, -0.382623, -0.245046}, {0.0153802, 0.0408047, 0.0548321, 0.0765604,
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   0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
LinearPositive_18 → {{1., 0.684111, 0.404792, 0.132384, -0.0606279, -0.245961, -0.350448,
   -0.425923, -0.382524, -0.255803}, {0.0115844, 0.0455792, 0.0534286, 0.068487, 0.0918771,
   0.107837, 0.137609, 0.144956, 0.162508, 0.185864, 0.206224, 0.229689, 0.232407, 0.261637,
   0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}}, LinearPositive_19 →
 {{1., 0.699244, 0.422015, 0.147958, -0.0782255, -0.271984, -0.378351, -0.423859, -0.372331, -0.244467},
  {0.0205961, 0.045526, 0.0569898, 0.0724948, 0.0867427, 0.105806, 0.12769, 0.145665, 0.170669, 0.180276,
   0.216792, 0.223063, 0.241101, 0.270774, 0.282283, 0.293887, 0.315058, 0.334039, 0.359611, 0.369743}},
LinearPositive_20 → {{1., 0.688016, 0.40477, 0.139957, -0.0641909, -0.253801, -0.356399,
   -0.421886, -0.383325, -0.253142}, {0.00952752, 0.0286979, 0.0547226, 0.0709501,
   0.0958101, 0.109505, 0.135844, 0.152431, 0.165158, 0.182651, 0.210505, 0.231304,
   0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
LinearNegative_1 → {{1., 0.673224, 0.369988, 0.16643, -0.0528454, -0.267876, -0.344135,
   -0.386855, -0.398952, -0.258979}, {-0.0218046, -0.0446169, -0.0612231, -0.0738948,
   -0.109733, -0.115191, -0.124469, -0.148293, -0.159758, -0.176361, -0.217843, -0.224298,
   -0.23172, -0.273794, -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733}},
LinearNegative_2 → {{1., 0.718864, 0.411059, 0.143266, -0.0889583, -0.258744, -0.387112,
   -0.428789, -0.383953, -0.225632}, {-0.0137543, -0.0552134, -0.0387902, -0.0787876,
   -0.0972777, -0.0993326, -0.131634, -0.158204, -0.178021, -0.176063, -0.209858, -0.230763,
   -0.248781, -0.268592, -0.290148, -0.294015, -0.319548, -0.339092, -0.343638, -0.357122}},
LinearNegative_3 → {{1., 0.695443, 0.413074, 0.135843, -0.0603693, -0.278633, -0.356048,
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```
    -0.428273, -0.379744, -0.241293}, {-0.0283384, -0.0528281, -0.0527884, -0.0740599,
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    -0.237918, -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
LinearNegative_4 → {{1., 0.70622, 0.413682, 0.144538, -0.0787741, -0.262683, -0.377072,
    -0.426136, -0.382069, -0.237706}, {-0.0158873, -0.0248133, -0.0382326, -0.0881019,
    -0.0887054, -0.128386, -0.128859, -0.161147, -0.159022, -0.205319, -0.200777, -0.210411,
    -0.243003, -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844}},
LinearNegative_5 → {{1., 0.695149, 0.415546, 0.14541, -0.0777504, -0.261286, -0.377478,
    -0.42141, -0.375396, -0.242784}, {-0.0201624, -0.0405386, -0.0436406, -0.0738225,
    -0.0817467, -0.105404, -0.114359, -0.154377, -0.169473, -0.174198, -0.212011, -0.225376,
    -0.230144, -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}},
LinearNegative_6 → {{1., 0.710813, 0.403309, 0.156324, -0.0838182, -0.26453, -0.382078,
    -0.414541, -0.391916, -0.233563}, {-0.0267223, -0.0446999, -0.0523138, -0.0699606,
    -0.0987645, -0.126896, -0.126614, -0.165572, -0.172297, -0.184872, -0.208135, -0.237294,
    -0.243037, -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481}},
LinearNegative_7 → {{1., 0.663466, 0.386219, 0.130453, -0.0667799, -0.202002, -0.344284,
    -0.412292, -0.388106, -0.266675}, {-0.00172329, -0.032268, -0.068173, -0.0857129,
    -0.0881686, -0.107137, -0.140409, -0.14992, -0.182962, -0.175511, -0.200764, -0.226349,
    -0.23516, -0.248536, -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923}},
LinearNegative_8 → {{1., 0.68559, 0.393357, 0.116198, -0.0737183, -0.19817, -0.356351,
    -0.4352, -0.384484, -0.247221}, {-0.0170306, -0.0378539, -0.0394845, -0.0767312,
    -0.0942537, -0.105065, -0.146528, -0.134698, -0.186411, -0.174071, -0.194782, -0.232787,
    -0.238911, -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
LinearNegative_9 → {{1., 0.727431, 0.441921, 0.165601, -0.117365, -0.295226, -0.425995,
    -0.417171, -0.362191, -0.217006}, {-0.0287969, -0.0189698, -0.0530075, -0.0828922,
    -0.0936032, -0.115414, -0.114422, -0.130851, -0.167598, -0.173937, -0.198609, -0.23569,
    -0.258977, -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
LinearNegative_10 → {{1., 0.687788, 0.40544, 0.149372, -0.0839568, -0.246869, -0.382425,
    -0.408004, -0.38429, -0.237054}, {-0.00155633, -0.0271325, -0.0625737, -0.0744387,
    -0.0901925, -0.0932579, -0.138846, -0.15092, -0.157289, -0.198281, -0.189392, -0.206968,
    -0.259028, -0.273261, -0.270544, -0.29133, -0.328913, -0.352948, -0.335503, -0.37816}},
LinearNegative_11 → {{1., 0.685633, 0.419008, 0.142601, -0.0776993, -0.250946, -0.371237,
    -0.423968, -0.370177, -0.253216}, {-0.0105542, -0.0364589, -0.0515525, -0.0708746,
    -0.0862196, -0.118392, -0.123851, -0.151596, -0.176372, -0.191037, -0.213033, -0.221631,
    -0.235518, -0.271564, -0.288178, -0.293001, -0.310129, -0.328328, -0.364455, -0.366174}},
LinearNegative_12 → {{1., 0.6859, 0.411865, 0.146543, -0.068964, -0.260943, -0.364731,
    -0.417759, -0.377761, -0.254151}, {-0.0105234, -0.0459122, -0.0631169, -0.0780043,
    -0.0883748, -0.108962, -0.137461, -0.144887, -0.163604, -0.184293, -0.210166, -0.217602,
    -0.245066, -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
LinearNegative_13 → {{1., 0.687634, 0.41526, 0.160988, -0.0789249, -0.269234, -0.379628,
    -0.408674, -0.373174, -0.254248}, {-0.01186, -0.0431645, -0.0590873, -0.0756374,
    -0.0887624, -0.1144, -0.121973, -0.156462, -0.165726, -0.190329, -0.20958, -0.216046,
    -0.244405, -0.264186, -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596}},
LinearNegative_14 → {{1., 0.698483, 0.40025, 0.137965, -0.0764922, -0.233283, -0.368005,
    -0.424699, -0.389474, -0.244744}, {-0.0187992, -0.0431131, -0.0473458, -0.070655,
    -0.0879629, -0.116006, -0.12521, -0.152395, -0.170415, -0.184268, -0.196593, -0.22289,
    -0.23237, -0.26046, -0.276864, -0.301954, -0.319987, -0.336453, -0.361973, -0.377956}},
LinearNegative_15 → {{1., 0.698242, 0.413727, 0.160344, -0.0838212, -0.26722, -0.384303,
    -0.411359, -0.379422, -0.246188}, {-0.0162872, -0.0293132, -0.0552218, -0.0807767,
    -0.0935334, -0.121112, -0.124004, -0.147926, -0.165828, -0.191582, -0.205406, -0.219926,
    -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
LinearNegative_16 → {{1., 0.705906, 0.399473, 0.148052, -0.0809578, -0.246103, -0.375664,
    -0.418512, -0.393935, -0.23826}, {-0.0225164, -0.0461677, -0.0473716, -0.067817,
    -0.0986701, -0.119505, -0.130459, -0.1556, -0.169469, -0.1814, -0.198572, -0.221935,
    -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}},
LinearNegative_17 → {{1., 0.6918, 0.419808, 0.147985, -0.0770053, -0.262617, -0.374688,
    -0.421881, -0.372487, -0.250915}, {-0.0130003, -0.0309644, -0.0613334, -0.0794837,
    -0.0865967, -0.117058, -0.128048, -0.153332, -0.167054, -0.192254, -0.208455, -0.223898,
    -0.240133, -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}},
LinearNegative_18 → {{1., 0.711405, 0.408735, 0.137687, -0.0797323, -0.250175, -0.375031,
    -0.432083, -0.386514, -0.234292}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
    -0.0895021, -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921,
    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
LinearNegative_19 → {{1., 0.701587, 0.403604, 0.149795, -0.0748901, -0.261202, -0.370664,
    -0.417371, -0.388875, -0.241985}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
    -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
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      -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
    LinearNegative_20 → {{1., 0.719202, 0.424049, 0.147735, -0.0860762, -0.28138, -0.388799,
      -0.429996, -0.37666, -0.228076}, {-0.024006, -0.0432239, -0.0496914, -0.0682004,
      -0.0867373, -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
      -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}}|>,
  Lag2 → <|Sinusoidal2_11 → {{1., -0.829017, 0.411475, 0.0518138, -0.383639, 0.499898, -0.425247,
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      0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
    Sinusoidal2_12 → {{1., -0.827495, 0.408054, 0.0563599, -0.387693, 0.499755, -0.421128,
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      0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668, 0.262301,
      0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
    Sinusoidal2_13 → {{1., -0.825073, 0.400234, 0.0655333, -0.392815, 0.499765, -0.415903,
      0.24337, -0.0915142, 0.0164021}, {-0.0918789, -0.259087, 0.253065, 0.103093,
      -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
      0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
    Sinusoidal2_14 → {{1., -0.826536, 0.403507, 0.0631351, -0.392153, 0.499693, -0.416543,
      0.245954, -0.0948107, 0.0177539}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
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      0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
    Sinusoidal2_15 → {{1., -0.827029, 0.405272, 0.0597795, -0.388886, 0.499885, -0.41996,
      0.249171, -0.0963681, 0.0181355}, {-0.0939856, -0.25429, 0.25073, 0.100441, -0.313599,
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      0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
    Sinusoidal2_16 → {{1., -0.826789, 0.40402, 0.0617558, -0.390026, 0.499811, -0.418687,
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      0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
    Sinusoidal2_17 → {{1., -0.829423, 0.412383, 0.0514215, -0.383565, 0.499829, -0.425344,
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      -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
      0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
    Sinusoidal2_18 → {{1., -0.829612, 0.4128, 0.0513889, -0.383356, 0.499706, -0.425626,
      0.257431, -0.103777, 0.0210469}, {-0.102994, -0.260616, 0.250831, 0.0989794,
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      0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
    Sinusoidal2_19 → {{1., -0.826718, 0.406773, 0.0553693, -0.385566, 0.499858, -0.4233,
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      0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
    Sinusoidal2_20 → {{1., -0.826669, 0.406268, 0.0554359, -0.384538, 0.499874, -0.424262,
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      0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
  Lag3 → <|Sinusoidal1_1 → {{1., -0.365567, -0.60478, 0.637641, 0.0868436, -0.497813, 0.219718,
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      0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
    Sinusoidal1_2 → {{1., -0.377431, -0.587587, 0.631483, 0.0839954, -0.497517, 0.222815,
      0.173993, -0.217656, 0.0679047}, {-0.153886, -0.0875347, 0.297854, -0.276583,
      0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
      -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
    Sinusoidal1_3 → {{1., -0.379784, -0.563877, 0.601353, 0.084444, -0.497158, 0.222198,
      0.202874, -0.241895, 0.0718442}, {-0.187066, -0.0732084, 0.32812, -0.266161, 0.00567862,
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      0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
    Sinusoidal1_4 → {{1., -0.367387, -0.611005, 0.64816, 0.077089, -0.491174, 0.226609, 0.151457,
      -0.191943, 0.0581946}, {-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004,
      0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987, -0.322486,
      0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
    Sinusoidal1_5 → {{1., -0.376989, -0.584927, 0.613138, 0.109618, -0.498752, 0.200097,
      0.19047, -0.21979, 0.0671353}, {-0.20104, -0.101657, 0.31364, -0.234517, -0.0163677,
      0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444, -0.303865,
      0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
    Sinusoidal1_6 → {{1., -0.371524, -0.581557, 0.597048, 0.120868, -0.497326, 0.183924,
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    0.206732, -0.222088, 0.0639235}, {-0.17526, -0.106684, 0.304186, -0.27676, -0.0299081,
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    0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
Sinusoidal1_7 → {{1., -0.375639, -0.577798, 0.618602, 0.0741057, -0.49482, 0.233494,
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    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
Sinusoidal1_8 → {{1., -0.379407, -0.572587, 0.590636, 0.126297, -0.495521, 0.178471,
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    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
Sinusoidal1_9 → {{1., -0.380951, -0.588209, 0.652018, 0.0612232, -0.496484, 0.242324,
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    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
Sinusoidal1_10 → {{1., -0.391996, -0.560476, 0.635962, 0.0550537, -0.49764, 0.252074,
    0.167733, -0.246635, 0.0859254}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}},
Sinusoidal3_21 → {{1., -0.381208, -0.579584, 0.629022, 0.0787856, -0.499824, 0.230141,
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    0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
Sinusoidal3_22 → {{1., -0.376226, -0.58733, 0.627303, 0.0856048, -0.499971, 0.22335, 0.181486,
    -0.221474, 0.0672594}, {0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846,
    0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523, 0.303756,
    0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{1., -0.378143, -0.5853, 0.625298, 0.0908286, -0.499829, 0.218061,
    0.183491, -0.223512, 0.0691063}, {0.18264, -0.0994704, -0.295137, -0.250857,
    0.00157044, 0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036,
    0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{1., -0.378566, -0.586256, 0.632954, 0.0800441, -0.499837, 0.228864,
    0.175825, -0.222525, 0.0694974}, {0.183018, -0.0977985, -0.296248, -0.251125,
    -0.00333361, 0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939,
    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
Sinusoidal3_25 → {{1., -0.377984, -0.58515, 0.626182, 0.0892764, -0.499875, 0.219613,
    0.182395, -0.223596, 0.0691384}, {0.191347, -0.0982886, -0.29771, -0.261082,
    0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
    0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
Sinusoidal3_26 → {{1., -0.377304, -0.584241, 0.621687, 0.0916051, -0.499861, 0.217264,
    0.18715, -0.224608, 0.0683061}, {0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724,
    0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444, 0.296927,
    0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
Sinusoidal3_27 → {{1., -0.377192, -0.585229, 0.625396, 0.0868114, -0.499964, 0.222146,
    0.183464, -0.22362, 0.0681866}, {0.185809, -0.10192, -0.303748, -0.261172, 0.000202029,
    0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227, 0.302676,
    0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
Sinusoidal3_28 → {{1., -0.3773, -0.586621, 0.624841, 0.0923776, -0.499873, 0.21662, 0.183954,
    -0.222327, 0.0683283}, {0.187562, -0.10053, -0.297144, -0.250552, 0.00476677,
    0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453, 0.301104,
    0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
Sinusoidal3_29 → {{1., -0.380157, -0.582694, 0.63157, 0.0792219, -0.499885, 0.2297, 0.177145,
    -0.226176, 0.0712749}, {0.189755, -0.100643, -0.295957, -0.251445, -0.0055221,
    0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546, 0.296096,
    0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
Sinusoidal3_30 → {{1., -0.37831, -0.585112, 0.628653, 0.0847426, -0.499952, 0.224143,
    0.18015, -0.22375, 0.0694368}, {0.186539, -0.100579, -0.301622, -0.251977, 0.00452805,
    0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063, 0.296225,
    0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>|>
```

In[6]:= `Query[All, Length]@classificationInterpolatedAutocorrelationDeltaT`

Out[6]= `<|SpikeMax → 20, SpikeMin → 20, Lag1 → 40, Lag2 → 10, Lag3 → 20|>`

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InterpolationOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

InterpolationOptions allows us to pass options for the internal Interpolation function used. This assumes the Method option has been set for "InterpolatedAutocorrelation". For example we can change the InterpolationOrder option. First we need to generate the data to use:

For example, we can provide cutoffs for different lags (we use the same main example, and background noise example for 20 timepoints):

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
timePointsExample = Range[20];
```

We can use the background to determine our data cutoffs for the "InterpolatedAutocorrelation" method. We work with the QuantileEstimator function to generate a value for the AutocorrelationCutoffs, by default using the 0.95th quantile. (N.B. the following computaiton may be time consuming depending on number of samples in the background simulation).:

In[3]:=
```
bootstrapQ95InterpolatedAutocorrelationOrder3 = QuantileEstimator[backgroundExample, timePointsExample ,
  Method → "InterpolatedAutocorrelation", InterpolationOptions → {InterpolationOrder → 3}]
```

Out[3]=
```
{0.303188, 0.296659, 0.287586, 0.281611, 0.274524, 0.268483, 0.262192, 0.254505, 0.245366, 0.239768,
 0.227267, 0.215607, 0.200545, 0.185658, 0.171387, 0.15369, 0.132348, 0.108645, 0.079037}
```

We can work again with the QuantileEstimator function to also generate a value for the SpikeCutoffs:

In[4]:=
```
bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"]
```

Out[4]=
```
<|20 → {0.42185, -0.421758}|>
```

Let's perform the classification, setting the InterpolationDeltaT to 2:

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In[5]:=
```
classificationInterpolatedAutocorrelationOrder3 =
 TimeSeriesClassification[classificationExample1, timePointsExample, AutocorrelationCutoffs →
   bootstrapQ95InterpolatedAutocorrelationOrder3, SpikeCutoffs → bootstrapQ95Spikes,
  Method → "InterpolatedAutocorrelation", InterpolationOptions → {InterpolationOrder → 3}]
```

Method → "InterpolatedAutocorrelation"

Out[5]=
```
<| SpikeMax →
  <| SpikePositive_1 → {{1., -0.0829057, 0.00040893, 0.00713647, -0.0831192, 0.0737441, -0.0413379, 0.0130211,
      -0.0175846, 0.0654331, -0.0225876, -0.00392938, -0.0528106, -0.0128336, -0.0169535, -0.0930537,
      -0.0542933, -0.0216233, -0.0806804, -0.0760309}, {0.970569, -0.0988615, -0.0240026, -0.0115612,
      -0.0977222, 0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224,
      -0.055411, -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{1., 0.000158644, -0.00795959, 0.0515558, -0.0291068, 0.0483314, -0.00591426,
      -0.0981006, -0.078311, -0.0387618, 0.0252972, -0.0916473, -0.052656, -0.108454, -0.107867, 0.0179604,
      -0.0701124, 0.0200393, -0.00231356, 0.0278615}, {0.973207, 0.00872172, -0.00191539, 0.0695064,
      -0.00641562, 0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666,
      -0.00648697, -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{1., 0.089534, 0.0952262, 0.0221336, -0.0170007, -0.0562672, -0.112552,
      -0.0609559, -0.0664499, 0.0860571, 0.067277, 0.0284007, 0.00100325, 0.0370133, -0.0910503,
      -0.0954548, -0.0861248, -0.118416, -0.111234, -0.11114}, {0.95896, 0.0348607, 0.0657694, 0.0097693,
      -0.0146057, -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763,
      -0.00816843, 0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{1., -0.00637208, 0.0274577, 0.0850603, 0.0605054, -0.0675975, 0.0256527,
      -0.10735, -0.0364457, 0.0333519, -0.0858393, -0.0871813, -0.0371184, 0.0174961, 0.0149864, -0.12483,
      -0.112055, 0.0201852, -0.129091, 0.00918542}, {0.958583, 0.00400217, 0.0429904, 0.0838796,
      0.0778033, -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858,
      0.0195539, 0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{1., -0.018243, 0.00703195, 0.0200047, 0.0640766, 0.0349022, 0.0598126,
      0.00932457, -0.0215913, -0.101708, -0.0849453, 0.0224546, -0.110791, 0.0402995, -0.104482, -0.067085,
      -0.112343, -0.0262379, -0.125582, 0.0151022}, {0.966833, -0.0172757, -0.0101601, 0.0449156,
      0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
      -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{1., -0.0857767, -0.0433111, -0.0393968, -0.079762, -0.0115756, -0.0720682,
      -0.0240194, 0.00862958, -0.036558, 0.0333122, 0.019709, 0.046871, 0.0615058, -0.115273, -0.0169599,
      0.0195664, -0.10028, -0.0701365, 0.00552322}, {0.971085, -0.0737213, -0.0183259, -0.0280164,
      -0.0370416, 0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791,
      0.0886387, 0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{1., -0.0389747, -0.0267932, 0.0356737, 0.00493848, -0.0535228, -0.0336027,
      0.0000646491, -0.0771895, -0.00116161, 0.0367309, 0.00838664, 0.00181294, 0.0355048, -0.0189124,
      -0.0310215, -0.136519, -0.132601, 0.0235617, -0.0963755}, {0.973634, -0.0197451, 0.00381691,
      0.0632199, 0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
      0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{1., -0.0498892, 0.00569434, 0.0525829, -0.0276404, -0.0225072,
      -0.0204974, -0.0639724, -0.079573, 0.0539101, -0.0909182, -0.0860885, -0.0516648,
      -0.10555, -0.0618739, -0.00732326, 0.0333824, 0.023962, 0.0397857, -0.0418197},
     {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677, -0.0238371,
      -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
      -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{1., -0.0388329, -0.0364709, 0.00555867, -0.0600205, 0.11361, -0.0285306,
      -0.0103586, -0.0508265, -0.063406, 0.023537, -0.0222665, -0.056719, -0.062707, -0.105077, 0.00153685,
      0.00897393, -0.00461782, -0.0612345, -0.0521491}, {0.979998, -0.049438, -0.0488434, 0.00681623,
      -0.062095, 0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267,
      -0.0503857, -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{1., -0.10299, -0.00625346, 0.0187041, 0.0105549, 0.0435659, -0.0188147,
      0.0287845, -0.109404, -0.0164167, -0.122764, -0.091056, 0.0600743, -0.0630775, -0.0922395, 0.0601883,
      -0.0922895, -0.0639819, 0.041124, 0.0162916}, {0.961551, -0.0906575, 0.00581915, 0.00875268,
      0.0455119, 0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431,
      0.101266, -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{1., -0.0252805, 0.0751799, -0.00977573, -0.102989, 0.0253495, -0.0428297,
      0.0636324, -0.0792322, -0.0380079, -0.0695781, -0.0126896, -0.00994757, -0.0468254, -0.0574888,
      -0.0488202, -0.160838, 0.0423057, -0.00232819, 0.000163028}, {0.0696283, 0.0251021, 0.968196,
      0.0511374, 0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
      -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{1., -0.114796, 0.0123203, 0.0497409, 0.0682909, -0.121107, 0.07003, -0.11022,
      0.043144, -0.100916, -0.0206145, -0.00774724, 0.0429704, -0.115509, -0.00827139, -0.0957671,
```

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```
      -0.0433478, -0.054675, 0.00569054, 0.000784489}, {0.0427773, -0.0204301, 0.972226, -0.00645026,
      0.0200803, 0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808,
      0.00471403, 0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
   SpikePositive_13 → {{1., 0.010788, -0.175038, -0.0595551, -0.0726882, 0.0905362, -0.0592104,
      0.0188561, 0.0575894, -0.0668446, 0.0458708, 0.0314406, -0.125494, -0.123434, -0.105443, 0.0661682,
      0.0515828, -0.0938117, 0.00159562, 0.00709075}, {-0.0343175, -0.0155132, 0.955818, 0.0636753,
      -0.0900903, -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626,
      0.0398952, 0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
   SpikePositive_14 → {{1., -0.146257, 0.0898353, 0.0620822, -0.00675877, -0.0241766, -0.0229316,
      -0.0824982, 0.0306996, -0.109258, -0.067984, -0.0632565, -0.132622, 0.0203788, 0.0212707, -0.0628653,
      -0.0331826, 0.0298752, -0.00321041, 0.000859144}, {0.0757209, -0.0202174, 0.968597, -0.0798072,
      0.0669311, 0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164,
      -0.0464562, -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
   SpikePositive_15 → {{1., -0.0891417, -0.0669202, 0.0133757, 0.0639883, -0.10497, 0.0138498,
      0.0383513, 0.022042, 0.00768769, 0.0251438, -0.0596496, -0.13082, -0.0740195, -0.107679, 0.0436447,
      -0.139503, 0.0444339, 0.0010135, -0.000826739}, {0.0367157, 0.00909492, 0.955211, -0.0373177,
      -0.0545922, 0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346,
      0.0584456, -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
   SpikePositive_16 → {{1., 0.0619093, -0.0811079, -0.100739, 0.00690859, -0.083394, 0.0156456,
      -0.0398845, 0.0548407, -0.0264353, -0.0778217, -0.0673814, 0.0432855, -0.00177617,
      -0.0948292, -0.0990838, -0.0179445, 0.00651696, 0.00132317, -0.0000325663},
     {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223, -0.00461306,
      -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381, -0.0588352,
      -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
   SpikePositive_17 → {{1., -0.308291, 0.0368668, 0.0708828, -0.0995177, 0.0377104, 0.0347984,
      -0.0390797, -0.0285037, 0.0406767, -0.15296, 0.053668, 0.0295606, -0.0679747, -0.00679,
      0.0204712, -0.105663, -0.0213386, 0.00622363, -0.000741028}, {0.0894556, -0.0939456, 0.955206,
      -0.0721055, 0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
      -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
   SpikePositive_18 → {{1., 0.0176341, -0.179643, -0.0639626, 0.0145391, -0.030203, 0.0623805,
      -0.118843, -0.109145, -0.0202256, 0.0141673, 0.0147488, -0.0680384, -0.0368559, 0.03698, 0.0681757,
      -0.0100084, -0.107953, 0.00733095, 0.00892167}, {-0.0361007, -0.0216285, 0.964135, 0.085142,
      -0.0857144, -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
      0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
   SpikePositive_19 → {{1., -0.0497285, -0.0610777, -0.0825769, -0.0109207, 0.0379495,
      -0.0371235, -0.0431269, -0.0770761, 0.0570927, -0.124799, 0.0179696, -0.0495028,
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      -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
   SpikePositive_20 → {{1., -0.113509, -0.0251942, -0.0654097, -0.0733454, 0.0868586,
      -0.0822755, 0.0549689, -0.100258, -0.0813179, 0.0613956, -0.100971, -0.000366274,
      -0.0455853, 0.0409148, -0.0558407, -0.0163248, 0.0184595, -0.0023035, 0.000102651},
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      0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{1., -0.0578427, -0.056229, 0.0113341, 0.0664772, 0.0629189,
      -0.104036, -0.0182135, 0.0670416, -0.0917389, 0.0261831, -0.0747941, 0.00134751,
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      0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
   SpikeNegative_2 → {{1., 0.0113655, 0.0828504, -0.100257, 0.0341282, 0.0170601, 0.0137485,
      0.0504148, -0.106829, -0.0364211, 0.000580082, 0.0171607, -0.017316, -0.0694273,
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   SpikeNegative_3 → {{1., -0.10065, -0.130339, 0.0573648, 0.0776776, -0.142795, -0.00396032,
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      -0.0384319, -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
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SpikeNegative_5 → {{1., 0.0287821, -0.0238913, -0.023378, 0.0837827, -0.0628705, 0.0611547,
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SpikeNegative_6 → {{1., -0.029236, -0.074812, 0.030229, -0.0142458, 0.06204, -0.028062,
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SpikeNegative_7 → {{1., -0.0286054, -0.127639, 0.0481525, 0.0589468, -0.110098, 0.0321937,
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SpikeNegative_8 → {{1., 0.0915046, 0.0249483, -0.0530743, -0.0303541, 0.0651667, -0.0508778,
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SpikeNegative_9 → {{1., 0.00504013, 0.0180484, -0.125757, 0.0249134, -0.0691307, 0.0335256,
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SpikeNegative_10 → {{1., -0.0268062, 0.0435122, 0.0611982, 0.045413, -0.0337753, 0.0363176,
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SpikeNegative_11 → {{1., -0.0272544, -0.0925908, 0.0637475, -0.0101278, 0.0195276,
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SpikeNegative_12 → {{1., -0.0328545, -0.0524229, -0.0801562, -0.0769035, -0.00280053,
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SpikeNegative_13 → {{1., -0.002932, -0.0811098, -0.0953748, -0.016938, -0.0501992, 0.0705982,
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SpikeNegative_14 → {{1., -0.0282876, 0.0599456, -0.0490142, 0.00141084, -0.0489796,
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SpikeNegative_15 → {{1., -0.0533932, -0.0392353, -0.0215225, 0.0733335, -0.0501356,
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SpikeNegative_16 → {{1., -0.0731179, -0.0416662, 0.00225728, -0.0571636, -0.0199014,
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Lag1 → <|LinearPositive_1 → {{1., 0.84935, 0.699686, 0.555868, 0.414693, 0.279153, 0.151819,
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  LinearPositive_4 → {{1., 0.848146, 0.699299, 0.554107, 0.414547, 0.281336, 0.153127,
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  LinearPositive_5 → {{1., 0.849996, 0.700775, 0.555186, 0.413672, 0.279375, 0.152519,
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      0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
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  LinearPositive_8 → {{1., 0.848013, 0.700589, 0.556702, 0.416024, 0.280146, 0.149859,
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  LinearPositive_14 → {{1., 0.853189, 0.696868, 0.551152, 0.413612, 0.271755, 0.14462,
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  LinearPositive_20 → {{1., 0.849301, 0.698334, 0.548901, 0.409285, 0.280316, 0.151052,
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LinearNegative_2 → {{1., 0.848252, 0.723909, 0.564221, 0.422921, 0.293574, 0.148311, 0.024294,
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LinearNegative_6 → {{1., 0.833676, 0.69017, 0.554105, 0.409712, 0.254649, 0.143761, 0.0362799,
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LinearNegative_11 → {{1., 0.847922, 0.692912, 0.552191, 0.416704, 0.282559, 0.154323, 0.0226993,
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LinearNegative_13 → {{1., 0.840973, 0.696087, 0.557274, 0.420566, 0.27625, 0.156577, 0.0278414,
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LinearNegative_17 → {{1., 0.846843, 0.692271, 0.549426, 0.413897, 0.275105, 0.151522, 0.0334252,
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    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
LinearNegative_19 → {{1., 0.844039, 0.693719, 0.547442, 0.411931, 0.289635, 0.15698, 0.0382691,
    -0.0709944, -0.168877, -0.264245, -0.319365, -0.368274, -0.39847, -0.410094, -0.393795,
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    -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
    -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
LinearNegative_20 → {{1., 0.859512, 0.720391, 0.570337, 0.423131, 0.288439, 0.154227, 0.0228425,
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    -0.0867373, -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
    -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}},
Sinusoidal3_21 → {{1., 0.526276, -0.313093, -0.81386, -0.623575, 0.0380469, 0.585502, 0.603459,
    0.148314, -0.354542, -0.499799, -0.232979, 0.160613, 0.347299, 0.223134, -0.0381001,
    -0.185269, -0.136953, 0.00421195, 0.0613158}, {0.18867, -0.0972321, -0.306583, -0.251354,
    -0.00388461, 0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096,
    0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
Sinusoidal3_22 → {{1., 0.530102, -0.311646, -0.818511, -0.627495, 0.0342222, 0.588451,
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    0.00419846, 0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523,
    0.303756, 0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{1., 0.529872, -0.31129, -0.820928, -0.627833, 0.0338845, 0.586732,
    0.610712, 0.154856, -0.351498, -0.499849, -0.23614, 0.1541, 0.340062, 0.222061, -0.0338969,
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    0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{1., 0.529434, -0.312514, -0.820436, -0.625573, 0.0373198, 0.590454,
    0.607322, 0.146033, -0.356064, -0.499862, -0.231568, 0.162957, 0.343404, 0.218373, -0.0373224,
    -0.183222, -0.130414, 0.00350322, 0.0581752}, {0.183018, -0.0977985, -0.296248, -0.251125,
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    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
Sinusoidal3_25 → {{1., 0.527106, -0.313576, -0.822091, -0.623397, 0.0359993, 0.589535,
    0.609359, 0.148505, -0.355766, -0.499829, -0.231879, 0.160384, 0.341443, 0.219112, -0.0359426,
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    0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
    0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
Sinusoidal3_26 → {{1., 0.529654, -0.314084, -0.82045, -0.625813, 0.0362957, 0.587287, 0.606545,
    0.150413, -0.354134, -0.499858, -0.233575, 0.158426, 0.344414, 0.221568, -0.0364127,
    -0.183002, -0.130323, 0.00506948, 0.0579813}, {0.185284, -0.0936261, -0.306395, -0.25385,
    0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
    0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
Sinusoidal3_27 → {{1., 0.529156, -0.311923, -0.819859, -0.624586, 0.03525, 0.585185, 0.606511,
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    Sinusoidal3_28 → {{1., 0.527642, -0.309688, -0.818151, -0.627934, 0.0325232, 0.583418, 0.60936,
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    Sinusoidal3_30 → {{1., 0.529088, -0.311587, -0.819511, -0.626983, 0.0348907, 0.587005,
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        0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
Lag3 → <|Sinusoidal1_1 → {{1., -0.522677, -0.306569, 0.82793, -0.620097, -0.0349623, 0.596332,
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    Sinusoidal1_2 → {{1., -0.538639, -0.315707, 0.828717, -0.615896, -0.0489264, 0.592582,
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        -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
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    Sinusoidal1_4 → {{1., -0.532036, -0.302356, 0.831106, -0.629711, -0.0371085, 0.596985,
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    Sinusoidal1_6 → {{1., -0.522957, -0.301441, 0.809437, -0.612822, -0.0160013, 0.558882,
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    Sinusoidal1_8 → {{1., -0.52831, -0.312186, 0.813182, -0.627885, -0.016639, 0.560325, -0.614633,
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        -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
    Sinusoidal1_10 → {{1., -0.521088, -0.326836, 0.8189, -0.615252, -0.0525415, 0.601327,
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Sinusoidal2_12 → {{1., -0.276885, -0.737128, 0.678704, 0.262136, -0.750132, 0.200574, 0.536952,
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Sinusoidal2_14 → {{1., -0.277698, -0.734459, 0.679775, 0.25739, -0.752569, 0.204627, 0.532738,
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    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
Sinusoidal2_19 → {{1., -0.278939, -0.739103, 0.678303, 0.262313, -0.749557, 0.201567, 0.535642,
    -0.474427, -0.185995, 0.499913, -0.123017, -0.334357, 0.273147, 0.107268, -0.250189,
    0.0465856, 0.130499, -0.069647, -0.030009}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
Sinusoidal2_20 → {{1., -0.279393, -0.736615, 0.67888, 0.261362, -0.748114, 0.198363, 0.533023,
    -0.473514, -0.187235, 0.499877, -0.121687, -0.335325, 0.275714, 0.110577, -0.251599,
    0.0475096, 0.129987, -0.0722285, -0.0295813}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
    -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>|>
```

In[6]:=
```
Query[All, Length]@classificationInterpolatedAutocorrelationOrder3
```

Out[6]=
```
<|SpikeMax → 20, SpikeMin → 20, Lag1 → 50, Lag3 → 20|>
```

Method (6)

In[1]:=
```
Needs["MathIOmica`"]
```

We may choose differnet methods for the calculations (usually depending on the downstream application). First let's generate the data for the examples, background noise for 20 timepoints:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
timePointsExample = Range[20];
```

Method: "LombScargle" (1)

This is the default Method. It can also be set by the option. We need to also have values for the appropriate cutoffs. We may base these on the background noise and use the QuantileEstimation for this:

In[8]:=
```
bootstrapQ95 = QuantileEstimator[backgroundExample, timePointsExample];
bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

Let's perform the classification:

In[119]:=
```
classification1 = TimeSeriesClassification[classificationExample1, timePointsExample,
  LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes, Method → "LombScargle"]
```

Method → "LombScargle"

Out[119]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
      0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
      -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
      0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
      0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
      0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
      0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
      0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
      0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
      0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
      0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
      -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
```

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```
    0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
  SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
    0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
    -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
    -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
  SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
    0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
    0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
  SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
    0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
    0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
  SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
    0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
    0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
    0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
  SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
    0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
    0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
  SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
    0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
    -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
    0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
  SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
    0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
    0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
  SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
    0.156306, 0.49338, 0.197723}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
    0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
    -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
  SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
    0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
    -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
    -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
  SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
    0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
    0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
    0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
  SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
    0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
    -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
    0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
    0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
    -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
    0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
    -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
    0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
    0.469391, 0.294777, 0.463012, 0.279525}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
    -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
    -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
  SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
    0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
    -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
    -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
    0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
    0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
    -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
  SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
```

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```
    0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
    -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
    0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
    0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
    0.341117, 0.381366, 0.325221}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
    -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
    0.214233, 0.523873, 0.243986}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
    0.0874465, -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
    0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
    -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
    0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
  SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
    0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
    -0.0488362, -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052,
    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
    0.35716, 0.304919, 0.374001}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
    0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
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  SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
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    -0.245066, -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
  LinearNegative_13 → {{0.98451, 0.16303, 0.0227595, 0.00132012, 0.00348595, 0.0126863,
    0.0149005, 0.0329653, 0.0281054, 0.0370164}, {-0.01186, -0.0431645, -0.0590873, -0.0756374,
    -0.0887624, -0.1144, -0.121973, -0.156462, -0.165726, -0.190329, -0.20958, -0.216046,
```

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```
    -0.244405, -0.264186, -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596}},
  LinearNegative_14 → {{0.978579, 0.195677, 0.0313545, 0.00267509, 0.00341515, 0.0129726,
    0.0194829, 0.0277661, 0.0277908, 0.0316459}, {-0.0187992, -0.0431131, -0.0473458, -0.070655,
    -0.0879629, -0.116006, -0.12521, -0.152395, -0.170415, -0.184268, -0.196593, -0.22289,
    -0.23237, -0.26046, -0.276864, -0.301954, -0.319987, -0.336453, -0.361973, -0.377956}},
  LinearNegative_15 → {{0.987412, 0.147538, 0.0327634, 0.00558518, 0.00366499, 0.00919838,
    0.0134794, 0.0247462, 0.0207871, 0.0286609}, {-0.0162872, -0.0293132, -0.0552218, -0.0807767,
    -0.0935334, -0.121112, -0.124004, -0.147926, -0.165828, -0.191582, -0.205406, -0.219926,
    -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
  LinearNegative_16 → {{0.979857, 0.186118, 0.0444944, 0.00475256, 0.00394217, 0.0176745,
    0.0237503, 0.0289162, 0.0192921, 0.033722}, {-0.0225164, -0.0461677, -0.0473716, -0.067817,
    -0.0986701, -0.119505, -0.130459, -0.1556, -0.169469, -0.1814, -0.198572, -0.221935,
    -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}},
  LinearNegative_17 → {{0.983395, 0.171344, 0.0310503, 0.00202654, 0.00193992, 0.00923842,
    0.0176563, 0.0269516, 0.0227712, 0.0310183}, {-0.0130003, -0.0309644, -0.0613334, -0.0794837,
    -0.0865967, -0.117058, -0.128048, -0.153332, -0.167054, -0.192254, -0.208455, -0.223898,
    -0.240133, -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}},
  LinearNegative_18 → {{0.981857, 0.181794, 0.0372624, 0.00157464, 0.00102441, 0.00691753,
    0.0240936, 0.0170077, 0.0123945, 0.0210674}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
    -0.0895021, -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921,
    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
  LinearNegative_19 → {{0.986834, 0.144628, 0.035256, 0.00310318, 0.000702006, 0.0165652,
    0.0245304, 0.0352455, 0.0134744, 0.0410912}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
    -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
    -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
  LinearNegative_20 → {{0.985534, 0.158105, 0.0328843, 0.00243514, 0.000101469, 0.0195265,
    0.0175251, 0.026453, 0.0180484, 0.0303906}, {-0.024006, -0.0432239, -0.0496914, -0.0682004,
    -0.0867373, -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
    -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}}|>,
f3 → <|Sinusoidal3_21 → {{0.003093, 0.067983, 0.992591, 0.0880879, 0.0381938, 0.0201564,
    0.0111428, 0.00371032, 0.0191542, 0.00156895}, {0.18867, -0.0972321, -0.306583, -0.251354,
    -0.00388461, 0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096,
    0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
  Sinusoidal3_22 → {{0.00318631, 0.0730881, 0.992797, 0.0819348, 0.0379624, 0.0193048,
    0.00904049, 0.00285594, 0.0196066, 0.00109025}, {0.181513, -0.0928691, -0.305475, -0.251164,
    0.00419846, 0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523,
    0.303756, 0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
  Sinusoidal3_23 → {{0.00295231, 0.0765523, 0.992363, 0.0843288, 0.0378838, 0.0169649,
    0.00808632, 0.0027773, 0.0209207, 0.000957331}, {0.18264, -0.0994704, -0.295137, -0.250857,
    0.00157044, 0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036,
    0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
  Sinusoidal3_24 → {{0.00314279, 0.0708784, 0.992955, 0.0826235, 0.0361366, 0.0195659,
    0.00754111, 0.00268053, 0.020647, 0.000914497}, {0.183018, -0.0977985, -0.296248, -0.251125,
    -0.00333361, 0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939,
    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
  Sinusoidal3_25 → {{0.00289275, 0.0722254, 0.992563, 0.084147, 0.0394916, 0.0185649, 0.00643529,
    0.00207684, 0.0237235, 0.000529693}, {0.191347, -0.0982886, -0.29771, -0.261082,
    0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
    0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
  Sinusoidal3_26 → {{0.0035927, 0.0724177, 0.992482, 0.0865873, 0.0377177, 0.018194, 0.00903366,
    0.0026512, 0.0195294, 0.000949465}, {0.185284, -0.0936261, -0.306395, -0.25385,
    0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
    0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{0.00356621, 0.0718347, 0.992461, 0.086876, 0.0384877, 0.0168536, 0.00812238,
    0.00246869, 0.0215147, 0.000777483}, {0.185809, -0.10192, -0.303748, -0.261172,
    0.000202029, 0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227,
    0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.00292996, 0.0773356, 0.991977, 0.0880559, 0.0367946, 0.0176203,
    0.00875596, 0.00325153, 0.0220462, 0.00118298}, {0.187562, -0.10053, -0.297144, -0.250552,
    0.00476677, 0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453,
    0.301104, 0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{0.00262506, 0.0711674, 0.99281, 0.0827274, 0.0380578, 0.0177335, 0.00874852,
    0.00232562, 0.0238141, 0.000654616}, {0.189755, -0.100643, -0.295957, -0.251445,
    -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
    0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
  Sinusoidal3_30 → {{0.00427552, 0.071229, 0.992804, 0.0839262, 0.0365748, 0.018534, 0.00877504,
```

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    0.00265531, 0.0209496, 0.000906179}, {0.186539, -0.100579, -0.301622, -0.251977,
    0.00452805, 0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
    0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
    0.0294955, 0.00418398, 0.028168, 0.00135728}, {-0.0952089, -0.252202, 0.25704, 0.097318,
    -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
    0.00565905, 0.0259503, 0.00224675}, {-0.101498, -0.25529, 0.251653, 0.0972642,
    -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
    0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395,
    0.00472652, 0.0285215, 0.00169662}, {-0.0918789, -0.259087, 0.253065, 0.103093,
    -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
    0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735,
    0.00386219, 0.0290145, 0.00118185}, {-0.0939856, -0.25429, 0.25073, 0.100441,
    -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
    0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
    0.00582096, 0.0271664, 0.00231721}, {-0.0916775, -0.260977, 0.251061, 0.104141,
    -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
    0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
    0.00436252, 0.0286975, 0.00143738}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
    -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868,
    0.00399143, 0.0293851, 0.00124852}, {-0.102994, -0.260616, 0.250831, 0.0989794,
    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
    0.00452946, 0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
    0.00512062, 0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
    -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
    0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
    -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
    -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
    0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
    0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
    -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
    0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
    0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
    -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
  Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
    0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
    0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
    -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
    0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
    0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
    -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
```

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```
    -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

If we want the classes produced, we can query the keys:

```
In[120]:= Query[Keys]@classification1
Out[120]= {SpikeMax, SpikeMin, f1, f3, f5, f6}
```

For the members in each class we have:

```
In[121]:= Query[All, Length]@classification1
Out[121]= <|SpikeMax → 20, SpikeMin → 20, f1 → 40, f3 → 10, f5 → 10, f6 → 10|>
```

The actual value of the possible frequencies can also be obtained if necessary using any of the signals and looking at its LombScargle transformation. In the example considered we have:

```
In[122]:= frequenciesPossible = LombScargle[classificationExample1[[1]], timePointsExample, FrequenciesOnly → True]
Out[122]= <|f1 → 0.0554017, f2 → 0.110803, f3 → 0.166205, f4 → 0.221607, f5 → 0.277008,
  f6 → 0.33241, f7 → 0.387812, f8 → 0.443213, f9 → 0.498615, f10 → 0.554017|>
```

Method: "Autocorrelation" (1)

We can evaluate the appropriate cutoffs to be used with this method using QuantileEstimation for autocorrelations and spikes:

```
In[123]:= bootstrapQ95Autocorrelation =
  QuantileEstimator[backgroundExample, timePointsExample , Method → "Autocorrelation"]
Out[123]= {0.104569, 0.750865, 0.330876, 0.582844, 0.384145, 0.476242, 0.361702, 0.407732, 0.30536}
```

```
In[124]:= bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

Let's perform the classification:

```
In[128]:= classificationAutocorrelation1 = TimeSeriesClassification[classificationExample1,
    timePointsExample, AutocorrelationCutoffs → bootstrapQ95Autocorrelation,
    SpikeCutoffs → bootstrapQ95Spikes, Method → "Autocorrelation"]
```

Method → "Autocorrelation"

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```
Out[128]= <|SpikeMax →
  <|SpikePositive_1 → {{1., -0.452395, 0.219937, -0.141456, -0.040982, 0.0671421, -0.0204863, -0.0225783,
      0.00336149, 0.0248339}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
      0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{1., -0.33332, 0.178978, -0.043203, 0.0330959, 0.0187841, 0.0643953,
      -0.167683, -0.0783794, -0.134626}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{1., -0.150943, 0.25591, -0.077747, 0.03904, -0.112386, -0.130446,
      -0.111423, -0.0923815, 0.0100807}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{1., -0.329658, 0.231525, 0.0162836, 0.164488, -0.166715, 0.0989705,
      -0.163788, -0.0754534, 0.0143191}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{1., -0.354501, 0.199318, -0.099174, 0.199, -0.0363005, 0.158313,
      -0.0231566, 0.0362299, -0.135361}, {0.966833, -0.0172757, -0.0101601, 0.0449156,
      0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
      -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{1., -0.466257, 0.137607, -0.192065, -0.0315355, -0.0729004, -0.0550543,
      -0.104833, 0.0601693, -0.0827568}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{1., -0.389552, 0.144053, -0.0395178, 0.0603777, -0.112134, -0.0357364,
      -0.00620881, -0.073946, -0.0864452}, {0.973634, -0.0197451, 0.00381691, 0.0632199,
      0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
      0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{1., -0.394532, 0.210425, -0.0366925, 0.0213409, -0.067476, 0.000171715,
      -0.0864154, -0.128194, 0.0081353}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{1., -0.400547, 0.143122, -0.118456, -0.00900312, 0.125105, 0.0177367,
      -0.061955, -0.00116964, -0.150973}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
      0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{1., -0.486387, 0.214384, -0.107572, 0.107945, 0.0130167, 0.0145573,
      0.0233586, -0.0802024, -0.127062}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
      0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
      -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{1., -0.338874, 0.300856, -0.187073, -0.0720043, -0.0204714, -0.0156668,
      0.0397913, -0.0000121023, -0.147044}, {0.0696283, 0.0251021, 0.968196, 0.0511374,
      0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
      -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{1., -0.490403, 0.230471, -0.02836, 0.158686, -0.26022, 0.158602,
      -0.177464, 0.0371373, -0.0785755}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
   SpikePositive_13 → {{1., -0.380553, -0.0954718, -0.150478, -0.0658297, 0.106079, -0.0357483,
      -0.0423526, 0.134218, -0.0648447}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
      -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
      0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
   SpikePositive_14 → {{1., -0.526563, 0.402071, -0.0816825, 0.0766719, -0.117882, 0.0465972,
      -0.195255, 0.0724303, -0.107586}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
      0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
      -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
   SpikePositive_15 → {{1., -0.498776, 0.12023, -0.0909257, 0.179612, -0.241152, 0.0697987,
      0.00693521, 0.0904771, -0.0399131}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
      0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
      -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
   SpikePositive_16 → {{1., -0.252346, -0.0181276, -0.202654, 0.0588694, -0.165692, 0.058152,
      -0.0733224, 0.0688338, 0.00969476}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
      -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
      -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
   SpikePositive_17 → {{1., -0.868718, 0.44914, -0.120491, -0.0616033, -0.0228913, 0.14139,
```

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      -0.0932499, -0.0473214, 0.036701}, {0.0894556, -0.0939456, 0.955206, -0.0721055,
      0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
      -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
   SpikePositive_18 → {{1., -0.362902, -0.122098, -0.129486, 0.0562719, -0.0830183, 0.122331,
      -0.122383, -0.180395, -0.0773557}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
      -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
      0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
   SpikePositive_19 → {{1., -0.42077, 0.0763867, -0.227391, 0.0475263, 0.0245878, -0.0251915,
      -0.0584293, -0.118635, 0.0240546}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
      -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
      0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
   SpikePositive_20 → {{1., -0.507801, 0.163243, -0.238989, -0.0407895, 0.101176, -0.0803686,
      0.0171814, 0.00408016, -0.268402}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
      -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
      0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{1., -0.423906, 0.0870199, -0.0546103, 0.153795, 0.0753404,
      -0.11792, -0.102237, 0.144444, -0.0974828}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
      -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
      -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
   SpikeNegative_2 → {{1., -0.254883, 0.246154, -0.281797, 0.168139, -0.0510077, 0.0696523,
      0.044741, -0.0493091, -0.173802}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
      -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
      -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
   SpikeNegative_3 → {{1., -0.52844, 0.0128591, 0.0401754, 0.156405, -0.25313, 0.0143667,
      -0.105044, 0.0118936, -0.135968}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
      0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
      -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
   SpikeNegative_4 → {{1., -0.261291, 0.197729, -0.0669671, -0.0489197, 0.019136, -0.0777287,
      -0.0858975, 0.0311934, -0.0488232}, {-0.978499, -0.0375369, -0.0308657, -0.0197828,
      0.087556, -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659,
      -0.0303762, 0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
   SpikeNegative_5 → {{1., -0.275359, 0.08563, -0.0927664, 0.179004, -0.137792, 0.112485,
      -0.0158152, -0.046442, -0.180954}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
      0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
      -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
   SpikeNegative_6 → {{1., -0.398833, 0.0778628, -0.044104, 0.0333735, 0.0658697, -0.0029231,
      -0.0938463, -0.0655049, -0.0116685}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
      -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
      0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
   SpikeNegative_7 → {{1., -0.42086, -0.00214872, 0.0208358, 0.127917, -0.202863, 0.0631005,
      -0.00894861, 0.0102268, 0.000991105}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
      0.0874465, -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
      -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
   SpikeNegative_8 → {{1., -0.167986, 0.132625, -0.161643, 0.0190856, 0.0689723, -0.0356912,
      -0.0774932, -0.0382031, -0.110421}, {-0.971714, -0.0689738, -0.0116232, 0.0693961,
      0.0405887, -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389,
      0.06932, -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
   SpikeNegative_9 → {{1., -0.280681, 0.131522, -0.27773, 0.125519, -0.158639, 0.0827061,
      -0.0794961, -0.159761, -0.0325458}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
      0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
      -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
   SpikeNegative_10 → {{1., -0.351869, 0.262355, -0.0376404, 0.155982, -0.124093, 0.105999,
      -0.0645218, 0.0405128, 0.0335434}, {-0.972673, -0.00291876, -0.0540171, -0.0812638,
      -0.0617025, 0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018,
      -0.0213425, -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
   SpikeNegative_11 → {{1., -0.413539, 0.0679203, 0.00410847, 0.0261914, -0.0181218, 0.0852791,
      -0.0436318, -0.0440867, -0.13617}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
      -0.0488362, -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052,
      0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
   SpikeNegative_12 → {{1., -0.395846, 0.0894882, -0.237998, -0.0446471, -0.0524744, 0.0771359,
      -0.0422126, -0.134419, 0.0146231}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
      0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
      -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
   SpikeNegative_13 → {{1., -0.343983, 0.00454468, -0.205612, 0.0119525, -0.102592, 0.103107,
      0.0746079, -0.0154823, -0.032091}, {0.089408, -0.00831708, -0.964283, -0.0122152,
      -0.0196036, 0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
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    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{1., -0.332802, 0.244793, -0.20513, 0.0810854, -0.132165, -0.0116365,
    -0.109746, -0.0688768, -0.10264}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594,
    0.0528555, 0.00336549, 0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{1., -0.409677, 0.104665, -0.110113, 0.152765, -0.103758, -0.130233,
    -0.0168568, 0.0773673, -0.0765506}, {-0.00121514, -0.0078406, -0.978821, -0.0221297,
    -0.026309, 0.000455216, -0.0829657, 0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281,
    0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{1., -0.458875, 0.142195, -0.117197, -0.0328704, -0.0724729, 0.062644,
    0.0215451, -0.0873599, 0.0313895}, {-0.00639921, 0.0369683, -0.976295, 0.0340422,
    0.0583464, 0.0166785, 0.0680268, 0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101,
    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{1., -0.28948, 0.0899977, -0.14795, 0.137414, -0.00541154, 0.0773486,
    0.045355, -0.117622, -0.0110899}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
    0.0616787, -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667,
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  SpikeNegative_18 → {{1., -0.219411, 0.0906106, -0.0586132, 0.117458, -0.0973521, -0.064392,
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  SpikeNegative_19 → {{1., -0.25374, 0.0112197, -0.122395, -0.0226519, -0.0591994, -0.111793,
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  SpikeNegative_20 → {{1., -0.223368, 0.0633665, -0.177509, 0.103343, 0.0332846, -0.0776252,
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Lag1 → <|LinearPositive_1 → {{1., 0.812153, 0.688835, 0.540544, 0.408977, 0.277736,
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  LinearPositive_2 → {{1., 0.812426, 0.690113, 0.540471, 0.410253, 0.280388, 0.156519,
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  LinearPositive_5 → {{1., 0.813098, 0.689554, 0.539503, 0.407967, 0.278017, 0.155904,
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  LinearPositive_6 → {{1., 0.812702, 0.691452, 0.540319, 0.407464, 0.275268, 0.153852,
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  LinearPositive_7 → {{1., 0.812932, 0.68944, 0.541059, 0.410632, 0.279722, 0.156421,
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    0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
  LinearPositive_8 → {{1., 0.811593, 0.690699, 0.541512, 0.410794, 0.279002, 0.153279,
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  LinearPositive_9 → {{1., 0.814527, 0.692284, 0.539635, 0.407699, 0.277329, 0.156518,
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  LinearPositive_10 → {{1., 0.812617, 0.690354, 0.540412, 0.408665, 0.278245, 0.15546,
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LinearPositive_11 → {{1., 0.804492, 0.685812, 0.542844, 0.417517, 0.287434, 0.157954,
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LinearPositive_18 → {{1., 0.808358, 0.691342, 0.539614, 0.409352, 0.280974, 0.150255,
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LinearPositive_20 → {{1., 0.811999, 0.686267, 0.532886, 0.404237, 0.279336, 0.155285,
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LinearNegative_1 → {{1., 0.816083, 0.69022, 0.532722, 0.391788, 0.275312, 0.170471, 0.0446087,
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LinearNegative_2 → {{1., 0.821326, 0.717404, 0.546117, 0.420827, 0.293304, 0.153503,
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LinearNegative_3 → {{1., 0.7994, 0.689563, 0.54124, 0.413475, 0.28062, 0.146429, 0.0329069,
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LinearNegative_4 → {{1., 0.810147, 0.673108, 0.506627, 0.392328, 0.257163, 0.143303,
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LinearNegative_5 → {{1., 0.824394, 0.693531, 0.533655, 0.410999, 0.263856, 0.139629,
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LinearNegative_6 → {{1., 0.798686, 0.686017, 0.542515, 0.404526, 0.253837, 0.145439,
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LinearNegative_7 → {{1., 0.794993, 0.672705, 0.521019, 0.397866, 0.258824, 0.137151,
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LinearNegative_8 → {{1., 0.809117, 0.687749, 0.52855, 0.409176, 0.285162, 0.144781, 0.0442807,
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LinearNegative_9 → {{1., 0.822069, 0.699828, 0.550014, 0.43437, 0.295909, 0.177084, 0.052593,
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LinearNegative_10 → {{1., 0.793864, 0.690767, 0.539565, 0.408436, 0.282279, 0.155187,
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LinearNegative_11 → {{1., 0.808637, 0.681433, 0.538256, 0.411633, 0.281455, 0.159477,
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LinearNegative_13 → {{1., 0.805711, 0.688968, 0.545194, 0.415927, 0.275731, 0.160197,
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LinearNegative_14 → {{1., 0.813584, 0.690966, 0.53621, 0.402116, 0.265448, 0.150454,
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LinearNegative_15 → {{1., 0.80731, 0.678574, 0.536884, 0.408767, 0.281237, 0.169746,
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LinearNegative_16 → {{1., 0.816224, 0.694855, 0.53266, 0.392939, 0.271184, 0.156789,
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LinearNegative_17 → {{1., 0.808181, 0.680533, 0.535776, 0.40837, 0.273865, 0.154831,
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LinearNegative_18 → {{1., 0.819864, 0.693802, 0.543666, 0.404933, 0.275224, 0.145932,
    0.0398621, -0.0573997, -0.157583}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
    -0.0895021, -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921,
    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
LinearNegative_19 → {{1., 0.80655, 0.684193, 0.531796, 0.408803, 0.289272, 0.161874,
    0.0485676, -0.0588794, -0.150081}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
    -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
    -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
LinearNegative_20 → {{1., 0.826495, 0.708181, 0.552333, 0.416142, 0.286253, 0.158391,
    0.0329808, -0.0709138, -0.160329}, {-0.024006, -0.0432239, -0.0496914, -0.0682004,
    -0.0867373, -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
    -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}},
Sinusoidal3_21 → {{1., 0.247123, -0.557445, -0.939795, -0.653303, 0.0229178, 0.617163,
    0.727312, 0.357869, -0.205849}, {0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461,
    0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096, 0.29637,
    0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
Sinusoidal3_22 → {{1., 0.25169, -0.557413, -0.944049, -0.656755, 0.0183542, 0.61891,
    0.732724, 0.361424, -0.20497}, {0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846,
    0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523, 0.303756,
    0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{1., 0.251844, -0.557571, -0.947176, -0.65663, 0.0177201, 0.617109,
    0.73334, 0.36597, -0.200787}, {0.18264, -0.0994704, -0.295137, -0.250857, 0.00157044,
    0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036, 0.298633,
    0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{1., 0.25092, -0.558801, -0.94624, -0.654133, 0.0216276, 0.621752, 0.731812,
```

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```
    0.356685, -0.208697}, {0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361,
    0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939, 0.304721,
    0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
  Sinusoidal3_25 → {{1., 0.248531, -0.559984, -0.948885, -0.651591, 0.0192409, 0.621271,
    0.733629, 0.360855, -0.207618}, {0.191347, -0.0982886, -0.29771, -0.261082, 0.00611569,
    0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799, 0.302028,
    0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
  Sinusoidal3_26 → {{1., 0.250536, -0.560428, -0.945524, -0.654639, 0.0206229, 0.618008,
    0.729843, 0.360449, -0.204321}, {0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724,
    0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444, 0.296927,
    0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{1., 0.25091, -0.557951, -0.945799, -0.653107, 0.0190659, 0.616088,
    0.729145, 0.361895, -0.203958}, {0.185809, -0.10192, -0.303748, -0.261172, 0.000202029,
    0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227, 0.302676,
    0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{1., 0.250094, -0.554849, -0.945719, -0.657297, 0.0161014, 0.61427,
    0.731466, 0.368519, -0.19556}, {0.187562, -0.10053, -0.297144, -0.250552, 0.00476677,
    0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453, 0.301104,
    0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{1., 0.24794, -0.557153, -0.947197, -0.653095, 0.0208478, 0.622396,
    0.732075, 0.361144, -0.208204}, {0.189755, -0.100643, -0.295957, -0.251445, -0.0055221,
    0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546, 0.296096,
    0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
  Sinusoidal3_30 → {{1., 0.250844, -0.557432, -0.945813, -0.655932, 0.0188606, 0.618245,
    0.729494, 0.359139, -0.206123}, {0.186539, -0.100579, -0.301622, -0.251977, 0.00452805,
    0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063, 0.296225,
    0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
Lag3 → <|Sinusoidal1_1 → {{1., -1.62035, 0.360419, 1.21497, -1.21821, -0.141878, 1.2192,
    -0.78073, -0.461427, 1.00856}, {-0.20264, -0.107877, 0.278896, -0.289184, -0.0168796,
    0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701, -0.331998,
    0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{1., -1.66532, 0.355438, 1.22652, -1.2175, -0.172353, 1.22186, -0.77432,
    -0.462836, 1.00478}, {-0.153886, -0.0875347, 0.297854, -0.276583, 0.004457,
    0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307, -0.288819,
    0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{1., -1.64445, 0.326285, 1.20792, -1.19633, -0.166442, 1.18651, -0.75412,
    -0.488243, 1.0025}, {-0.187066, -0.0732084, 0.32812, -0.266161, 0.00567862,
    0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439, -0.297199,
    0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
  Sinusoidal1_4 → {{1., -1.64431, 0.377649, 1.22081, -1.23917, -0.150641, 1.23362, -0.812858,
    -0.479352, 1.02686}, {-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004,
    0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987, -0.322486,
    0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{1., -1.63326, 0.350694, 1.19562, -1.24989, -0.119703, 1.19466, -0.824007,
    -0.44053, 1.03035}, {-0.20104, -0.101657, 0.31364, -0.234517, -0.0163677,
    0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444, -0.303865,
    0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{1., -1.61745, 0.362188, 1.18112, -1.19845, -0.108432, 1.16148, -0.801294,
    -0.406369, 1.00513}, {-0.17526, -0.106684, 0.304186, -0.27676, -0.0299081,
    0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573, -0.282169,
    0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{1., -1.62603, 0.364189, 1.15957, -1.20495, -0.116659, 1.18331, -0.778645,
    -0.412438, 0.991653}, {-0.179672, -0.126709, 0.328842, -0.280026, -0.0129078,
    0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949, -0.27099,
    0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{1., -1.63516, 0.349888, 1.18931, -1.23013, -0.107577, 1.16798, -0.826875,
    -0.408475, 1.00889}, {-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322,
    0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394, -0.280218,
    0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{1., -1.63545, 0.3389, 1.19087, -1.23845, -0.122747, 1.21239, -0.803972,
    -0.441409, 1.00971}, {-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817,
    0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813, -0.323289,
    0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{1., -1.62154, 0.318378, 1.205, -1.20671, -0.172296, 1.21745, -0.763933,
    -0.495003, 1.01357}, {-0.203834, -0.0722574, 0.294696, -0.254799, 0.00423677,
    0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167, -0.291561,
```

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```
    0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}},
  Sinusoidal2_11 → {{1., -1.17252, -0.601542, 1.19408, 0.25188, -1.13858, 0.0704528, 0.976677,
    -0.291154, -0.781135}, {-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852,
    0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865, 0.258725,
    0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{1., -1.16785, -0.598321, 1.19453, 0.248915, -1.13786, 0.0682078, 0.978793,
    -0.291032, -0.776961}, {-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067,
    0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668, 0.262301,
    0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{1., -1.17536, -0.59477, 1.20107, 0.24206, -1.14339, 0.0770172, 0.974134,
    -0.300202, -0.775021}, {-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667,
    0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963, 0.254435,
    0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{1., -1.1688, -0.593543, 1.19507, 0.242189, -1.14297, 0.0748801, 0.976008,
    -0.300757, -0.77767}, {-0.0971308, -0.259618, 0.249762, 0.0996953, -0.311793,
    0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698, 0.256122,
    0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{1., -1.17333, -0.597548, 1.19893, 0.246055, -1.14361, 0.077823, 0.976081,
    -0.300583, -0.777469}, {-0.0939856, -0.25429, 0.25073, 0.100441, -0.313599,
    0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627, 0.255722,
    0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{1., -1.17552, -0.594542, 1.19905, 0.240051, -1.13983, 0.0800883, 0.973032,
    -0.306018, -0.774319}, {-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132,
    0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968, 0.256443,
    0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{1., -1.16939, -0.601413, 1.1928, 0.254696, -1.14293, 0.0645867, 0.979436,
    -0.29009, -0.783073}, {-0.0991608, -0.252958, 0.255513, 0.0985052, -0.309591,
    0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{1., -1.16579, -0.598353, 1.19062, 0.252474, -1.13536, 0.0710946, 0.973451,
    -0.292364, -0.776772}, {-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724,
    0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{1., -1.17252, -0.600788, 1.19475, 0.249722, -1.13835, 0.070574, 0.977201,
    -0.28997, -0.779946}, {-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977,
    0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469, 0.251806,
    0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{1., -1.17271, -0.596923, 1.19503, 0.249005, -1.13678, 0.0667731, 0.972508,
    -0.289316, -0.780821}, {-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484,
    0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815,
    0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>|>
```

If we want the classes produced, we can query the keys:

```
In[129]:= Query[Keys]@classificationAutocorrelation1
Out[129]= {SpikeMax, SpikeMin, Lag1, Lag3}
```

For the members in each class we have:

```
In[130]:= Query[All, Length]@classificationAutocorrelation1
Out[130]= <|SpikeMax → 20, SpikeMin → 20, Lag1 → 50, Lag3 → 20|>
```

Method: "InterpolatedAutocorrelation" (1)

We can evaluate the appropriate cutoffs to be used with this method using QuantileEstimation for autocorrelations and spikes:

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In[131]:=
```
bootstrapQ95InterpolatedAutocorrelation =
 QuantileEstimator[backgroundExample, timePointsExample , Method → "InterpolatedAutocorrelation"]
```

Out[131]=
```
{0.303188, 0.296659, 0.287586, 0.281611, 0.274524, 0.268483, 0.262192, 0.254505, 0.245366, 0.239768,
 0.227267, 0.215607, 0.200545, 0.185658, 0.171387, 0.15369, 0.132348, 0.108645, 0.079037}
```

In[8]:=
```
bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

Let's perform the classification:

In[135]:=
```
classificationIntepolatedAutocorrelation1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, AutocorrelationCutoffs → bootstrapQ95InterpolatedAutocorrelation,
  SpikeCutoffs → bootstrapQ95Spikes, Method → "InterpolatedAutocorrelation"]
```

Method → "InterpolatedAutocorrelation"

Out[135]=
```
<| SpikeMax →
  <| SpikePositive_1 → {{1., -0.0829057, 0.00040893, 0.00713647, -0.0831192, 0.0737441, -0.0413379, 0.0130211,
      -0.0175846, 0.0654331, -0.0225876, -0.00392938, -0.0528106, -0.0128336, -0.0169535, -0.0930537,
      -0.0542933, -0.0216233, -0.0806804, -0.0760309}, {0.970569, -0.0988615, -0.0240026, -0.0115612,
      -0.0977222, 0.0813682, -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224,
      -0.055411, -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{1., 0.000158644, -0.00795959, 0.0515558, -0.0291068, 0.0483314, -0.00591426,
      -0.0981006, -0.078311, -0.0387618, 0.0252972, -0.0916473, -0.052656, -0.108454, -0.107867, 0.0179604,
      -0.0701124, 0.0200393, -0.00231356, 0.0278615}, {0.973207, 0.00872172, -0.00191539, 0.0695064,
      -0.00641562, 0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666,
      -0.00648697, -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{1., 0.089534, 0.0952262, 0.0221336, -0.0170007, -0.0562672, -0.112552,
      -0.0609559, -0.0664499, 0.0860571, 0.067277, 0.0284007, 0.00100325, 0.0370133, -0.0910503,
      -0.0954548, -0.0861248, -0.118416, -0.111234, -0.11114}, {0.95896, 0.0348607, 0.0657694, 0.0097693,
      -0.0146057, -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763,
      -0.00816843, 0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{1., -0.00637208, 0.0274577, 0.0850603, 0.0605054, -0.0675975, 0.0256527,
      -0.10735, -0.0364457, 0.0333519, -0.0858393, -0.0871813, -0.0371184, 0.0174961, 0.0149864, -0.12483,
      -0.112055, 0.0201852, -0.129091, 0.00918542}, {0.958583, 0.00400217, 0.0429904, 0.0838796,
      0.0778033, -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858,
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SpikeNegative_12 → {{1., -0.0328545, -0.0524229, -0.0801562, -0.0769035, -0.00280053,
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     -0.237918, -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
  LinearNegative_4 → {{1., 0.846899, 0.690567, 0.523353, 0.396597, 0.259456, 0.140683, 0.0318825,
     -0.0649947, -0.150808, -0.214597, -0.29397, -0.348757, -0.389391, -0.412022, -0.412155,
     -0.383837, -0.343184, -0.247781, -0.127942}, {-0.0158873, -0.0248133, -0.0382326, -0.0881019,
     -0.0887054, -0.128386, -0.128859, -0.161147, -0.159022, -0.205319, -0.200777, -0.210411,
     -0.243003, -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844}},
  LinearNegative_5 → {{1., 0.858201, 0.711131, 0.550497, 0.418649, 0.266884, 0.139287, 0.0261681,
     -0.0691814, -0.163856, -0.256859, -0.312375, -0.363868, -0.411894, -0.425272, -0.41827,
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     -0.0817467, -0.105404, -0.114359, -0.154377, -0.169473, -0.174198, -0.212011, -0.225376,
     -0.230144, -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}},
  LinearNegative_6 → {{1., 0.833676, 0.69017, 0.554105, 0.409712, 0.254649, 0.143761, 0.0362799,
     -0.0574299, -0.1625, -0.245544, -0.306622, -0.348646, -0.392721, -0.410218, -0.421791,
     -0.379059, -0.316139, -0.239419, -0.142263}, {-0.0267223, -0.0446999, -0.0523138, -0.0699606,
     -0.0987645, -0.126896, -0.126614, -0.165572, -0.172297, -0.184872, -0.208135, -0.237294,
     -0.243037, -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481}},
  LinearNegative_7 → {{1., 0.833055, 0.680617, 0.534437, 0.401427, 0.259636, 0.135783, 0.0364103,
     -0.062167, -0.141257, -0.228439, -0.288165, -0.345655, -0.382117, -0.412999, -0.413752,
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     -0.0775795, -0.167073, -0.247187, -0.314756, -0.372011, -0.397247, -0.422964, -0.398028,
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     -0.238911, -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
  LinearNegative_9 → {{1., 0.855482, 0.712228, 0.563097, 0.437965, 0.296759, 0.173276, 0.0373694,
     -0.0946609, -0.201367, -0.293044, -0.358412, -0.401409, -0.411065, -0.40372, -0.395398,
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     -0.258977, -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
  LinearNegative_10 → {{1., 0.827869, 0.690649, 0.552611, 0.409803, 0.281342, 0.150281, 0.0361065,
     -0.0820813, -0.172951, -0.225626, -0.316643, -0.377192, -0.396081, -0.408577, -0.397328,
     -0.376822, -0.317332, -0.23459, -0.14344}, {-0.00155633, -0.0271325, -0.0625737, -0.0744387,
     -0.0901925, -0.0932579, -0.138846, -0.15092, -0.157289, -0.198281, -0.189392, -0.206968,
     -0.259028, -0.273261, -0.270544, -0.29133, -0.328913, -0.352948, -0.335503, -0.37816}},
  LinearNegative_11 → {{1., 0.847922, 0.692912, 0.552191, 0.416704, 0.282559, 0.154323, 0.0226993,
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     -0.0862196, -0.118392, -0.123851, -0.151596, -0.176372, -0.191037, -0.213033, -0.221631,
     -0.235518, -0.271564, -0.288178, -0.293001, -0.310129, -0.328328, -0.364455, -0.366174}},
  LinearNegative_12 → {{1., 0.846616, 0.702339, 0.561016, 0.420952, 0.278946, 0.149793, 0.0369446,
     -0.0763804, -0.17106, -0.259783, -0.320982, -0.373741, -0.401019, -0.418482, -0.409708,
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    -0.245066, -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
LinearNegative_13 → {{1., 0.840973, 0.696087, 0.557274, 0.420566, 0.27625, 0.156577, 0.0278414,
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    -0.244405, -0.264186, -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596}},
LinearNegative_14 → {{1., 0.848321, 0.70257, 0.552277, 0.408715, 0.267635, 0.147708, 0.026818,
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LinearNegative_15 → {{1., 0.847116, 0.690023, 0.550188, 0.413916, 0.282106, 0.165532, 0.036334,
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LinearNegative_16 → {{1., 0.851131, 0.706606, 0.551864, 0.399581, 0.273328, 0.153411, 0.033393,
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    -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}},
LinearNegative_17 → {{1., 0.846843, 0.692271, 0.549426, 0.413897, 0.275105, 0.151522, 0.0334252,
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LinearNegative_18 → {{1., 0.858284, 0.707, 0.562096, 0.412442, 0.278079, 0.142895, 0.0339196,
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    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
LinearNegative_19 → {{1., 0.844039, 0.693719, 0.547442, 0.411931, 0.289635, 0.15698, 0.0382691,
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LinearNegative_20 → {{1., 0.859512, 0.720391, 0.570337, 0.423131, 0.288439, 0.154227, 0.0228425,
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Sinusoidal3_21 → {{1., 0.526276, -0.313093, -0.81386, -0.623575, 0.0380469, 0.585502, 0.603459,
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Sinusoidal3_22 → {{1., 0.530102, -0.311646, -0.818511, -0.627495, 0.0342222, 0.588451,
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    0.303756, 0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{1., 0.529872, -0.31129, -0.820928, -0.627833, 0.0338845, 0.586732,
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    0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{1., 0.529434, -0.312514, -0.820436, -0.625573, 0.0373198, 0.590454,
    0.607322, 0.146033, -0.356064, -0.499862, -0.231568, 0.162957, 0.343404, 0.218373, -0.0373224,
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    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
Sinusoidal3_25 → {{1., 0.527106, -0.313576, -0.822091, -0.623397, 0.0359993, 0.589535,
    0.609359, 0.148505, -0.355766, -0.499829, -0.231879, 0.160384, 0.341443, 0.219112, -0.0359426,
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    Sinusoidal3_26 → {{1., 0.529654, -0.314084, -0.82045, -0.625813, 0.0362957, 0.587287, 0.606545,
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    Sinusoidal3_27 → {{1., 0.529156, -0.311923, -0.819859, -0.624586, 0.03525, 0.585185, 0.606511,
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    Sinusoidal3_29 → {{1., 0.526094, -0.311715, -0.819411, -0.624478, 0.0373058, 0.589773,
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    Sinusoidal3_30 → {{1., 0.529088, -0.311587, -0.819511, -0.626983, 0.0348907, 0.587005,
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Lag3 → <| Sinusoidal1_1 → {{1., -0.522677, -0.306569, 0.82793, -0.620097, -0.0349623, 0.596332,
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    Sinusoidal1_3 → {{1., -0.530347, -0.325215, 0.817467, -0.606563, -0.0498757, 0.581319,
        -0.589923, 0.122749, 0.369791, -0.496883, 0.214177, 0.183285, -0.356379, 0.223113, 0.052763,
        -0.198601, 0.126545, 0.0167961, -0.0542183}, {-0.187066, -0.0732084, 0.32812, -0.266161,
        0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
        -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
    Sinusoidal1_4 → {{1., -0.532036, -0.302356, 0.831106, -0.629711, -0.0371085, 0.596985,
        -0.62075, 0.142423, 0.36295, -0.493594, 0.221724, 0.162571, -0.324237, 0.20497, 0.0344758,
        -0.17362, 0.112388, -0.00622156, -0.0499598}, {-0.151568, -0.0998564, 0.265085, -0.275486,
        0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
        -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
    Sinusoidal1_5 → {{1., -0.527309, -0.312887, 0.817769, -0.63784, -0.0237078, 0.577367,
        -0.621324, 0.164028, 0.351345, -0.49821, 0.231947, 0.142714, -0.32515, 0.225656, 0.0251669,
        -0.165949, 0.127976, 0.00513716, -0.0567312}, {-0.20104, -0.101657, 0.31364, -0.234517,
        -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
        -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
    Sinusoidal1_6 → {{1., -0.522957, -0.301441, 0.809437, -0.612822, -0.0160013, 0.558882,
        -0.600183, 0.170944, 0.335272, -0.496822, 0.24924, 0.134325, -0.346461, 0.245466, 0.0145607,
        -0.191767, 0.137294, -0.00655488, -0.0604127}, {-0.17526, -0.106684, 0.304186, -0.27676,
        -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
        -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
    Sinusoidal1_7 → {{1., -0.527071, -0.299918, 0.797362, -0.616678, -0.0186254, 0.569954,
        -0.58735, 0.161401, 0.333202, -0.495766, 0.248661, 0.144045, -0.35774, 0.231849, 0.0182884,
        -0.187509, 0.148033, -0.00582717, -0.0563091}, {-0.179672, -0.126709, 0.328842, -0.280026,
        -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
        -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
    Sinusoidal1_8 → {{1., -0.52831, -0.312186, 0.813182, -0.627885, -0.016639, 0.560325, -0.614633,
        0.175931, 0.327078, -0.496677, 0.257476, 0.129162, -0.331267, 0.243627, 0.0177458,
        -0.176866, 0.132737, 0.0049543, -0.0577547}, {-0.187929, -0.0921767, 0.316032, -0.235549,
        -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
        -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
    Sinusoidal1_9 → {{1., -0.527694, -0.317952, 0.813259, -0.632253, -0.0233934, 0.587889,
```

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```
    -0.612342, 0.159447, 0.339318, -0.495163, 0.24501, 0.14516, -0.334143, 0.215821, 0.0263486,
    -0.171203, 0.127942, 0.00973395, -0.0557843}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
Sinusoidal1_10 → {{1., -0.521088, -0.326836, 0.8189, -0.615252, -0.0525415, 0.601327,
    -0.603279, 0.126784, 0.373577, -0.497758, 0.21052, 0.180427, -0.342998, 0.204147, 0.0532366,
    -0.191766, 0.12733, 0.019034, -0.0637605}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}},
Sinusoidal2_11 → {{1., -0.278894, -0.739438, 0.677729, 0.263549, -0.74964, 0.201433, 0.535198,
    -0.475396, -0.186387, 0.49992, -0.122659, -0.333427, 0.273702, 0.107559, -0.250224,
    0.0454066, 0.131084, -0.0694275, -0.030086}, {-0.0952089, -0.252202, 0.25704, 0.097318,
    -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
Sinusoidal2_12 → {{1., -0.276885, -0.737128, 0.678704, 0.262136, -0.750132, 0.200574, 0.536952,
    -0.475301, -0.182598, 0.499836, -0.126407, -0.333557, 0.271968, 0.108371, -0.24965,
    0.0467672, 0.130088, -0.0716985, -0.0320403}, {-0.101498, -0.25529, 0.251653, 0.0972642,
    -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
    0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
Sinusoidal2_13 → {{1., -0.280504, -0.736435, 0.682899, 0.257454, -0.751962, 0.205634, 0.530699,
    -0.478309, -0.178941, 0.499795, -0.130022, -0.330384, 0.277981, 0.103314, -0.247611,
    0.0512805, 0.125921, -0.0722738, -0.0285358}, {-0.0918789, -0.259087, 0.253065, 0.103093,
    -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
Sinusoidal2_14 → {{1., -0.277698, -0.734459, 0.679775, 0.25739, -0.752569, 0.204627, 0.532738,
    -0.480375, -0.180008, 0.49979, -0.128977, -0.32842, 0.27605, 0.104385, -0.247127,
    0.0514268, 0.128902, -0.0743448, -0.0311064}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
Sinusoidal2_15 → {{1., -0.279353, -0.737749, 0.681322, 0.260133, -0.752558, 0.206477, 0.532246,
    -0.479743, -0.180504, 0.499899, -0.128441, -0.329137, 0.276611, 0.102509, -0.247286,
    0.0487821, 0.127648, -0.0711713, -0.0296864}, {-0.0939856, -0.25429, 0.25073, 0.100441,
    -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
    0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
Sinusoidal2_16 → {{1., -0.280699, -0.736087, 0.681775, 0.255957, -0.749566, 0.20752, 0.528795,
    -0.481535, -0.176093, 0.499812, -0.13287, -0.327138, 0.279884, 0.101395, -0.25011,
    0.0529545, 0.126976, -0.0725898, -0.0283783}, {-0.0916775, -0.260977, 0.251061, 0.104141,
    -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
    0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
Sinusoidal2_17 → {{1., -0.277518, -0.738773, 0.676889, 0.265432, -0.753017, 0.198194, 0.537938,
    -0.476343, -0.186949, 0.49987, -0.122055, -0.33252, 0.270923, 0.110716, -0.246744,
    0.0434958, 0.131953, -0.0700124, -0.0314804}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
    -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
Sinusoidal2_18 → {{1., -0.276063, -0.736479, 0.676457, 0.263789, -0.748125, 0.201591, 0.533508,
    -0.475374, -0.183134, 0.49978, -0.125875, -0.333564, 0.275277, 0.107277, -0.251652,
    0.0452349, 0.132409, -0.0722365, -0.0328205}, {-0.102994, -0.260616, 0.250831, 0.0989794,
    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
Sinusoidal2_19 → {{1., -0.278939, -0.739103, 0.678303, 0.262313, -0.749557, 0.201567, 0.535642,
    -0.474427, -0.185995, 0.499913, -0.123017, -0.334357, 0.273147, 0.107268, -0.250189,
    0.0465856, 0.130499, -0.069647, -0.030009}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
Sinusoidal2_20 → {{1., -0.279393, -0.736615, 0.67888, 0.261362, -0.748114, 0.198363, 0.533023,
    -0.473514, -0.187235, 0.499877, -0.121687, -0.335325, 0.275714, 0.110577, -0.251599,
    0.0475096, 0.129987, -0.0722285, -0.0295813}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
    -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>|>
```

If we want the classes produced, we can query the keys:

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In[136]:=
```
Query[Keys]@classificationIntepolatedAutocorrelation1
```

Out[136]=
```
{SpikeMax, SpikeMin, Lag1, Lag3}
```

For the members in each class we have:

In[137]:=
```
Query[All, Length]@classificationIntepolatedAutocorrelation1
```

Out[137]=
```
<|SpikeMax → 20, SpikeMin → 20, Lag1 → 50, Lag3 → 20|>
```

Method: "TimeSeriesModelAggregate" (1)

This method does not utilize cutoffs, but fits the data to Mathematica's inbuilt time-series processes and classifies the data by model family:

In[138]:=
```
classificationTimeSeriesModelAggregate1 =
 TimeSeriesClassification[classificationExample1, timePointsExample, Method → "TimeSeriesModelAggregate"]
```

```
Method → "TimeSeriesModelAggregate"
```

Out[138]=
```
<|MAProcess →
  <|SpikePositive_1 → {{0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682, -0.0371416,
      0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411, -0.00869189,
      -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732},
     {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682, -0.0371416,
      0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411, -0.00869189,
      -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829,
      0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543},
     {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829, 0.017722,
      -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993,
      -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977},
     {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993, -0.0955887,
      -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843, 0.0402401,
      -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033, -0.0772898, 0.0399612,
      -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539, 0.0509389, 0.0608363, -0.0848876,
      -0.0715063, 0.0612102, -0.0887476, 0.0558859}, {0.958583, 0.00400217, 0.0429904, 0.0838796,
      0.0778033, -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858,
      0.0195539, 0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663, 0.0676522, 0.0605738,
      0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931, 0.0796911, -0.0701274,
      -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}, {0.966833, -0.0172757, -0.0101601,
      0.0449156, 0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
      -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416, 0.0326082,
      -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387, 0.0872339, -0.0766939,
      0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}, {0.971085, -0.0737213, -0.0183259,
      -0.0280164, -0.0370416, 0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791,
      0.0886387, 0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442, -0.00304927,
      0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801, 0.0872978, 0.0241062,
      0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}, {0.973634, -0.0197451, 0.00381691,
      0.0632199, 0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
      0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677,
      -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
      -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763},
     {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677, -0.0238371,
```

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```
    -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
    -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
SpikePositive_9 → {{0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483,
    -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062},
   {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483, -0.0385902,
    -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
SpikePositive_10 → {{0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367,
    -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457},
   {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367, -0.0143555,
    0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266, -0.0322946,
    -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
SpikePositive_11 → {{0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068, 0.0325846, -0.0861631,
    0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531, 0.0377134, 0.0259428, 0.0165473,
    0.00876485, 0.0104191, -0.0990718, 0.101205}, {0.0696283, 0.0251021, 0.968196, 0.0511374,
    0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
    -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
SpikePositive_12 → {{0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803, 0.0850629,
    0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826},
   {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803, 0.0850629, 0.0791585,
    -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403, 0.0350351,
    0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
SpikePositive_13 → {{-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903, -0.0475178,
    -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952, 0.0310687, -0.0939468,
    -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}, {-0.0343175, -0.0155132, 0.955818,
    0.0636753, -0.0900903, -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626,
    0.0398952, 0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
SpikePositive_14 → {{0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311, 0.0642856,
    -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114},
   {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311, 0.0642856, -0.00120334,
    -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562, -0.044588,
    -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
SpikePositive_15 → {{0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922, 0.0322486,
    0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456, -0.0576246, -0.101699,
    -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}, {0.0367157, 0.00909492, 0.955211,
    -0.0373177, -0.0545922, 0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346,
    0.0584456, -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
SpikePositive_16 → {{-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223,
    -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381, -0.0588352,
    -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908},
   {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223, -0.00461306,
    -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381, -0.0588352,
    -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
SpikePositive_17 → {{0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444, 0.09185, -0.0309321,
    0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902, 0.101663, 0.086855,
    0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}, {0.0894556, -0.0939456, 0.955206,
    -0.0721055, 0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
    -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
SpikePositive_18 → {{-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144, -0.0566396,
    0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424, 0.0179427,
    0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999},
   {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144, -0.0566396, 0.00932272,
    -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424, 0.0179427, 0.0577408,
    -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
SpikePositive_19 → {{-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727, -0.0813174,
    0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065},
   {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727, -0.0813174, 0.0169025,
    0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997, 0.0704534,
    -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
SpikePositive_20 → {{0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833, -0.0790448,
    -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909,
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    -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381},
   {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833, -0.0790448, -0.0883667,
    0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909,
    -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}},
 SpikeNegative_1 → {{-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627,
    0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467, -0.0370811,
    0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511},
   {-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627, 0.0839417,
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    0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
 SpikeNegative_2 → {{-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113, -0.0217826,
    -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501, -0.0295528,
    0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342},
   {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113, -0.0217826, -0.0407702,
    -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501, -0.0295528,
    0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
 SpikeNegative_3 → {{-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095, 0.102466,
    -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
    -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636},
   {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095, 0.102466, -0.0311731,
    0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319, -0.00382691,
    -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
 SpikeNegative_4 → {{-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556, -0.0455452,
    0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411},
   {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556, -0.0455452, 0.0806517,
    0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762, 0.065436,
    -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
 SpikeNegative_5 → {{-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968, 0.0456577,
    -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712},
   {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968, 0.0456577, -0.0741938,
    0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812, -0.0509291,
    -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
 SpikeNegative_6 → {{-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953, -0.058058,
    0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539},
   {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953, -0.058058, 0.0371483,
    0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694, 0.00809772,
    0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
 SpikeNegative_7 → {{-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109, 0.0874465,
    -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901},
   {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109, 0.0874465, -0.0578879,
    -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136, -0.0870922,
    -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
 SpikeNegative_8 → {{-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887, -0.0684695,
    0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666},
   {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887, -0.0684695, 0.0552479,
    0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932, -0.0311677,
    -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
 SpikeNegative_9 → {{-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416, 0.0325626,
    -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653},
   {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416, 0.0325626, -0.0841603,
    0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441, -0.0901265,
    -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
 SpikeNegative_10 → {{-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025, 0.0119404,
    -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664},
   {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025, 0.0119404, -0.0700182,
    -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425, -0.020989,
    0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
 SpikeNegative_11 → {{-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755, -0.0488362,
    -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052, 0.0300314,
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    0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954},
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    -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052, 0.0300314, 0.0700943,
    -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
 SpikeNegative_12 → {{0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571, 0.0770767,
    0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
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   {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571, 0.0770767, 0.070194,
    -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504, -0.0981713,
    -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
 SpikeNegative_13 → {{0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036, 0.0881039,
    0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538, -0.028162,
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   {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036, 0.0881039, 0.0257902,
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    0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
 SpikeNegative_14 → {{-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594, 0.0528555,
    0.00336549, 0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977},
   {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594, 0.0528555, 0.00336549,
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    0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
 SpikeNegative_15 → {{-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309, 0.000455216,
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    0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439},
   {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309, 0.000455216, -0.0829657,
    0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281, 0.0312967, 0.0228599,
    -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
 SpikeNegative_16 → {{-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464, 0.0166785,
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    -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422},
   {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464, 0.0166785, 0.0680268,
    0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101, 0.0309736,
    -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
 SpikeNegative_17 → {{-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312, 0.0616787,
    -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667, 0.022695,
    0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092},
   {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312, 0.0616787, -0.0836702,
    -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667, 0.022695, 0.0217809,
    0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
 SpikeNegative_18 → {{0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604, 0.0000556895,
    -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971, 0.099183, 0.0322089,
    0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389},
   {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604, 0.0000556895, -0.0637593,
    0.0386416, 0.0568781, -0.0191067, -0.0633971, 0.099183, 0.0322089, 0.0782449,
    0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
 SpikeNegative_19 → {{-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693, 0.0216656,
    0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588,
    -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696},
   {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693, 0.0216656, 0.0247419,
    -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588, -0.0116062,
    0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
 SpikeNegative_20 → {{-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452, 0.057722,
    -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007,
    -0.0175827, 0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368},
   {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452, 0.057722, -0.0391361,
    -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007, -0.0175827,
    0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}},
 Sinusoidal1_3 → {{-0.187066, -0.0732084, 0.32812, -0.266161, 0.00567862, 0.253731, -0.305231,
    0.119463, 0.171259, -0.307063, 0.163206, 0.095439, -0.297199, 0.229651, -0.00688215,
    -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}, {-0.187066, -0.0732084, 0.32812,
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 Sinusoidal1_4 → {{-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004, 0.261223, -0.285188,
    0.110899, 0.212223, -0.322869, 0.206654, 0.11987, -0.322486, 0.240951, 0.0208141, -0.225578,
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      0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
      -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
   Sinusoidal1_8 → {{-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322, 0.285866, -0.282711,
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   Sinusoidal1_9 → {{-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817, 0.286427, -0.303775,
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      -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
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      0.121391, 0.20297, -0.328442, 0.171305, 0.113167, -0.291561, 0.268582, 0.0225742, -0.256505,
      0.297837, -0.104109, -0.200599, 0.310941}, {-0.203834, -0.0722574, 0.294696, -0.254799,
      0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
      -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>,
SARIMAProcess → <|LinearPositive_1 → {{0.018415, 0.0377122, 0.0574444, 0.0761646, 0.0918826,
      0.112863, 0.131264, 0.149525, 0.166786, 0.18659, 0.205188, 0.223266, 0.241367,
      0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, 0.373425},
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      0.205188, 0.223266, 0.241367, 0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, 0.373425}},
   LinearPositive_2 → {{0.0183904, 0.0374466, 0.0550304, 0.0738563, 0.0928923, 0.110677,
      0.130133, 0.148914, 0.167272, 0.186766, 0.206807, 0.224025, 0.242161, 0.261728, 0.280689,
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      0.224025, 0.242161, 0.261728, 0.280689, 0.29779, 0.316418, 0.335012, 0.355339, 0.375155}},
   LinearPositive_3 → {{0.0204364, 0.0388961, 0.055949, 0.0753517, 0.0937248, 0.112155,
      0.1288, 0.150982, 0.166685, 0.187482, 0.204397, 0.22244, 0.241027,
      0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089},
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      0.204397, 0.22244, 0.241027, 0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}},
   LinearPositive_4 → {{0.0188591, 0.0384796, 0.0552706, 0.0761382, 0.0941127, 0.11255,
      0.131257, 0.150426, 0.166514, 0.185049, 0.206061, 0.222052, 0.24344, 0.261751, 0.281444,
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      0.222052, 0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}},
   LinearPositive_6 → {{0.0186014, 0.0381755, 0.0550572, 0.074646, 0.0932816, 0.113886, 0.132134,
      0.149767, 0.168659, 0.185415, 0.205262, 0.222624, 0.242621, 0.260049, 0.279298, 0.299912,
      0.319378, 0.335084, 0.353279, 0.374138}, {0.0186014, 0.0381755, 0.0550572, 0.074646,
      0.0932816, 0.113886, 0.132134, 0.149767, 0.168659, 0.185415, 0.205262, 0.222624,
      0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
   LinearPositive_7 → {{0.0186204, 0.0363314, 0.0569047, 0.0757329, 0.092018, 0.111558,
      0.130244, 0.148133, 0.167451, 0.186409, 0.204805, 0.22423, 0.241912, 0.261689, 0.28065,
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      0.0757329, 0.092018, 0.111558, 0.130244, 0.148133, 0.167451, 0.186409, 0.204805, 0.22423,
      0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
   LinearPositive_8 → {{0.0170019, 0.0382694, 0.0569482, 0.0754625, 0.0914347, 0.110031,
      0.132014, 0.15073, 0.169121, 0.188274, 0.205265, 0.223358, 0.242529, 0.260421, 0.281319,
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      0.0754625, 0.0914347, 0.110031, 0.132014, 0.15073, 0.169121, 0.188274, 0.205265, 0.223358,
      0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}},
   LinearPositive_9 → {{0.0185501, 0.0388643, 0.0547098, 0.0747468, 0.0938687, 0.113558,
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      0.241691, 0.261072, 0.279055, 0.298507, 0.318632, 0.337602, 0.353993, 0.372608}},
   LinearPositive_10 → {{0.0174864, 0.0370712, 0.0572236, 0.0748823, 0.0926627, 0.111129,
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      0.223211, 0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
   LinearPositive_11 → {{0.013623, 0.0406398, 0.0607801, 0.0781742, 0.0921015, 0.112119,
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    0.216208, 0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, 0.373621}},
LinearPositive_12 → {{0.0219335, 0.0431422, 0.0502095, 0.0696589, 0.0884956, 0.116468,
    0.123447, 0.151797, 0.168869, 0.179094, 0.204522, 0.228042, 0.240546, 0.269187, 0.279387,
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    0.240546, 0.269187, 0.279387, 0.302162, 0.315899, 0.330232, 0.349931, 0.381055}},
LinearPositive_13 → {{0.022617, 0.0284408, 0.0607512, 0.0795972, 0.0880775, 0.119613,
    0.134238, 0.152698, 0.169261, 0.181713, 0.197855, 0.217149, 0.241086, 0.263228, 0.284546,
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    0.241086, 0.263228, 0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}},
LinearPositive_15 → {{0.0152129, 0.0390101, 0.0602871, 0.0702062, 0.091338, 0.118718,
    0.136185, 0.146481, 0.161128, 0.179922, 0.215359, 0.218444, 0.250473, 0.25777, 0.279989,
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    0.250473, 0.25777, 0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}},
LinearPositive_16 → {{0.0164478, 0.0360481, 0.048135, 0.0712245, 0.101186, 0.114916,
    0.129433, 0.153936, 0.164281, 0.192697, 0.203977, 0.223277, 0.236402,
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    0.203977, 0.223277, 0.236402, 0.257694, 0.277977, 0.296096, 0.311924, 0.344353, 0.357433, 0.375096}},
LinearPositive_17 → {{0.0153802, 0.0408047, 0.0548321, 0.0765604, 0.0991872, 0.117741,
    0.128177, 0.147496, 0.159869, 0.189666, 0.195939, 0.215447, 0.240506, 0.262803, 0.283339,
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    0.0765604, 0.0991872, 0.117741, 0.128177, 0.147496, 0.159869, 0.189666, 0.195939,
    0.215447, 0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
LinearPositive_18 → {{0.0115844, 0.0455792, 0.0534286, 0.068487, 0.0918771, 0.107837,
    0.137609, 0.144956, 0.162508, 0.185864, 0.206224, 0.229689, 0.232407, 0.261637, 0.285165,
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    0.068487, 0.0918771, 0.107837, 0.137609, 0.144956, 0.162508, 0.185864, 0.206224, 0.229689,
    0.232407, 0.261637, 0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}},
LinearPositive_20 → {{0.00952752, 0.0286979, 0.0547226, 0.0709501, 0.0958101, 0.109505,
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    0.0709501, 0.0958101, 0.109505, 0.135844, 0.152431, 0.165158, 0.182651, 0.210505,
    0.231304, 0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
LinearNegative_1 → {{-0.0218046, -0.0446169, -0.0612231, -0.0738948, -0.109733, -0.115191,
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    -0.273794, -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733},
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    -0.148293, -0.159758, -0.176361, -0.217843, -0.224298, -0.23172, -0.273794,
    -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733}},
LinearNegative_3 → {{-0.0283384, -0.0528281, -0.0527884, -0.0740599, -0.0921776, -0.0948819,
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LinearNegative_5 → {{-0.0201624, -0.0405386, -0.0436406, -0.0738225, -0.0817467, -0.105404,
    -0.114359, -0.154377, -0.169473, -0.174198, -0.212011, -0.225376, -0.230144,
    -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219},
   {-0.0201624, -0.0405386, -0.0436406, -0.0738225, -0.0817467, -0.105404, -0.114359,
    -0.154377, -0.169473, -0.174198, -0.212011, -0.225376, -0.230144, -0.247108,
    -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}},
LinearNegative_6 → {{-0.0267223, -0.0446999, -0.0523138, -0.0699606, -0.0987645, -0.126896,
    -0.126614, -0.165572, -0.172297, -0.184872, -0.208135, -0.237294, -0.243037,
    -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481},
   {-0.0267223, -0.0446999, -0.0523138, -0.0699606, -0.0987645, -0.126896, -0.126614,
    -0.165572, -0.172297, -0.184872, -0.208135, -0.237294, -0.243037, -0.24423,
    -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481}},
LinearNegative_7 → {{-0.00172329, -0.032268, -0.068173, -0.0857129, -0.0881686, -0.107137,
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    -0.248536, -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923},
   {-0.00172329, -0.032268, -0.068173, -0.0857129, -0.0881686, -0.107137, -0.140409,
    -0.14992, -0.182962, -0.175511, -0.200764, -0.226349, -0.23516, -0.248536,
    -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923}},
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    LinearNegative_8 → {{-0.0170306, -0.0378539, -0.0394845, -0.0767312, -0.0942537, -0.105065,
        -0.146528, -0.134698, -0.186411, -0.174071, -0.194782, -0.232787, -0.238911,
        -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678},
      {-0.0170306, -0.0378539, -0.0394845, -0.0767312, -0.0942537, -0.105065, -0.146528,
        -0.134698, -0.186411, -0.174071, -0.194782, -0.232787, -0.238911, -0.261139,
        -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
    LinearNegative_10 → {{-0.00155633, -0.0271325, -0.0625737, -0.0744387, -0.0901925,
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    LinearNegative_11 → {{-0.0105542, -0.0364589, -0.0515525, -0.0708746, -0.0862196, -0.118392,
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  ARIMAProcess → <|LinearPositive_5 → {{0.0196474, 0.0375735, 0.0561861, 0.0745382, 0.094777,
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LinearNegative_14 → {{-0.0187992, -0.0431131, -0.0473458, -0.070655, -0.0879629, -0.116006,
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LinearNegative_16 → {{-0.0225164, -0.0461677, -0.0473716, -0.067817, -0.0986701, -0.119505,
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Sinusoidal3_21 → {{0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461, 0.254971, 0.296206,
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Sinusoidal3_22 → {{0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846, 0.258728, 0.299815,
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Sinusoidal3_24 → {{0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361, 0.252171, 0.301387,
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Sinusoidal3_25 → {{0.191347, -0.0982886, -0.29771, -0.261082, 0.00611569, 0.249936, 0.298887,
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Sinusoidal3_26 → {{0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724, 0.255415, 0.302354,
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      -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}, {-0.153886, -0.0875347, 0.297854,
      -0.276583, 0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
      -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_6 → {{-0.17526, -0.106684, 0.304186, -0.27676, -0.0299081, 0.264665, -0.287699,
      0.0895741, 0.174449, -0.288889, 0.206239, 0.11573, -0.282169, 0.247232, 0.00318229,
      -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}, {-0.17526, -0.106684, 0.304186,
      -0.27676, -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
      -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}}|>,
GARCHProcess → <|Sinusoidal2_11 → {{-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852,
      0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
      0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889},
     {-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852, 0.0940832, 0.259478,
      -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865, 0.258725, 0.0998843,
      -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067, 0.0980672, 0.250394,
      -0.261387, -0.102951, 0.313615, -0.102471, -0.251668, 0.262301, 0.0921143, -0.316076, 0.0956623,
      0.258148, -0.257012, -0.0945577, 0.317903}, {-0.101498, -0.25529, 0.251653, 0.0972642,
      -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
      0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667, 0.104182, 0.258366,
      -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963, 0.254435, 0.0947659, -0.322671,
      0.099541, 0.251173, -0.252867, -0.092285, 0.311489}, {-0.0918789, -0.259087, 0.253065,
      0.103093, -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
      0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{-0.0971308, -0.259618, 0.249762, 0.0996953, -0.311793, 0.0980176, 0.26024,
      -0.249275, -0.100238, 0.318125, -0.100697, -0.257698, 0.256122, 0.0982282, -0.320808,
      0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}, {-0.0971308, -0.259618, 0.249762,
```

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```
    0.0996953, -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
Sinusoidal2_15 → {{-0.0939856, -0.25429, 0.25073, 0.100441, -0.313599, 0.0944084, 0.258905,
    -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627, 0.255722, 0.0993267, -0.321786,
    0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}, {-0.0939856, -0.25429, 0.25073, 0.100441,
    -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
    0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
Sinusoidal2_16 → {{-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132, 0.0966092, 0.262552,
    -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968, 0.256443, 0.0917731, -0.314379,
    0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}, {-0.0916775, -0.260977, 0.251061,
    0.104141, -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
    0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
Sinusoidal2_17 → {{-0.0991608, -0.252958, 0.255513, 0.0985052, -0.309591, 0.0946333, 0.259341,
    -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912, 0.259191, 0.0930131, -0.318952,
    0.0920208, 0.256431, -0.252563, -0.102318, 0.317}, {-0.0991608, -0.252958, 0.255513,
    0.0985052, -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735,
    -0.25912, 0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
Sinusoidal2_18 → {{-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724, 0.0944222, 0.259447,
    -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843, 0.258552, 0.0991506, -0.312675,
    0.10202, 0.254956, -0.252332, -0.102226, 0.317809}, {-0.102994, -0.260616, 0.250831,
    0.0989794, -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167,
    -0.251843, 0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
Sinusoidal2_19 → {{-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977, 0.0989163, 0.249498,
    -0.259273, -0.103637, 0.311237, -0.101011, -0.258469, 0.251806, 0.101187, -0.319249, 0.100504,
    0.251478, -0.255713, -0.0973637, 0.309885}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
Sinusoidal2_20 → {{-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484, 0.101942, 0.254089,
    -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815, 0.0941545, -0.321907,
    0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}, {-0.0946325, -0.259177, 0.259154,
    0.0992225, -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>|>
```

If we want the classes produced, we can query the keys:

```
In[139]:= Query[Keys]@classificationTimeSeriesModelAggregate1

Out[139]= {MAProcess, SARIMAProcess, ARIMAProcess, SARMAProcess, ARProcess, GARCHProcess}
```

For the members in each class we have:

```
In[140]:= Query[All, Length]@classificationTimeSeriesModelAggregate1

Out[140]= <|MAProcess → 45, SARIMAProcess → 28, ARIMAProcess → 22, SARMAProcess → 3, ARProcess → 2, GARCHProcess → 10|>
```

Method: "TimeSeriesModelDetailed" (1)

This method does not utilize cutoffs, but fits the data to Mathematica's inbuilt time-series processes and classifies the data by model family and parameters:

```
In[141]:= classificationTimeSeriesModelAggregate1 =
  TimeSeriesClassification[classificationExample1, timePointsExample, Method → "TimeSeriesModelDetailed"]

  Method → "TimeSeriesModelDetailed"

Out[141]= <|ARIMAProcess[0, 1, 1] →
    <|LinearPositive_14 → {{-0.581486}, {0.0276601, 0.0348994, 0.0578995, 0.0764811, 0.0865063,
        0.115217, 0.136395, 0.15157, 0.16455, 0.180615, 0.213666, 0.215142, 0.243638,
        0.254281, 0.280739, 0.299298, 0.313921, 0.336645, 0.361637, 0.373861}},
     LinearNegative_9 → {{-0.446399}, {-0.0287969, -0.0189698, -0.0530075, -0.0828922, -0.0936032,
        -0.115414, -0.114422, -0.130851, -0.167598, -0.173937, -0.198609, -0.23569, -0.258977,
        -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
```

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```
  LinearNegative_12 → {{-0.289577}, {-0.0105234, -0.0459122, -0.0631169, -0.0780043, -0.0883748,
      -0.108962, -0.137461, -0.144887, -0.163604, -0.184293, -0.210166, -0.217602, -0.245066,
      -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
  LinearNegative_17 → {{-0.553142}, {-0.0130003, -0.0309644, -0.0613334, -0.0794837, -0.0865967,
      -0.117058, -0.128048, -0.153332, -0.167054, -0.192254, -0.208455, -0.223898, -0.240133,
      -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}}|>,
ARIMAProcess[0, 4, 1] → <|Sinusoidal3_25 → {{0.455474}, {0.191347, -0.0982886, -0.29771, -0.261082,
      0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
      0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}}|>,
ARIMAProcess[0, 5, 1] → <|Sinusoidal3_21 → {{0.344018}, {0.18867, -0.0972321, -0.306583, -0.251354,
      -0.00388461, 0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096,
      0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
  Sinusoidal3_22 → {{0.434402}, {0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846,
      0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523, 0.303756,
      0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
  Sinusoidal3_23 → {{0.381462}, {0.18264, -0.0994704, -0.295137, -0.250857, 0.00157044,
      0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036, 0.298633,
      0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
  Sinusoidal3_24 → {{0.285474}, {0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361,
      0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939, 0.304721,
      0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
  Sinusoidal3_26 → {{0.466283}, {0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724,
      0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444, 0.296927,
      0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{0.387691}, {0.185809, -0.10192, -0.303748, -0.261172, 0.000202029,
      0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227, 0.302676,
      0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.455829}, {0.187562, -0.10053, -0.297144, -0.250552, 0.00476677,
      0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453, 0.301104,
      0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}}|>,
ARIMAProcess[0, 6, 0] → <|Sinusoidal3_29 → {{109}, {0.189755, -0.100643, -0.295957, -0.251445,
      -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
      0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}}|>,
ARIMAProcess[1, 1, 0] → <|LinearPositive_5 → {{-0.669385}, {0.0196474, 0.0375735, 0.0561861,
      0.0745382, 0.094777, 0.113054, 0.132423, 0.150372, 0.169563, 0.188068, 0.205612,
      0.225889, 0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
  LinearNegative_14 → {{-0.6417}, {-0.0187992, -0.0431131, -0.0473458, -0.070655, -0.0879629,
      -0.116006, -0.12521, -0.152395, -0.170415, -0.184268, -0.196593, -0.22289, -0.23237,
      -0.26046, -0.276864, -0.301954, -0.319987, -0.336453, -0.361973, -0.377956}}|>,
ARIMAProcess[1, 1, 1] → <|LinearPositive_19 → {{-0.080681, -0.893891},
     {0.0205961, 0.045526, 0.0569898, 0.0724948, 0.0867427, 0.105806, 0.12769, 0.145665, 0.170669, 0.180276,
      0.216792, 0.223063, 0.241101, 0.270774, 0.282283, 0.293887, 0.315058, 0.334039, 0.359611, 0.369743}},
  LinearNegative_4 → {{-0.488986, -0.686262}, {-0.0158873, -0.0248133, -0.0382326, -0.0881019,
      -0.0887054, -0.128386, -0.128859, -0.161147, -0.159022, -0.205319, -0.200777, -0.210411,
      -0.243003, -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844}},
  LinearNegative_15 → {{-0.16501, -0.892412}, {-0.0162872, -0.0293132, -0.0552218, -0.0807767,
      -0.0935334, -0.121112, -0.124004, -0.147926, -0.165828, -0.191582, -0.205406, -0.219926,
      -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
  LinearNegative_19 → {{-0.133156, -0.633589}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
      -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
      -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}}|>,
ARIMAProcess[2, 1, 0] → <|LinearNegative_2 → {{-0.786493, -0.488014}, {-0.0137543, -0.0552134,
      -0.0387902, -0.0787876, -0.0972777, -0.0993326, -0.131634, -0.158204, -0.178021, -0.176063, -0.209858,
      -0.230763, -0.248781, -0.268592, -0.290148, -0.294015, -0.319548, -0.339092, -0.343638, -0.357122}}|>,
ARIMAProcess[2, 1, 1] → <|LinearNegative_16 → {{0.0606033, -0.37368, -0.937769}, {-0.0225164, -0.0461677,
      -0.0473716, -0.067817, -0.0986701, -0.119505, -0.130459, -0.1556, -0.169469, -0.1814, -0.198572,
      -0.221935, -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}}|>,
ARIMAProcess[4, 7, 1] → <|Sinusoidal3_30 → {{-0.645761, 0.325783, -0.71686, -0.956465, 0.182246},
     {0.186539, -0.100579, -0.301622, -0.251977, 0.00452805, 0.258968, 0.30446,
      0.103392, -0.185935, -0.314134, -0.188321, 0.10063, 0.296225, 0.252222,
      -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
ARProcess[3] → <|Sinusoidal1_2 → {{-0.787653, -0.596135, 0.350312}, {-0.153886, -0.0875347,
      0.297854, -0.276583, 0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389,
      0.0667307, -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_6 → {{-0.659125, -0.424289, 0.504182}, {-0.17526, -0.106684, 0.304186, -0.27676,
      -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
```

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```
      -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}}|>,
GARCHProcess[0, 1] → <|Sinusoidal2_11 → {{0.206862}, {-0.0952089, -0.252202, 0.25704, 0.097318,
      -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
      0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{0.20692}, {-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067,
      0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668, 0.262301,
      0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{0.206862}, {-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667,
      0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963, 0.254435,
      0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{0.206973}, {-0.0971308, -0.259618, 0.249762, 0.0996953, -0.311793,
      0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698, 0.256122,
      0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{0.206862}, {-0.0939856, -0.25429, 0.25073, 0.100441, -0.313599, 0.0944084,
      0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627, 0.255722,
      0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{0.206862}, {-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132,
      0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968, 0.256443,
      0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{0.206869}, {-0.0991608, -0.252958, 0.255513, 0.0985052, -0.309591,
      0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
      0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.206811}, {-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724,
      0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
      0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{0.206862}, {-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977,
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      0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{0.206802}, {-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484,
      0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824, 0.252815,
      0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
MAProcess[0] → <|SpikePositive_1 → {{1}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222,
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      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
  SpikePositive_2 → {{2}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829,
      0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
  SpikePositive_3 → {{3}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993,
      -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
  SpikePositive_4 → {{4}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033, -0.0772898,
      0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
  SpikePositive_5 → {{5}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663, 0.0676522,
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  SpikePositive_6 → {{6}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416, 0.0326082,
      -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
  SpikePositive_7 → {{7}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442, -0.00304927,
      0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
  SpikePositive_8 → {{8}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677,
      -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
      -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
  SpikePositive_9 → {{9}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483,
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      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
  SpikePositive_10 → {{10}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367,
      -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
      -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
  SpikePositive_11 → {{11}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068, 0.0325846,
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  SpikePositive_12 → {{12}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803, 0.0850629,
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    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
  SpikePositive_13 → {{13}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
    -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
    0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
  SpikePositive_14 → {{14}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311, 0.0642856,
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    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
  SpikePositive_15 → {{15}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
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  SpikePositive_16 → {{16}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223,
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    -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
  SpikePositive_17 → {{17}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444, 0.09185,
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  SpikePositive_18 → {{18}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144, -0.0566396,
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    0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{19}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727, -0.0813174,
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    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{20}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833, -0.0790448,
    -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909,
    -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}},
  SpikeNegative_1 → {{21}, {-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627,
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  SpikeNegative_2 → {{22}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113, -0.0217826,
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  SpikeNegative_3 → {{23}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095, 0.102466,
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  SpikeNegative_4 → {{24}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556, -0.0455452,
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    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{25}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968, 0.0456577,
    -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{26}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953, -0.058058,
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    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{27}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109, 0.0874465,
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  SpikeNegative_8 → {{28}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
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  SpikeNegative_9 → {{29}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416, 0.0325626,
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  SpikeNegative_10 → {{30}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
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    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
  SpikeNegative_11 → {{31}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755, -0.0488362,
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    0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{32}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571, 0.0770767,
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    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{33}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
    0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{34}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594, 0.0528555,
    0.00336549, 0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
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      0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
    SpikeNegative_15 → {{35}, {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309,
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      0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
    SpikeNegative_16 → {{36}, {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464, 0.0166785,
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    SpikeNegative_17 → {{37}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312, 0.0616787,
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      0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
    SpikeNegative_18 → {{38}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
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      0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
    SpikeNegative_19 → {{39}, {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693, 0.0216656,
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      -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
    SpikeNegative_20 → {{40}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
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  MAProcess[1] → <|Sinusoidal1_3 → {{-0.921682}, {-0.187066, -0.0732084, 0.32812, -0.266161,
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      -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
    Sinusoidal1_4 → {{-0.907748}, {-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004,
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      0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
    Sinusoidal1_8 → {{-0.909422}, {-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322,
      0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394, -0.280218,
      0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
    Sinusoidal1_9 → {{-0.912675}, {-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817,
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      0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
    Sinusoidal1_10 → {{-0.909464}, {-0.203834, -0.0722574, 0.294696, -0.254799, 0.00423677,
      0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167, -0.291561,
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  SARIMAProcess[{0, 1, 0}, {1, 2, 0}5] → <|LinearPositive_18 → {{-1.94005}, {0.0115844, 0.0455792,
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  SARIMAProcess[{0, 1, 0}, {1, 2, 1}4] → <|LinearPositive_17 → {{-0.614529, -0.743646}, {0.0153802,
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      0.195939, 0.215447, 0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
    LinearNegative_5 → {{-0.128252, -0.936477}, {-0.0201624, -0.0405386, -0.0436406, -0.0738225,
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      -0.230144, -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}}|>,
  SARIMAProcess[{0, 1, 1}, {0, 2, 0}4] → <|LinearPositive_20 → {{-0.650559}, {0.00952752, 0.0286979,
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      0.231304, 0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
    LinearNegative_20 → {{-0.718729}, {-0.024006, -0.0432239, -0.0496914, -0.0682004, -0.0867373,
      -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471, -0.23997,
      -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}}|>,
  SARIMAProcess[{0, 1, 1}, {0, 2, 0}7] → <|LinearNegative_13 → {{-0.729423}, {-0.01186, -0.0431645,
      -0.0590873, -0.0756374, -0.0887624, -0.1144, -0.121973, -0.156462, -0.165726, -0.190329, -0.20958,
      -0.216046, -0.244405, -0.264186, -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596}}|>,
  SARIMAProcess[{0, 1, 1}, {1, 2, 0}4] → <|LinearPositive_1 → {{-0.773912, -0.375283},
     {0.018415, 0.0377122, 0.0574444, 0.0761646, 0.0918826, 0.112863, 0.131264, 0.149525, 0.166786, 0.18659,
      0.205188, 0.223266, 0.241367, 0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, 0.373425}},
    LinearNegative_10 → {{-0.877087, -0.799045}, {-0.00155633, -0.0271325, -0.0625737, -0.0744387,
      -0.0901925, -0.0932579, -0.138846, -0.15092, -0.157289, -0.198281, -0.189392, -0.206968,
      -0.259028, -0.273261, -0.270544, -0.29133, -0.328913, -0.352948, -0.335503, -0.37816}},
    LinearNegative_11 → {{-0.612293, -0.885838}, {-0.0105542, -0.0364589, -0.0515525, -0.0708746,
      -0.0862196, -0.118392, -0.123851, -0.151596, -0.176372, -0.191037, -0.213033, -0.221631,
      -0.235518, -0.271564, -0.288178, -0.293001, -0.310129, -0.328328, -0.364455, -0.366174}},
    LinearNegative_18 → {{-0.65323, -0.71236}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
      -0.0895021, -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921,
      -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}}|>,
  SARIMAProcess[{0, 1, 1}, {2, 2, 0}4] → <|LinearPositive_15 → {{-0.979205, -1.11667, -1.18764}, {0.0152129,
      0.0390101, 0.0602871, 0.0702062, 0.091338, 0.118718, 0.136185, 0.146481, 0.161128, 0.179922,
```

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```
      0.215359, 0.218444, 0.250473, 0.25777, 0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}}|>,
SARIMAProcess[{0, 1, 2}, {0, 1, 0}10] → <|LinearPositive_13 → {{-0.900987, 0.508086}, {0.022617, 0.0284408,
      0.0607512, 0.0795972, 0.0880775, 0.119613, 0.134238, 0.152698, 0.169261, 0.181713, 0.197855,
      0.217149, 0.241086, 0.263228, 0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}}|>,
SARIMAProcess[{0, 1, 2}, {0, 2, 0}7] → <|LinearPositive_4 → {{-1.2093, 0.614432}, {0.0188591,
      0.0384796, 0.0552706, 0.0761382, 0.0941127, 0.11255, 0.131257, 0.150426, 0.166514, 0.185049,
      0.206061, 0.222052, 0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}}|>,
SARIMAProcess[{0, 1, 2}, {2, 2, 0}4] → <|LinearPositive_7 →
    {{-1.21538, 0.633917, -0.59951, 0.499365}, {0.0186204, 0.0363314, 0.0569047, 0.0757329,
      0.092018, 0.111558, 0.130244, 0.148133, 0.167451, 0.186409, 0.204805, 0.22423,
      0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}}|>,
SARIMAProcess[{1, 1, 0}, {0, 2, 1}4] → <|LinearNegative_6 → {{-0.538386, -0.74313}, {-0.0267223, -0.0446999,
      -0.0523138, -0.0699606, -0.0987645, -0.126896, -0.126614, -0.165572, -0.172297, -0.184872, -0.208135,
      -0.237294, -0.243037, -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481}}|>,
SARIMAProcess[{1, 1, 0}, {1, 2, 0}5] → <|LinearPositive_8 → {{-0.533171, -1.39731}, {0.0170019,
      0.0382694, 0.0569482, 0.0754625, 0.0914347, 0.110031, 0.132014, 0.15073, 0.169121, 0.188274,
      0.205265, 0.223358, 0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}}|>,
SARIMAProcess[{1, 1, 1}, {0, 2, 0}5] → <|LinearPositive_3 → {{-0.606636, -0.866162},
     {0.0204364, 0.0388961, 0.055949, 0.0753517, 0.0937248, 0.112155, 0.1288, 0.150982, 0.166685, 0.187482,
      0.204397, 0.22244, 0.241027, 0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}}|>,
SARIMAProcess[{1, 1, 1}, {0, 2, 0}6] → <|LinearPositive_10 → {{-0.435232, -0.809816}, {0.0174864,
      0.0370712, 0.0572236, 0.0748823, 0.0926627, 0.111129, 0.130239, 0.148771, 0.168913, 0.186275,
      0.206359, 0.223211, 0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
  LinearPositive_12 → {{-0.316876, -0.683206}, {0.0219335, 0.0431422, 0.0502095, 0.0696589,
      0.0884956, 0.116468, 0.123447, 0.151797, 0.168869, 0.179094, 0.204522, 0.228042,
      0.240546, 0.269187, 0.279387, 0.302162, 0.315899, 0.330232, 0.349931, 0.381055}},
  LinearPositive_16 → {{-0.0645979, -0.915949}, {0.0164478, 0.0360481, 0.048135, 0.0712245,
      0.101186, 0.114916, 0.129433, 0.153936, 0.164281, 0.192697, 0.203977, 0.223277,
      0.236402, 0.257694, 0.277977, 0.296096, 0.311924, 0.344353, 0.357433, 0.375096}}|>,
SARIMAProcess[{1, 1, 1}, {0, 2, 0}7] → <|LinearNegative_1 → {{0.0303832, -0.905139}, {-0.0218046, -0.0446169,
      -0.0612231, -0.0738948, -0.109733, -0.115191, -0.124469, -0.148293, -0.159758, -0.176361, -0.217843,
      -0.224298, -0.23172, -0.273794, -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733}}|>,
SARIMAProcess[{1, 1, 1}, {0, 4, 0}4] → <|LinearPositive_6 → {{-0.155278, -0.936152}, {0.0186014,
      0.0381755, 0.0550572, 0.074646, 0.0932816, 0.113886, 0.132134, 0.149767, 0.168659, 0.185415, 0.205262,
      0.222624, 0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}}|>,
SARIMAProcess[{2, 1, 0}, {0, 2, 0}5] → <|LinearNegative_8 → {{-0.999592, -0.397806}, {-0.0170306, -0.0378539,
      -0.0394845, -0.0767312, -0.0942537, -0.105065, -0.146528, -0.134698, -0.186411, -0.174071, -0.194782,
      -0.232787, -0.238911, -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}}|>,
SARIMAProcess[{2, 1, 1}, {1, 2, 0}4] → <|LinearPositive_9 →
    {{-0.349892, -0.769229, -0.989904, -0.936068}, {0.0185501, 0.0388643, 0.0547098, 0.0747468,
      0.0938687, 0.113558, 0.129413, 0.148929, 0.168743, 0.186495, 0.204247, 0.225298,
      0.241691, 0.261072, 0.279055, 0.298507, 0.318632, 0.337602, 0.353993, 0.372608}}|>,
SARIMAProcess[{2, 1, 2}, {0, 2, 0}4] → <|LinearNegative_3 → {{-0.619078, -0.587516, -0.333018, -0.592526},
     {-0.0283384, -0.0528281, -0.0527884, -0.0740599, -0.0921776, -0.0948819,
      -0.146225, -0.165182, -0.160057, -0.18686, -0.220224, -0.211812, -0.237918,
      -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}}|>,
SARIMAProcess[{2, 1, 2}, {0, 2, 0}5] → <|LinearPositive_11 →
    {{-0.520206, -0.586619, -0.0210872, -0.886317}, {0.013623, 0.0406398, 0.0607801, 0.0781742,
      0.0921015, 0.112119, 0.128868, 0.151429, 0.171509, 0.192449, 0.211181, 0.216208,
      0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, 0.373621}}|>,
SARIMAProcess[{3, 1, 0}, {0, 3, 0}5] → <|LinearNegative_7 → {{-0.159037, 3.21246, -3.0529},
     {-0.00172329, -0.032268, -0.068173, -0.0857129, -0.0881686, -0.107137,
      -0.140409, -0.14992, -0.182962, -0.175511, -0.200764, -0.226349, -0.23516,
      -0.248536, -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923}}|>,
SARIMAProcess[{3, 1, 3}, {0, 2, 0}6] → <|LinearPositive_2 →
    {{1.37645, -1.42021, 1.44122, 0.0637764, -0.570932, -0.436994}, {0.0183904, 0.0374466,
      0.0550304, 0.0738563, 0.0928923, 0.110677, 0.130133, 0.148914, 0.167272, 0.186766, 0.206807,
      0.224025, 0.242161, 0.261728, 0.280689, 0.29779, 0.316418, 0.335012, 0.355339, 0.375155}}|>,
SARMAProcess[{0, 1}, {0, 1}4] → <|Sinusoidal1_5 → {{-0.382618, -0.461833}, {-0.20104, -0.101657,
      0.31364, -0.234517, -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134,
      0.118444, -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}}|>,
SARMAProcess[{0, 1}, {1, 0}4] → <|Sinusoidal1_1 → {{-0.371824, -0.781599}, {-0.20264, -0.107877,
      0.278896, -0.289184, -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752,
      0.0908701, -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}}|>,
SARMAProcess[{0, 1}, {1, 0}10] → <|Sinusoidal1_7 → {{-0.520119, -0.946197}, {-0.179672, -0.126709,
      0.328842, -0.280026, -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866,
```

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If we want the classes produced, we can query the keys:

In[142]:=
```
Query[Keys]@classificationTimeSeriesModelAggregate1
```

Out[142]=
```
{ARIMAProcess[0, 1, 1], ARIMAProcess[0, 4, 1], ARIMAProcess[0, 5, 1],
 ARIMAProcess[0, 6, 0], ARIMAProcess[1, 1, 0], ARIMAProcess[1, 1, 1],
 ARIMAProcess[2, 1, 0], ARIMAProcess[2, 1, 1], ARIMAProcess[4, 7, 1], ARProcess[3],
 GARCHProcess[0, 1], MAProcess[0], MAProcess[1], SARIMAProcess[{0, 1, 0}, {1, 2, 0}_5],
 SARIMAProcess[{0, 1, 0}, {1, 2, 1}_4], SARIMAProcess[{0, 1, 1}, {0, 2, 0}_4],
 SARIMAProcess[{0, 1, 1}, {0, 2, 0}_7], SARIMAProcess[{0, 1, 1}, {1, 2, 0}_4],
 SARIMAProcess[{0, 1, 1}, {2, 2, 0}_4], SARIMAProcess[{0, 1, 2}, {0, 1, 0}_10],
 SARIMAProcess[{0, 1, 2}, {0, 2, 0}_7], SARIMAProcess[{0, 1, 2}, {2, 2, 0}_4],
 SARIMAProcess[{1, 1, 0}, {0, 2, 1}_4], SARIMAProcess[{1, 1, 0}, {1, 2, 0}_5],
 SARIMAProcess[{1, 1, 1}, {0, 2, 0}_5], SARIMAProcess[{1, 1, 1}, {0, 2, 0}_6],
 SARIMAProcess[{1, 1, 1}, {0, 2, 0}_7], SARIMAProcess[{1, 1, 1}, {0, 4, 0}_4],
 SARIMAProcess[{2, 1, 0}, {0, 2, 0}_5], SARIMAProcess[{2, 1, 1}, {1, 2, 0}_4],
 SARIMAProcess[{2, 1, 2}, {0, 2, 0}_4], SARIMAProcess[{2, 1, 2}, {0, 2, 0}_5],
 SARIMAProcess[{3, 1, 0}, {0, 3, 0}_5], SARIMAProcess[{3, 1, 3}, {0, 2, 0}_6],
 SARMAProcess[{0, 1}, {0, 1}_4], SARMAProcess[{0, 1}, {1, 0}_4], SARMAProcess[{0, 1}, {1, 0}_10]}
```

For the members in each class we have:

In[143]:=
```
Query[All, Length]@classificationTimeSeriesModelAggregate1
```

Out[143]=
```
<|ARIMAProcess[0, 1, 1] → 4, ARIMAProcess[0, 4, 1] → 1, ARIMAProcess[0, 5, 1] → 7,
 ARIMAProcess[0, 6, 0] → 1, ARIMAProcess[1, 1, 0] → 2, ARIMAProcess[1, 1, 1] → 4,
 ARIMAProcess[2, 1, 0] → 1, ARIMAProcess[2, 1, 1] → 1, ARIMAProcess[4, 7, 1] → 1, ARProcess[3] → 2,
 GARCHProcess[0, 1] → 10, MAProcess[0] → 40, MAProcess[1] → 5, SARIMAProcess[{0, 1, 0}, {1, 2, 0}_5] → 1,
 SARIMAProcess[{0, 1, 0}, {1, 2, 1}_4] → 2, SARIMAProcess[{0, 1, 1}, {0, 2, 0}_4] → 2,
 SARIMAProcess[{0, 1, 1}, {0, 2, 0}_7] → 1, SARIMAProcess[{0, 1, 1}, {1, 2, 0}_4] → 4,
 SARIMAProcess[{0, 1, 1}, {2, 2, 0}_4] → 1, SARIMAProcess[{0, 1, 2}, {0, 1, 0}_10] → 1,
 SARIMAProcess[{0, 1, 2}, {0, 2, 0}_7] → 1, SARIMAProcess[{0, 1, 2}, {2, 2, 0}_4] → 1,
 SARIMAProcess[{1, 1, 0}, {0, 2, 1}_4] → 1, SARIMAProcess[{1, 1, 0}, {1, 2, 0}_5] → 1,
 SARIMAProcess[{1, 1, 1}, {0, 2, 0}_5] → 1, SARIMAProcess[{1, 1, 1}, {0, 2, 0}_6] → 3,
 SARIMAProcess[{1, 1, 1}, {0, 2, 0}_7] → 1, SARIMAProcess[{1, 1, 1}, {0, 4, 0}_4] → 1,
 SARIMAProcess[{2, 1, 0}, {0, 2, 0}_5] → 1, SARIMAProcess[{2, 1, 1}, {1, 2, 0}_4] → 1,
 SARIMAProcess[{2, 1, 2}, {0, 2, 0}_4] → 1, SARIMAProcess[{2, 1, 2}, {0, 2, 0}_5] → 1,
 SARIMAProcess[{3, 1, 0}, {0, 3, 0}_5] → 1, SARIMAProcess[{3, 1, 3}, {0, 2, 0}_6] → 1,
 SARMAProcess[{0, 1}, {0, 1}_4] → 1, SARMAProcess[{0, 1}, {1, 0}_4] → 1, SARMAProcess[{0, 1}, {1, 0}_10] → 1|>
```

LombScargleCutoff (1)

In[1]:=
```
Needs["MathIOmica`"]
```

LombScargleCutoff provides a cutoff for filtering based on highest frequency spectrum intensity in the "LombScargle" Method. The cutoff is user - provided and typically calculated through simulation, or may be manually selected. For example we can set the cutoff based on simulation (note that we still must provide cutoffs for spikes as well):

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
timePointsExample = Range[20];
```

In[3]:=
```
bootstrapQ95 = QuantileEstimator[backgroundExample, timePointsExample];
bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

In[4]:=
```
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes]
```

```
Method → "LombScargle"
```

Out[4]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
      0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
      -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
      0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
      0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
      0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
      0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
      0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
      0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
      0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
      0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
      -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
      0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
      0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
      0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
      0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
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    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
  SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
    0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
    0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
    0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
  SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
    0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
    0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
  SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
    0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
    -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
    0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
  SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
    0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
    0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
  SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
    0.156306, 0.49338, 0.197723}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
    0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
    -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
  SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
    0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
    -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
    -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
  SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
    0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
    0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
    0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
  SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
    0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
    -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
    0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
    0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
    -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
    0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
    -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
    0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
    0.469391, 0.294777, 0.463012, 0.279525}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
    -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
    -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
  SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
    0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
    -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
    -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
    0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
    0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
    -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
  SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
    0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
    -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
    0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
    0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
    0.341117, 0.381366, 0.325221}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
    -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
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    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
    0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
    -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
    0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
  SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
    0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
    -0.0488362, -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052,
    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
    0.35716, 0.304919, 0.374001}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
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    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{0.173083, 0.379193, 0.338228, 0.384591, 0.344256, 0.301779, 0.172933,
    0.337034, 0.332955, 0.316239}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
    0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{0.369536, 0.475376, 0.186202, 0.236301, 0.19825, 0.237895, 0.260777,
    0.276741, 0.472509, 0.288441}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594,
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    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
    0.315364, 0.382839, 0.290684}, {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309,
    0.000455216, -0.0829657, 0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281,
    0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
    0.404761, 0.291284, 0.418924}, {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464,
    0.0166785, 0.0680268, 0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101,
    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{0.197001, 0.246358, 0.358498, 0.402863, 0.27067, 0.34906, 0.104226,
    0.386107, 0.331869, 0.380125}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
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    0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
    0.16152, 0.319203, 0.158339}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
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    0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
  SpikeNegative_19 → {{0.392542, 0.277194, 0.303304, 0.316005, 0.451557, 0.178107, 0.336152,
    0.30277, 0.204908, 0.308124}, {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693,
    0.0216656, 0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588,
    -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{0.373567, 0.348518, 0.182641, 0.399653, 0.340024, 0.197691, 0.337761,
    0.284486, 0.34594, 0.276612}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
    0.057722, -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007,
    -0.0175827, 0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}}|>,
f1 → <|LinearPositive_1 → {{0.984043, 0.16711, 0.0316771, 0.00181032, 0.00174073,
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  LinearPositive_2 → {{0.984661, 0.162755, 0.0313267, 0.0020944, 0.00156008, 0.011475,
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    0.242161, 0.261728, 0.280689, 0.29779, 0.316418, 0.335012, 0.355339, 0.375155}},
  LinearPositive_3 → {{0.983778, 0.169007, 0.0312598, 0.00266983, 0.0014985,
    0.0109335, 0.01999, 0.0270723, 0.0199171, 0.0313541},
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    0.204397, 0.22244, 0.241027, 0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}},
LinearPositive_4 → {{0.984544, 0.162861, 0.0316916, 0.00219377, 0.00149925, 0.011724,
    0.0216336, 0.0306627, 0.0181213, 0.0355609}, {0.0188591, 0.0384796, 0.0552706,
    0.0761382, 0.0941127, 0.11255, 0.131257, 0.150426, 0.166514, 0.185049, 0.206061,
    0.222052, 0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}},
LinearPositive_5 → {{0.983951, 0.167274, 0.0329686, 0.00225602, 0.00179127, 0.0107481,
    0.0213666, 0.0279768, 0.0186733, 0.0325615}, {0.0196474, 0.0375735, 0.0561861, 0.0745382,
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    0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
LinearPositive_6 → {{0.982932, 0.171949, 0.0327492, 0.00164224, 0.002379, 0.0113266,
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    0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
LinearPositive_7 → {{0.98472, 0.163134, 0.0312689, 0.00212913, 0.0016404, 0.0102459,
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    0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
LinearPositive_8 → {{0.98371, 0.168572, 0.0284284, 0.00170281, 0.00185745, 0.010751,
    0.0232594, 0.0297876, 0.0184231, 0.0346602}, {0.0170019, 0.0382694, 0.0569482, 0.0754625,
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LinearPositive_9 → {{0.98365, 0.168058, 0.033981, 0.00241806, 0.00210287, 0.0115589,
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LinearPositive_10 → {{0.983876, 0.167373, 0.0315427, 0.00211686, 0.00191546, 0.0115056,
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LinearPositive_11 → {{0.985278, 0.159772, 0.0170525, 0.00324467, 0.00218142, 0.0151391,
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LinearPositive_12 → {{0.985678, 0.154732, 0.0287579, 0.00132291, 0.00382878, 0.0177303,
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LinearPositive_13 → {{0.980798, 0.186414, 0.0294262, 0.00278288, 0.00330631, 0.0108519,
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LinearPositive_15 → {{0.984521, 0.158493, 0.0449595, 0.00110501, 0.00265532, 0.0107268,
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LinearPositive_17 → {{0.983915, 0.163837, 0.0268448, 0.00291022, 0.00438077, 0.0123819,
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LinearPositive_18 → {{0.983959, 0.16518, 0.0329124, 0.00150854, 0.000803325, 0.0135443,
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LinearPositive_19 → {{0.987202, 0.147191, 0.027074, 0.00249316, 0.000777253,
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LinearPositive_20 → {{0.983551, 0.167679, 0.0393618, 0.00233188, 0.0011172, 0.0161293,
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 LinearNegative_1 → {{0.984203, 0.159785, 0.0568416, 0.00506241, 0.000881747, 0.023661,
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 LinearNegative_2 → {{0.983975, 0.157281, 0.0272884, 0.00492376, 0.00030144, 0.0209059,
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 LinearNegative_3 → {{0.981452, 0.174458, 0.0229664, 0.001764, 0.000281227, 0.0288508,
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 LinearNegative_6 → {{0.978811, 0.190012, 0.0393558, 0.000605398, 0.0150579, 0.015651,
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 LinearNegative_8 → {{0.982135, 0.172786, 0.0318874, 0.00532189, 0.00125899, 0.00528407,
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 LinearNegative_13 → {{0.98451, 0.16303, 0.0227595, 0.00132012, 0.00348595, 0.0126863,
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 LinearNegative_15 → {{0.987412, 0.147538, 0.0327634, 0.00558518, 0.00366499, 0.00919838,
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    0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
    0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{0.00356621, 0.0718347, 0.992461, 0.086876, 0.0384877, 0.0168536, 0.00812238,
    0.00246869, 0.0215147, 0.000777483}, {0.185809, -0.10192, -0.303748, -0.261172,
    0.000202029, 0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227,
    0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.00292996, 0.0773356, 0.991977, 0.0880559, 0.0367946, 0.0176203,
    0.00875596, 0.00325153, 0.0220462, 0.00118298}, {0.187562, -0.10053, -0.297144, -0.250552,
    0.00476677, 0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453,
    0.301104, 0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{0.00262506, 0.0711674, 0.99281, 0.0827274, 0.0380578, 0.0177335, 0.00874852,
    0.00232562, 0.0238141, 0.000654616}, {0.189755, -0.100643, -0.295957, -0.251445,
    -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
    0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
  Sinusoidal3_30 → {{0.00427552, 0.071229, 0.992804, 0.0839262, 0.0365748, 0.018534, 0.00877504,
    0.00265531, 0.0209496, 0.000906179}, {0.186539, -0.100579, -0.301622, -0.251977,
    0.00452805, 0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
    0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
    0.0294955, 0.00418398, 0.028168, 0.00135728}, {-0.0952089, -0.252202, 0.25704, 0.097318,
    -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
    0.00565905, 0.0259503, 0.00224675}, {-0.101498, -0.25529, 0.251653, 0.0972642,
    -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
    0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395,
```

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    0.00472652, 0.0285215, 0.00169662}, {-0.0918789, -0.259087, 0.253065, 0.103093,
    -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
    0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735,
    0.00386219, 0.0290145, 0.00118185}, {-0.0939856, -0.25429, 0.25073, 0.100441,
    -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
    0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
    0.00582096, 0.0271664, 0.00231721}, {-0.0916775, -0.260977, 0.251061, 0.104141,
    -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
    0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
    0.00436252, 0.0286975, 0.00143738}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
    -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868,
    0.00399143, 0.0293851, 0.00124852}, {-0.102994, -0.260616, 0.250831, 0.0989794,
    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
    0.00452946, 0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
    0.00512062, 0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
    -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
    0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
    -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
    -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
    0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
    0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
    -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
    0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
    0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
    -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
  Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
    0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
    0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
    -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
    0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
    0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
    -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
    -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
```

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```
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

In[5]:=
```
Query[All, Length]@classification1
```

Out[5]=
```
<|SpikeMax → 20, SpikeMin → 20, f1 → 40, f3 → 10, f5 → 10, f6 → 10|>
```

We can also set this cutoff to any value, say 0.5:

In[6]:=
```
classification1Cutoff = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.5, SpikeCutoffs → bootstrapQ95Spikes]
```

```
Method → "LombScargle"
```

Out[6]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
    0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
    -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
    -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
    0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
    -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
    0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
    0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
    -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
    0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
    0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
    -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
    -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
    0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
    0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
    0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
    0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
    0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
    0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
    0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
    0.156306, 0.49338, 0.197723}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
    0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
    -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
   SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
    0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
    -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
    -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
   SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
    0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
    0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
    0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
   SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
    0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
    -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
    0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
   SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
    0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
    -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
```

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```
      0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
    SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
      0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
      -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
      0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
  SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
      0.469391, 0.294777, 0.463012, 0.279525}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
      -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
      -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
    SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
      0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
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    SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
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    SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
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    SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
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    SpikeNegative_13 → {{0.173083, 0.379193, 0.338228, 0.384591, 0.344256, 0.301779, 0.172933,
      0.337034, 0.332955, 0.316239}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
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      -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
    SpikeNegative_14 → {{0.369536, 0.475376, 0.186202, 0.236301, 0.19825, 0.237895, 0.260777,
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      0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
    SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
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    SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
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    SpikeNegative_17 → {{0.197001, 0.246358, 0.358498, 0.402863, 0.27067, 0.34906, 0.104226,
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    SpikeNegative_19 → {{0.392542, 0.277194, 0.303304, 0.316005, 0.451557, 0.178107, 0.336152,
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    SpikeNegative_20 → {{0.373567, 0.348518, 0.182641, 0.399653, 0.340024, 0.197691, 0.337761,
      0.284486, 0.34594, 0.276612}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
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  f1 → <|SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
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    LinearPositive_1 → {{0.984043, 0.16711, 0.0316771, 0.00181032, 0.00174073,
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    LinearPositive_2 → {{0.984661, 0.162755, 0.0313267, 0.0020944, 0.00156008, 0.011475,
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    LinearPositive_3 → {{0.983778, 0.169007, 0.0312598, 0.00266983, 0.0014985,
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 LinearPositive_6 → {{0.982932, 0.171949, 0.0327492, 0.00164224, 0.002379, 0.0113266,
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 LinearPositive_10 → {{0.983876, 0.167373, 0.0315427, 0.00211686, 0.00191546, 0.0115056,
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 LinearPositive_11 → {{0.985278, 0.159772, 0.0170525, 0.00324467, 0.00218142, 0.0151391,
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    0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, 0.373621}},
 LinearPositive_12 → {{0.985678, 0.154732, 0.0287579, 0.00132291, 0.00382878, 0.0177303,
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 LinearPositive_13 → {{0.980798, 0.186414, 0.0294262, 0.00278288, 0.00330631, 0.0108519,
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 LinearPositive_14 → {{0.981111, 0.181783, 0.0375471, 0.00148453, 0.000312388,
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 LinearPositive_15 → {{0.984521, 0.158493, 0.0449595, 0.00110501, 0.00265532, 0.0107268,
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 LinearPositive_16 → {{0.979313, 0.188576, 0.0419809, 0.00521628, 0.000903989,
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 LinearPositive_17 → {{0.983915, 0.163837, 0.0268448, 0.00291022, 0.00438077, 0.0123819,
    0.0293441, 0.032835, 0.0286218, 0.0375256}, {0.0153802, 0.0408047, 0.0548321,
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 LinearPositive_18 → {{0.983959, 0.16518, 0.0329124, 0.00150854, 0.000803325, 0.0135443,
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 LinearPositive_19 → {{0.987202, 0.147191, 0.027074, 0.00249316, 0.000777253,
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LinearNegative_1 → {{0.984203, 0.159785, 0.0568416, 0.00506241, 0.000881747, 0.023661,
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LinearNegative_2 → {{0.983975, 0.157281, 0.0272884, 0.00492376, 0.00030144, 0.0209059,
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LinearNegative_3 → {{0.981452, 0.174458, 0.0229664, 0.001764, 0.000281227, 0.0288508,
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LinearNegative_4 → {{0.97237, 0.220138, 0.0433705, 0.00935025, 0.000670999, 0.00240098,
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LinearNegative_5 → {{0.977089, 0.200269, 0.0364024, 0.00199978, 0.00231623, 0.00860671,
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LinearNegative_6 → {{0.978811, 0.190012, 0.0393558, 0.000605398, 0.0150579, 0.015651,
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LinearNegative_7 → {{0.974629, 0.205946, 0.0323035, 0.00710776, 0.0022957, 0.0115893,
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LinearNegative_8 → {{0.982135, 0.172786, 0.0318874, 0.00532189, 0.00125899, 0.00528407,
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LinearNegative_9 → {{0.992163, 0.105938, 0.0360944, 0.0064934, 0.00217633, 0.00513993,
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    -0.258977, -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
LinearNegative_10 → {{0.983194, 0.163431, 0.0236169, 0.0117059, 0.0187534, 0.0128491,
    0.0464304, 0.0333413, 0.0244635, 0.039273}, {-0.00155633, -0.0271325, -0.0625737, -0.0744387,
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LinearNegative_11 → {{0.984307, 0.167887, 0.0231976, 0.00646005, 0.000895278, 0.0137762,
    0.0124029, 0.0261219, 0.0206864, 0.0303092}, {-0.0105542, -0.0364589, -0.0515525, -0.0708746,
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    -0.235518, -0.271564, -0.288178, -0.293001, -0.310129, -0.328328, -0.364455, -0.366174}},
LinearNegative_12 → {{0.984685, 0.160376, 0.0299467, 0.000604418, 0.00378349, 0.00929028,
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    -0.0883748, -0.108962, -0.137461, -0.144887, -0.163604, -0.184293, -0.210166, -0.217602,
    -0.245066, -0.261694, -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
LinearNegative_13 → {{0.98451, 0.16303, 0.0227595, 0.00132012, 0.00348595, 0.0126863,
    0.0149005, 0.0329653, 0.0281054, 0.0370164}, {-0.01186, -0.0431645, -0.0590873, -0.0756374,
    -0.0887624, -0.1144, -0.121973, -0.156462, -0.165726, -0.190329, -0.20958, -0.216046,
    -0.244405, -0.264186, -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596}},
LinearNegative_14 → {{0.978579, 0.195677, 0.0313545, 0.00267509, 0.00341515, 0.0129726,
    0.0194829, 0.0277661, 0.0277908, 0.0316459}, {-0.0187992, -0.0431131, -0.0473458, -0.070655,
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LinearNegative_15 → {{0.987412, 0.147538, 0.0327634, 0.00558518, 0.00366499, 0.00919838,
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    -0.0935334, -0.121112, -0.124004, -0.147926, -0.165828, -0.191582, -0.205406, -0.219926,
    -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
LinearNegative_16 → {{0.979857, 0.186118, 0.0444944, 0.00475256, 0.00394217, 0.0176745,
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    0.0237503, 0.0289162, 0.0192921, 0.033722}, {-0.0225164, -0.0461677, -0.0473716, -0.067817,
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  LinearNegative_17 → {{0.983395, 0.171344, 0.0310503, 0.00202654, 0.00193992, 0.00923842,
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  LinearNegative_18 → {{0.981857, 0.181794, 0.0372624, 0.00157464, 0.00102441, 0.00691753,
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    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
  LinearNegative_19 → {{0.986834, 0.144628, 0.035256, 0.00310318, 0.000702006, 0.0165652,
    0.0245304, 0.0352455, 0.0134744, 0.0410912}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
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    -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
  LinearNegative_20 → {{0.985534, 0.158105, 0.0328843, 0.00243514, 0.000101469, 0.0195265,
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f3 → <|Sinusoidal3_21 → {{0.003093, 0.067983, 0.992591, 0.0880879, 0.0381938, 0.0201564,
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    0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
  Sinusoidal3_22 → {{0.00318631, 0.0730881, 0.992797, 0.0819348, 0.0379624, 0.0193048,
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    0.303756, 0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
  Sinusoidal3_23 → {{0.00295231, 0.0765523, 0.992363, 0.0843288, 0.0378838, 0.0169649,
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    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
  Sinusoidal3_25 → {{0.00289275, 0.0722254, 0.992563, 0.084147, 0.0394916, 0.0185649, 0.00643529,
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    0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
  Sinusoidal3_26 → {{0.0035927, 0.0724177, 0.992482, 0.0865873, 0.0377177, 0.018194, 0.00903366,
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    0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{0.00356621, 0.0718347, 0.992461, 0.086876, 0.0384877, 0.0168536, 0.00812238,
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    0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.00292996, 0.0773356, 0.991977, 0.0880559, 0.0367946, 0.0176203,
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    0.301104, 0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{0.00262506, 0.0711674, 0.99281, 0.0827274, 0.0380578, 0.0177335, 0.00874852,
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  Sinusoidal3_30 → {{0.00427552, 0.071229, 0.992804, 0.0839262, 0.0365748, 0.018534, 0.00877504,
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    0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
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  Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
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  Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
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  Sinusoidal2_13 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395,
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    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
    0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735,
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  Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
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  Sinusoidal2_17 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
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    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868,
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  Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
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  Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
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f6 → <|SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
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    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
    0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
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    -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
    0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
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    -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
    0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
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    -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
  Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
    0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
    0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
    -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
    0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
    0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
    -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
    -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
```

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```
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>,
f7 → <|SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
    0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
    -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
    0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}}|>,
f9 → <|SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
    0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
    0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
    -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
  SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
    0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
    -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
    0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
  SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
    0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
    0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
    0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
  SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
    0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
    0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
    0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
  SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
    0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
    0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
  SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
    0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
    0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
  SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
    0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
    -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
    -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
    0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
    0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
    0.214233, 0.523873, 0.243986}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
    0.0874465, -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
    0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}}|>|>
```

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The choice of cutoff affects the classification:

In[7]:=
```
Query[All, Length]@classification1Cutoff
```

Out[7]=
```
<|SpikeMax → 13, SpikeMin → 12, f1 → 41, f3 → 10, f5 → 11, f6 → 11, f7 → 1, f9 → 11|>
```

LombScargleOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

LombScargleOptions allow us to pass options to the internal LombScargle function in the case that the Method "LombScargle" is used. The default values are {PairReturn→ False, NormalizeIntensities→ True}. These are a minimum requirement for the classification to work and it is not recommended that they are modified. Other modifications can include for example `OversamplingRate`. We still need to also provide values for the appropriate cutoffs. We may base these on the background noise and use the QuantileEstimation for this:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
timePointsExample = Range[20];
```

In[3]:=
```
bootstrapQ95 = QuantileEstimator[backgroundExample, timePointsExample];
bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

We oversample here by a factor of 1.5 and carry out the classification for the default "LombScargle" method:

In[4]:=
```
classification1Oversampled = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes,
  LombScargleOptions → {PairReturn → False, NormalizeIntensities → True, OversamplingRate → 1.5}]
```

Method → "LombScargle"

Out[4]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0678541, 0.302594, 0.246107, 0.185357, 0.234538, 0.280871, 0.147606, 0.201517,
      0.347562, 0.278747, 0.353075, 0.317987, 0.330584, 0.281159},
     {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682, -0.0371416,
      0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411, -0.00869189,
      -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.346053, 0.221697, 0.164731, 0.214458, 0.345568, 0.174021, 0.205273,
      0.26395, 0.288467, 0.275747, 0.23845, 0.206956, 0.438437, 0.212831},
     {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829, 0.017722,
      -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.0898986, 0.610283, 0.166199, 0.0994118, 0.229683, 0.26221, 0.107904, 0.246643,
```

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```
    0.16192, 0.226838, 0.201733, 0.296135, 0.337451, 0.260856}, {0.95896, 0.0348607, 0.0657694, 0.0097693,
    -0.0146057, -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763,
    -0.00816843, 0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
SpikePositive_4 → {{0.23556, 0.282703, 0.122257, 0.141988, 0.170251, 0.30547, 0.12403, 0.292406,
    0.377764, 0.0539234, 0.227994, 0.249246, 0.528711, 0.258935}, {0.958583, 0.00400217, 0.0429904,
    0.0838796, 0.0778033, -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858,
    0.0195539, 0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
SpikePositive_5 → {{0.177052, 0.199419, 0.110588, 0.280232, 0.211542, 0.218709, 0.222727, 0.233681,
    0.224357, 0.220986, 0.135329, 0.377405, 0.4876, 0.379017}, {0.966833, -0.0172757, -0.0101601,
    0.0449156, 0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
    -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
SpikePositive_6 → {{0.0816531, 0.380744, 0.165692, 0.233528, 0.222749, 0.268947, 0.152854, 0.315337,
    0.132768, 0.368321, 0.228599, 0.258895, 0.436132, 0.242576}, {0.971085, -0.0737213, -0.0183259,
    -0.0280164, -0.0370416, 0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791,
    0.0886387, 0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
SpikePositive_7 → {{0.0906862, 0.421194, 0.113679, 0.222125, 0.243623, 0.182073, 0.360144,
    0.262567, 0.217604, 0.308503, 0.180972, 0.290919, 0.374774, 0.246162}, {0.973634, -0.0197451,
    0.00381691, 0.0632199, 0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389,
    0.0440781, 0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
SpikePositive_8 → {{0.358191, 0.146095, 0.276759, 0.146988, 0.21361, 0.268076, 0.182958,
    0.272914, 0.351919, 0.211636, 0.279917, 0.273582, 0.386041, 0.236304},
   {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677, -0.0238371,
    -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
    -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
SpikePositive_9 → {{0.210147, 0.195151, 0.247938, 0.240597, 0.338998, 0.248879, 0.19591,
    0.238215, 0.244304, 0.378658, 0.281973, 0.256644, 0.349096, 0.236849},
   {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483, -0.0385902,
    -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
SpikePositive_10 → {{0.26524, 0.139914, 0.113253, 0.282985, 0.211303, 0.20324, 0.265987,
    0.256831, 0.245025, 0.234617, 0.333858, 0.32633, 0.415035, 0.298679},
   {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367, -0.0143555,
    0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266, -0.0322946,
    -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
SpikePositive_11 → {{0.261308, 0.278444, 0.188245, 0.382743, 0.116208, 0.139856, 0.247786,
    0.136972, 0.307717, 0.248729, 0.360105, 0.301076, 0.312437, 0.290758}, {0.0696283, 0.0251021,
    0.968196, 0.0511374, 0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872,
    0.0156503, -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
SpikePositive_12 → {{0.2304, 0.264384, 0.0850278, 0.25109, 0.15742, 0.21572, 0.356092, 0.267008, 0.389796,
    0.2088, 0.212363, 0.151088, 0.493812, 0.173249}, {0.0427773, -0.0204301, 0.972226, -0.00645026,
    0.0200803, 0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808,
    0.00471403, 0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
SpikePositive_13 → {{0.163675, 0.164354, 0.382191, 0.223143, 0.470633, 0.195965, 0.374111, 0.199321,
    0.144054, 0.454757, 0.167237, 0.135349, 0.151586, 0.118018}, {-0.0343175, -0.0155132, 0.955818,
    0.0636753, -0.0900903, -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626,
    0.0398952, 0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
SpikePositive_14 → {{0.342758, 0.122298, 0.187399, 0.148743, 0.121992, 0.204762, 0.235536,
    0.202919, 0.320949, 0.364561, 0.226446, 0.272888, 0.467516, 0.276812},
   {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311, 0.0642856, -0.00120334,
    -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562, -0.044588,
    -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
SpikePositive_15 → {{0.179525, 0.150734, 0.271157, 0.141828, 0.232171, 0.195672, 0.393548, 0.27732,
    0.244352, 0.225177, 0.128118, 0.318112, 0.432963, 0.334593}, {0.0367157, 0.00909492, 0.955211,
    -0.0373177, -0.0545922, 0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346,
    0.0584456, -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
SpikePositive_16 → {{0.234491, 0.284544, 0.29509, 0.433976, 0.143114, 0.426325, 0.189656,
    0.273994, 0.215373, 0.171373, 0.141053, 0.171516, 0.341813, 0.182907},
   {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223, -0.00461306,
    -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381, -0.0588352,
    -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
SpikePositive_17 → {{0.108379, 0.126465, 0.0782491, 0.197527, 0.127047, 0.121307, 0.226148,
    0.158604, 0.505886, 0.277964, 0.34406, 0.33517, 0.396334, 0.314619}, {0.0894556, -0.0939456,
    0.955206, -0.0721055, 0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614,
    0.063305, -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
SpikePositive_18 → {{0.225404, 0.230346, 0.227488, 0.259527, 0.549379, 0.136364, 0.34609,
    0.321043, 0.250127, 0.195732, 0.100908, 0.166487, 0.263149, 0.16046},
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      {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144, -0.0566396, 0.00932272,
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       -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
   SpikePositive_19 → {{0.251984, 0.196794, 0.253918, 0.286924, 0.355138, 0.287124, 0.234716,
       0.186895, 0.337213, 0.159449, 0.351, 0.264712, 0.25443, 0.235047}, {-0.0584325, 0.0880122, 0.972312,
       -0.0409534, 0.0540727, -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323,
       -0.0924997, 0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
   SpikePositive_20 → {{0.227795, 0.162974, 0.219041, 0.320667, 0.285898, 0.193613, 0.244303,
       0.254406, 0.17843, 0.337739, 0.502677, 0.134561, 0.308566, 0.123302},
      {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833, -0.0790448, -0.0883667,
       0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909, -0.0700673,
       0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.154333, 0.204895, 0.254337, 0.138336, 0.26054, 0.427018,
       0.34149, 0.152002, 0.199055, 0.409261, 0.259545, 0.120947, 0.403699, 0.0913658},
      {-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627, 0.0839417,
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       0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
   SpikeNegative_2 → {{0.163748, 0.315934, 0.118047, 0.334067, 0.226037, 0.139811, 0.200666, 0.160262,
       0.142772, 0.134096, 0.26485, 0.351941, 0.512237, 0.3413}, {-0.969717, -0.0281117, -0.0848724,
       0.0813594, -0.068113, -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293,
       -0.0520501, -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
   SpikeNegative_3 → {{0.197306, 0.186462, 0.182456, 0.184519, 0.149738, 0.303737, 0.485797,
       0.188338, 0.365384, 0.23819, 0.084972, 0.177429, 0.46769, 0.158561}, {-0.953174, 0.0687073, 0.081267,
       -0.0893468, -0.0891095, 0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647,
       -0.0384319, -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
   SpikeNegative_4 → {{0.280244, 0.333716, 0.285785, 0.200175, 0.249477, 0.239156, 0.271945, 0.126991,
       0.337245, 0.302964, 0.292723, 0.227244, 0.312227, 0.196227}, {-0.978499, -0.0375369, -0.0308657,
       -0.0197828, 0.087556, -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659,
       -0.0303762, 0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
   SpikeNegative_5 → {{0.187255, 0.298153, 0.164555, 0.31498, 0.246671, 0.222539, 0.344009, 0.242966,
       0.186925, 0.233706, 0.0867489, 0.239149, 0.509005, 0.220548}, {-0.975409, -0.0426067, 0.018748,
       0.0233455, -0.0851968, 0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457,
       0.0411812, -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
   SpikeNegative_6 → {{0.212614, 0.26489, 0.175795, 0.228956, 0.340532, 0.331878, 0.157524, 0.361507,
       0.242562, 0.308534, 0.294481, 0.20339, 0.328044, 0.173114}, {-0.980123, 0.0414029, 0.0844458,
       -0.0197615, 0.0300953, -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521,
       0.00178694, 0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
   SpikeNegative_7 → {{0.160075, 0.168287, 0.334578, 0.121955, 0.207132, 0.378679, 0.275428,
       0.387103, 0.251777, 0.223857, 0.082115, 0.241012, 0.423288, 0.222988},
      {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109, 0.0874465, -0.0578879,
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       -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
   SpikeNegative_8 → {{0.336378, 0.256767, 0.341833, 0.250793, 0.333179, 0.261346, 0.224909, 0.107167,
       0.205717, 0.327532, 0.200965, 0.250044, 0.323527, 0.206445}, {-0.971714, -0.0689738, -0.0116232,
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       0.06932, -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
   SpikeNegative_9 → {{0.181707, 0.301812, 0.252502, 0.222929, 0.290547, 0.243364, 0.134646, 0.220938,
       0.217971, 0.114006, 0.179221, 0.314234, 0.526803, 0.288022}, {-0.964652, -0.0492164, -0.044027,
       0.0970846, -0.0799416, 0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659,
       -0.0888441, -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
   SpikeNegative_10 → {{0.133028, 0.271276, 0.166323, 0.192028, 0.103905, 0.27389, 0.246824,
       0.143401, 0.355307, 0.212472, 0.0869953, 0.379928, 0.471166, 0.362738},
      {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025, 0.0119404, -0.0700182,
       -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425, -0.020989,
       0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
   SpikeNegative_11 → {{0.342312, 0.107185, 0.237995, 0.284172, 0.28897, 0.240077, 0.310085, 0.334623,
       0.321104, 0.280545, 0.238389, 0.170807, 0.294531, 0.173512}, {-0.03227, 0.0360081, -0.974536,
       -0.0562723, 0.0838755, -0.0488362, -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817,
       0.050052, 0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
   SpikeNegative_12 → {{0.111251, 0.362529, 0.13587, 0.422317, 0.271414, 0.212472, 0.186409, 0.242311,
       0.322249, 0.196789, 0.241577, 0.297007, 0.285967, 0.276026}, {0.0228997, -0.0356184, -0.973634,
       0.0493933, 0.0107571, 0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636,
       0.029504, -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
   SpikeNegative_13 → {{0.156945, 0.238608, 0.368838, 0.306692, 0.405098, 0.147115, 0.312158,
       0.340108, 0.220308, 0.156809, 0.31596, 0.117788, 0.30191, 0.107194}, {0.089408, -0.00831708,
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    -0.0365538, -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{0.338205, 0.235134, 0.270334, 0.170415, 0.284974, 0.199545, 0.181441, 0.285828,
    0.187278, 0.238667, 0.285606, 0.256251, 0.432448, 0.257448}, {-0.0381839, 0.0217806, -0.963264,
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    -0.0718374, 0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{0.230428, 0.268994, 0.189861, 0.254909, 0.20066, 0.327683, 0.417379,
    0.185262, 0.269711, 0.143, 0.424354, 0.116807, 0.343567, 0.111355},
   {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309, 0.000455216, -0.0829657,
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    -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{0.128986, 0.294526, 0.206968, 0.287866, 0.274161, 0.198366, 0.217553,
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    -0.0727101, 0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{0.195236, 0.289067, 0.179047, 0.355286, 0.369905, 0.225113, 0.268245,
    0.290194, 0.253966, 0.103292, 0.341057, 0.209998, 0.328896, 0.180568}, {-0.0701592, 0.0172702,
    -0.96504, -0.0844552, 0.0472312, 0.0616787, -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417,
    -0.0836667, 0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{0.468283, 0.151489, 0.326548, 0.277173, 0.135528, 0.40808, 0.298197, 0.214267,
    0.200832, 0.233937, 0.214736, 0.126529, 0.279171, 0.139491}, {0.0700203, -0.100452, -0.962503,
    -0.0223616, -0.0879604, 0.0000556895, -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971,
    0.099183, 0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
  SpikeNegative_19 → {{0.342445, 0.212053, 0.397995, 0.264596, 0.313709, 0.203055, 0.393929,
    0.243432, 0.134066, 0.293252, 0.236288, 0.189964, 0.178758, 0.165614},
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    0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{0.322512, 0.311492, 0.236334, 0.15768, 0.535643, 0.188176, 0.293553,
    0.166752, 0.135515, 0.291599, 0.24881, 0.122974, 0.29866, 0.110983},
   {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452, 0.057722, -0.0391361,
    -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007, -0.0175827,
    0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}}|>,
f1 → <|LinearPositive_1 → {{0.919118, 0.371368, 0.0307895, 0.0295871, 0.0934124, 0.0529731,
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  LinearPositive_2 → {{0.921447, 0.365265, 0.0317003, 0.0293156, 0.0946825, 0.0517469, 0.00145993,
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  LinearPositive_3 → {{0.920994, 0.367597, 0.028473, 0.0292648, 0.0949086, 0.0480908,
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  LinearPositive_4 → {{0.919749, 0.3687, 0.0328616, 0.0296059, 0.0964523, 0.052151, 0.00140058,
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  LinearPositive_5 → {{0.919145, 0.371523, 0.0310285, 0.0307971, 0.0940662, 0.0501835, 0.00167329,
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    0.205612, 0.225889, 0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
  LinearPositive_6 → {{0.917506, 0.37623, 0.0292168, 0.0305693, 0.0897342, 0.0512376, 0.00222065,
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  LinearPositive_7 → {{0.921714, 0.364823, 0.0313546, 0.0292682, 0.0949564, 0.0515273, 0.00153544,
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    0.204805, 0.22423, 0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
  LinearPositive_8 → {{0.919316, 0.370807, 0.0289568, 0.0265675, 0.0943534, 0.0535206, 0.00173586,
    0.0205048, 0.0434189, 0.0217368, 7.12964×10^-6, 0.0255558, 0.0172171, 0.0178334}, {0.0170019,
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LinearPositive_9 → {{0.920093, 0.370033, 0.0301475, 0.0317854, 0.0919466, 0.0474319, 0.00196699,
    0.0187588, 0.0441419, 0.020199, 7.12166×10^-6, 0.0235807, 0.0188877, 0.0160283}, {0.0185501,
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LinearPositive_10 → {{0.919472, 0.37052, 0.0303643, 0.0294779, 0.0939605, 0.0506934, 0.00179007,
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    0.206359, 0.223211, 0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
LinearPositive_11 → {{0.920556, 0.360944, 0.0294048, 0.0159323, 0.114277, 0.0561181, 0.00203813,
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    0.216208, 0.237083, 0.269021, 0.288161, 0.295793, 0.313062, 0.329161, 0.35343, 0.373621}},
LinearPositive_12 → {{0.931044, 0.342009, 0.0289796, 0.0271639, 0.0843681, 0.0502788, 0.00361656,
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LinearPositive_13 → {{0.912182, 0.388619, 0.0250656, 0.0273676, 0.0939409, 0.0495665, 0.003075,
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LinearPositive_17 → {{0.917154, 0.373962, 0.0330411, 0.0250233, 0.101434, 0.0486711, 0.00408352,
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      0.0614225, 0.13762, 0.984363, 0.0826936, 0.0259915, 0.00426577, 0.0120459, 0.00536434},
     {-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817, 0.286427, -0.303775,
      0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813, -0.323289, 0.257909,
      0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{0.00205965, 0.00181269, 0.0111244, 0.0167429, 0.00207872, 0.013522,
      0.0610545, 0.156255, 0.98313, 0.0612961, 0.0269466, 0.00604549, 0.0117925, 0.00737077},
     {-0.203834, -0.0722574, 0.294696, -0.254799, 0.00423677, 0.247448, -0.272648,
      0.121391, 0.20297, -0.328442, 0.171305, 0.113167, -0.291561, 0.268582,
      0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|⟩
```

In[5]:=
```
Query[All, Length]@classification1Oversampled
```

Out[5]=
```
⟨|SpikeMax → 20, SpikeMin → 20, f1 → 38, f9 → 10|⟩
```

ReturnAllSpikes (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ReturnAllSpikes is an option for Methods that classify Spikes, such as "Autocorrelation",

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"InterpolatedAutocorrelation", and the default "LombScargle". The default value is False, which means each signal has unique class membership in either SpikeMax or SpikeMin. First spike maxima are classified, and only signals found not to belong to spike maxima are then considered for membership in the spike minima class. We still need to generate cutoffs for our example, using the default "LombScargle" Method:

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
          Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["Sinusoidal2_" <> ToString[i] →
             5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
            {i, 21, 30}]]];
        backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
        timePointsExample = Range[20];

In[3]:= bootstrapQ95 = QuantileEstimator[backgroundExample, timePointsExample];

In[4]:= bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

For illustration purposes we set the SpikeCutoffs to low absolute values:

```
In[5]:= allSpikesCutoff = <|20 → {0.1, -0.1}|>;

In[6]:= classification1UniqueSpikes = TimeSeriesClassification[classificationExample1, timePointsExample,
          LombScargleCutoff → bootstrapQ95, SpikeCutoffs → allSpikesCutoff, ReturnAllSpikes → False]
```

Method → "LombScargle"

```
Out[6]= <|SpikeMax →
          <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
              0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
              -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
              -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
           SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
              0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
              0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
              -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
           SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
              0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
              -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
              0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
           SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
              0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
              -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
              0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
           SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
              0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
              0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
              0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
           SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
              0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
              0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
              0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
           SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
```

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```
    0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
    -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
    0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
  SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
    0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
    -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
    -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
  SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
    0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
    0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
  SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
    0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
    0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
  SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
    0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
    0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
    0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
  SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
    0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
    0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
  SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
    0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
    -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
    0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
  SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
    0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
    0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
  SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
    0.156306, 0.49338, 0.197723}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
    0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
    -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
  SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
    0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
    -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
    -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
  SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
    0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
    0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
    0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
  SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
    0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
    -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
    0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
    0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
    -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
    0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
    -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
    0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}},
  SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
    0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
    0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
    -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
    0.469391, 0.294777, 0.463012, 0.279525}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
    -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
    -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
  SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
    0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
    -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
```

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```
    -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
    0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
    -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
    0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
    0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
    0.341117, 0.381366, 0.325221}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
    -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
    0.214233, 0.523873, 0.243986}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
    0.0874465, -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
    0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
    -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
    0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
  SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
    0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
    -0.0488362, -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052,
    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
    0.35716, 0.304919, 0.374001}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
    0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{0.173083, 0.379193, 0.338228, 0.384591, 0.344256, 0.301779, 0.172933,
    0.337034, 0.332955, 0.316239}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
    0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
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  SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
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  SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
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  SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
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  SpikeNegative_20 → {{0.373567, 0.348518, 0.182641, 0.399653, 0.340024, 0.197691, 0.337761,
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  LinearPositive_2 → {{0.984661, 0.162755, 0.0313267, 0.0020944, 0.00156008, 0.011475,
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  LinearPositive_4 → {{0.984544, 0.162861, 0.0316916, 0.00219377, 0.00149925, 0.011724,
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  LinearPositive_6 → {{0.982932, 0.171949, 0.0327492, 0.00164224, 0.002379, 0.0113266,
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  LinearPositive_7 → {{0.98472, 0.163134, 0.0312689, 0.00212913, 0.0016404, 0.0102459,
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  LinearPositive_8 → {{0.98371, 0.168572, 0.0284284, 0.00170281, 0.00185745, 0.010751,
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  LinearPositive_9 → {{0.98365, 0.168058, 0.033981, 0.00241806, 0.00210287, 0.0115589,
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  LinearPositive_14 → {{0.981111, 0.181783, 0.0375471, 0.00148453, 0.000312388,
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LinearPositive_19 → {{0.987202, 0.147191, 0.027074, 0.00249316, 0.000777253,
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LinearPositive_20 → {{0.983551, 0.167679, 0.0393618, 0.00233188, 0.0011172, 0.0161293,
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LinearNegative_1 → {{0.984203, 0.159785, 0.0568416, 0.00506241, 0.000881747, 0.023661,
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LinearNegative_2 → {{0.983975, 0.157281, 0.0272884, 0.00492376, 0.00030144, 0.0209059,
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LinearNegative_3 → {{0.981452, 0.174458, 0.0229664, 0.001764, 0.000281227, 0.0288508,
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LinearNegative_4 → {{0.97237, 0.220138, 0.0433705, 0.00935025, 0.000670999, 0.00240098,
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LinearNegative_5 → {{0.977089, 0.200269, 0.0364024, 0.00199978, 0.00231623, 0.00860671,
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LinearNegative_6 → {{0.978811, 0.190012, 0.0393558, 0.000605398, 0.0150579, 0.015651,
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LinearNegative_7 → {{0.974629, 0.205946, 0.0323035, 0.00710776, 0.0022957, 0.0115893,
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LinearNegative_9 → {{0.992163, 0.105938, 0.0360944, 0.0064934, 0.00217633, 0.00513993,
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LinearNegative_10 → {{0.983194, 0.163431, 0.0236169, 0.0117059, 0.0187534, 0.0128491,
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LinearNegative_11 → {{0.984307, 0.167887, 0.0231976, 0.00646005, 0.000895278, 0.0137762,
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LinearNegative_12 → {{0.984685, 0.160376, 0.0299467, 0.000604418, 0.00378349, 0.00929028,
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LinearNegative_13 → {{0.98451, 0.16303, 0.0227595, 0.00132012, 0.00348595, 0.0126863,
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    -0.0887624, -0.1144, -0.121973, -0.156462, -0.165726, -0.190329, -0.20958, -0.216046,
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  LinearNegative_14 → {{0.978579, 0.195677, 0.0313545, 0.00267509, 0.00341515, 0.0129726,
    0.0194829, 0.0277661, 0.0277908, 0.0316459}, {-0.0187992, -0.0431131, -0.0473458, -0.070655,
    -0.0879629, -0.116006, -0.12521, -0.152395, -0.170415, -0.184268, -0.196593, -0.22289,
    -0.23237, -0.26046, -0.276864, -0.301954, -0.319987, -0.336453, -0.361973, -0.377956}},
  LinearNegative_15 → {{0.987412, 0.147538, 0.0327634, 0.00558518, 0.00366499, 0.00919838,
    0.0134794, 0.0247462, 0.0207871, 0.0286609}, {-0.0162872, -0.0293132, -0.0552218, -0.0807767,
    -0.0935334, -0.121112, -0.124004, -0.147926, -0.165828, -0.191582, -0.205406, -0.219926,
    -0.248657, -0.269473, -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
  LinearNegative_16 → {{0.979857, 0.186118, 0.0444944, 0.00475256, 0.00394217, 0.0176745,
    0.0237503, 0.0289162, 0.0192921, 0.033722}, {-0.0225164, -0.0461677, -0.0473716, -0.067817,
    -0.0986701, -0.119505, -0.130459, -0.1556, -0.169469, -0.1814, -0.198572, -0.221935,
    -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}},
  LinearNegative_17 → {{0.983395, 0.171344, 0.0310503, 0.00202654, 0.00193992, 0.00923842,
    0.0176563, 0.0269516, 0.0227712, 0.0310183}, {-0.0130003, -0.0309644, -0.0613334, -0.0794837,
    -0.0865967, -0.117058, -0.128048, -0.153332, -0.167054, -0.192254, -0.208455, -0.223898,
    -0.240133, -0.259044, -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}},
  LinearNegative_18 → {{0.981857, 0.181794, 0.0372624, 0.00157464, 0.00102441, 0.00691753,
    0.0240936, 0.0170077, 0.0123945, 0.0210674}, {-0.0251341, -0.0366273, -0.0488411, -0.0708482,
    -0.0895021, -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921,
    -0.243131, -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
  LinearNegative_19 → {{0.986834, 0.144628, 0.035256, 0.00310318, 0.000702006, 0.0165652,
    0.0245304, 0.0352455, 0.0134744, 0.0410912}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
    -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
    -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
  LinearNegative_20 → {{0.985534, 0.158105, 0.0328843, 0.00243514, 0.000101469, 0.0195265,
    0.0175251, 0.026453, 0.0180484, 0.0303906}, {-0.024006, -0.0432239, -0.0496914, -0.0682004,
    -0.0867373, -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
    -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}}|>,
f3 → <|Sinusoidal3_21 → {{0.003093, 0.067983, 0.992591, 0.0880879, 0.0381938, 0.0201564,
    0.0111428, 0.00371032, 0.0191542, 0.00156895}, {0.18867, -0.0972321, -0.306583, -0.251354,
    -0.00388461, 0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096,
    0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
  Sinusoidal3_22 → {{0.00318631, 0.0730881, 0.992797, 0.0819348, 0.0379624, 0.0193048,
    0.00904049, 0.00285594, 0.0196066, 0.00109025}, {0.181513, -0.0928691, -0.305475, -0.251164,
    0.00419846, 0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523,
    0.303756, 0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
  Sinusoidal3_23 → {{0.00295231, 0.0765523, 0.992363, 0.0843288, 0.0378838, 0.0169649,
    0.00808632, 0.0027773, 0.0209207, 0.000957331}, {0.18264, -0.0994704, -0.295137, -0.250857,
    0.00157044, 0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036,
    0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
  Sinusoidal3_24 → {{0.00314279, 0.0708784, 0.992955, 0.0826235, 0.0361366, 0.0195659,
    0.00754111, 0.00268053, 0.020647, 0.000914497}, {0.183018, -0.0977985, -0.296248, -0.251125,
    -0.00333361, 0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939,
    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
  Sinusoidal3_25 → {{0.00289275, 0.0722254, 0.992563, 0.084147, 0.0394916, 0.0185649, 0.00643529,
    0.00207684, 0.0237235, 0.000529693}, {0.191347, -0.0982886, -0.29771, -0.261082,
    0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
    0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
  Sinusoidal3_26 → {{0.0035927, 0.0724177, 0.992482, 0.0865873, 0.0377177, 0.018194, 0.00903366,
    0.0026512, 0.0195294, 0.000949465}, {0.185284, -0.0936261, -0.306395, -0.25385,
    0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
    0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{0.00356621, 0.0718347, 0.992461, 0.086876, 0.0384877, 0.0168536, 0.00812238,
    0.00246869, 0.0215147, 0.000777483}, {0.185809, -0.10192, -0.303748, -0.261172,
    0.000202029, 0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227,
    0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.00292996, 0.0773356, 0.991977, 0.0880559, 0.0367946, 0.0176203,
    0.00875596, 0.00325153, 0.0220462, 0.00118298}, {0.187562, -0.10053, -0.297144, -0.250552,
    0.00476677, 0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453,
    0.301104, 0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{0.00262506, 0.0711674, 0.99281, 0.0827274, 0.0380578, 0.0177335, 0.00874852,
    0.00232562, 0.0238141, 0.000654616}, {0.189755, -0.100643, -0.295957, -0.251445,
    -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
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      0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
    Sinusoidal3_30 → {{0.00427552, 0.071229, 0.992804, 0.0839262, 0.0365748, 0.018534, 0.00877504,
      0.00265531, 0.0209496, 0.000906179}, {0.186539, -0.100579, -0.301622, -0.251977,
      0.00452805, 0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
      0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
      0.0294955, 0.00418398, 0.028168, 0.00135728}, {-0.0952089, -0.252202, 0.25704, 0.097318,
      -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
      0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
    Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
      0.00565905, 0.0259503, 0.00224675}, {-0.101498, -0.25529, 0.251653, 0.0972642,
      -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
      0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
    Sinusoidal2_13 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395,
      0.00472652, 0.0285215, 0.00169662}, {-0.0918789, -0.259087, 0.253065, 0.103093,
      -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
      0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
    Sinusoidal2_14 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
      0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
      -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
      0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
    Sinusoidal2_15 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735,
      0.00386219, 0.0290145, 0.00118185}, {-0.0939856, -0.25429, 0.25073, 0.100441,
      -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
      0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
    Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
      0.00582096, 0.0271664, 0.00231721}, {-0.0916775, -0.260977, 0.251061, 0.104141,
      -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
      0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
    Sinusoidal2_17 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
      0.00436252, 0.0286975, 0.00143738}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
      -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
      0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
    Sinusoidal2_18 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868,
      0.00399143, 0.0293851, 0.00124852}, {-0.102994, -0.260616, 0.250831, 0.0989794,
      -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
      0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
    Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
      0.00452946, 0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358,
      -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
      0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
    Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
      0.00512062, 0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
      -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
      0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
      0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
      -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
      -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
    Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
      0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
      0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
      -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
    Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
      0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
      0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
      -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
    Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
      0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
      0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
      -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
    Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
      0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
      -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
      -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
    Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
```

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```
    0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
    -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
    -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

In[7]:=
```
Query[All, Length]@classification1
```

Out[7]=
```
<|SpikeMax → 20, SpikeMin → 20, f1 → 40, f3 → 10, f5 → 10, f6 → 10|>
```

In[8]:=
```
classification1AllSpikes = TimeSeriesClassification[classificationExample1, timePointsExample,
  LombScargleCutoff → bootstrapQ95, SpikeCutoffs → allSpikesCutoff, ReturnAllSpikes → True]
  Method → "LombScargle"
```

Out[8]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
    0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
    -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
    -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
  SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
    0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
    0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
    -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
  SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
    0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
    -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
    0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
  SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
    0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
    -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
    0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
  SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
    0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
    0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
    0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
  SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
    0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
    0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
    0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
  SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
    0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
    -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
    0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
  SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
    0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
    -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
    -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
  SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
    0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
    0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
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    SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
       0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
       0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
       -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
    SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
       0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
       0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
       0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
    SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
       0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
       0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
       0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
    SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
       0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
       -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
       0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
    SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
       0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
       0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
       -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
    SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
       0.156306, 0.49338, 0.197723}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
       0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
       -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
    SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
       0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
       -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
       -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
    SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
       0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
       0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
       0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
    SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
       0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
       -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
       0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
    SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
       0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
       -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
       0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
    SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
       0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
       -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
       0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}},
    SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
       0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
       0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
       -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}}|>,
  SpikeMin → <|SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607,
       0.256599, 0.156306, 0.49338, 0.197723}, {0.0367157, 0.00909492, 0.955211, -0.0373177,
       -0.0545922, 0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346,
       0.0584456, -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
    SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985, 0.469391,
       0.294777, 0.463012, 0.279525}, {-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075,
       -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467, -0.0370811,
       0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
    SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
       0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
       -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
       -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
    SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
       0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
       0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
       -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
    SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
       0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
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    -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
    0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
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    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
    0.341117, 0.381366, 0.325221}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
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    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
    0.214233, 0.523873, 0.243986}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
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    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
    0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
    -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
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    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
    0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
    0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
    -0.0488362, -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052,
    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
    0.35716, 0.304919, 0.374001}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
    0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
SpikeNegative_13 → {{0.173083, 0.379193, 0.338228, 0.384591, 0.344256, 0.301779, 0.172933,
    0.337034, 0.332955, 0.316239}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
    0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
SpikeNegative_14 → {{0.369536, 0.475376, 0.186202, 0.236301, 0.19825, 0.237895, 0.260777,
    0.276741, 0.472509, 0.288441}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594,
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    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
    0.315364, 0.382839, 0.290684}, {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309,
    0.000455216, -0.0829657, 0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281,
    0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
    0.404761, 0.291284, 0.418924}, {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464,
    0.0166785, 0.0680268, 0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101,
    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
SpikeNegative_17 → {{0.197001, 0.246358, 0.358498, 0.402863, 0.27067, 0.34906, 0.104226,
    0.386107, 0.331869, 0.380125}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
    0.0616787, -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667,
    0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
    0.16152, 0.319203, 0.158339}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
    0.0000556895, -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971, 0.099183,
    0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
SpikeNegative_19 → {{0.392542, 0.277194, 0.303304, 0.316005, 0.451557, 0.178107, 0.336152,
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  LinearPositive_14 → {{0.981111, 0.181783, 0.0375471, 0.00148453, 0.000312388,
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  LinearPositive_16 → {{0.979313, 0.188576, 0.0419809, 0.00521628, 0.000903989,
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LinearPositive_19 → {{0.987202, 0.147191, 0.027074, 0.00249316, 0.000777253,
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LinearNegative_1 → {{0.984203, 0.159785, 0.0568416, 0.00506241, 0.000881747, 0.023661,
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LinearNegative_6 → {{0.978811, 0.190012, 0.0393558, 0.000605398, 0.0150579, 0.015651,
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LinearNegative_7 → {{0.974629, 0.205946, 0.0323035, 0.00710776, 0.0022957, 0.0115893,
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LinearNegative_8 → {{0.982135, 0.172786, 0.0318874, 0.00532189, 0.00125899, 0.00528407,
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LinearNegative_9 → {{0.992163, 0.105938, 0.0360944, 0.0064934, 0.00217633, 0.00513993,
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LinearNegative_10 → {{0.983194, 0.163431, 0.0236169, 0.0117059, 0.0187534, 0.0128491,
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LinearNegative_11 → {{0.984307, 0.167887, 0.0231976, 0.00646005, 0.000895278, 0.0137762,
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LinearNegative_12 → {{0.984685, 0.160376, 0.0299467, 0.000604418, 0.00378349, 0.00929028,
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LinearNegative_13 → {{0.98451, 0.16303, 0.0227595, 0.00132012, 0.00348595, 0.0126863,
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    LinearNegative_16 → {{0.979857, 0.186118, 0.0444944, 0.00475256, 0.00394217, 0.0176745,
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    LinearNegative_17 → {{0.983395, 0.171344, 0.0310503, 0.00202654, 0.00193992, 0.00923842,
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       0.0245304, 0.0352455, 0.0134744, 0.0410912}, {-0.0210969, -0.0344615, -0.0471464, -0.078958,
       -0.100694, -0.103899, -0.130428, -0.144859, -0.170748, -0.178648, -0.21371, -0.229276,
       -0.241033, -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
    LinearNegative_20 → {{0.985534, 0.158105, 0.0328843, 0.00243514, 0.000101469, 0.0195265,
       0.0175251, 0.026453, 0.0180484, 0.0303906}, {-0.024006, -0.0432239, -0.0496914, -0.0682004,
       -0.0867373, -0.103335, -0.12376, -0.155984, -0.167494, -0.179829, -0.214247, -0.231471,
       -0.23997, -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}}|>,
f3 → <|Sinusoidal3_21 → {{0.003093, 0.067983, 0.992591, 0.0880879, 0.0381938, 0.0201564,
       0.0111428, 0.00371032, 0.0191542, 0.00156895}, {0.18867, -0.0972321, -0.306583, -0.251354,
       -0.00388461, 0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096,
       0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
    Sinusoidal3_22 → {{0.00318631, 0.0730881, 0.992797, 0.0819348, 0.0379624, 0.0193048,
       0.00904049, 0.00285594, 0.0196066, 0.00109025}, {0.181513, -0.0928691, -0.305475, -0.251164,
       0.00419846, 0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523,
       0.303756, 0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
    Sinusoidal3_23 → {{0.00295231, 0.0765523, 0.992363, 0.0843288, 0.0378838, 0.0169649,
       0.00808632, 0.0027773, 0.0209207, 0.000957331}, {0.18264, -0.0994704, -0.295137, -0.250857,
       0.00157044, 0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036,
       0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
    Sinusoidal3_24 → {{0.00314279, 0.0708784, 0.992955, 0.0826235, 0.0361366, 0.0195659,
       0.00754111, 0.00268053, 0.020647, 0.000914497}, {0.183018, -0.0977985, -0.296248, -0.251125,
       -0.00333361, 0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939,
       0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
    Sinusoidal3_25 → {{0.00289275, 0.0722254, 0.992563, 0.084147, 0.0394916, 0.0185649, 0.00643529,
       0.00207684, 0.0237235, 0.000529693}, {0.191347, -0.0982886, -0.29771, -0.261082,
       0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
       0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
    Sinusoidal3_26 → {{0.0035927, 0.0724177, 0.992482, 0.0865873, 0.0377177, 0.018194, 0.00903366,
       0.0026512, 0.0195294, 0.000949465}, {0.185284, -0.0936261, -0.306395, -0.25385,
       0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
       0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
    Sinusoidal3_27 → {{0.00356621, 0.0718347, 0.992461, 0.086876, 0.0384877, 0.0168536, 0.00812238,
       0.00246869, 0.0215147, 0.000777483}, {0.185809, -0.10192, -0.303748, -0.261172,
       0.000202029, 0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227,
       0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
    Sinusoidal3_28 → {{0.00292996, 0.0773356, 0.991977, 0.0880559, 0.0367946, 0.0176203,
       0.00875596, 0.00325153, 0.0220462, 0.00118298}, {0.187562, -0.10053, -0.297144, -0.250552,
       0.00476677, 0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453,
       0.301104, 0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
    Sinusoidal3_29 → {{0.00262506, 0.0711674, 0.99281, 0.0827274, 0.0380578, 0.0177335, 0.00874852,
       0.00232562, 0.0238141, 0.000654616}, {0.189755, -0.100643, -0.295957, -0.251445,
       -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
       0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
    Sinusoidal3_30 → {{0.00427552, 0.071229, 0.992804, 0.0839262, 0.0365748, 0.018534, 0.00877504,
       0.00265531, 0.0209496, 0.000906179}, {0.186539, -0.100579, -0.301622, -0.251977,
```

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```
      0.00452805, 0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
      0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
      0.0294955, 0.00418398, 0.028168, 0.00135728}, {-0.0952089, -0.252202, 0.25704, 0.097318,
      -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
      0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
      0.00565905, 0.0259503, 0.00224675}, {-0.101498, -0.25529, 0.251653, 0.0972642,
      -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
      0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395,
      0.00472652, 0.0285215, 0.00169662}, {-0.0918789, -0.259087, 0.253065, 0.103093,
      -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
      0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
      0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
      -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
      0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735,
      0.00386219, 0.0290145, 0.00118185}, {-0.0939856, -0.25429, 0.25073, 0.100441,
      -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
      0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
      0.00582096, 0.0271664, 0.00231721}, {-0.0916775, -0.260977, 0.251061, 0.104141,
      -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
      0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
      0.00436252, 0.0286975, 0.00143738}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
      -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
      0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868,
      0.00399143, 0.0293851, 0.00124852}, {-0.102994, -0.260616, 0.250831, 0.0989794,
      -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
      0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
      0.00452946, 0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358,
      -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
      0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
      0.00512062, 0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
      -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
      0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
      0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
      -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
      -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
      0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
      0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
      -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
      0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
      0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
      -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
  Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
      0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
      0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
      -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
      0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
      -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
      -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
      0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
      -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
      -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
```

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```
Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

```
In[9]:= Query[All, Length]@classification1AllSpikes
Out[9]= <|SpikeMax → 21, SpikeMin → 21, f1 → 40, f3 → 10, f5 → 10, f6 → 10|>
```

We see that in this case the SpikeMin class displays signals that also belong in the SpikeMax Class.

ReturnData (1)

```
In[1]:= Needs["MathIOmica`"]
```

ReturnData is an option to either return labels and data for each class membership (default, set to True), or only return the keys of the input data in the classification (if set to False).

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
      Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["Sinusoidal2_" <> ToString[i] →
         5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
        {i, 21, 30}]]];
 backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
 timePointsExample = Range[20];
```

We need to also have values for the appropriate cutoffs. We may base these on the background noise and use the QuantileEstimation for this:

```
In[3]:= bootstrapQ95 = QuantileEstimator[backgroundExample, timePointsExample];
        bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

Let's perform the classification:

```
In[4]:= classification1 = TimeSeriesClassification[classificationExample1, timePointsExample,
          LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes, ReturnData → True]
```

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```
Method → "LombScargle"
```

Out[4]=

```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
      0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
      -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
      0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
      0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
      0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
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      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
      0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
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      0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
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      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
      0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
      -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
      0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
      0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
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   SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
      0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
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      -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
      0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
      0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
      0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
      0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
   SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
      0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
      -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
      0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
   SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
      0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
      0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
      -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
   SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
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   SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
      0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
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    -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
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  SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
    0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
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    0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
  SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
    0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
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    0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
    0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
    -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
    0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
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    0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
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    -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
    -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
  SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
    0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
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    -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
    0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
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    -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
  SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
    0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
    -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
    0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
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    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
    0.341117, 0.381366, 0.325221}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
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    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
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    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
    0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
    -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
    0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
  SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
    0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
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    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
    0.35716, 0.304919, 0.374001}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
    0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
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    SpikeNegative_13 → {{0.173083, 0.379193, 0.338228, 0.384591, 0.344256, 0.301779, 0.172933,
       0.337034, 0.332955, 0.316239}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
       0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
       -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
    SpikeNegative_14 → {{0.369536, 0.475376, 0.186202, 0.236301, 0.19825, 0.237895, 0.260777,
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       0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
    SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
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       0.000455216, -0.0829657, 0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281,
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    SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
       0.404761, 0.291284, 0.418924}, {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464,
       0.0166785, 0.0680268, 0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101,
       0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
    SpikeNegative_17 → {{0.197001, 0.246358, 0.358498, 0.402863, 0.27067, 0.34906, 0.104226,
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       0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
    SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
       0.16152, 0.319203, 0.158339}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
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       0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
    SpikeNegative_19 → {{0.392542, 0.277194, 0.303304, 0.316005, 0.451557, 0.178107, 0.336152,
       0.30277, 0.204908, 0.308124}, {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693,
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       -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
    SpikeNegative_20 → {{0.373567, 0.348518, 0.182641, 0.399653, 0.340024, 0.197691, 0.337761,
       0.284486, 0.34594, 0.276612}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
       0.057722, -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007,
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f1 → <|LinearPositive_1 → {{0.984043, 0.16711, 0.0316771, 0.00181032, 0.00174073,
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    LinearPositive_2 → {{0.984661, 0.162755, 0.0313267, 0.0020944, 0.00156008, 0.011475,
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    LinearPositive_3 → {{0.983778, 0.169007, 0.0312598, 0.00266983, 0.0014985,
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    LinearPositive_7 → {{0.98472, 0.163134, 0.0312689, 0.00212913, 0.0016404, 0.0102459,
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    LinearPositive_8 → {{0.98371, 0.168572, 0.0284284, 0.00170281, 0.00185745, 0.010751,
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LinearPositive_12 → {{0.985678, 0.154732, 0.0287579, 0.00132291, 0.00382878, 0.0177303,
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LinearPositive_14 → {{0.981111, 0.181783, 0.0375471, 0.00148453, 0.000312388,
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LinearPositive_15 → {{0.984521, 0.158493, 0.0449595, 0.00110501, 0.00265532, 0.0107268,
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LinearPositive_16 → {{0.979313, 0.188576, 0.0419809, 0.00521628, 0.000903989,
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LinearPositive_17 → {{0.983915, 0.163837, 0.0268448, 0.00291022, 0.00438077, 0.0123819,
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LinearPositive_18 → {{0.983959, 0.16518, 0.0329124, 0.00150854, 0.000803325, 0.0135443,
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LinearPositive_19 → {{0.987202, 0.147191, 0.027074, 0.00249316, 0.000777253,
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LinearPositive_20 → {{0.983551, 0.167679, 0.0393618, 0.00233188, 0.0011172, 0.0161293,
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LinearNegative_1 → {{0.984203, 0.159785, 0.0568416, 0.00506241, 0.000881747, 0.023661,
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LinearNegative_2 → {{0.983975, 0.157281, 0.0272884, 0.00492376, 0.00030144, 0.0209059,
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LinearNegative_3 → {{0.981452, 0.174458, 0.0229664, 0.001764, 0.000281227, 0.0288508,
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LinearNegative_4 → {{0.97237, 0.220138, 0.0433705, 0.00935025, 0.000670999, 0.00240098,
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LinearNegative_5 → {{0.977089, 0.200269, 0.0364024, 0.00199978, 0.00231623, 0.00860671,
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LinearNegative_7 → {{0.974629, 0.205946, 0.0323035, 0.00710776, 0.0022957, 0.0115893,
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LinearNegative_8 → {{0.982135, 0.172786, 0.0318874, 0.00532189, 0.00125899, 0.00528407,
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LinearNegative_9 → {{0.992163, 0.105938, 0.0360944, 0.0064934, 0.00217633, 0.00513993,
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LinearNegative_13 → {{0.98451, 0.16303, 0.0227595, 0.00132012, 0.00348595, 0.0126863,
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LinearNegative_14 → {{0.978579, 0.195677, 0.0313545, 0.00267509, 0.00341515, 0.0129726,
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LinearNegative_15 → {{0.987412, 0.147538, 0.0327634, 0.00558518, 0.00366499, 0.00919838,
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LinearNegative_16 → {{0.979857, 0.186118, 0.0444944, 0.00475256, 0.00394217, 0.0176745,
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LinearNegative_17 → {{0.983395, 0.171344, 0.0310503, 0.00202654, 0.00193992, 0.00923842,
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LinearNegative_19 → {{0.986834, 0.144628, 0.035256, 0.00310318, 0.000702006, 0.0165652,
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  Sinusoidal3_23 → {{0.00295231, 0.0765523, 0.992363, 0.0843288, 0.0378838, 0.0169649,
    0.00808632, 0.0027773, 0.0209207, 0.000957331}, {0.18264, -0.0994704, -0.295137, -0.250857,
    0.00157044, 0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036,
    0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
  Sinusoidal3_24 → {{0.00314279, 0.0708784, 0.992955, 0.0826235, 0.0361366, 0.0195659,
    0.00754111, 0.00268053, 0.020647, 0.000914497}, {0.183018, -0.0977985, -0.296248, -0.251125,
    -0.00333361, 0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939,
    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
  Sinusoidal3_25 → {{0.00289275, 0.0722254, 0.992563, 0.084147, 0.0394916, 0.0185649, 0.00643529,
    0.00207684, 0.0237235, 0.000529693}, {0.191347, -0.0982886, -0.29771, -0.261082,
    0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
    0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
  Sinusoidal3_26 → {{0.0035927, 0.0724177, 0.992482, 0.0865873, 0.0377177, 0.018194, 0.00903366,
    0.0026512, 0.0195294, 0.000949465}, {0.185284, -0.0936261, -0.306395, -0.25385,
    0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
    0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{0.00356621, 0.0718347, 0.992461, 0.086876, 0.0384877, 0.0168536, 0.00812238,
    0.00246869, 0.0215147, 0.000777483}, {0.185809, -0.10192, -0.303748, -0.261172,
    0.000202029, 0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227,
    0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.00292996, 0.0773356, 0.991977, 0.0880559, 0.0367946, 0.0176203,
    0.00875596, 0.00325153, 0.0220462, 0.00118298}, {0.187562, -0.10053, -0.297144, -0.250552,
    0.00476677, 0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453,
    0.301104, 0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{0.00262506, 0.0711674, 0.99281, 0.0827274, 0.0380578, 0.0177335, 0.00874852,
    0.00232562, 0.0238141, 0.000654616}, {0.189755, -0.100643, -0.295957, -0.251445,
    -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
    0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
  Sinusoidal3_30 → {{0.00427552, 0.071229, 0.992804, 0.0839262, 0.0365748, 0.018534, 0.00877504,
    0.00265531, 0.0209496, 0.000906179}, {0.186539, -0.100579, -0.301622, -0.251977,
    0.00452805, 0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
    0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
    0.0294955, 0.00418398, 0.028168, 0.00135728}, {-0.0952089, -0.252202, 0.25704, 0.097318,
    -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
    0.00565905, 0.0259503, 0.00224675}, {-0.101498, -0.25529, 0.251653, 0.0972642,
    -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
    0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395,
    0.00472652, 0.0285215, 0.00169662}, {-0.0918789, -0.259087, 0.253065, 0.103093,
    -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
    0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735,
    0.00386219, 0.0290145, 0.00118185}, {-0.0939856, -0.25429, 0.25073, 0.100441,
    -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
    0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
    0.00582096, 0.0271664, 0.00231721}, {-0.0916775, -0.260977, 0.251061, 0.104141,
    -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
    0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
    0.00436252, 0.0286975, 0.00143738}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
    -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868,
    0.00399143, 0.0293851, 0.00124852}, {-0.102994, -0.260616, 0.250831, 0.0989794,
    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
```

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```
    Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
       0.00452946, 0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358,
       -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
       0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
    Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
       0.00512062, 0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
       -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
       0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
  f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
       0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
       -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
       -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
    Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
       0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
       0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
       -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
    Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
       0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
       0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
       -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
    Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
       0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
       0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
       -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
    Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
       0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
       -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
       -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
    Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
       0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
       -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
       -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
    Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
       0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
       -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
       -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
    Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
       0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
       -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
       -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
    Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
       0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
       -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
       -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
    Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
       0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
       0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
       -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

In[5]:=
```
classification1LabelsOnly = TimeSeriesClassification[classificationExample1, timePointsExample,
  LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes, ReturnData → False]
```

```
Method → "LombScargle"
```

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```
Out[5]= ⟨|SpikeMax → {SpikePositive_1, SpikePositive_2, SpikePositive_3, SpikePositive_4, SpikePositive_5,
    SpikePositive_6, SpikePositive_7, SpikePositive_8, SpikePositive_9, SpikePositive_10,
    SpikePositive_11, SpikePositive_12, SpikePositive_13, SpikePositive_14, SpikePositive_15,
    SpikePositive_16, SpikePositive_17, SpikePositive_18, SpikePositive_19, SpikePositive_20},
  SpikeMin → {SpikeNegative_1, SpikeNegative_2, SpikeNegative_3, SpikeNegative_4, SpikeNegative_5,
    SpikeNegative_6, SpikeNegative_7, SpikeNegative_8, SpikeNegative_9, SpikeNegative_10,
    SpikeNegative_11, SpikeNegative_12, SpikeNegative_13, SpikeNegative_14, SpikeNegative_15,
    SpikeNegative_16, SpikeNegative_17, SpikeNegative_18, SpikeNegative_19, SpikeNegative_20},
  f1 → {LinearPositive_1, LinearPositive_2, LinearPositive_3, LinearPositive_4, LinearPositive_5,
    LinearPositive_6, LinearPositive_7, LinearPositive_8, LinearPositive_9, LinearPositive_10,
    LinearPositive_11, LinearPositive_12, LinearPositive_13, LinearPositive_14, LinearPositive_15,
    LinearPositive_16, LinearPositive_17, LinearPositive_18, LinearPositive_19, LinearPositive_20,
    LinearNegative_1, LinearNegative_2, LinearNegative_3, LinearNegative_4, LinearNegative_5,
    LinearNegative_6, LinearNegative_7, LinearNegative_8, LinearNegative_9, LinearNegative_10,
    LinearNegative_11, LinearNegative_12, LinearNegative_13, LinearNegative_14, LinearNegative_15,
    LinearNegative_16, LinearNegative_17, LinearNegative_18, LinearNegative_19, LinearNegative_20},
  f3 → {Sinusoidal3_21, Sinusoidal3_22, Sinusoidal3_23, Sinusoidal3_24, Sinusoidal3_25,
    Sinusoidal3_26, Sinusoidal3_27, Sinusoidal3_28, Sinusoidal3_29, Sinusoidal3_30},
  f5 → {Sinusoidal2_11, Sinusoidal2_12, Sinusoidal2_13, Sinusoidal2_14, Sinusoidal2_15,
    Sinusoidal2_16, Sinusoidal2_17, Sinusoidal2_18, Sinusoidal2_19, Sinusoidal2_20},
  f6 → {Sinusoidal1_1, Sinusoidal1_2, Sinusoidal1_3, Sinusoidal1_4, Sinusoidal1_5,
    Sinusoidal1_6, Sinusoidal1_7, Sinusoidal1_8, Sinusoidal1_9, Sinusoidal1_10}|⟩
```

If we want the classes produced, we can query the keys and see that these are still the same:

```
In[6]:= Query[Keys][#] & /@ {classification1, classification1LabelsOnly}
Out[6]= {{SpikeMax, SpikeMin, f1, f3, f5, f6}, {SpikeMax, SpikeMin, f1, f3, f5, f6}}
```

For the members in each class we have:

```
In[7]:= Query[All, Length][#] & /@ {classification1, classification1LabelsOnly}
Out[7]= {⟨|SpikeMax → 20, SpikeMin → 20, f1 → 40, f3 → 10, f5 → 10, f6 → 10|⟩,
  ⟨|SpikeMax → 20, SpikeMin → 20, f1 → 40, f3 → 10, f5 → 10, f6 → 10|⟩}
```

ReturnModels (1)

```
In[1]:= Needs["MathIOmica`"]
```

ReturnModels can be set to True (default value is False), to return the models as well as the classification information for the input data.

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
  backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
  timePointsExample = Range[20];
```

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Let's perform the classification:

In[3]:=
```
classificationTimeSeriesModelAggregate1Models = TimeSeriesClassification[classificationExample1,
  timePointsExample, Method → "TimeSeriesModelAggregate", ReturnModels → True]
```

```
Method → "TimeSeriesModelAggregate"
```

Out[3]=
```
⟨|TimeSeriesClasses →
  ⟨|MAProcess → ⟨|SpikePositive_1 → {{0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
        -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
        -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732},
       {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682, -0.0371416,
        0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411, -0.00869189,
        -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
     SpikePositive_2 → {{0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829,
        0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
        -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543},
       {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829, 0.017722,
        -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
        -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
     SpikePositive_3 → {{0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993,
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        -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
     SpikePositive_4 → {{0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033, -0.0772898,
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        0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
     SpikePositive_5 → {{0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663, 0.0676522,
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        0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368},
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     SpikePositive_6 → {{0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416, 0.0326082,
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     SpikePositive_7 → {{0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442, -0.00304927, 0.016839,
        0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801, 0.0872978, 0.0241062, 0.0100416,
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        0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
        0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
     SpikePositive_8 → {{0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677,
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     SpikePositive_9 → {{0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483,
        -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
        -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062},
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        -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
     SpikePositive_10 → {{0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367,
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    {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367, -0.0143555,
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  SpikePositive_11 → {{0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068, 0.0325846, -0.0861631,
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  SpikePositive_12 → {{0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803, 0.0850629,
     0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
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  SpikePositive_13 → {{-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903, -0.0475178,
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  SpikePositive_14 → {{0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311, 0.0642856,
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     -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
  SpikePositive_15 → {{0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922, 0.0322486,
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     -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
  SpikePositive_16 → {{-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223,
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    {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223, -0.00461306,
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  SpikePositive_17 → {{0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444, 0.09185,
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     -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
  SpikePositive_18 → {{-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144, -0.0566396,
     0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424, 0.0179427,
     0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999},
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     -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424, 0.0179427, 0.0577408,
     -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727, -0.0813174,
     0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
     0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065},
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     -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833, -0.0790448,
     -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909,
     -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381},
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     0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909,
     -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}},
  SpikeNegative_1 → {{-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627,
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     0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511},
    {-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627, 0.0839417,
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    0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
SpikeNegative_2 → {{-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113, -0.0217826,
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    0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342},
  {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113, -0.0217826, -0.0407702,
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    0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
SpikeNegative_3 → {{-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095, 0.102466,
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  {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095, 0.102466, -0.0311731,
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SpikeNegative_4 → {{-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556, -0.0455452,
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SpikeNegative_5 → {{-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968, 0.0456577,
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  {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968, 0.0456577, -0.0741938,
    0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812, -0.0509291,
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SpikeNegative_6 → {{-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953, -0.058058,
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    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539},
  {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953, -0.058058, 0.0371483,
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SpikeNegative_7 → {{-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109, 0.0874465,
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    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901},
  {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109, 0.0874465, -0.0578879,
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SpikeNegative_8 → {{-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887, -0.0684695,
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SpikeNegative_9 → {{-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416, 0.0325626,
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SpikeNegative_10 → {{-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025, 0.0119404,
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SpikeNegative_11 → {{-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755, -0.0488362,
    -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052, 0.0300314,
    0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954},
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    -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052, 0.0300314, 0.0700943,
    -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
SpikeNegative_12 → {{0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571, 0.0770767,
    0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734},
  {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571, 0.0770767, 0.070194,
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    -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036, 0.0881039,
     0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538, -0.028162,
     0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681},
    {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036, 0.0881039, 0.0257902,
     0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538, -0.028162,
     0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594, 0.0528555,
     0.00336549, 0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
     0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977},
    {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594, 0.0528555, 0.00336549,
     0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374, 0.0379646,
     0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309, 0.000455216,
     -0.0829657, 0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281, 0.0312967,
     0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439},
    {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309, 0.000455216, -0.0829657,
     0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281, 0.0312967, 0.0228599,
     -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464, 0.0166785,
     0.0680268, 0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101, 0.0309736,
     -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422},
    {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464, 0.0166785, 0.0680268,
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  SpikeNegative_17 → {{-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312, 0.0616787,
     -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667, 0.022695,
     0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092},
    {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312, 0.0616787, -0.0836702,
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     0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604, 0.0000556895,
     -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971, 0.099183, 0.0322089,
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     0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
  SpikeNegative_19 → {{-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693, 0.0216656,
     0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588,
     -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696},
    {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693, 0.0216656, 0.0247419,
     -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588, -0.0116062,
     0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452, 0.057722,
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    {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452, 0.057722, -0.0391361,
     -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007, -0.0175827,
     0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}},
  Sinusoidal1_3 → {{-0.187066, -0.0732084, 0.32812, -0.266161, 0.00567862, 0.253731, -0.305231,
     0.119463, 0.171259, -0.307063, 0.163206, 0.095439, -0.297199, 0.229651, -0.00688215,
     -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}, {-0.187066, -0.0732084, 0.32812,
     -0.266161, 0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
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  Sinusoidal1_4 → {{-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004, 0.261223, -0.285188,
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  Sinusoidal1_8 → {{-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322, 0.285866, -0.282711,
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     -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817, 0.286427, -0.303775,
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  Sinusoidal1_10 → {{-0.203834, -0.0722574, 0.294696, -0.254799, 0.00423677, 0.247448,
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SARIMAProcess → <|LinearPositive_1 → {{0.018415, 0.0377122, 0.0574444, 0.0761646, 0.0918826,
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  LinearPositive_2 → {{0.0183904, 0.0374466, 0.0550304, 0.0738563, 0.0928923, 0.110677,
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  LinearPositive_3 → {{0.0204364, 0.0388961, 0.055949, 0.0753517, 0.0937248, 0.112155,
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    0.241027, 0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}},
  LinearPositive_4 → {{0.0188591, 0.0384796, 0.0552706, 0.0761382, 0.0941127, 0.11255,
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  LinearPositive_6 → {{0.0186014, 0.0381755, 0.0550572, 0.074646, 0.0932816, 0.113886,
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    0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
  LinearPositive_7 → {{0.0186204, 0.0363314, 0.0569047, 0.0757329, 0.092018, 0.111558,
    0.130244, 0.148133, 0.167451, 0.186409, 0.204805, 0.22423, 0.241912, 0.261689, 0.28065,
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    0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
  LinearPositive_8 → {{0.0170019, 0.0382694, 0.0569482, 0.0754625, 0.0914347, 0.110031,
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  LinearPositive_9 → {{0.0185501, 0.0388643, 0.0547098, 0.0747468, 0.0938687, 0.113558,
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  LinearPositive_10 → {{0.0174864, 0.0370712, 0.0572236, 0.0748823, 0.0926627, 0.111129,
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    0.223211, 0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
  LinearPositive_11 → {{0.013623, 0.0406398, 0.0607801, 0.0781742, 0.0921015, 0.112119,
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  LinearPositive_12 → {{0.0219335, 0.0431422, 0.0502095, 0.0696589, 0.0884956, 0.116468,
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  LinearPositive_13 → {{0.022617, 0.0284408, 0.0607512, 0.0795972, 0.0880775, 0.119613,
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  LinearPositive_16 → {{0.0164478, 0.0360481, 0.048135, 0.0712245, 0.101186, 0.114916,
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    0.232407, 0.261637, 0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}},
  LinearPositive_20 → {{0.00952752, 0.0286979, 0.0547226, 0.0709501, 0.0958101, 0.109505,
    0.135844, 0.152431, 0.165158, 0.182651, 0.210505, 0.231304, 0.235391, 0.267585, 0.28298,
    0.294497, 0.314251, 0.344366, 0.352473, 0.366536}, {0.00952752, 0.0286979, 0.0547226,
    0.0709501, 0.0958101, 0.109505, 0.135844, 0.152431, 0.165158, 0.182651, 0.210505,
    0.231304, 0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
  LinearNegative_1 → {{-0.0218046, -0.0446169, -0.0612231, -0.0738948, -0.109733, -0.115191,
    -0.124469, -0.148293, -0.159758, -0.176361, -0.217843, -0.224298, -0.23172,
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   {-0.0218046, -0.0446169, -0.0612231, -0.0738948, -0.109733, -0.115191, -0.124469,
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    -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733}},
  LinearNegative_3 → {{-0.0283384, -0.0528281, -0.0527884, -0.0740599, -0.0921776, -0.0948819,
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    -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769},
   {-0.0283384, -0.0528281, -0.0527884, -0.0740599, -0.0921776, -0.0948819, -0.146225,
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    -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
  LinearNegative_5 → {{-0.0201624, -0.0405386, -0.0436406, -0.0738225, -0.0817467, -0.105404,
    -0.114359, -0.154377, -0.169473, -0.174198, -0.212011, -0.225376, -0.230144,
    -0.247108, -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219},
   {-0.0201624, -0.0405386, -0.0436406, -0.0738225, -0.0817467, -0.105404, -0.114359,
    -0.154377, -0.169473, -0.174198, -0.212011, -0.225376, -0.230144, -0.247108,
    -0.279263, -0.313397, -0.310044, -0.355813, -0.367062, -0.365219}},
  LinearNegative_6 → {{-0.0267223, -0.0446999, -0.0523138, -0.0699606, -0.0987645, -0.126896,
    -0.126614, -0.165572, -0.172297, -0.184872, -0.208135, -0.237294, -0.243037,
    -0.24423, -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481},
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    -0.165572, -0.172297, -0.184872, -0.208135, -0.237294, -0.243037, -0.24423,
    -0.267876, -0.316863, -0.31725, -0.320163, -0.342501, -0.381481}},
  LinearNegative_7 → {{-0.00172329, -0.032268, -0.068173, -0.0857129, -0.0881686, -0.107137,
    -0.140409, -0.14992, -0.182962, -0.175511, -0.200764, -0.226349, -0.23516,
    -0.248536, -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923},
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    -0.14992, -0.182962, -0.175511, -0.200764, -0.226349, -0.23516, -0.248536,
    -0.268245, -0.303398, -0.321997, -0.349618, -0.352678, -0.371923}},
  LinearNegative_8 → {{-0.0170306, -0.0378539, -0.0394845, -0.0767312, -0.0942537, -0.105065,
    -0.146528, -0.134698, -0.186411, -0.174071, -0.194782, -0.232787, -0.238911,
    -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678},
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    -0.134698, -0.186411, -0.174071, -0.194782, -0.232787, -0.238911, -0.261139,
    -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
  LinearNegative_10 → {{-0.00155633, -0.0271325, -0.0625737, -0.0744387, -0.0901925,
    -0.0932579, -0.138846, -0.15092, -0.157289, -0.198281, -0.189392, -0.206968,
    -0.259028, -0.273261, -0.270544, -0.29133, -0.328913, -0.352948, -0.335503, -0.37816},
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      {-0.00155633, -0.0271325, -0.0625737, -0.0744387, -0.0901925, -0.0932579,
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    LinearNegative_11 → {{-0.0105542, -0.0364589, -0.0515525, -0.0708746, -0.0862196,
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       -0.271564, -0.288178, -0.293001, -0.310129, -0.328328, -0.364455, -0.366174},
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    LinearNegative_13 → {{-0.01186, -0.0431645, -0.0590873, -0.0756374, -0.0887624, -0.1144,
       -0.121973, -0.156462, -0.165726, -0.190329, -0.20958, -0.216046, -0.244405,
       -0.264186, -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596},
      {-0.01186, -0.0431645, -0.0590873, -0.0756374, -0.0887624, -0.1144, -0.121973,
       -0.156462, -0.165726, -0.190329, -0.20958, -0.216046, -0.244405, -0.264186,
       -0.273481, -0.307757, -0.312755, -0.331563, -0.35751, -0.373596}},
    LinearNegative_18 → {{-0.0251341, -0.0366273, -0.0488411, -0.0708482, -0.0895021,
       -0.108048, -0.135017, -0.151934, -0.16602, -0.187332, -0.199435, -0.229921, -0.243131,
       -0.254831, -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752},
      {-0.0251341, -0.0366273, -0.0488411, -0.0708482, -0.0895021, -0.108048, -0.135017,
       -0.151934, -0.16602, -0.187332, -0.199435, -0.229921, -0.243131, -0.254831,
       -0.285694, -0.295132, -0.326762, -0.328866, -0.362472, -0.367752}},
    LinearNegative_20 → {{-0.024006, -0.0432239, -0.0496914, -0.0682004, -0.0867373, -0.103335,
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       -0.270233, -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106},
      {-0.024006, -0.0432239, -0.0496914, -0.0682004, -0.0867373, -0.103335, -0.12376,
       -0.155984, -0.167494, -0.179829, -0.214247, -0.231471, -0.23997, -0.270233,
       -0.283577, -0.29212, -0.319745, -0.341763, -0.35111, -0.366106}}|>,
  ARIMAProcess → <|LinearPositive_5 → {{0.0196474, 0.0375735, 0.0561861, 0.0745382, 0.094777,
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       0.225889, 0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
    LinearPositive_14 → {{0.0276601, 0.0348994, 0.0578995, 0.0764811, 0.0865063, 0.115217,
       0.136395, 0.15157, 0.16455, 0.180615, 0.213666, 0.215142, 0.243638, 0.254281, 0.280739,
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       0.0764811, 0.0865063, 0.115217, 0.136395, 0.15157, 0.16455, 0.180615, 0.213666, 0.215142,
       0.243638, 0.254281, 0.280739, 0.299298, 0.313921, 0.336645, 0.361637, 0.373861}},
    LinearPositive_19 → {{0.0205961, 0.045526, 0.0569898, 0.0724948, 0.0867427, 0.105806,
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       0.0724948, 0.0867427, 0.105806, 0.12769, 0.145665, 0.170669, 0.180276, 0.216792, 0.223063,
       0.241101, 0.270774, 0.282283, 0.293887, 0.315058, 0.334039, 0.359611, 0.369743}},
    LinearNegative_2 → {{-0.0137543, -0.0552134, -0.0387902, -0.0787876, -0.0972777, -0.0993326,
       -0.131634, -0.158204, -0.178021, -0.176063, -0.209858, -0.230763, -0.248781,
       -0.268592, -0.290148, -0.294015, -0.319548, -0.339092, -0.343638, -0.357122},
      {-0.0137543, -0.0552134, -0.0387902, -0.0787876, -0.0972777, -0.0993326, -0.131634,
       -0.158204, -0.178021, -0.176063, -0.209858, -0.230763, -0.248781, -0.268592,
       -0.290148, -0.294015, -0.319548, -0.339092, -0.343638, -0.357122}},
    LinearNegative_4 → {{-0.0158873, -0.0248133, -0.0382326, -0.0881019, -0.0887054, -0.128386,
       -0.128859, -0.161147, -0.159022, -0.205319, -0.200777, -0.210411, -0.243003,
       -0.248744, -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844},
      {-0.0158873, -0.0248133, -0.0382326, -0.0881019, -0.0887054, -0.128386, -0.128859,
       -0.161147, -0.159022, -0.205319, -0.200777, -0.210411, -0.243003, -0.248744,
       -0.287693, -0.296322, -0.315419, -0.341857, -0.361551, -0.363844}},
    LinearNegative_9 → {{-0.0287969, -0.0189698, -0.0530075, -0.0828922, -0.0936032, -0.115414,
       -0.114422, -0.130851, -0.167598, -0.173937, -0.198609, -0.23569, -0.258977,
       -0.272337, -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269},
      {-0.0287969, -0.0189698, -0.0530075, -0.0828922, -0.0936032, -0.115414, -0.114422,
       -0.130851, -0.167598, -0.173937, -0.198609, -0.23569, -0.258977, -0.272337,
       -0.282281, -0.313212, -0.310016, -0.342252, -0.33673, -0.371269}},
    LinearNegative_12 → {{-0.0105234, -0.0459122, -0.0631169, -0.0780043, -0.0883748,
       -0.108962, -0.137461, -0.144887, -0.163604, -0.184293, -0.210166, -0.217602, -0.245066,
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      {-0.0105234, -0.0459122, -0.0631169, -0.0780043, -0.0883748, -0.108962, -0.137461,
       -0.144887, -0.163604, -0.184293, -0.210166, -0.217602, -0.245066, -0.261694,
       -0.278017, -0.302052, -0.320586, -0.338539, -0.357344, -0.365709}},
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LinearNegative_14 → {{-0.0187992, -0.0431131, -0.0473458, -0.070655, -0.0879629,
    -0.116006, -0.12521, -0.152395, -0.170415, -0.184268, -0.196593, -0.22289, -0.23237,
    -0.26046, -0.276864, -0.301954, -0.319987, -0.336453, -0.361973, -0.377956},
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    -0.276864, -0.301954, -0.319987, -0.336453, -0.361973, -0.377956}},
LinearNegative_15 → {{-0.0162872, -0.0293132, -0.0552218, -0.0807767, -0.0935334,
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    -0.277195, -0.295945, -0.318029, -0.32797, -0.357333, -0.372295}},
LinearNegative_16 → {{-0.0225164, -0.0461677, -0.0473716, -0.067817, -0.0986701, -0.119505,
    -0.130459, -0.1556, -0.169469, -0.1814, -0.198572, -0.221935, -0.24543, -0.26292, -0.27777,
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    -0.067817, -0.0986701, -0.119505, -0.130459, -0.1556, -0.169469, -0.1814, -0.198572, -0.221935,
    -0.24543, -0.26292, -0.27777, -0.290757, -0.323084, -0.338468, -0.356158, -0.371628}},
LinearNegative_17 → {{-0.0130003, -0.0309644, -0.0613334, -0.0794837, -0.0865967,
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    -0.153332, -0.167054, -0.192254, -0.208455, -0.223898, -0.240133, -0.259044,
    -0.280559, -0.29661, -0.315863, -0.337898, -0.355985, -0.370276}},
LinearNegative_19 → {{-0.0210969, -0.0344615, -0.0471464, -0.078958, -0.100694, -0.103899,
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    -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137},
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    -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
Sinusoidal3_21 → {{0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461, 0.254971, 0.296206,
    0.0966543, -0.185492, -0.313443, -0.183529, 0.10096, 0.29637, 0.252844, -0.00335276, -0.262031,
    -0.296035, -0.102293, 0.188443, 0.324183}, {0.18867, -0.0972321, -0.306583, -0.251354,
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    0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
Sinusoidal3_22 → {{0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846, 0.258728,
    0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523, 0.303756,
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    -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{0.18264, -0.0994704, -0.295137, -0.250857, 0.00157044, 0.256486, 0.297096,
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    0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361, 0.252171,
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    -0.251125, -0.00333361, 0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939,
    0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
Sinusoidal3_25 → {{0.191347, -0.0982886, -0.29771, -0.261082, 0.00611569, 0.249936, 0.298887,
    0.101714, -0.1867, -0.321641, -0.191881, 0.0933799, 0.302028, 0.251166, -0.00172715,
    -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}, {0.191347, -0.0982886, -0.29771,
    -0.261082, 0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
    0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
Sinusoidal3_26 → {{0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724, 0.255415, 0.302354,
    0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444, 0.296927, 0.253991, 0.00087675,
    -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}, {0.185284, -0.0936261, -0.306395,
    -0.25385, 0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
    0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
Sinusoidal3_27 → {{0.185809, -0.10192, -0.303748, -0.261172, 0.000202029, 0.258446, 0.299423,
    0.0942508, -0.180597, -0.31495, -0.188893, 0.100227, 0.302676, 0.24961, -0.00174468, -0.2545,
    -0.305591, -0.0963953, 0.182678, 0.311459}, {0.185809, -0.10192, -0.303748, -0.261172,
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    0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
Sinusoidal3_28 → {{0.187562, -0.10053, -0.297144, -0.250552, 0.00476677, 0.261432, 0.296623,
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    0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453, 0.301104, 0.258413, 0.0054441, -0.255345,
    -0.298729, -0.095819, 0.181572, 0.323712}, {0.187562, -0.10053, -0.297144, -0.250552,
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  Sinusoidal3_29 → {{0.189755, -0.100643, -0.295957, -0.251445, -0.0055221, 0.252696, 0.29864,
    0.0975281, -0.189706, -0.322914, -0.187404, 0.103546, 0.296096, 0.252167, -0.00435421,
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  Sinusoidal3_30 → {{0.186539, -0.100579, -0.301622, -0.251977, 0.00452805, 0.258968, 0.30446,
    0.103392, -0.185935, -0.314134, -0.188321, 0.10063, 0.296225, 0.252222, -0.00565741,
    -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}, {0.186539, -0.100579, -0.301622,
    -0.251977, 0.00452805, 0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
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    0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146},
   {-0.20264, -0.107877, 0.278896, -0.289184, -0.0168796, 0.24783, -0.330128,
    0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701, -0.331998, 0.269056,
    0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_5 → {{-0.20104, -0.101657, 0.31364, -0.234517, -0.0163677, 0.270631, -0.291058,
    0.116837, 0.181012, -0.326971, 0.209134, 0.118444, -0.303865, 0.241156, -0.0144953, -0.269088,
    0.287857, -0.110143, -0.16922, 0.282537}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_7 → {{-0.179672, -0.126709, 0.328842, -0.280026, -0.0129078, 0.249841, -0.321504,
    0.0766221, 0.171569, -0.295035, 0.186866, 0.091949, -0.27099, 0.269353, 0.0293645, -0.238668,
    0.285517, -0.11389, -0.190549, 0.31436}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}}|>,
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    -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}, {-0.153886, -0.0875347, 0.297854,
    -0.276583, 0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
    -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_6 → {{-0.17526, -0.106684, 0.304186, -0.27676, -0.0299081, 0.264665, -0.287699,
    0.0895741, 0.174449, -0.288889, 0.206239, 0.11573, -0.282169, 0.247232, 0.00318229,
    -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}, {-0.17526, -0.106684, 0.304186,
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GARCHProcess → <|Sinusoidal2_11 → {{-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852,
    0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889},
   {-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852, 0.0940832, 0.259478,
    -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865, 0.258725, 0.0998843,
    -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067, 0.0980672, 0.250394,
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    0.258148, -0.257012, -0.0945577, 0.317903}, {-0.101498, -0.25529, 0.251653, 0.0972642,
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    0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667, 0.104182, 0.258366,
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    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{-0.0971308, -0.259618, 0.249762, 0.0996953, -0.311793, 0.0980176, 0.26024,
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    0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}, {-0.0971308, -0.259618, 0.249762,
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  Sinusoidal2_15 → {{-0.0939856, -0.25429, 0.25073, 0.100441, -0.313599, 0.0944084, 0.258905,
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    Sinusoidal2_16 → {{-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132, 0.0966092, 0.262552,
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        0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}, {-0.0916775, -0.260977, 0.251061,
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    Sinusoidal2_17 → {{-0.0991608, -0.252958, 0.255513, 0.0985052, -0.309591, 0.0946333, 0.259341,
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    Sinusoidal2_18 → {{-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724, 0.0944222, 0.259447,
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        -0.259273, -0.103637, 0.311237, -0.101011, -0.258469, 0.251806, 0.101187, -0.319249, 0.100504,
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        0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
    Sinusoidal2_20 → {{-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484, 0.101942,
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        0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467},
      {-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484, 0.101942, 0.254089,
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SpikePositive_15 → TimeSeriesModel[ Family: MA Order: {0} ],
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SpikePositive_17 → TimeSeriesModel[ Family: MA Order: {0} ],
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LinearPositive_2 →
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LinearPositive_4 →
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LinearPositive_5 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 0} ],
LinearPositive_6 →
 TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 4, 0}_4} ],
LinearPositive_7 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 2}, {2, 2, 0}_4} ],
LinearPositive_8 →
 TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 0}, {1, 2, 0}_5} ],
LinearPositive_9 → TimeSeriesModel[ Family: SARIMA, Order: {{2, 1, 1}, {1, 2, 0}_4} ],
LinearPositive_10 →
 TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 2, 0}_6} ],
LinearPositive_11 → TimeSeriesModel[ Family: SARIMA, Order: {{2, 1, 2}, {0, 2, 0}_5} ],
LinearPositive_12 →
 TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 2, 0}_6} ],
LinearPositive_13 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 2}, {0, 1, 0}_10} ],
LinearPositive_14 →
 TimeSeriesModel[ Family: ARIMA, Order: {0, 1, 1} ],
LinearPositive_15 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {2, 2, 0}_4} ],
LinearPositive_16 →
 TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 2, 0}_6} ],
LinearPositive_17 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 0}, {1, 2, 1}_4} ],
LinearPositive_18 →
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LinearPositive_19 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 1} ],
LinearPositive_20 →
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LinearNegative_2 →
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LinearNegative_3 → TimeSeriesModel[ Family: SARIMA, Order: {{2, 1, 2}, {0, 2, 0}4} ],
LinearNegative_4 →
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LinearNegative_5 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 0}, {1, 2, 1}4} ],
LinearNegative_6 →
 TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 0}, {0, 2, 1}4} ],
LinearNegative_7 → TimeSeriesModel[ Family: SARIMA, Order: {{3, 1, 0}, {0, 3, 0}5} ],
LinearNegative_8 →
 TimeSeriesModel[ Family: SARIMA, Order: {{2, 1, 0}, {0, 2, 0}5} ],
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LinearNegative_11 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {1, 2, 0}4} ],
LinearNegative_12 →
 TimeSeriesModel[ Family: ARIMA, Order: {0, 1, 1} ],
LinearNegative_13 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {0, 2, 0}7} ],
LinearNegative_14 →
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LinearNegative_15 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 1} ],
LinearNegative_16 →
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LinearNegative_18 →
 TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {1, 2, 0}4} ],
LinearNegative_19 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 1} ],
LinearNegative_20 →
 TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {0, 2, 0}4} ],
Sinusoidal1_1 → TimeSeriesModel[ Family: SARMA, Order: {{0, 1}, {1, 0}4} ],
Sinusoidal1_2 →
 TimeSeriesModel[ Family: AR, Order: {3} ],
Sinusoidal1_3 → TimeSeriesModel[ Family: MA, Order: {1} ],
Sinusoidal1_4 →
 TimeSeriesModel[ Family: MA, Order: {1} ],
Sinusoidal1_5 → TimeSeriesModel[ Family: SARMA, Order: {{0, 1}, {0, 1}4} ],
Sinusoidal1_6 →
 TimeSeriesModel[ Family: AR, Order: {3} ],
Sinusoidal1_7 → TimeSeriesModel[ Family: SARMA, Order: {{0, 1}, {1, 0}10} ],
Sinusoidal1_8 →
 TimeSeriesModel[ Family: MA, Order: {1} ],
Sinusoidal1_9 → TimeSeriesModel[ Family: MA, Order: {1} ],
Sinusoidal1_10 →
 TimeSeriesModel[ Family: MA, Order: {1} ],
```

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```
Sinusoidal2_11 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_12 →
 TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_13 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_14 →
 TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_15 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_16 →
 TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_17 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_18 →
 TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_19 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_20 →
 TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal3_21 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_22 →
 TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_23 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_24 →
 TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_25 → TimeSeriesModel[ Family: ARIMA Order: {0, 4, 1} ],
Sinusoidal3_26 →
 TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
```

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```
Sinusoidal3_27 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_28 →
 TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_29 → TimeSeriesModel[ Family: ARIMA Order: {0, 6, 0} ],
Sinusoidal3_30 →
 TimeSeriesModel[ Family: ARIMA Order: {4, 7, 1} ] |> |>
```

In[4]:=
```
Keys@classificationTimeSeriesModelAggregate1Models
```

Out[4]=
```
{TimeSeriesClasses, Models}
```

In[5]:=
```
classificationTimeSeriesModelAggregate1Models["TimeSeriesClasses"]
```

Out[5]=
```
<| MAProcess →
  <| SpikePositive_1 → {{0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682, -0.0371416,
      0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411, -0.00869189,
      -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732},
     {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682, -0.0371416,
      0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411, -0.00869189,
      -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829,
      0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543},
     {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562, 0.0574829, 0.017722,
      -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993,
      -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977},
     {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057, -0.0359993, -0.0955887,
      -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843, 0.0402401,
      -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033, -0.0772898, 0.0399612,
      -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539, 0.0509389, 0.0608363, -0.0848876,
      -0.0715063, 0.0612102, -0.0887476, 0.0558859}, {0.958583, 0.00400217, 0.0429904, 0.0838796,
      0.0778033, -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858,
      0.0195539, 0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663, 0.0676522, 0.0605738,
      0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931, 0.0796911, -0.0701274,
      -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}, {0.966833, -0.0172757, -0.0101601,
      0.0449156, 0.0804663, 0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823,
      -0.064931, 0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416, 0.0326082,
      -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387, 0.0872339, -0.0766939,
      0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}, {0.971085, -0.0737213, -0.0183259,
      -0.0280164, -0.0370416, 0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791,
      0.0886387, 0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442, -0.00304927,
      0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801, 0.0872978, 0.0241062,
      0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}, {0.973634, -0.0197451, 0.00381691,
      0.0632199, 0.0519442, -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781,
      0.0525801, 0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677,
      -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
      -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763},
     {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775, -0.0116677, -0.0238371,
```

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```
    -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273, -0.0192342,
    -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
 SpikePositive_9 → {{0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483,
    -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062},
   {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095, 0.0935483, -0.0385902,
    -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
    -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
 SpikePositive_10 → {{0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367,
    -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
    -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457},
   {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119, 0.0618367, -0.0143555,
    0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266, -0.0322946,
    -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
 SpikePositive_11 → {{0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068, 0.0325846, -0.0861631,
    0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531, 0.0377134, 0.0259428, 0.0165473,
    0.00876485, 0.0104191, -0.0990718, 0.101205}, {0.0696283, 0.0251021, 0.968196, 0.0511374,
    0.0825068, 0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503,
    -0.036531, 0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
 SpikePositive_12 → {{0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803, 0.0850629,
    0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
    0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826},
   {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803, 0.0850629, 0.0791585,
    -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403, 0.0350351,
    0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
 SpikePositive_13 → {{-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903, -0.0475178,
    -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952, 0.0310687, -0.0939468,
    -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}, {-0.0343175, -0.0155132, 0.955818,
    0.0636753, -0.0900903, -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626,
    0.0398952, 0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
 SpikePositive_14 → {{0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311, 0.0642856,
    -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
    -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114},
   {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311, 0.0642856, -0.00120334,
    -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562, -0.044588,
    -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
 SpikePositive_15 → {{0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922, 0.0322486,
    0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456, -0.0576246, -0.101699,
    -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}, {0.0367157, 0.00909492, 0.955211,
    -0.0373177, -0.0545922, 0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346,
    0.0584456, -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
 SpikePositive_16 → {{-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223,
    -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381, -0.0588352,
    -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908},
   {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647, -0.0912223, -0.00461306,
    -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381, -0.0588352,
    -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
 SpikePositive_17 → {{0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444, 0.09185, -0.0309321,
    0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902, 0.101663, 0.086855,
    0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}, {0.0894556, -0.0939456, 0.955206,
    -0.0721055, 0.0609444, 0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305,
    -0.0823902, 0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
 SpikePositive_18 → {{-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144, -0.0566396,
    0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424, 0.0179427,
    0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999},
   {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144, -0.0566396, 0.00932272,
    -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424, 0.0179427, 0.0577408,
    -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
 SpikePositive_19 → {{-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727, -0.0813174,
    0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
    0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065},
   {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727, -0.0813174, 0.0169025,
    0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997, 0.0704534,
    -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
 SpikePositive_20 → {{0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833, -0.0790448,
    -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909,
```

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    -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381},
   {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833, -0.0790448, -0.0883667,
    0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731, 0.0759909,
    -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}},
 SpikeNegative_1 → {{-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627,
    0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467, -0.0370811,
    0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511},
   {-0.972238, 0.0262336, 0.0376581, -0.0481536, -0.0795075, -0.0819627, 0.0839417,
    -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467, -0.0370811,
    0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
 SpikeNegative_2 → {{-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113, -0.0217826,
    -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501, -0.0295528,
    0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342},
   {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113, -0.0217826, -0.0407702,
    -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501, -0.0295528,
    0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
 SpikeNegative_3 → {{-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095, 0.102466,
    -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
    -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636},
   {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095, 0.102466, -0.0311731,
    0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319, -0.00382691,
    -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
 SpikeNegative_4 → {{-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556, -0.0455452,
    0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
    0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411},
   {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556, -0.0455452, 0.0806517,
    0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762, 0.065436,
    -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
 SpikeNegative_5 → {{-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968, 0.0456577,
    -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712},
   {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968, 0.0456577, -0.0741938,
    0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812, -0.0509291,
    -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
 SpikeNegative_6 → {{-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953, -0.058058,
    0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539},
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    0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694, 0.00809772,
    0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
 SpikeNegative_7 → {{-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109, 0.0874465,
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    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901},
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 SpikeNegative_8 → {{-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887, -0.0684695,
    0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666},
   {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887, -0.0684695, 0.0552479,
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    -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
 SpikeNegative_9 → {{-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416, 0.0325626,
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    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653},
   {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416, 0.0325626, -0.0841603,
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 SpikeNegative_10 → {{-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025, 0.0119404,
    -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664},
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    0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
 SpikeNegative_11 → {{-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755, -0.0488362,
    -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052, 0.0300314,
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    0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954},
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    -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
 SpikeNegative_12 → {{0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571, 0.0770767,
    0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734},
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 SpikeNegative_13 → {{0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036, 0.0881039,
    0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538, -0.028162,
    0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681},
   {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036, 0.0881039, 0.0257902,
    0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538, -0.028162,
    0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
 SpikeNegative_14 → {{-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594, 0.0528555,
    0.00336549, 0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977},
   {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594, 0.0528555, 0.00336549,
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    0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
 SpikeNegative_15 → {{-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309, 0.000455216,
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    0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439},
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    -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
 SpikeNegative_16 → {{-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464, 0.0166785,
    0.0680268, 0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101, 0.0309736,
    -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422},
   {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464, 0.0166785, 0.0680268,
    0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101, 0.0309736,
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 SpikeNegative_17 → {{-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312, 0.0616787,
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    0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
 SpikeNegative_18 → {{0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604, 0.0000556895,
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    0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
 SpikeNegative_19 → {{-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693, 0.0216656,
    0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588,
    -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696},
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    0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
 SpikeNegative_20 → {{-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452, 0.057722,
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   {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452, 0.057722, -0.0391361,
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 Sinusoidal1_3 → {{-0.187066, -0.0732084, 0.32812, -0.266161, 0.00567862, 0.253731, -0.305231,
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 Sinusoidal1_4 → {{-0.151568, -0.0998564, 0.265085, -0.275486, 0.0223004, 0.261223, -0.285188,
    0.110899, 0.212223, -0.322869, 0.206654, 0.11987, -0.322486, 0.240951, 0.0208141, -0.225578,
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   Sinusoidal1_8 → {{-0.187929, -0.0921767, 0.316032, -0.235549, -0.0280322, 0.285866, -0.282711,
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   Sinusoidal1_9 → {{-0.179756, -0.0938318, 0.280617, -0.224439, -0.0137817, 0.286427, -0.303775,
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SARIMAProcess → <|LinearPositive_1 → {{0.018415, 0.0377122, 0.0574444, 0.0761646, 0.0918826,
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   LinearPositive_2 → {{0.0183904, 0.0374466, 0.0550304, 0.0738563, 0.0928923, 0.110677,
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   LinearPositive_3 → {{0.0204364, 0.0388961, 0.055949, 0.0753517, 0.0937248, 0.112155,
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   LinearPositive_6 → {{0.0186014, 0.0381755, 0.0550572, 0.074646, 0.0932816, 0.113886, 0.132134,
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      0.223211, 0.241838, 0.260952, 0.279399, 0.29785, 0.318882, 0.336928, 0.35463, 0.373419}},
   LinearPositive_11 → {{0.013623, 0.0406398, 0.0607801, 0.0781742, 0.0921015, 0.112119,
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  LinearPositive_12 → {{0.0219335, 0.0431422, 0.0502095, 0.0696589, 0.0884956, 0.116468,
    0.123447, 0.151797, 0.168869, 0.179094, 0.204522, 0.228042, 0.240546, 0.269187, 0.279387,
    0.302162, 0.315899, 0.330232, 0.349931, 0.381055}, {0.0219335, 0.0431422, 0.0502095,
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  LinearPositive_13 → {{0.022617, 0.0284408, 0.0607512, 0.0795972, 0.0880775, 0.119613,
    0.134238, 0.152698, 0.169261, 0.181713, 0.197855, 0.217149, 0.241086, 0.263228, 0.284546,
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  LinearPositive_15 → {{0.0152129, 0.0390101, 0.0602871, 0.0702062, 0.091338, 0.118718,
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    0.250473, 0.25777, 0.279989, 0.293839, 0.316027, 0.338974, 0.359625, 0.369849}},
  LinearPositive_16 → {{0.0164478, 0.0360481, 0.048135, 0.0712245, 0.101186, 0.114916,
    0.129433, 0.153936, 0.164281, 0.192697, 0.203977, 0.223277, 0.236402,
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  LinearPositive_17 → {{0.0153802, 0.0408047, 0.0548321, 0.0765604, 0.0991872, 0.117741,
    0.128177, 0.147496, 0.159869, 0.189666, 0.195939, 0.215447, 0.240506, 0.262803, 0.283339,
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    0.215447, 0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
  LinearPositive_18 → {{0.0115844, 0.0455792, 0.0534286, 0.068487, 0.0918771, 0.107837,
    0.137609, 0.144956, 0.162508, 0.185864, 0.206224, 0.229689, 0.232407, 0.261637, 0.285165,
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    0.232407, 0.261637, 0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}},
  LinearPositive_20 → {{0.00952752, 0.0286979, 0.0547226, 0.0709501, 0.0958101, 0.109505,
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    0.294497, 0.314251, 0.344366, 0.352473, 0.366536}, {0.00952752, 0.0286979, 0.0547226,
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    0.231304, 0.235391, 0.267585, 0.28298, 0.294497, 0.314251, 0.344366, 0.352473, 0.366536}},
  LinearNegative_1 → {{-0.0218046, -0.0446169, -0.0612231, -0.0738948, -0.109733, -0.115191,
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  LinearNegative_5 → {{-0.0201624, -0.0405386, -0.0436406, -0.0738225, -0.0817467, -0.105404,
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  LinearNegative_6 → {{-0.0267223, -0.0446999, -0.0523138, -0.0699606, -0.0987645, -0.126896,
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  LinearNegative_7 → {{-0.00172329, -0.032268, -0.068173, -0.0857129, -0.0881686, -0.107137,
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    LinearNegative_8 → {{-0.0170306, -0.0378539, -0.0394845, -0.0767312, -0.0942537, -0.105065,
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    LinearNegative_10 → {{-0.00155633, -0.0271325, -0.0625737, -0.0744387, -0.0901925,
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    LinearNegative_11 → {{-0.0105542, -0.0364589, -0.0515525, -0.0708746, -0.0862196, -0.118392,
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    LinearNegative_20 → {{-0.024006, -0.0432239, -0.0496914, -0.0682004, -0.0867373, -0.103335,
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  ARIMAProcess → <|LinearPositive_5 → {{0.0196474, 0.0375735, 0.0561861, 0.0745382, 0.094777,
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    LinearPositive_14 → {{0.0276601, 0.0348994, 0.0578995, 0.0764811, 0.0865063, 0.115217,
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    LinearPositive_19 → {{0.0205961, 0.045526, 0.0569898, 0.0724948, 0.0867427, 0.105806,
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    LinearNegative_9 → {{-0.0287969, -0.0189698, -0.0530075, -0.0828922, -0.0936032, -0.115414,
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LinearNegative_12 → {{-0.0105234, -0.0459122, -0.0631169, -0.0780043, -0.0883748, -0.108962,
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LinearNegative_14 → {{-0.0187992, -0.0431131, -0.0473458, -0.070655, -0.0879629, -0.116006,
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LinearNegative_15 → {{-0.0162872, -0.0293132, -0.0552218, -0.0807767, -0.0935334, -0.121112,
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LinearNegative_17 → {{-0.0130003, -0.0309644, -0.0613334, -0.0794837, -0.0865967, -0.117058,
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LinearNegative_19 → {{-0.0210969, -0.0344615, -0.0471464, -0.078958, -0.100694, -0.103899,
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   -0.263307, -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137},
  {-0.0210969, -0.0344615, -0.0471464, -0.078958, -0.100694, -0.103899, -0.130428,
   -0.144859, -0.170748, -0.178648, -0.21371, -0.229276, -0.241033, -0.263307,
   -0.281329, -0.291554, -0.315673, -0.329753, -0.355337, -0.38137}},
Sinusoidal3_21 → {{0.18867, -0.0972321, -0.306583, -0.251354, -0.00388461, 0.254971, 0.296206,
   0.0966543, -0.185492, -0.313443, -0.183529, 0.10096, 0.29637, 0.252844, -0.00335276, -0.262031,
   -0.296035, -0.102293, 0.188443, 0.324183}, {0.18867, -0.0972321, -0.306583, -0.251354,
   -0.00388461, 0.254971, 0.296206, 0.0966543, -0.185492, -0.313443, -0.183529, 0.10096,
   0.29637, 0.252844, -0.00335276, -0.262031, -0.296035, -0.102293, 0.188443, 0.324183}},
Sinusoidal3_22 → {{0.181513, -0.0928691, -0.305475, -0.251164, 0.00419846, 0.258728, 0.299815,
   0.101596, -0.183948, -0.320966, -0.180033, 0.102523, 0.303756, 0.256723, -0.00539331,
   -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}, {0.181513, -0.0928691, -0.305475,
   -0.251164, 0.00419846, 0.258728, 0.299815, 0.101596, -0.183948, -0.320966, -0.180033, 0.102523,
   0.303756, 0.256723, -0.00539331, -0.253514, -0.294842, -0.0929271, 0.184499, 0.320941}},
Sinusoidal3_23 → {{0.18264, -0.0994704, -0.295137, -0.250857, 0.00157044, 0.256486, 0.297096,
   0.103377, -0.186093, -0.321512, -0.189976, 0.0988036, 0.298633, 0.258092, 0.00508974, -0.253346,
   -0.304932, -0.0954742, 0.18711, 0.317813}, {0.18264, -0.0994704, -0.295137, -0.250857,
   0.00157044, 0.256486, 0.297096, 0.103377, -0.186093, -0.321512, -0.189976, 0.0988036,
   0.298633, 0.258092, 0.00508974, -0.253346, -0.304932, -0.0954742, 0.18711, 0.317813}},
Sinusoidal3_24 → {{0.183018, -0.0977985, -0.296248, -0.251125, -0.00333361, 0.252171, 0.301387,
   0.101024, -0.190512, -0.312491, -0.18742, 0.100939, 0.304721, 0.252809, -0.00469484, -0.254372,
   -0.306416, -0.0944326, 0.190532, 0.318758}, {0.183018, -0.0977985, -0.296248, -0.251125,
   -0.00333361, 0.252171, 0.301387, 0.101024, -0.190512, -0.312491, -0.18742, 0.100939,
   0.304721, 0.252809, -0.00469484, -0.254372, -0.306416, -0.0944326, 0.190532, 0.318758}},
Sinusoidal3_25 → {{0.191347, -0.0982886, -0.29771, -0.261082, 0.00611569, 0.249936, 0.298887,
   0.101714, -0.1867, -0.321641, -0.191881, 0.0933799, 0.302028, 0.251166, -0.00172715,
   -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}, {0.191347, -0.0982886, -0.29771,
   -0.261082, 0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
   0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
Sinusoidal3_26 → {{0.185284, -0.0936261, -0.306395, -0.25385, 0.00597724, 0.255415, 0.302354,
   0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444, 0.296927, 0.253991, 0.00087675,
   -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}, {0.185284, -0.0936261, -0.306395,
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      -0.25385, 0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
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  Sinusoidal3_27 → {{0.185809, -0.10192, -0.303748, -0.261172, 0.000202029, 0.258446, 0.299423,
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      0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.187562, -0.10053, -0.297144, -0.250552, 0.00476677, 0.261432, 0.296623,
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      -0.251445, -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
      0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
  Sinusoidal3_30 → {{0.186539, -0.100579, -0.301622, -0.251977, 0.00452805, 0.258968, 0.30446,
      0.103392, -0.185935, -0.314134, -0.188321, 0.10063, 0.296225, 0.252222, -0.00565741,
      -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}, {0.186539, -0.100579, -0.301622,
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      0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
SARMAProcess → <|Sinusoidal1_1 → {{-0.20264, -0.107877, 0.278896, -0.289184, -0.0168796, 0.24783,
      -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701, -0.331998, 0.269056, 0.00609382,
      -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}, {-0.20264, -0.107877, 0.278896,
      -0.289184, -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
      -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_5 → {{-0.20104, -0.101657, 0.31364, -0.234517, -0.0163677, 0.270631, -0.291058,
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  Sinusoidal1_7 → {{-0.179672, -0.126709, 0.328842, -0.280026, -0.0129078, 0.249841, -0.321504,
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      0.285517, -0.11389, -0.190549, 0.31436}, {-0.179672, -0.126709, 0.328842, -0.280026,
      -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
      -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}}|>,
ARProcess → <|Sinusoidal1_2 → {{-0.153886, -0.0875347, 0.297854, -0.276583, 0.004457, 0.260377,
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      -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}, {-0.153886, -0.0875347, 0.297854,
      -0.276583, 0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
      -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_6 → {{-0.17526, -0.106684, 0.304186, -0.27676, -0.0299081, 0.264665, -0.287699,
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      -0.27676, -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
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GARCHProcess → <|Sinusoidal2_11 → {{-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852,
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     {-0.0952089, -0.252202, 0.25704, 0.097318, -0.313852, 0.0940832, 0.259478,
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      -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{-0.101498, -0.25529, 0.251653, 0.0972642, -0.315067, 0.0980672, 0.250394,
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      0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{-0.0918789, -0.259087, 0.253065, 0.103093, -0.320667, 0.104182, 0.258366,
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  Sinusoidal2_14 → {{-0.0971308, -0.259618, 0.249762, 0.0996953, -0.311793, 0.0980176, 0.26024,
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    0.0996953, -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
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  Sinusoidal2_16 → {{-0.0916775, -0.260977, 0.251061, 0.104141, -0.322132, 0.0966092, 0.262552,
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  Sinusoidal2_18 → {{-0.102994, -0.260616, 0.250831, 0.0989794, -0.318724, 0.0944222, 0.259447,
    -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843, 0.258552, 0.0991506, -0.312675,
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    -0.251843, 0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{-0.0979953, -0.254783, 0.260889, 0.100358, -0.321977, 0.0989163, 0.249498,
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  Sinusoidal2_20 → {{-0.0946325, -0.259177, 0.259154, 0.0992225, -0.320484, 0.101942, 0.254089,
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In[6]:=
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classificationTimeSeriesModelAggregate1Models["Models"]
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Out[6]=
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 SpikePositive_2 → TimeSeriesModel[ Family: MA Order: {0} ],
 SpikePositive_3 → TimeSeriesModel[ Family: MA Order: {0} ],
 SpikePositive_4 → TimeSeriesModel[ Family: MA Order: {0} ],
 SpikePositive_5 → TimeSeriesModel[ Family: MA Order: {0} ],
 SpikePositive_6 → TimeSeriesModel[ Family: MA Order: {0} ],
 SpikePositive_7 → TimeSeriesModel[ Family: MA Order: {0} ],
 SpikePositive_8 → TimeSeriesModel[ Family: MA Order: {0} ],
 SpikePositive_9 → TimeSeriesModel[ Family: MA Order: {0} ],
```

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SpikePositive_10 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_11 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_12 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_13 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_14 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_15 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_16 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_17 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_18 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_19 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikePositive_20 → TimeSeriesModel[ Family: MA Order: {0} ],
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SpikeNegative_4 → TimeSeriesModel[ Family: MA Order: {0} ],
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SpikeNegative_6 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_7 → TimeSeriesModel[ Family: MA Order: {0} ],
```

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```
SpikeNegative_8 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_9 → TimeSeriesModel[ Family: MA Order: {0} ],
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SpikeNegative_11 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_12 → TimeSeriesModel[ Family: MA Order: {0} ],
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SpikeNegative_14 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_15 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_16 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_17 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_18 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_19 → TimeSeriesModel[ Family: MA Order: {0} ],
SpikeNegative_20 → TimeSeriesModel[ Family: MA Order: {0} ],
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LinearPositive_2 → TimeSeriesModel[ Family: SARIMA Order: {{3, 1, 3}, {0, 2, 0}_6} ],
LinearPositive_3 → TimeSeriesModel[ Family: SARIMA Order: {{1, 1, 1}, {0, 2, 0}_5} ],
LinearPositive_4 → TimeSeriesModel[ Family: SARIMA Order: {{0, 1, 2}, {0, 2, 0}_7} ],
LinearPositive_5 → TimeSeriesModel[ Family: ARIMA Order: {1, 1, 0} ],
```

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```
LinearPositive_6 → TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 4, 0}_4} ],
LinearPositive_7 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 2}, {2, 2, 0}_4} ],
LinearPositive_8 → TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 0}, {1, 2, 0}_5} ],
LinearPositive_9 → TimeSeriesModel[ Family: SARIMA, Order: {{2, 1, 1}, {1, 2, 0}_4} ],
LinearPositive_10 → TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 2, 0}_6} ],
LinearPositive_11 → TimeSeriesModel[ Family: SARIMA, Order: {{2, 1, 2}, {0, 2, 0}_5} ],
LinearPositive_12 → TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 2, 0}_6} ],
LinearPositive_13 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 2}, {0, 1, 0}_10} ],
LinearPositive_14 → TimeSeriesModel[ Family: ARIMA, Order: {0, 1, 1} ],
LinearPositive_15 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {2, 2, 0}_4} ],
LinearPositive_16 → TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 2, 0}_6} ],
LinearPositive_17 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 0}, {1, 2, 1}_4} ],
LinearPositive_18 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 0}, {1, 2, 0}_5} ],
LinearPositive_19 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 1} ],
LinearPositive_20 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {0, 2, 0}_4} ],
LinearNegative_1 → TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 1}, {0, 2, 0}_7} ],
LinearNegative_2 → TimeSeriesModel[ Family: ARIMA, Order: {2, 1, 0} ],
LinearNegative_3 → TimeSeriesModel[ Family: SARIMA, Order: {{2, 1, 2}, {0, 2, 0}_4} ],
```

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```
LinearNegative_4 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 1} ],
LinearNegative_5 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 0}, {1, 2, 1}4} ],
LinearNegative_6 → TimeSeriesModel[ Family: SARIMA, Order: {{1, 1, 0}, {0, 2, 1}4} ],
LinearNegative_7 → TimeSeriesModel[ Family: SARIMA, Order: {{3, 1, 0}, {0, 3, 0}5} ],
LinearNegative_8 → TimeSeriesModel[ Family: SARIMA, Order: {{2, 1, 0}, {0, 2, 0}5} ],
LinearNegative_9 → TimeSeriesModel[ Family: ARIMA, Order: {0, 1, 1} ],
LinearNegative_10 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {1, 2, 0}4} ],
LinearNegative_11 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {1, 2, 0}4} ],
LinearNegative_12 → TimeSeriesModel[ Family: ARIMA, Order: {0, 1, 1} ],
LinearNegative_13 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {0, 2, 0}7} ],
LinearNegative_14 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 0} ],
LinearNegative_15 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 1} ],
LinearNegative_16 → TimeSeriesModel[ Family: ARIMA, Order: {2, 1, 1} ],
LinearNegative_17 → TimeSeriesModel[ Family: ARIMA, Order: {0, 1, 1} ],
LinearNegative_18 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {1, 2, 0}4} ],
LinearNegative_19 → TimeSeriesModel[ Family: ARIMA, Order: {1, 1, 1} ],
LinearNegative_20 → TimeSeriesModel[ Family: SARIMA, Order: {{0, 1, 1}, {0, 2, 0}4} ],
Sinusoidal1_1 → TimeSeriesModel[ Family: SARMA, Order: {{0, 1}, {1, 0}4} ],
```

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```
Sinusoidal1_2 → TimeSeriesModel[ Family: AR Order: {3} ], Sinusoidal1_3 → TimeSeriesModel[ Family: MA Order: {1} ],
Sinusoidal1_4 → TimeSeriesModel[ Family: MA Order: {1} ],
Sinusoidal1_5 → TimeSeriesModel[ Family: SARMA Order: {{0, 1}, {0, 1}4} ],
Sinusoidal1_6 → TimeSeriesModel[ Family: AR Order: {3} ],
Sinusoidal1_7 → TimeSeriesModel[ Family: SARMA Order: {{0, 1}, {1, 0}10} ],
Sinusoidal1_8 → TimeSeriesModel[ Family: MA Order: {1} ], Sinusoidal1_9 → TimeSeriesModel[ Family: MA Order: {1} ],
Sinusoidal1_10 → TimeSeriesModel[ Family: MA Order: {1} ],
Sinusoidal2_11 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_12 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_13 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_14 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_15 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_16 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_17 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_18 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_19 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal2_20 → TimeSeriesModel[ Family: GARCH Order: {0, 1} ],
Sinusoidal3_21 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
```

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```
Sinusoidal3_22 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_23 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_24 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_25 → TimeSeriesModel[ Family: ARIMA Order: {0, 4, 1} ],
Sinusoidal3_26 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_27 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_28 → TimeSeriesModel[ Family: ARIMA Order: {0, 5, 1} ],
Sinusoidal3_29 → TimeSeriesModel[ Family: ARIMA Order: {0, 6, 0} ],
Sinusoidal3_30 → TimeSeriesModel[ Family: ARIMA Order: {4, 7, 1} ] |⟩
```

SpikeCutoffs (1)

```
In[1]:= Needs["MathIOmica`"]
```

SpikeCutoffs provides a cutoff Association with number, n, of data points as keys, and values corresponding to cutoffs, in the form <|n → {Maximum Spike Cutoff_n, Maximum Spike Cutoff_n}|> used to call spike maxima and minima for a time series with this number of datapoints. The values are provided by the user depending on data approach based on simulation. We consider the example:

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
 backgroundExample = Normalize[#] & /@ RandomReal[{-.1, .1}, {10^5, 20}];
 timePointsExample = Range[20];
```

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In[3]:=
```
bootstrapQ95 = QuantileEstimator[backgroundExample, timePointsExample];
bootstrapQ95Spikes = QuantileEstimator[backgroundExample, timePointsExample, Method → "Spikes"];
```

The spike cutoff is given the above calculation for series of length 20 for maxima and minima:

In[4]:=
```
bootstrapQ95Spikes
```

Out[4]=
```
<|20 → {0.42185, -0.421758}|>
```

We can now perform the classification based on the cutoff:

In[5]:=
```
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → bootstrapQ95, SpikeCutoffs → bootstrapQ95Spikes]
```

Method → "LombScargle"

Out[5]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
      0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
      -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
      0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_3 → {{0.125418, 0.359591, 0.13869, 0.303377, 0.150537, 0.286138, 0.316463,
      0.387482, 0.47078, 0.408939}, {0.95896, 0.0348607, 0.0657694, 0.0097693, -0.0146057,
      -0.0359993, -0.0955887, -0.0573438, -0.0695415, 0.089338, 0.0614405, 0.00535763, -0.00816843,
      0.0402401, -0.0812913, -0.0771292, -0.0621431, -0.0944407, -0.0920576, -0.0932977}},
   SpikePositive_4 → {{0.311141, 0.158973, 0.187546, 0.412209, 0.163826, 0.30463, 0.0712251,
      0.168013, 0.698351, 0.179431}, {0.958583, 0.00400217, 0.0429904, 0.0838796, 0.0778033,
      -0.0772898, 0.0399612, -0.0865925, -0.0313674, 0.0653022, -0.078399, -0.0771858, 0.0195539,
      0.0509389, 0.0608363, -0.0848876, -0.0715063, 0.0612102, -0.0887476, 0.0558859}},
   SpikePositive_5 → {{0.238423, 0.0985576, 0.377368, 0.235579, 0.29993, 0.155657, 0.297585,
      0.200919, 0.656615, 0.247551}, {0.966833, -0.0172757, -0.0101601, 0.0449156, 0.0804663,
      0.0676522, 0.0605738, 0.0193896, -0.0145715, -0.0841473, -0.0457237, 0.0680823, -0.064931,
      0.0796911, -0.0701274, -0.0338009, -0.07913, 0.0127139, -0.0810818, 0.0638368}},
   SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
      0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
      0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
      -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
      0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
      0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
      0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_10 → {{0.282245, 0.113914, 0.301127, 0.236475, 0.283039, 0.473724, 0.249659,
      0.311891, 0.441642, 0.318723}, {0.961551, -0.0906575, 0.00581915, 0.00875268, 0.0455119,
      0.0618367, -0.0143555, 0.0373711, -0.0970219, 0.00655522, -0.0944221, -0.0442431, 0.101266,
      -0.0322946, -0.0461255, 0.0966287, -0.0517594, -0.00829841, 0.0959418, 0.0674457}},
   SpikePositive_11 → {{0.300133, 0.338666, 0.43961, 0.211333, 0.284602, 0.289242, 0.285686,
      0.293154, 0.358859, 0.310342}, {0.0696283, 0.0251021, 0.968196, 0.0511374, 0.0825068,
      0.0325846, -0.0861631, 0.0484829, -0.0239985, 0.102042, -0.0409872, 0.0156503, -0.036531,
      0.0377134, 0.0259428, 0.0165473, 0.00876485, 0.0104191, -0.0990718, 0.101205}},
   SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
```

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```
      0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
  SpikePositive_13 → {{0.192165, 0.417017, 0.261983, 0.253189, 0.439228, 0.23303, 0.533912,
      0.211578, 0.177971, 0.218412}, {-0.0343175, -0.0155132, 0.955818, 0.0636753, -0.0900903,
      -0.0475178, -0.0708036, 0.0962073, -0.0355342, 0.0473543, 0.067386, -0.045626, 0.0398952,
      0.0310687, -0.0939468, -0.0977753, -0.0940704, 0.0758018, 0.0877875, -0.0540773}},
  SpikePositive_14 → {{0.387971, 0.174644, 0.168364, 0.280804, 0.266606, 0.184848, 0.412651,
      0.269436, 0.529186, 0.289168}, {0.0757209, -0.0202174, 0.968597, -0.0798072, 0.0669311,
      0.0642856, -0.00120334, -0.0296223, -0.023198, -0.0497165, 0.0535985, -0.077164, -0.0464562,
      -0.044588, -0.0886026, 0.0684105, 0.0666712, -0.0212333, 0.0128158, 0.0790114}},
  SpikePositive_15 → {{0.204577, 0.367487, 0.161619, 0.304898, 0.448465, 0.3607, 0.256599,
      0.156306, 0.49338, 0.197723}, {0.0367157, 0.00909492, 0.955211, -0.0373177, -0.0545922,
      0.0322486, 0.0966403, -0.0489349, 0.0728429, 0.084504, 0.0771998, 0.0399346, 0.0584456,
      -0.0576246, -0.101699, -0.0479939, -0.0786055, 0.0824405, -0.0864275, 0.0957378}},
  SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
      0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
      -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
      -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
  SpikePositive_17 → {{0.119917, 0.0985653, 0.218556, 0.153386, 0.250224, 0.498057, 0.307556,
      0.382157, 0.438528, 0.401243}, {0.0894556, -0.0939456, 0.955206, -0.0721055, 0.0609444,
      0.09185, -0.0309321, 0.0925898, 0.0610032, 0.0181723, 0.0260614, 0.063305, -0.0823902,
      0.101663, 0.086855, 0.000889116, 0.0519813, 0.0723495, -0.0396682, 0.0309544}},
  SpikePositive_18 → {{0.265006, 0.191214, 0.305125, 0.419551, 0.406897, 0.437639, 0.230122,
      0.237816, 0.309383, 0.24852}, {-0.0361007, -0.0216285, 0.964135, 0.085142, -0.0857144,
      -0.0566396, 0.00932272, -0.0627836, 0.0853683, -0.0927231, -0.0835222, -0.0206424,
      0.0179427, 0.0577408, -0.0317543, 0.00348765, 0.0583858, 0.0970094, 0.0427967, -0.0649999}},
  SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
      0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
      -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
      0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}},
  SpikePositive_20 → {{0.271467, 0.235399, 0.382144, 0.340438, 0.291139, 0.194548, 0.402488,
      0.320275, 0.367722, 0.294209}, {0.0411315, -0.0931735, 0.964126, 0.020519, -0.0485833,
      -0.0790448, -0.0883667, 0.0638796, -0.0652838, 0.0409636, -0.0779777, -0.0895731,
      0.0759909, -0.0700673, 0.0119244, -0.0203333, 0.0694876, -0.0174003, 0.010671, 0.051381}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
      0.469391, 0.294777, 0.463012, 0.279525}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
      -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
      -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
  SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
      0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
      -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
      -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
  SpikeNegative_3 → {{0.22085, 0.148273, 0.206537, 0.227322, 0.543766, 0.327858, 0.266613,
      0.19901, 0.523498, 0.21679}, {-0.953174, 0.0687073, 0.081267, -0.0893468, -0.0891095,
      0.102466, -0.0311731, 0.0363503, -0.043063, 0.0536749, -0.0580462, -0.0930647, -0.0384319,
      -0.00382691, -0.0686129, -0.0608866, -0.0628233, -0.0858682, -0.078135, 0.0855636}},
  SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
      0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
      -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
      0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
  SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
      0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
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      -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
      0.341117, 0.381366, 0.325221}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
      -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
      0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
      0.214233, 0.523873, 0.243986}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
      0.0874465, -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
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  SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
      0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
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    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
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  SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
    0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
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    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
    0.35716, 0.304919, 0.374001}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
    0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{0.173083, 0.379193, 0.338228, 0.384591, 0.344256, 0.301779, 0.172933,
    0.337034, 0.332955, 0.316239}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
    0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{0.369536, 0.475376, 0.186202, 0.236301, 0.19825, 0.237895, 0.260777,
    0.276741, 0.472509, 0.288441}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594,
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    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
    0.315364, 0.382839, 0.290684}, {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309,
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    0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
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    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{0.197001, 0.246358, 0.358498, 0.402863, 0.27067, 0.34906, 0.104226,
    0.386107, 0.331869, 0.380125}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
    0.0616787, -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667,
    0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
    0.16152, 0.319203, 0.158339}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
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    0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
  SpikeNegative_19 → {{0.392542, 0.277194, 0.303304, 0.316005, 0.451557, 0.178107, 0.336152,
    0.30277, 0.204908, 0.308124}, {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693,
    0.0216656, 0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588,
    -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{0.373567, 0.348518, 0.182641, 0.399653, 0.340024, 0.197691, 0.337761,
    0.284486, 0.34594, 0.276612}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
    0.057722, -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007,
    -0.0175827, 0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}}|>,
f1 → <|LinearPositive_1 → {{0.984043, 0.16711, 0.0316771, 0.00181032, 0.00174073,
    0.0106378, 0.0207385, 0.0279534, 0.0184004, 0.0325683},
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  LinearPositive_2 → {{0.984661, 0.162755, 0.0313267, 0.0020944, 0.00156008, 0.011475,
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  LinearPositive_3 → {{0.983778, 0.169007, 0.0312598, 0.00266983, 0.0014985,
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  LinearPositive_4 → {{0.984544, 0.162861, 0.0316916, 0.00219377, 0.00149925, 0.011724,
    0.0216336, 0.0306627, 0.0181213, 0.0355609}, {0.0188591, 0.0384796, 0.0552706,
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  LinearPositive_5 → {{0.983951, 0.167274, 0.0329686, 0.00225602, 0.00179127, 0.0107481,
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LinearPositive_6 → {{0.982932, 0.171949, 0.0327492, 0.00164224, 0.002379, 0.0113266,
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LinearPositive_7 → {{0.98472, 0.163134, 0.0312689, 0.00212913, 0.0016404, 0.0102459,
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LinearPositive_8 → {{0.98371, 0.168572, 0.0284284, 0.00170281, 0.00185745, 0.010751,
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LinearPositive_9 → {{0.98365, 0.168058, 0.033981, 0.00241806, 0.00210287, 0.0115589,
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LinearPositive_10 → {{0.983876, 0.167373, 0.0315427, 0.00211686, 0.00191546, 0.0115056,
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LinearPositive_11 → {{0.985278, 0.159772, 0.0170525, 0.00324467, 0.00218142, 0.0151391,
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LinearPositive_12 → {{0.985678, 0.154732, 0.0287579, 0.00132291, 0.00382878, 0.0177303,
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LinearPositive_13 → {{0.980798, 0.186414, 0.0294262, 0.00278288, 0.00330631, 0.0108519,
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LinearPositive_14 → {{0.981111, 0.181783, 0.0375471, 0.00148453, 0.000312388,
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LinearPositive_15 → {{0.984521, 0.158493, 0.0449595, 0.00110501, 0.00265532, 0.0107268,
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LinearPositive_16 → {{0.979313, 0.188576, 0.0419809, 0.00521628, 0.000903989,
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LinearPositive_17 → {{0.983915, 0.163837, 0.0268448, 0.00291022, 0.00438077, 0.0123819,
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    0.215447, 0.240506, 0.262803, 0.283339, 0.30483, 0.3159, 0.337001, 0.349837, 0.380979}},
LinearPositive_18 → {{0.983959, 0.16518, 0.0329124, 0.00150854, 0.000803325, 0.0135443,
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LinearPositive_19 → {{0.987202, 0.147191, 0.027074, 0.00249316, 0.000777253,
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LinearPositive_20 → {{0.983551, 0.167679, 0.0393618, 0.00233188, 0.0011172, 0.0161293,
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LinearNegative_1 → {{0.984203, 0.159785, 0.0568416, 0.00506241, 0.000881747, 0.023661,
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    -0.23172, -0.273794, -0.262471, -0.299402, -0.322831, -0.348108, -0.361357, -0.357733}},
  LinearNegative_2 → {{0.983975, 0.157281, 0.0272884, 0.00492376, 0.00030144, 0.0209059,
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  LinearNegative_3 → {{0.981452, 0.174458, 0.0229664, 0.001764, 0.000281227, 0.0288508,
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  LinearNegative_4 → {{0.97237, 0.220138, 0.0433705, 0.00935025, 0.000670999, 0.00240098,
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  LinearNegative_5 → {{0.977089, 0.200269, 0.0364024, 0.00199978, 0.00231623, 0.00860671,
    0.0111157, 0.0372061, 0.025344, 0.04037}, {-0.0201624, -0.0405386, -0.0436406, -0.0738225,
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  LinearNegative_6 → {{0.978811, 0.190012, 0.0393558, 0.000605398, 0.0150579, 0.015651,
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  LinearNegative_7 → {{0.974629, 0.205946, 0.0323035, 0.00710776, 0.0022957, 0.0115893,
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  LinearNegative_8 → {{0.982135, 0.172786, 0.0318874, 0.00532189, 0.00125899, 0.00528407,
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    -0.238911, -0.261139, -0.29695, -0.295252, -0.309714, -0.332549, -0.365044, -0.365678}},
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  LinearNegative_12 → {{0.984685, 0.160376, 0.0299467, 0.000604418, 0.00378349, 0.00929028,
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f3 → <|Sinusoidal3_21 → {{0.003093, 0.067983, 0.992591, 0.0880879, 0.0381938, 0.0201564,
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  Sinusoidal3_26 → {{0.0035927, 0.0724177, 0.992482, 0.0865873, 0.0377177, 0.018194, 0.00903366,
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  Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
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f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
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    0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
    -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
    0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
    0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
    -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
    -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
  Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
  Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

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In[6]:=
```
Query[All, Length]@classification1
```

Out[6]=
```
⟨|SpikeMax → 20, SpikeMin → 20, f1 → 40, f3 → 10, f5 → 10, f6 → 10|⟩
```

We can also set the cutoff to other values, for example say 0.97 for maxima, and -0.96 for minima:

In[7]:=
```
classification1SpikeCutoffs = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → bootstrapQ95, SpikeCutoffs → <|20 → {0.97, -0.96}|>]
  Method → "LombScargle"
```

Out[7]=
```
⟨|SpikeMax →
  <|SpikePositive_1 → {{0.0854621, 0.256297, 0.233457, 0.333126, 0.18591, 0.2626, 0.351082, 0.426463,
      0.41637, 0.423696}, {0.970569, -0.0988615, -0.0240026, -0.0115612, -0.0977222, 0.0813682,
      -0.0371416, 0.0201554, -0.00963618, 0.0739698, -0.0117404, -0.0110224, -0.055411,
      -0.00869189, -0.0220374, -0.0981645, -0.0457957, -0.015177, -0.0708976, -0.0557732}},
   SpikePositive_2 → {{0.39753, 0.312339, 0.24636, 0.312095, 0.235808, 0.387442, 0.316765,
      0.112284, 0.503656, 0.118252}, {0.973207, 0.00872172, -0.00191539, 0.0695064, -0.00641562,
      0.0574829, 0.017722, -0.0788988, -0.0302812, 0.000120193, 0.0715816, -0.036666, -0.00648697,
      -0.0492696, -0.0508375, 0.0801151, -0.00760663, 0.0845842, 0.0616622, 0.0905543}},
   SpikePositive_6 → {{0.103935, 0.254831, 0.297255, 0.188346, 0.194566, 0.282781, 0.468831,
      0.273102, 0.555147, 0.282891}, {0.971085, -0.0737213, -0.0183259, -0.0280164, -0.0370416,
      0.0326082, -0.0159531, 0.0348121, 0.0534494, 0.0216255, 0.0804326, 0.0596791, 0.0886387,
      0.0872339, -0.0766939, 0.0301023, 0.0613835, -0.0471675, -0.00566043, 0.0700102}},
   SpikePositive_7 → {{0.0976109, 0.152855, 0.239087, 0.31988, 0.387645, 0.388764, 0.33206,
      0.331779, 0.403391, 0.350929}, {0.973634, -0.0197451, 0.00381691, 0.0632199, 0.0519442,
      -0.00304927, 0.016839, 0.0443557, -0.0384471, 0.0417391, 0.0828389, 0.0440781, 0.0525801,
      0.0872978, 0.0241062, 0.0100416, -0.0831706, -0.07202, 0.0810017, -0.0303004}},
   SpikePositive_8 → {{0.381308, 0.304162, 0.156474, 0.259269, 0.194766, 0.42643, 0.225295,
      0.338817, 0.410956, 0.340837}, {0.973714, -0.0655433, 0.00410752, 0.0489941, -0.0178775,
      -0.0116677, -0.0238371, -0.0535769, -0.0499596, 0.0754105, -0.0540901, -0.0502273,
      -0.0192342, -0.0671247, -0.0139847, 0.0441607, 0.0880889, 0.0756489, 0.0843008, 0.0055763}},
   SpikePositive_9 → {{0.265804, 0.256951, 0.30432, 0.230395, 0.247797, 0.278285, 0.478947,
      0.276317, 0.441555, 0.279417}, {0.979998, -0.049438, -0.0488434, 0.00681623, -0.062095,
      0.0935483, -0.0385902, -0.0121923, -0.0467585, -0.0497611, 0.0208798, -0.0177267, -0.0503857,
      -0.0452555, -0.0820684, 0.0238864, 0.0314146, 0.0154229, -0.0374286, -0.0235062}},
   SpikePositive_12 → {{0.257185, 0.242852, 0.280281, 0.196583, 0.397489, 0.407275, 0.233074,
      0.196311, 0.55122, 0.192616}, {0.0427773, -0.0204301, 0.972226, -0.00645026, 0.0200803,
      0.0850629, 0.0791585, -0.0803568, 0.0732716, -0.0715285, 0.0380143, -0.0641808, 0.00471403,
      0.0350351, 0.0835748, -0.0637685, 0.0295574, -0.0532574, -0.00306441, -0.00749826}},
   SpikePositive_16 → {{0.267047, 0.419577, 0.494227, 0.34463, 0.215987, 0.299169, 0.195166,
      0.173899, 0.389268, 0.183297}, {-0.0123015, 0.0180774, 0.974876, 0.0737459, -0.0312647,
      -0.0912223, -0.00461306, -0.0920869, 0.0225014, -0.0374179, 0.0631067, -0.0121381,
      -0.0588352, -0.0599035, 0.0534693, 0.023468, -0.0578208, -0.0666874, 0.0118325, 0.0383908}},
   SpikePositive_19 → {{0.264427, 0.233828, 0.301093, 0.374105, 0.246306, 0.280227, 0.167322,
      0.452758, 0.266994, 0.448693}, {-0.0584325, 0.0880122, 0.972312, -0.0409534, 0.0540727,
      -0.0813174, 0.0169025, 0.03397, -0.00559207, -0.0334793, -0.0310815, 0.0706323, -0.0924997,
      0.0704534, -0.0265679, 0.0101062, 0.0719713, 0.00823026, 0.0613141, 0.0188065}}|>,
 SpikeMin → <|SpikeNegative_1 → {{0.177008, 0.147567, 0.158661, 0.342802, 0.391663, 0.225985,
      0.469391, 0.294777, 0.463012, 0.279525}, {-0.972238, 0.0262336, 0.0376581, -0.0481536,
      -0.0795075, -0.0819627, 0.0839417, -0.0119792, -0.0857077, 0.0528728, -0.0532664, 0.0409467,
      -0.0370811, 0.0327396, -0.0300333, -0.0152624, -0.0554391, 0.0311268, -0.0239962, 0.08511}},
   SpikeNegative_2 → {{0.199996, 0.282162, 0.408018, 0.183037, 0.245086, 0.194463, 0.163781,
      0.273687, 0.625629, 0.298968}, {-0.969717, -0.0281117, -0.0848724, 0.0813594, -0.068113,
      -0.0217826, -0.0407702, -0.084133, 0.0802461, -0.00904831, -0.0324293, -0.0520501,
      -0.0295528, 0.0389368, 0.0814642, 0.01828, 0.080829, -0.0461636, -0.00536829, -0.053342}},
   SpikeNegative_4 → {{0.343628, 0.244378, 0.24545, 0.165624, 0.333452, 0.325818, 0.371486,
      0.345512, 0.382845, 0.336487}, {-0.978499, -0.0375369, -0.0308657, -0.0197828, 0.087556,
      -0.0455452, 0.0806517, 0.0250558, -0.0209028, 0.0431483, 0.0919507, -0.0395659, -0.0303762,
      0.065436, -0.0030997, -0.0450637, -0.0215948, 0.0513989, 0.0151152, 0.00353411}},
   SpikeNegative_5 → {{0.210559, 0.158318, 0.35418, 0.314872, 0.38682, 0.218758, 0.262791,
      0.22287, 0.57235, 0.249425}, {-0.975409, -0.0426067, 0.018748, 0.0233455, -0.0851968,
      0.0456577, -0.0741938, 0.0264271, 0.0456206, 0.088312, -0.0633969, -0.0109457, 0.0411812,
```

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```
    -0.0509291, -0.00236205, 0.0497791, 0.0587988, 0.00117985, -0.0369538, 0.0685712}},
  SpikeNegative_6 → {{0.247173, 0.223138, 0.266171, 0.38547, 0.183128, 0.374061, 0.358684,
    0.341117, 0.381366, 0.325221}, {-0.980123, 0.0414029, 0.0844458, -0.0197615, 0.0300953,
    -0.058058, 0.0371483, 0.0651484, 0.0408842, -0.0299411, 0.03411, 0.0584521, 0.00178694,
    0.00809772, 0.0467893, 0.0530045, -0.0402163, 0.0704483, -0.0004514, -0.0377539}},
  SpikeNegative_7 → {{0.198113, 0.215208, 0.150935, 0.40997, 0.340877, 0.388275, 0.277051,
    0.214233, 0.523873, 0.243986}, {-0.972269, 0.00651176, 0.0927783, -0.0613428, -0.0810109,
    0.0874465, -0.0578879, -0.00819073, -0.0383373, -0.0320487, -0.0135205, 0.0745984, 0.0537136,
    -0.0870922, -0.00729996, -0.0225152, -0.0304264, -0.0351082, -0.00219264, 0.0566901}},
  SpikeNegative_8 → {{0.382276, 0.1371, 0.285013, 0.376504, 0.255597, 0.175343, 0.372224,
    0.343217, 0.367671, 0.352812}, {-0.971714, -0.0689738, -0.0116232, 0.0693961, 0.0405887,
    -0.0684695, 0.0552479, 0.0457732, 0.0555352, 0.0837797, 0.0580096, 0.0416389, 0.06932,
    -0.0311677, -0.0666678, -0.0111359, 0.00668498, 0.0430054, -0.0159963, 0.0829666}},
  SpikeNegative_9 → {{0.210675, 0.126038, 0.258468, 0.32602, 0.156111, 0.361702, 0.13218,
    0.31825, 0.610785, 0.345867}, {-0.964652, -0.0492164, -0.044027, 0.0970846, -0.0799416,
    0.0325626, -0.0841603, 0.0168915, 0.0698974, -0.0870238, -0.01715, 0.0126659, -0.0888441,
    -0.0901265, -0.0600632, -0.0839437, 0.00247871, -0.00450166, -0.0244654, 0.0251653}},
  SpikeNegative_10 → {{0.167365, 0.198233, 0.241593, 0.20746, 0.310533, 0.394156, 0.267315,
    0.251277, 0.592782, 0.305791}, {-0.972673, -0.00291876, -0.0540171, -0.0812638, -0.0617025,
    0.0119404, -0.0700182, -0.0156325, -0.0802783, -0.0231158, 0.0565453, -0.0704018, -0.0213425,
    -0.020989, 0.0829298, -0.0344473, 0.0917352, -0.0374081, -0.00270892, 0.0369664}},
  SpikeNegative_11 → {{0.379975, 0.229368, 0.315438, 0.223374, 0.344202, 0.53369, 0.311411,
    0.147776, 0.326936, 0.15688}, {-0.03227, 0.0360081, -0.974536, -0.0562723, 0.0838755,
    -0.0488362, -0.00265125, -0.0251548, -0.0391332, -0.00182196, 0.0410817, 0.050052,
    0.0300314, 0.0700943, -0.0249284, 0.0702143, 0.0797224, -0.0976145, -0.0118769, -0.039954}},
  SpikeNegative_12 → {{0.118624, 0.355945, 0.450306, 0.289323, 0.198763, 0.358884, 0.209831,
    0.35716, 0.304919, 0.374001}, {0.0228997, -0.0356184, -0.973634, 0.0493933, 0.0107571,
    0.0770767, 0.070194, -0.0097991, -0.0308696, 0.0352361, 0.0717955, -0.0786636, 0.029504,
    -0.0981713, -0.00791646, 0.00308272, 0.0687897, 0.0648618, 0.060538, 0.00167734}},
  SpikeNegative_13 → {{0.173083, 0.379193, 0.338228, 0.384591, 0.344256, 0.301779, 0.172933,
    0.337034, 0.332955, 0.316239}, {0.089408, -0.00831708, -0.964283, -0.0122152, -0.0196036,
    0.0881039, 0.0257902, 0.061572, -0.0890889, -0.0422681, 0.0222449, -0.0365538,
    -0.028162, 0.0473609, 0.087596, 0.090452, -0.0514811, 0.0871678, -0.0077697, 0.092681}},
  SpikeNegative_14 → {{0.369536, 0.475376, 0.186202, 0.236301, 0.19825, 0.237895, 0.260777,
    0.276741, 0.472509, 0.288441}, {-0.0381839, 0.0217806, -0.963264, 0.03797, -0.0196594,
    0.0528555, 0.00336549, 0.0661326, 0.0745322, 0.0881123, 0.09305, -0.00683978, -0.0718374,
    0.0379646, 0.0825702, 0.0964842, 0.0853888, 0.0167248, -0.0516422, -0.0786977}},
  SpikeNegative_15 → {{0.256767, 0.282131, 0.284047, 0.36522, 0.465087, 0.261131, 0.159345,
    0.315364, 0.382839, 0.290684}, {-0.00121514, -0.0078406, -0.978821, -0.0221297, -0.026309,
    0.000455216, -0.0829657, 0.0349969, 0.0713349, -0.0385142, -0.0365053, -0.00194281,
    0.0312967, 0.0228599, -0.0781757, 0.065398, -0.0982247, 0.054356, 0.0124281, -0.000440439}},
  SpikeNegative_16 → {{0.133102, 0.330529, 0.297052, 0.270643, 0.224495, 0.384054, 0.299127,
    0.404761, 0.291284, 0.418924}, {-0.00639921, 0.0369683, -0.976295, 0.0340422, 0.0583464,
    0.0166785, 0.0680268, 0.0212457, -0.0297585, -0.00701137, 0.0550893, -0.0727101,
    0.0309736, -0.0185729, 0.0728985, 0.0169522, 0.0805641, 0.0812958, 0.020356, 0.0764422}},
  SpikeNegative_17 → {{0.197001, 0.246358, 0.358498, 0.402863, 0.27067, 0.34906, 0.104226,
    0.386107, 0.331869, 0.380125}, {-0.0701592, 0.0172702, -0.96504, -0.0844552, 0.0472312,
    0.0616787, -0.0836702, -0.0161946, -0.0731278, -0.0394508, 0.0730417, -0.0836667,
    0.022695, 0.0217809, 0.00120993, 0.0625404, -0.0147936, 0.0900253, 0.0565877, 0.0859092}},
  SpikeNegative_18 → {{0.535433, 0.39154, 0.316918, 0.315364, 0.340957, 0.13881, 0.267482,
    0.16152, 0.319203, 0.158339}, {0.0700203, -0.100452, -0.962503, -0.0223616, -0.0879604,
    0.0000556895, -0.0637593, 0.0386416, 0.0568781, -0.0191067, -0.0633971, 0.099183,
    0.0322089, 0.0782449, 0.028811, 0.0378332, 0.0155804, 0.0561767, -0.069519, -0.0984389}},
  SpikeNegative_19 → {{0.392542, 0.277194, 0.303304, 0.316005, 0.451557, 0.178107, 0.336152,
    0.30277, 0.204908, 0.308124}, {-0.023199, -0.0672119, -0.973318, -0.0764401, 0.0302693,
    0.0216656, 0.0247419, -0.00361092, 0.0780475, -0.0859501, 0.0123732, 0.0421864, 0.0105588,
    -0.0116062, 0.0548142, -0.054358, -0.0879987, -0.0771945, -0.0664945, -0.00039696}},
  SpikeNegative_20 → {{0.373567, 0.348518, 0.182641, 0.399653, 0.340024, 0.197691, 0.337761,
    0.284486, 0.34594, 0.276612}, {-0.0543654, -0.0510581, -0.970055, -0.0636564, -0.000413452,
    0.057722, -0.0391361, -0.0430423, 0.0864043, 0.0923014, 0.0161379, 0.0137631, -0.0810007,
    -0.0175827, 0.0290342, 0.068689, -0.0389952, -0.048178, -0.0799885, 0.0596368}}|>,
f1 → <|LinearPositive_1 → {{0.984043, 0.16711, 0.0316771, 0.00181032, 0.00174073,
    0.0106378, 0.0207385, 0.0279534, 0.0184004, 0.0325683},
   {0.018415, 0.0377122, 0.0574444, 0.0761646, 0.0918826, 0.112863, 0.131264, 0.149525, 0.166786, 0.18659,
    0.205188, 0.223266, 0.241367, 0.260842, 0.280501, 0.297673, 0.318898, 0.33502, 0.356116, 0.373425}},
  LinearPositive_2 → {{0.984661, 0.162755, 0.0313267, 0.0020944, 0.00156008, 0.011475,
```

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    0.0216011, 0.0294057, 0.0183423, 0.0341563}, {0.0183904, 0.0374466, 0.0550304, 0.0738563,
    0.0928923, 0.110677, 0.130133, 0.148914, 0.167272, 0.186766, 0.206807, 0.224025,
    0.242161, 0.261728, 0.280689, 0.29779, 0.316418, 0.335012, 0.355339, 0.375155}},
LinearPositive_3 → {{0.983778, 0.169007, 0.0312598, 0.00266983, 0.0014985,
    0.0109335, 0.01999, 0.0270723, 0.0199171, 0.0313541},
   {0.0204364, 0.0388961, 0.055949, 0.0753517, 0.0937248, 0.112155, 0.1288, 0.150982, 0.166685, 0.187482,
    0.204397, 0.22244, 0.241027, 0.262217, 0.279814, 0.299561, 0.317724, 0.336804, 0.355812, 0.372089}},
LinearPositive_4 → {{0.984544, 0.162861, 0.0316916, 0.00219377, 0.00149925, 0.011724,
    0.0216336, 0.0306627, 0.0181213, 0.0355609}, {0.0188591, 0.0384796, 0.0552706,
    0.0761382, 0.0941127, 0.11255, 0.131257, 0.150426, 0.166514, 0.185049, 0.206061,
    0.222052, 0.24344, 0.261751, 0.281444, 0.297053, 0.316607, 0.33422, 0.355535, 0.374989}},
LinearPositive_5 → {{0.983951, 0.167274, 0.0329686, 0.00225602, 0.00179127, 0.0107481,
    0.0213666, 0.0279768, 0.0186733, 0.0325615}, {0.0196474, 0.0375735, 0.0561861, 0.0745382,
    0.094777, 0.113054, 0.132423, 0.150372, 0.169563, 0.188068, 0.205612, 0.225889,
    0.242492, 0.261976, 0.279334, 0.298018, 0.316353, 0.33459, 0.353954, 0.372244}},
LinearPositive_6 → {{0.982932, 0.171949, 0.0327492, 0.00164224, 0.002379, 0.0113266,
    0.0211801, 0.0312088, 0.0185636, 0.0360772}, {0.0186014, 0.0381755, 0.0550572, 0.074646,
    0.0932816, 0.113886, 0.132134, 0.149767, 0.168659, 0.185415, 0.205262, 0.222624,
    0.242621, 0.260049, 0.279298, 0.299912, 0.319378, 0.335084, 0.353279, 0.374138}},
LinearPositive_7 → {{0.98472, 0.163134, 0.0312689, 0.00212913, 0.0016404, 0.0102459,
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    0.241912, 0.261689, 0.28065, 0.298137, 0.317804, 0.335795, 0.355386, 0.373923}},
LinearPositive_8 → {{0.98371, 0.168572, 0.0284284, 0.00170281, 0.00185745, 0.010751,
    0.0232594, 0.0297876, 0.0184231, 0.0346602}, {0.0170019, 0.0382694, 0.0569482, 0.0754625,
    0.0914347, 0.110031, 0.132014, 0.15073, 0.169121, 0.188274, 0.205265, 0.223358,
    0.242529, 0.260421, 0.281319, 0.297942, 0.317815, 0.334838, 0.35394, 0.373734}},
LinearPositive_9 → {{0.98365, 0.168058, 0.033981, 0.00241806, 0.00210287, 0.0115589,
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    0.241691, 0.261072, 0.279055, 0.298507, 0.318632, 0.337602, 0.353993, 0.372608}},
LinearPositive_10 → {{0.983876, 0.167373, 0.0315427, 0.00211686, 0.00191546, 0.0115056,
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LinearPositive_11 → {{0.985278, 0.159772, 0.0170525, 0.00324467, 0.00218142, 0.0151391,
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LinearPositive_12 → {{0.985678, 0.154732, 0.0287579, 0.00132291, 0.00382878, 0.0177303,
    0.0169859, 0.0320887, 0.0266783, 0.0361838}, {0.0219335, 0.0431422, 0.0502095, 0.0696589,
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LinearPositive_13 → {{0.980798, 0.186414, 0.0294262, 0.00278288, 0.00330631, 0.0108519,
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    0.241086, 0.263228, 0.284546, 0.295642, 0.328037, 0.336195, 0.347819, 0.374015}},
LinearPositive_14 → {{0.981111, 0.181783, 0.0375471, 0.00148453, 0.000312388,
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LinearPositive_15 → {{0.984521, 0.158493, 0.0449595, 0.00110501, 0.00265532, 0.0107268,
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LinearPositive_16 → {{0.979313, 0.188576, 0.0419809, 0.00521628, 0.000903989,
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LinearPositive_17 → {{0.983915, 0.163837, 0.0268448, 0.00291022, 0.00438077, 0.0123819,
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LinearPositive_18 → {{0.983959, 0.16518, 0.0329124, 0.00150854, 0.000803325, 0.0135443,
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    0.232407, 0.261637, 0.285165, 0.296501, 0.314692, 0.336003, 0.361032, 0.374183}},
LinearPositive_19 → {{0.987202, 0.147191, 0.027074, 0.00249316, 0.000777253,
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LinearPositive_20 → {{0.983551, 0.167679, 0.0393618, 0.00233188, 0.0011172, 0.0161293,
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LinearNegative_1 → {{0.984203, 0.159785, 0.0568416, 0.00506241, 0.000881747, 0.023661,
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LinearNegative_2 → {{0.983975, 0.157281, 0.0272884, 0.00492376, 0.00030144, 0.0209059,
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LinearNegative_3 → {{0.981452, 0.174458, 0.0229664, 0.001764, 0.000281227, 0.0288508,
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    -0.237918, -0.269893, -0.279738, -0.29544, -0.307248, -0.326599, -0.352095, -0.384769}},
LinearNegative_4 → {{0.97237, 0.220138, 0.0433705, 0.00935025, 0.000670999, 0.00240098,
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LinearNegative_5 → {{0.977089, 0.200269, 0.0364024, 0.00199978, 0.00231623, 0.00860671,
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LinearNegative_6 → {{0.978811, 0.190012, 0.0393558, 0.000605398, 0.0150579, 0.015651,
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LinearNegative_7 → {{0.974629, 0.205946, 0.0323035, 0.00710776, 0.0022957, 0.0115893,
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LinearNegative_8 → {{0.982135, 0.172786, 0.0318874, 0.00532189, 0.00125899, 0.00528407,
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LinearNegative_9 → {{0.992163, 0.105938, 0.0360944, 0.0064934, 0.00217633, 0.00513993,
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LinearNegative_10 → {{0.983194, 0.163431, 0.0236169, 0.0117059, 0.0187534, 0.0128491,
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LinearNegative_11 → {{0.984307, 0.167887, 0.0231976, 0.00646005, 0.000895278, 0.0137762,
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LinearNegative_13 → {{0.98451, 0.16303, 0.0227595, 0.00132012, 0.00348595, 0.0126863,
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LinearNegative_14 → {{0.978579, 0.195677, 0.0313545, 0.00267509, 0.00341515, 0.0129726,
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LinearNegative_15 → {{0.987412, 0.147538, 0.0327634, 0.00558518, 0.00366499, 0.00919838,
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  Sinusoidal3_25 → {{0.00289275, 0.0722254, 0.992563, 0.084147, 0.0394916, 0.0185649, 0.00643529,
      0.00207684, 0.0237235, 0.000529693}, {0.191347, -0.0982886, -0.29771, -0.261082,
      0.00611569, 0.249936, 0.298887, 0.101714, -0.1867, -0.321641, -0.191881, 0.0933799,
      0.302028, 0.251166, -0.00172715, -0.251226, -0.306921, -0.0943973, 0.181288, 0.31225}},
  Sinusoidal3_26 → {{0.0035927, 0.0724177, 0.992482, 0.0865873, 0.0377177, 0.018194, 0.00903366,
      0.0026512, 0.0195294, 0.000949465}, {0.185284, -0.0936261, -0.306395, -0.25385,
      0.00597724, 0.255415, 0.302354, 0.0997498, -0.183287, -0.320935, -0.184548, 0.0968444,
      0.296927, 0.253991, 0.00087675, -0.260548, -0.301546, -0.0937923, 0.184534, 0.312366}},
  Sinusoidal3_27 → {{0.00356621, 0.0718347, 0.992461, 0.086876, 0.0384877, 0.0168536, 0.00812238,
      0.00246869, 0.0215147, 0.000777483}, {0.185809, -0.10192, -0.303748, -0.261172,
      0.000202029, 0.258446, 0.299423, 0.0942508, -0.180597, -0.31495, -0.188893, 0.100227,
      0.302676, 0.24961, -0.00174468, -0.2545, -0.305591, -0.0963953, 0.182678, 0.311459}},
  Sinusoidal3_28 → {{0.00292996, 0.0773356, 0.991977, 0.0880559, 0.0367946, 0.0176203,
      0.00875596, 0.00325153, 0.0220462, 0.00118298}, {0.187562, -0.10053, -0.297144, -0.250552,
      0.00476677, 0.261432, 0.296623, 0.0971592, -0.185463, -0.316454, -0.187195, 0.0970453,
      0.301104, 0.258413, 0.0054441, -0.255345, -0.298729, -0.095819, 0.181572, 0.323712}},
  Sinusoidal3_29 → {{0.00262506, 0.0711674, 0.99281, 0.0827274, 0.0380578, 0.0177335, 0.00874852,
      0.00232562, 0.0238141, 0.000654616}, {0.189755, -0.100643, -0.295957, -0.251445,
      -0.0055221, 0.252696, 0.29864, 0.0975281, -0.189706, -0.322914, -0.187404, 0.103546,
      0.296096, 0.252167, -0.00435421, -0.251264, -0.306742, -0.0937399, 0.183149, 0.321756}},
  Sinusoidal3_30 → {{0.00427552, 0.071229, 0.992804, 0.0839262, 0.0365748, 0.018534, 0.00877504,
      0.00265531, 0.0209496, 0.000906179}, {0.186539, -0.100579, -0.301622, -0.251977,
      0.00452805, 0.258968, 0.30446, 0.103392, -0.185935, -0.314134, -0.188321, 0.10063,
      0.296225, 0.252222, -0.00565741, -0.259043, -0.300195, -0.0938519, 0.185551, 0.315355}}|>,
f5 → <|Sinusoidal2_11 → {{0.00230838, 0.0110527, 0.0326835, 0.0943866, 0.932969, 0.343193,
      0.0294955, 0.00418398, 0.028168, 0.00135728}, {-0.0952089, -0.252202, 0.25704, 0.097318,
      -0.313852, 0.0940832, 0.259478, -0.256641, -0.0914793, 0.315873, -0.0980687, -0.254865,
```

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```
    0.258725, 0.0998843, -0.312706, 0.0991076, 0.259575, -0.260583, -0.100952, 0.313889}},
  Sinusoidal2_12 → {{0.00189149, 0.012459, 0.0277361, 0.093648, 0.932514, 0.345316, 0.0276648,
    0.00565905, 0.0259503, 0.00224675}, {-0.101498, -0.25529, 0.251653, 0.0972642,
    -0.315067, 0.0980672, 0.250394, -0.261387, -0.102951, 0.313615, -0.102471, -0.251668,
    0.262301, 0.0921143, -0.316076, 0.0956623, 0.258148, -0.257012, -0.0945577, 0.317903}},
  Sinusoidal2_13 → {{0.00302482, 0.0103915, 0.0266546, 0.0922877, 0.927851, 0.357576, 0.032395,
    0.00472652, 0.0285215, 0.00169662}, {-0.0918789, -0.259087, 0.253065, 0.103093,
    -0.320667, 0.104182, 0.258366, -0.258047, -0.0982902, 0.313851, -0.103806, -0.251963,
    0.254435, 0.0947659, -0.322671, 0.099541, 0.251173, -0.252867, -0.092285, 0.311489}},
  Sinusoidal2_14 → {{0.00385172, 0.0107462, 0.0282079, 0.0891523, 0.928785, 0.356134, 0.0282387,
    0.00496481, 0.0287502, 0.00177599}, {-0.0971308, -0.259618, 0.249762, 0.0996953,
    -0.311793, 0.0980176, 0.26024, -0.249275, -0.100238, 0.318125, -0.100697, -0.257698,
    0.256122, 0.0982282, -0.320808, 0.0913426, 0.250138, -0.256866, -0.09199, 0.320685}},
  Sinusoidal2_15 → {{0.0026932, 0.0101216, 0.030085, 0.0918119, 0.927927, 0.357447, 0.0296735,
    0.00386219, 0.0290145, 0.00118185}, {-0.0939856, -0.25429, 0.25073, 0.100441,
    -0.313599, 0.0944084, 0.258905, -0.254543, -0.0972341, 0.315559, -0.0966098, -0.259627,
    0.255722, 0.0993267, -0.321786, 0.101782, 0.255048, -0.256369, -0.0960787, 0.315476}},
  Sinusoidal2_16 → {{0.003148, 0.00996957, 0.0300388, 0.0945344, 0.925585, 0.362719, 0.0316366,
    0.00582096, 0.0271664, 0.00231721}, {-0.0916775, -0.260977, 0.251061, 0.104141,
    -0.322132, 0.0966092, 0.262552, -0.25371, -0.0971277, 0.311801, -0.0924506, -0.261968,
    0.256443, 0.0917731, -0.314379, 0.0949053, 0.252655, -0.259249, -0.0962303, 0.31152}},
  Sinusoidal2_17 → {{0.00335507, 0.0110107, 0.0295784, 0.0923821, 0.934142, 0.341126, 0.0250062,
    0.00436252, 0.0286975, 0.00143738}, {-0.0991608, -0.252958, 0.255513, 0.0985052,
    -0.309591, 0.0946333, 0.259341, -0.255535, -0.0978051, 0.319359, -0.092735, -0.25912,
    0.259191, 0.0930131, -0.318952, 0.0920208, 0.256431, -0.252563, -0.102318, 0.317}},
  Sinusoidal2_18 → {{0.00202415, 0.0108971, 0.0308656, 0.0972822, 0.932475, 0.343945, 0.0277868,
    0.00399143, 0.0293851, 0.00124852}, {-0.102994, -0.260616, 0.250831, 0.0989794,
    -0.318724, 0.0944222, 0.259447, -0.255191, -0.0963472, 0.315993, -0.0910167, -0.251843,
    0.258552, 0.0991506, -0.312675, 0.10202, 0.254956, -0.252332, -0.102226, 0.317809}},
  Sinusoidal2_19 → {{0.00214984, 0.012162, 0.0315289, 0.093449, 0.933102, 0.343103, 0.0301723,
    0.00452946, 0.0280819, 0.00157968}, {-0.0979953, -0.254783, 0.260889, 0.100358,
    -0.321977, 0.0989163, 0.249498, -0.259273, -0.103637, 0.311237, -0.101011, -0.258469,
    0.251806, 0.101187, -0.319249, 0.100504, 0.251478, -0.255713, -0.0973637, 0.309885}},
  Sinusoidal2_20 → {{0.00309449, 0.00954196, 0.0289593, 0.0943463, 0.934502, 0.339107, 0.03217,
    0.00512062, 0.028429, 0.00188335}, {-0.0946325, -0.259177, 0.259154, 0.0992225,
    -0.320484, 0.101942, 0.254089, -0.254747, -0.0919231, 0.311874, -0.101528, -0.253824,
    0.252815, 0.0941545, -0.321907, 0.0941883, 0.258829, -0.253272, -0.0958086, 0.313467}}|>,
f6 → <|Sinusoidal1_1 → {{0.000130266, 0.0027885, 0.0179706, 0.0302482, 0.0840588, 0.990408,
    0.101662, 0.00530508, 0.02029, 0.00230239}, {-0.20264, -0.107877, 0.278896, -0.289184,
    -0.0168796, 0.24783, -0.330128, 0.0902745, 0.166638, -0.294918, 0.198752, 0.0908701,
    -0.331998, 0.269056, 0.00609382, -0.233219, 0.293224, -0.0806647, -0.163467, 0.297146}},
  Sinusoidal1_2 → {{0.000389779, 0.00299077, 0.0165636, 0.0257913, 0.101427, 0.98935, 0.0961514,
    0.00470133, 0.0261198, 0.00136317}, {-0.153886, -0.0875347, 0.297854, -0.276583,
    0.004457, 0.260377, -0.301933, 0.0953972, 0.197403, -0.299928, 0.215389, 0.0667307,
    -0.288819, 0.270239, 0.0126278, -0.251425, 0.317945, -0.0686757, -0.20361, 0.297505}},
  Sinusoidal1_3 → {{0.00340674, 0.00508842, 0.0178489, 0.0465591, 0.103046, 0.9903, 0.0757873,
    0.00950723, 0.0175918, 0.00455002}, {-0.187066, -0.0732084, 0.32812, -0.266161,
    0.00567862, 0.253731, -0.305231, 0.119463, 0.171259, -0.307063, 0.163206, 0.095439,
    -0.297199, 0.229651, -0.00688215, -0.263593, 0.325312, -0.0871722, -0.204097, 0.290263}},
  Sinusoidal1_4 → {{0.000733858, 0.000547266, 0.0102127, 0.0347934, 0.0643735, 0.990885,
    0.109754, 0.00394754, 0.0250031, 0.00112486}, {-0.151568, -0.0998564, 0.265085, -0.275486,
    0.0223004, 0.261223, -0.285188, 0.110899, 0.212223, -0.322869, 0.206654, 0.11987,
    -0.322486, 0.240951, 0.0208141, -0.225578, 0.322449, -0.0776279, -0.163026, 0.319719}},
  Sinusoidal1_5 → {{0.00646995, 0.0102704, 0.0136175, 0.0496609, 0.0781544, 0.988056,
    0.120877, 0.0081269, 0.0120366, 0.00409263}, {-0.20104, -0.101657, 0.31364, -0.234517,
    -0.0163677, 0.270631, -0.291058, 0.116837, 0.181012, -0.326971, 0.209134, 0.118444,
    -0.303865, 0.241156, -0.0144953, -0.269088, 0.287857, -0.110143, -0.16922, 0.282537}},
  Sinusoidal1_6 → {{0.000204058, 0.00548599, 0.0124195, 0.05148, 0.110751, 0.986179, 0.108302,
    0.00951716, 0.0226369, 0.00423213}, {-0.17526, -0.106684, 0.304186, -0.27676,
    -0.0299081, 0.264665, -0.287699, 0.0895741, 0.174449, -0.288889, 0.206239, 0.11573,
    -0.282169, 0.247232, 0.00318229, -0.241778, 0.326338, -0.0967336, -0.164922, 0.339059}},
  Sinusoidal1_7 → {{0.000429816, 0.0140511, 0.0266745, 0.036387, 0.106883, 0.987754, 0.0981615,
    0.00880076, 0.0309666, 0.00365231}, {-0.179672, -0.126709, 0.328842, -0.280026,
    -0.0129078, 0.249841, -0.321504, 0.0766221, 0.171569, -0.295035, 0.186866, 0.091949,
    -0.27099, 0.269353, 0.0293645, -0.238668, 0.285517, -0.11389, -0.190549, 0.31436}},
  Sinusoidal1_8 → {{0.00532892, 0.00608397, 0.016565, 0.051537, 0.108388, 0.984265, 0.127165,
```

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```
    0.0100832, 0.013261, 0.00545014}, {-0.187929, -0.0921767, 0.316032, -0.235549,
    -0.0280322, 0.285866, -0.282711, 0.113113, 0.192157, -0.332705, 0.191007, 0.0780394,
    -0.280218, 0.240298, -0.0186326, -0.253401, 0.314819, -0.106789, -0.174596, 0.305921}},
Sinusoidal1_9 → {{0.00224293, 0.0105492, 0.0276483, 0.0400171, 0.0902121, 0.987045, 0.121453,
    0.00677996, 0.017692, 0.00334242}, {-0.179756, -0.0938318, 0.280617, -0.224439,
    -0.0137817, 0.286427, -0.303775, 0.0717486, 0.192497, -0.303567, 0.212864, 0.0940813,
    -0.323289, 0.257909, 0.0296669, -0.234036, 0.290736, -0.116105, -0.214844, 0.309654}},
Sinusoidal1_10 → {{0.00288804, 0.00864521, 0.0234769, 0.0444373, 0.0856105, 0.991157,
    0.0859493, 0.00292657, 0.0165354, 0.000810259}, {-0.203834, -0.0722574, 0.294696, -0.254799,
    0.00423677, 0.247448, -0.272648, 0.121391, 0.20297, -0.328442, 0.171305, 0.113167,
    -0.291561, 0.268582, 0.0225742, -0.256505, 0.297837, -0.104109, -0.200599, 0.310941}}|>|>
```

The choice of cutoff affects the classification:

```
In[8]:= Query[All, Length]@classification1SpikeCutoffs
Out[8]= <|SpikeMax → 9, SpikeMin → 19, f1 → 40, f3 → 10, f5 → 10, f6 → 10|>
```

See Also

Autocorrelation ▪ **CreateTimeSeries** ▪ **LombScargle** ▪ **MatrixClusters** ▪ **SeriesApplier** ▪ **SeriesCompare** ▪ **SeriesInternalCompare** ▪ **TimeExtractor** ▪ **TimeSeriesClusters** ▪ **TimeSeriesModelFit**

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TimeSeriesClusters

`TimeSeriesClusters[data]`
performs clustering of time series data using two tiers of hierarchical clustering to identify groups and subgroups in the data.

Details

- TimeSeriesClusters[data] takes as input series data, where each data is comprised of two lists and performs clustering of the data to identify groups and subgroups based on similarities between the input series. The form of the input data is either an association of classes and members, where each member must have a list of two components, typically two vectors used in classification: $\{\{\text{classification vector}_1\}, \{\text{classification vector}_2\}\}$.

- In the most common case of using as input data that came from performing a TimeSeriesClassification, the $\{\text{classification vector}_2\}$ will correspond to input original data for the corresponding time series. In this case the input will have the form:

- $$\begin{aligned}
&\text{data} = \\
&\ \langle|\ \text{Class}_1 \to \langle|\text{Member}_{11} \to \{\{\text{classification vector}_{11}\}, \{\text{input data vector}_{11}\}\}, \\
&\qquad \text{Member}_{12} \to \{\{\text{classification vector}_{12}\}, \{\text{input data vector}_{12}\}\}, \ldots, \\
&\qquad \text{Member}_{1\,m_1} \to \{\{\text{classification vector}_{1\,m_1}\}, \{\text{input data vector}_{1\,m_1}\}\}|\rangle, \\
&\ \ \text{Class}_2 \to \langle|\text{Member}_{21} \text{->} \{\{\text{classification vector}_{21}\}, \{\text{input data vector}_{21}\}\}, \\
&\qquad \text{Member}_{22} \text{->} \{\{\text{classification vector}_{22}\}, \{\text{input data vector}_{22}\}\}, \ldots, \\
&\qquad \text{Member}_{2\,m_2} \to \{\{\text{classification vector}_{2\,m_2}\}, \{\text{input data vector}_{2\,m_2}\}\}|\rangle, \ \ldots, \\
&\ \ \text{Class}_M \to \langle|\text{Member}_{M1} \text{->} \{\{\text{classification vector}_{M1}\}, \{\text{input data vector}_{M1}\}\}, \\
&\qquad \text{Member}_{M2} \text{->} \{\{\text{classification vector}_{M2}\}, \{\text{input data vector}_{M2}\}\}, \ldots, \\
&\qquad \text{Member}_{Mm_M} \to \{\{\text{classification vector}_{Mm_M}\}, \{\text{input data vector}_{Mm_M}\}\}|\rangle|\rangle
\end{aligned}$$

- We note that in the cases where only one class of data is being considered, the input can also be provided as a list of associations, or a single association, or a list of associations, or a single list of lists.

- A two-tier hierarchical clustering of the data is performed, using $\{\{\text{classification vector}_1\}, \{\text{classification vector}_2\}\}$ for each series to cluster the data pairwise. Similarities at each tier are computed using in succession from each time series first $\{\text{classification vector}_1\}$, and subsequently $\{\text{classification vector}_2\}$ (corresponding to the $\{\text{input data vector}\}$ if the input is from TimeSeriesClassification).

- The number of groups and subgroups for each tier of clustering is automatically determined by using internally the "Silhouette" (default) or "Gap" as "SignificanceTest" methods (see also Partitioning Data into Clusters).

- The result is grouping of the data based on similarity, denoted as G#S#, where G denotes the group based on the first clustering, and S denotes the corresponding subgroup for that group. For example G2S3 denotes the 3rd subgroup of group 2.

- The output is always an association of associations, providing a summary of the two tier clustering results for each class provided in the input. The output has the form:

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```
output =
 <| Class1 → <|"Cluster" → cluster object1,
    "InitialSplitCluster" → {InitialSplitCluster11, InitialSplitCluster12 ...},
    "IntermediateClusters" → {IntermediateCluster11, IntermediateCluster12 ...},
    "SubsplitClusters" → {{SubsplitClusters11} {SubsplitClusters12}},
    "Data" → {{input data vector11} → Member11, ...,},
    "GroupAssociations" → <|"G1S1" → {member list G1S1},
      "G1S2" → {member list for G1S2},
      ...,
      "G2S1" → { ...}|>|>,
  Class2 → <|"Cluster" → cluster object2,
    "InitialSplitCluster" → {InitialSplitCluster21, InitialSplitCluster22 ...},
    "IntermediateClusters" → {IntermediateCluster21, IntermediateCluster22 ...},
    "SubsplitClusters" → {{SubsplitClusters21} {SubsplitClusters22}},
    "Data" → {{input data vector21} → Member21, ...,},
    "GroupAssociations" → <|"G1S1" → {member list G1S1},
      "G1S2" → {member list for G1S2},
      ...,
      "G2S1" → { ...}|>|>,
  ...,
  ClassM → <|"Cluster" → cluster objectM,
    "InitialSplitCluster" → {InitialSplitClusterM1, InitialSplitClusterM2 ...},
    "IntermediateClusters" → {IntermediateClusterM1, IntermediateClusterM2 ...},
    "SubsplitClusters" → {{subsplitClustersM1} {subsplitClustersM2}},
    "Data" → {{input data vectorM1} → MemberM1, ...,},
    "GroupAssociations" → <|"G1S1" → {member list G1S1},
      "G1S2" → {member list for G1S2},
      ...,
      "G2S1" → { ...}|>|>
 |>
```

- The keys of the output correspond to the following properties related to the two tier clustering results:

"Cluster"	Cluster generated using the input {classification $vector_1$} for similarity calculations.
"InitialSplitCluster"	Clusters resulting from splitting the initial cluster (reported by key "Cluster") into groups using the SignificanceCriterion to determine the number of clusters.
"IntermediateClusters"	Aglomerative clustering result of hierarchical clustering of each of the initial split clusters (reported by "InitialSplitCluster")
"SubsplitClusters"	Custers generated from splitting the clusters following the second tier clustering (reported by "IntermediateClusters") into subgroups using the SignificanceCriterion to determine the number of clusters.
"Data"	Data reported in the order of clustering results as rules of {classification $vector_2$} → label for each time series, sorted in order of the clustering results.

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"GroupAssociations"	Association denoting membership of each initial data label to groups and subgroups generated by the two tier clustering.

- The following options can be given:

ClusterLabeling	""	Additional label to append to each cluster being computed to prepend to the inbuilt G#S# labeling.
DendrogramPlotOptions	{}	Options passed to the DendrogramPlot function used internally to generate the dendrograms.
DistanceFunction	EuclideanDistance	Distance function to be used in calculating the similarities between different time series in the first tier of clustering.
LinkageMeasure	"Average"	Which linkage measure to use in computing fusion coefficients.
PrintDendrograms	False	Option to print dendrograms for the clustering computed.
ReturnDendrograms	False	Option to return the dendrograms as output.
SignificanceCriterion	"Silhouette"	Method used in determining the number of groups and subgroups at each tier of clustering.
SingleAssociationLabel	"1"	Label to use in case a list is provided to name the class of data produced.
SubclusteringDistanceFunction	EuclideanDistance	Distance function to be used in calculating the similarities between different time series in the second tier of clustering.

- For a given set of series, Mathematica provides various measures of distance similarity, DistanceAndSimilarityMeasures. Three of the most common measures are the the EuclideanDistance, CorrelationDistance, and the CosineDistance.

- EuclideanDistance (default for both clustering tiers in TimeSeriesClusters), uses the Euclidean distance between two arbitrary vectors U and V as $d_{\text{euc}}(U, V) = (\sum_i (U_i - V_i)^2)^{1/2}$, i.e. the Pythagorean distance between two vectors.

- CorrelationDistance measures the correlation distance between two arbitrary vectors U and V, as $d_{\text{corr}}(U, V) = 1 - \frac{(U - \langle U \rangle) \cdot (V - \langle V \rangle)}{\| U - \langle U \rangle \| \| V - \langle V \rangle \|}$ where * here denotes a dot product, <> denotes an average, and || || denotes a norm.

- The CosineDistance between two arbitrary vectors U and V is $d_{\cos}(U, V) = 1 - \frac{U \cdot V}{\| U \| \| V \|}$. It is equal to the correlation distance in the case that the averages of U and V are zero.

- For two clusters A and B, the average linkage fusion coefficient between the two clusters is defined to be $L(A,B) = \frac{1}{|A|} \frac{1}{|B|} \sum_{a_i \in A} \sum_{b_j \in B} d(a_i, b_j)$, and thus a larger fusion coefficient means the two clusters are more well-separated. So, when deciding how to optimally cluster a given set of variables into two subsets, one chooses the partition such that the average linkage fusion coefficient is maximized, and this is the optimal partitioning of this group of data into two separate clusters.

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- We also note a subtlety when performing clustering of data series that are based on absolute values of intensity, (e.g. from a power spectrum/periodogram). In such cases, the sense (sign/phase) of the original time series cannot be detected directly from the intensity values. Therefore, such data vectors cannot distinguish correlated data from anti-correlated data, for example that have the same time patterns. However, this can be taken care of by the second tier of clustering, which can potentially distinguish the sense of each series, particularly when using the original data as the $\{\texttt{classification vector}_2\}$ for each time series, and recommended EuclideanDistance for the sub-clustering (2nd tier) distance function.

- If using data output from TimeSeriesClassification where `Method → "TimeSeriesModelAggregate"`, then the function TimeSeriesSingleClusters should be used instead.

Examples (10)

Basic Examples (1)

First we need to load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

We create and classify the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.174197, 0.222483, 0.0828994, 0.239707, 0.254458, 0.248102, 0.177032, 0.351951,
      0.676023, 0.342499}, {0.97283, -0.0387132, 0.055721, 0.0132284, 0.0614186, -0.0777038,
      -0.0696757, -0.0293021, 0.0658526, 0.0791389, -0.021624, 0.0277745, 0.0541714,
      -0.00146743, 0.0588579, 0.000484094, 0.0542206, -0.074295, -0.0673881, 0.0453871}},
   SpikePositive_2 → {{0.108751, 0.0763838, 0.324977, 0.325669, 0.232918, 0.316074, 0.402004,
      0.280378, 0.526747, 0.314378}, {0.964483, -0.0169253, -0.0736427, 0.00645466, 0.0553771,
      0.103344, 0.0845537, -0.0534816, 0.0230555, 0.0244047, -0.0381847, 0.0983257, 0.00985552,
      0.103047, -0.0293736, 0.0346889, 0.0111729, -0.0953944, -0.0524849, 0.0570082}},
   SpikePositive_3 → {{0.277678, 0.387923, 0.205551, 0.19227, 0.158883, 0.254952, 0.20513,
      0.38277, 0.506082, 0.39779}, {0.97431, 0.0679348, 0.0871604, -0.00619511, 0.0373728,
      -0.0712141, -0.00609634, 0.0279141, -0.034471, 0.0744139, 0.00484242, 0.0184791, -0.0419258,
      0.0391348, -0.0773116, -0.0466285, 0.0709036, -0.0443387, 0.00962021, 0.0746188}},
   SpikePositive_4 → {{0.171249, 0.305682, 0.102348, 0.301153, 0.322873, 0.37488, 0.14987,
      0.317049, 0.569155, 0.290455}, {0.96433, 0.0918383, 0.0100238, 0.0482904, 0.076612,
      -0.0837564, -0.0233932, -0.00627954, 0.0279062, 0.0884688, 0.0908656, -0.0183345, 0.0908194,
      -0.0533065, 0.0816058, -0.0211097, 0.0552682, -0.0409222, -0.0203142, -0.0720743}},
```

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```
    SpikePositive_5 → {{0.142265, 0.216687, 0.291253, 0.42587, 0.31589, 0.261074, 0.329562,
       0.194855, 0.549312, 0.224377}, {0.982985, 0.0710984, -0.0482713, -0.0210652, 0.0343857,
       0.0314819, 0.036717, 0.0265302, 0.06007, 0.0249678, 0.0359909, 0.0071373, -0.0219947,
       0.090104, 0.0104813, 0.042377, -0.0471167, -0.0364902, -0.036008, 0.0274225}},
    SpikePositive_6 → {{0.144176, 0.165796, 0.265426, 0.3423, 0.179665, 0.159033, 0.320311,
       0.443218, 0.443465, 0.459164}, {0.959799, -0.101644, -0.0606777, -0.0631077, 0.0629834,
       0.0951693, -0.000293284, 0.0609238, -0.0288076, 0.0424747, -0.0263224, 0.0165039,
       -0.0964077, 0.105162, -0.0346764, -0.0393062, 0.083036, -0.0479605, 0.013395, 0.0893319}},
    SpikePositive_7 → {{0.269113, 0.192784, 0.320359, 0.627927, 0.27691, 0.125219, 0.198423,
       0.251279, 0.372026, 0.245387}, {0.972724, 0.0701913, -0.0695013, -0.0310904, 0.0444243,
       0.0796341, -0.0718864, -0.0236797, -0.0582082, 0.00707326, 0.0140497, -0.0334657, -0.0482015,
       0.0515321, 0.0705977, -0.0850799, -0.0667406, 0.048337, -0.0170658, 0.00106499}},
    SpikePositive_8 → {{0.233805, 0.270768, 0.225984, 0.257741, 0.28128, 0.35299, 0.249745,
       0.228786, 0.632824, 0.188728}, {0.97356, -0.040843, 0.0131409, 0.0884637, -0.0272013,
       -0.0474065, -0.0146978, -0.0480148, 0.0510134, -0.0150452, -0.0173491, -0.043164, 0.0672762,
       -0.0596514, 0.0377668, -0.0856008, -0.0298529, -0.0659683, -0.0453302, 0.088748}},
    SpikePositive_9 → {{0.110242, 0.157247, 0.229114, 0.213633, 0.227826, 0.217674, 0.193331,
       0.518044, 0.418157, 0.533947}, {0.975036, -0.0388919, 0.0521334, -0.0196278, 0.00194313,
       0.020888, 0.0720114, 0.0477332, -0.0613068, 0.073044, -0.0386716, 0.06721, -0.0763606,
       0.0151239, 0.0343056, -0.0864028, -0.00532846, -0.034586, -0.0147507, -0.0743855}},
    SpikePositive_10 → {{0.211113, 0.169909, 0.262405, 0.234576, 0.181243, 0.309446, 0.361017,
       0.205507, 0.685537, 0.177617}, {0.970269, -0.0322597, -0.0281979, -0.031376, -0.0655363,
       0.00813211, 0.0908113, -0.0832106, 0.025015, -0.0765968, 0.0378847, -0.0675155, 0.0321072,
       -0.0394683, 0.0671992, -0.021811, 0.0779899, -0.0914636, -0.0400586, 0.0103425}},
    SpikePositive_11 → {{0.370939, 0.184173, 0.366317, 0.224462, 0.264505, 0.330255, 0.411138,
       0.234548, 0.418371, 0.256514}, {0.0471266, 0.0673758, 0.964274, -0.00404236, 0.0720873,
       -0.0739788, 0.025735, 0.0526378, -0.0277241, -0.00732209, -0.0878028, -0.0836972, -0.0219667,
       -0.0520706, 0.0552389, -0.0312271, -0.0839864, 0.099519, -0.084892, -0.0487261}},
    SpikePositive_12 → {{0.333301, 0.239583, 0.431798, 0.335775, 0.195087, 0.280176, 0.360225,
       0.287175, 0.327807, 0.309951}, {0.0419257, -0.0545536, 0.966481, 0.0879187, -0.0441213,
       0.0267958, -0.0261954, 0.0592112, 0.0837965, -0.073521, -0.09057, -0.00672117, -0.00397084,
       0.0771113, -0.0688641, 0.0612941, -0.0139555, -0.0433866, 0.0562748, 0.0788225}},
    SpikePositive_13 → {{0.268775, 0.389457, 0.376696, 0.465566, 0.326149, 0.266876, 0.289755,
       0.155373, 0.31917, 0.172822}, {0.0101071, -0.0146239, 0.9777, 0.0935715, -0.0453447,
       -0.0110062, -0.0816039, 0.000365585, 0.024743, -0.0505891, 0.0138359, -0.00166466,
       0.00433109, 0.00704064, -0.0932488, 0.00814372, 0.036912, -0.027597, -0.0911807, 0.0596705}},
    SpikePositive_14 → {{0.265735, 0.346968, 0.295638, 0.444734, 0.191543, 0.355826, 0.227946,
       0.279108, 0.384484, 0.287782}, {-0.0522107, 0.0349213, 0.968137, -0.0799842, 0.047351,
       -0.0772822, -0.0568847, 0.0309335, 0.0507682, -0.0612697, -0.0765045, 0.0731327, 0.0117092,
       -0.0670623, -0.0766037, -0.0426758, 0.0122976, -0.027796, -0.0224364, 0.0931515}},
    SpikePositive_15 → {{0.286619, 0.3612, 0.249065, 0.300653, 0.255112, 0.124064, 0.357152,
       0.259258, 0.524374, 0.291108}, {0.0656926, 0.00614861, 0.959289, 0.0427671, 0.10067,
       -0.0657101, 0.0920392, -0.0490468, -0.0516995, 0.0582136, 0.0668126, -0.0431852, 0.0398872,
       -0.082955, -0.0876706, 0.0501437, -0.0866949, -0.0487603, -0.085344, -0.00345957}},
    SpikePositive_16 → {{0.0661555, 0.288845, 0.353124, 0.193937, 0.158139, 0.298623, 0.359976,
       0.372526, 0.467269, 0.386007}, {0.0727386, -0.0915534, 0.964029, -0.00870412, 0.0892189,
       -0.0283309, -0.0483322, 0.0176061, 0.0855619, 0.0544392, 0.0284692, 0.0521011, 0.0557799,
       0.0415927, 0.0340909, 0.0356042, -0.0543247, -0.0938607, -0.0787296, -0.0803162}},
    SpikePositive_17 → {{0.0831822, 0.343539, 0.441825, 0.223609, 0.425898, 0.38419, 0.477719,
       0.110077, 0.216837, 0.116231}, {-0.0840441, 0.0147189, 0.962498, 0.0604104, -0.0691647,
       0.0129371, -0.0228974, -0.0564719, 0.00541753, 0.0375024, 0.0881098, -0.0697517, 0.0860361,
       0.0318939, 0.089988, 0.0662331, -0.0985622, 0.00673175, 0.0155535, -0.0950476}},
    SpikePositive_18 → {{0.298028, 0.348304, 0.257821, 0.237428, 0.165698, 0.47727, 0.294932,
       0.275802, 0.419721, 0.269372}, {0.0518772, 0.0631826, 0.957434, -0.0726839, -0.0602182,
       -0.0740156, -0.0668018, -0.0706452, 0.000707298, -0.0921525, 0.0410152, 0.00995582,
       -0.0902115, -0.0955735, 0.0613123, -0.0535225, -0.0492724, 0.0115877, 0.0947696, -0.0841532}},
    SpikePositive_19 → {{0.212325, 0.276401, 0.292942, 0.192097, 0.309751, 0.437214, 0.282055,
       0.206749, 0.537987, 0.238687}, {0.082399, -0.0233214, 0.971905, -0.0522713, -0.0255951,
       0.019056, 0.0375396, -0.00987763, 0.00111419, -0.0612339, -0.0265535, 0.00612701, 0.0352205,
       0.0751191, 0.0802036, -0.0414755, -0.0830778, 0.0817304, -0.0370315, 0.0912559}},
    SpikePositive_20 → {{0.2098, 0.368854, 0.205882, 0.255021, 0.386228, 0.324407, 0.383924,
       0.193548, 0.483643, 0.198311}, {0.0792453, -0.0803456, 0.96782, -0.0386202, -0.0838908,
       0.0195002, -0.0125519, -0.0497516, -0.0842305, 0.0698628, 0.0465179, -0.0296323, 0.0419965,
       -0.0813624, 0.00922913, -0.0399197, -0.0568886, 0.0232157, -0.0319518, 0.0957638}}|>,
  SpikeMin → <|SpikeNegative_1 → {{0.22886, 0.209777, 0.203664, 0.263067, 0.154584, 0.301907,
       0.650649, 0.295245, 0.263602, 0.312874}, {-0.96325, -0.0686971, 0.0238526, -0.0560797,
```

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```
    0.0283688, -0.0714351, 0.00708076, 0.0367718, -0.0319639, 0.0256996, -0.0260659, 0.0516957,
    0.0546751, -0.0645426, 0.102893, 0.0167217, -0.101947, 0.095522, -0.0592421, 0.101605}},
  SpikeNegative_2 → {{0.157986, 0.0957101, 0.0833221, 0.37338, 0.426844, 0.358551, 0.213421,
    0.291431, 0.539667, 0.295041}, {-0.96436, 0.0317675, 0.0226355, -0.0706413, -0.0778315,
    0.0538323, 0.0844271, 0.0565189, -0.0661133, -0.0215318, 0.0814691, -0.00198118,
    -0.0469417, 0.0111147, -0.0910847, -0.0172907, 0.0592489, 0.082816, 0.0753491, 0.075991}},
  SpikeNegative_3 → {{0.324033, 0.253209, 0.365985, 0.337321, 0.327287, 0.319096, 0.340238,
    0.181753, 0.445053, 0.16538}, {-0.969083, -0.0299995, 0.0318652, -0.0774942, -0.0752303,
    -0.0845354, -0.0136504, 0.0245764, -0.0424409, 0.0617039, -0.0264156, 0.0516787,
    -0.048963, 0.0842407, 0.0756619, 0.0813517, 0.0274273, 0.0160103, -0.0822386, -0.0278675}},
  SpikeNegative_4 → {{0.18636, 0.304295, 0.31539, 0.483042, 0.153721, 0.374877, 0.236316,
    0.222572, 0.473257, 0.215305}, {-0.967537, 0.004474, 0.0869078, 0.04201, 0.0737576,
    -0.014903, -0.0477562, 0.00904532, -0.0908789, -0.0976678, 0.0368689, 0.066166, -0.0664155,
    -0.076783, -0.0949671, -0.00812532, -0.0249225, -0.0493766, -0.00836891, -0.0212938}},
  SpikeNegative_5 → {{0.0940305, 0.141021, 0.345758, 0.354263, 0.340763, 0.328329, 0.39429,
    0.260028, 0.459035, 0.261743}, {-0.973708, 0.0371776, 0.0861219, -0.0410561, -0.0039739,
    -0.0791863, 0.00893982, 0.0666451, 0.0396439, 0.012428, -0.0761545, -0.085143, -0.0456059,
    -0.0181448, -0.0048565, 0.0303542, 0.0584274, 0.0555674, 0.0628512, 0.044929}},
  SpikeNegative_6 → {{0.154915, 0.525116, 0.118969, 0.229778, 0.275573, 0.378472, 0.294946,
    0.168848, 0.512351, 0.190039}, {-0.96037, 0.0763183, 0.0829475, 0.00120554, 0.0882963,
    0.0927442, 0.0718016, 0.03158, -0.0373819, -0.0951905, -0.0898633, -0.00519375, 0.0307794,
    0.0625527, 0.0834457, -0.0733943, -0.00160957, -0.0714821, 0.0333189, 0.0209386}},
  SpikeNegative_7 → {{0.21995, 0.231635, 0.320858, 0.117688, 0.184228, 0.154146, 0.220892,
    0.375259, 0.605032, 0.40962}, {-0.977392, 0.0241445, -0.0343695, 0.0795507, 0.0172591,
    0.0570728, -0.0358055, -0.0469283, 0.023706, 0.0283048, 0.0543989, -0.0637894, 0.0234018,
    -0.0643923, 0.0374271, 0.0192802, -0.08256, -0.0605339, 0.0545289, 0.0355053}},
  SpikeNegative_8 → {{0.231654, 0.239167, 0.159979, 0.338465, 0.363404, 0.494257, 0.297164,
    0.298757, 0.306228, 0.318267}, {-0.96908, -0.0734138, 0.0143924, -0.0843529, 0.0647735,
    0.0312448, -0.0396305, -0.0258689, -0.0191025, -0.0821505, 0.0450642, 0.0398691, 0.0769912,
    -0.0120521, -0.088212, -0.0877402, 0.0447053, 0.0598747, -0.0195973, 0.0500554}},
  SpikeNegative_9 → {{0.305657, 0.305584, 0.282929, 0.39701, 0.464683, 0.25046, 0.41757,
    0.127466, 0.301753, 0.123283}, {-0.963652, -0.0637224, 0.0873957, -0.0605197, -0.0103375,
    -0.0336451, 0.0599783, -0.0298254, -0.0390614, 0.0922197, -0.0526079, 0.0857253,
    0.0661317, 0.0305371, 0.0573747, 0.0249666, 0.0962933, 0.0372283, -0.0901981, -0.0461058}},
  SpikeNegative_10 → {{0.306086, 0.212692, 0.266243, 0.361558, 0.387391, 0.279733, 0.284,
    0.218918, 0.486391, 0.256874}, {-0.974002, -0.0571374, 0.0391712, -0.0294228, -0.0800212,
    -0.0312323, -0.0248353, 0.0647683, -0.0480614, 0.0278797, 0.0892922, -0.031029, 0.0891268,
    0.0379227, 0.0606926, 0.0103639, 0.0850544, 0.00293672, -0.00203848, 0.0319621}},
  SpikeNegative_11 → {{0.333989, 0.271846, 0.300606, 0.171011, 0.262037, 0.427028, 0.508994,
    0.21836, 0.300429, 0.216591}, {-0.0187549, -0.0898277, -0.968927, 0.0104847, -0.0500292,
    -0.0368473, -0.00307596, -0.0885077, -0.015467, 0.0139027, 0.0186356, 0.045518, -0.0635376,
    0.00760694, -0.0623412, 0.069759, 0.0901373, -0.0880911, -0.0805062, 0.0536634}},
  SpikeNegative_12 → {{0.3005, 0.291062, 0.22742, 0.274657, 0.227006, 0.330872, 0.279916,
    0.374803, 0.40071, 0.396762}, {-0.0574451, 0.0168575, -0.968502, 0.00803548, -0.0709812,
    -0.0718516, 0.0746233, 0.0932977, 0.000249893, 0.0750274, 0.0407549, -0.0518824, 0.0580837,
    -0.0389375, 0.0548341, -0.0873062, -0.0650327, 0.0503463, 0.0365655, -0.0166916}},
  SpikeNegative_13 → {{0.297233, 0.321982, 0.230556, 0.222525, 0.438876, 0.370658, 0.440431,
    0.206396, 0.307553, 0.210095}, {0.069365, 0.0132473, -0.972201, -0.0633653, -0.102077,
    -0.0342126, -0.0494306, -0.0152837, 0.0458958, -0.0770176, -0.0246615, 0.0218576,
    -0.0489048, 0.0387558, -0.0454579, 0.0565847, 0.0525596, -0.10089, -0.0142677, 0.0111677}},
  SpikeNegative_14 → {{0.186307, 0.477852, 0.188738, 0.159485, 0.254568, 0.448408, 0.313142,
    0.281129, 0.403915, 0.264151}, {-0.0187251, -0.0919697, -0.96341, 0.0639618, -0.0733979,
    0.0208208, 0.0989907, 0.093802, 0.00125644, -0.0111341, -0.0799719, -0.0528286, -0.0418918,
    0.0270891, -0.0682311, 0.0792423, -0.0327227, -0.0409555, -0.0614677, 0.0725293}},
  SpikeNegative_15 → {{0.148393, 0.183822, 0.248604, 0.262099, 0.552042, 0.401287, 0.383,
    0.193468, 0.343912, 0.213339}, {-0.016671, -0.0284087, -0.974791, 0.0392289, 0.0573372,
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    -0.0390236, 0.0550118, -0.0183449, -0.000754719, -0.0419712, 0.065442, 0.0696531}},
  SpikeNegative_16 → {{0.176616, 0.520519, 0.183703, 0.375309, 0.298576, 0.353965, 0.27419,
    0.289003, 0.255232, 0.291509}, {0.0744193, -0.0353346, -0.970787, -0.0460693, -0.0133332,
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    -0.024943, 0.0481646, 0.0417251, 0.0228202, -0.0527538, -0.0397655, 0.0825021}},
  SpikeNegative_17 → {{0.120804, 0.439736, 0.230506, 0.192539, 0.231941, 0.266749, 0.256682,
    0.378206, 0.45204, 0.404495}, {-0.0790693, -0.0262901, -0.976638, 0.0415916, -0.0394312,
    0.0460245, -0.0047098, 0.0621946, 0.0120913, -0.0108207, -0.0709668, -0.0840572,
    0.0128283, -0.0859732, 0.00205691, 0.00751334, 0.0925499, 0.0270674, 0.0233521, 0.010782}},
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    SpikeNegative_18 → {{0.217188, 0.182764, 0.553284, 0.336429, 0.384562, 0.312531, 0.217697,
       0.178605, 0.368004, 0.199591}, {0.0657324, 0.074034, -0.967529, -0.0280721, 0.0645145,
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       -0.0240915, -0.00876646, -0.0584372, 0.0442301, 0.0882509, 0.0603172, -0.088479}},
    SpikeNegative_19 → {{0.290898, 0.349317, 0.411197, 0.502711, 0.210027, 0.384914, 0.158748,
       0.18323, 0.298324, 0.17752}, {0.0758233, -0.0735989, -0.961665, 0.00775562, 0.0758076,
       0.0888718, -0.0151953, -0.0105481, -0.0811796, 0.100363, 0.00592442, -0.022846,
       0.0545179, 0.0964283, 0.040605, 0.0989251, 0.0391439, 0.0838162, -0.00321667, 0.022232}},
    SpikeNegative_20 → {{0.289399, 0.168914, 0.178426, 0.48767, 0.326873, 0.270179, 0.511264,
       0.199918, 0.29825, 0.218873}, {0.0274711, -0.0646503, -0.973611, 0.0673836, -0.0273109,
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  f1 → <|LinearPositive_1 → {{0.984448, 0.16376, 0.0319117, 0.00177604, 0.00183218, 0.0109016,
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       0.243998, 0.259847, 0.280103, 0.299076, 0.318333, 0.334809, 0.353249, 0.37517}},
    LinearPositive_2 → {{0.982931, 0.173178, 0.0312212, 0.00226309, 0.00149734,
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       0.205516, 0.222653, 0.240711, 0.261552, 0.280634, 0.29786, 0.318635, 0.336406, 0.35532, 0.372719}},
    LinearPositive_3 → {{0.984119, 0.165514, 0.0327501, 0.0019974, 0.00181623,
       0.0118867, 0.0215181, 0.0297519, 0.0186917, 0.0345929},
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    LinearPositive_4 → {{0.983919, 0.167315, 0.0321394, 0.00202359, 0.00156857, 0.0107132,
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       0.243388, 0.260066, 0.281462, 0.298943, 0.316714, 0.335842, 0.353704, 0.373289}},
    LinearPositive_5 → {{0.984679, 0.162614, 0.0324677, 0.00244099, 0.0012482, 0.0102521,
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    LinearPositive_6 → {{0.983784, 0.168498, 0.0316791, 0.00238338, 0.00153327, 0.0102273,
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    LinearPositive_7 → {{0.983753, 0.167862, 0.0337261, 0.00207529, 0.00196266,
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    LinearPositive_8 → {{0.983464, 0.16943, 0.0336457, 0.00230069, 0.00195618,
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    LinearPositive_12 → {{0.983687, 0.166631, 0.0445253, 0.00127665, 0.00176685,
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LinearPositive_16 → {{0.981504, 0.18339, 0.0237401, 0.00247794, 0.00082838, 0.00577573,
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LinearPositive_17 → {{0.984472, 0.159711, 0.0477262, 0.00250262, 0.0014111,
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LinearPositive_19 → {{0.984649, 0.162548, 0.0293253, 0.00153615, 0.00403794, 0.0112793,
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LinearPositive_20 → {{0.986381, 0.154766, 0.0220035, 0.00463131, 0.0031809, 0.0101382,
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LinearNegative_1 → {{0.987139, 0.142956, 0.0569238, 0.0079298, 9.55071×10^-6, 0.0109799,
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LinearNegative_2 → {{0.96962, 0.219418, 0.0486819, 0.00111677, 0.00688809, 0.01931, 0.0262151,
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LinearNegative_3 → {{0.967884, 0.23171, 0.0469701, 0.00663008, 0.00479686, 0.0269489,
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LinearNegative_4 → {{0.986991, 0.148483, 0.0313687, 0.00362716, 0.00562016, 0.0130289,
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LinearNegative_5 → {{0.989859, 0.132839, 0.0250516, 0.00869797, 0.00673716, 0.00920269,
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LinearNegative_6 → {{0.983213, 0.165728, 0.0531206, 0.00200397, 0.0000125415, 0.0048337,
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LinearNegative_7 → {{0.984853, 0.155355, 0.0324022, 0.00587701, 0.00415764, 0.0162937,
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LinearNegative_8 → {{0.974164, 0.211553, 0.0368085, 0.0036533, 0.00889532, 0.0254786,
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LinearNegative_9 → {{0.988338, 0.145983, 0.0174139, 0.00023971, 0.0033213, 0.0175295,
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LinearNegative_10 → {{0.986408, 0.138051, 0.0245821, 0.00633433, 0.0039243, 0.0263066,
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  LinearNegative_15 → {{0.983605, 0.171777, 0.0348966, 0.00244296, 0.000361368, 0.014878,
    0.0197043, 0.0190264, 0.0171232, 0.0229112}, {-0.0170231, -0.0309271, -0.0627263, -0.0796228,
    -0.100154, -0.1126, -0.125679, -0.157209, -0.162764, -0.186542, -0.208024, -0.226347,
    -0.235315, -0.258272, -0.284822, -0.298344, -0.325242, -0.337329, -0.352753, -0.365028}},
  LinearNegative_16 → {{0.983699, 0.162496, 0.029878, 0.00369008, 0.00152678, 0.0139491,
    0.0289219, 0.0399111, 0.0163381, 0.0461625}, {-0.0169409, -0.0378766, -0.0637393, -0.0789792,
    -0.096412, -0.110829, -0.134565, -0.154913, -0.176555, -0.178773, -0.201738, -0.22632,
    -0.249968, -0.256785, -0.283061, -0.291758, -0.312766, -0.341087, -0.347204, -0.375314}},
  LinearNegative_17 → {{0.979615, 0.194486, 0.02314, 0.00162769, 0.0019067, 0.0102199, 0.0241717,
    0.0204383, 0.0165027, 0.0246689}, {-0.0223082, -0.0385322, -0.0640439, -0.0743739,
    -0.08446, -0.108322, -0.129556, -0.154037, -0.174605, -0.190325, -0.196689, -0.225239,
    -0.235193, -0.254259, -0.283464, -0.293308, -0.325079, -0.335208, -0.357971, -0.374627}},
  LinearNegative_18 → {{0.98187, 0.179182, 0.0345876, 0.00492913, 0.00251999, 0.00657599,
    0.0229875, 0.026188, 0.0202926, 0.0304719}, {-0.0219264, -0.0277344, -0.0477879, -0.0745452,
    -0.0964386, -0.115016, -0.137336, -0.150157, -0.167244, -0.192682, -0.197555, -0.219566,
    -0.24682, -0.265439, -0.279353, -0.301121, -0.315384, -0.333562, -0.351403, -0.374612}},
  LinearNegative_19 → {{0.981095, 0.179869, 0.0351907, 0.00168591, 0.00277299, 0.0101218,
    0.027189, 0.0340098, 0.0172151, 0.0394461}, {-0.0146473, -0.0462727, -0.06027, -0.0750068,
    -0.101207, -0.117554, -0.137214, -0.142087, -0.1612, -0.190043, -0.208851, -0.215854,
    -0.235111, -0.252768, -0.284368, -0.307504, -0.319681, -0.338197, -0.354863, -0.368648}},
  LinearNegative_20 → {{0.982978, 0.17463, 0.0381291, 0.00230909, 0.00235726, 0.0115947,
    0.0169125, 0.0206381, 0.0190803, 0.0241372}, {-0.0268322, -0.0299946, -0.0551747, -0.0714832,
    -0.0866237, -0.118598, -0.134838, -0.154978, -0.167431, -0.192744, -0.211158, -0.229616,
    -0.240512, -0.268104, -0.281693, -0.291355, -0.320036, -0.335781, -0.346191, -0.367394}}|>,
f3 → <|Sinusoidal3_21 → {{0.00349651, 0.0732136, 0.992332, 0.0869556, 0.0383968, 0.0189946,
    0.0087378, 0.00294149, 0.020534, 0.00106506}, {0.189773, -0.0981128, -0.302541, -0.250441,
    0.00586221, 0.256994, 0.300834, 0.0982355, -0.189623, -0.318449, -0.187375, 0.0982056,
    0.297105, 0.250114, -0.00096613, -0.258229, -0.302445, -0.0960746, 0.186068, 0.314515}},
  Sinusoidal3_22 → {{0.00313462, 0.0725749, 0.992377, 0.0885642, 0.0356586, 0.0158045,
    0.00862829, 0.0033168, 0.02142, 0.0012355}, {0.185279, -0.102138, -0.298856, -0.256122,
    -0.00419689, 0.260367, 0.298248, 0.0914015, -0.185444, -0.311836, -0.188881, 0.101155,
    0.301396, 0.249848, 0.00450712, -0.260102, -0.304731, -0.0939658, 0.182365, 0.319042}},
  Sinusoidal3_23 → {{0.00399696, 0.0730615, 0.992188, 0.0904002, 0.0348226, 0.0195025,
    0.00798103, 0.00343063, 0.0191378, 0.00138321}, {0.1872, -0.0938404, -0.303802, -0.257059,
    -0.00192035, 0.261528, 0.30321, 0.102729, -0.187358, -0.310853, -0.180287, 0.0925097,
    0.300332, 0.256398, 0.00281425, -0.256496, -0.303614, -0.100528, 0.181029, 0.311921}},
  Sinusoidal3_24 → {{0.00319758, 0.0727617, 0.992516, 0.0856087, 0.0377136, 0.0177523, 0.00758941,
    0.00226403, 0.0218425, 0.000673084}, {0.186015, -0.0995289, -0.297533, -0.260578,
    0.00471492, 0.256007, 0.301816, 0.100199, -0.184073, -0.314091, -0.185296, 0.102547,
    0.303136, 0.255483, 0.00106243, -0.252094, -0.301335, -0.0956296, 0.186846, 0.315293}},
  Sinusoidal3_25 → {{0.00258432, 0.0716056, 0.992651, 0.0848182, 0.0380729, 0.0201326,
    0.00754257, 0.00306615, 0.0198505, 0.00116429}, {0.187228, -0.102389, -0.304258, -0.255477,
    -0.00203168, 0.252402, 0.295637, 0.102831, -0.190504, -0.315925, -0.186254, 0.0972148,
    0.303949, 0.255376, -0.00138343, -0.251733, -0.30273, -0.0962015, 0.190099, 0.310936}},
  Sinusoidal3_26 → {{0.00262081, 0.0754953, 0.9921, 0.0886408, 0.0373648, 0.017477, 0.00841698,
    0.00287394, 0.0197938, 0.0010897}, {0.183286, -0.0979326, -0.297222, -0.258273,
    0.00608983, 0.255927, 0.295119, 0.098936, -0.189199, -0.316465, -0.190894, 0.0992358,
```

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```
    0.296856, 0.260011, 0.00584555, -0.258352, -0.299502, -0.0984744, 0.190601, 0.314451}},
  Sinusoidal3_27 → {{0.00245036, 0.0708241, 0.992326, 0.0909895, 0.0341751, 0.0177477, 0.00909287,
    0.00252721, 0.0203703, 0.000847081}, {0.184867, -0.0922002, -0.299228, -0.260702,
    -0.00508774, 0.255884, 0.300882, 0.0948556, -0.18848, -0.312343, -0.183162, 0.099808,
    0.295877, 0.261908, 0.0047932, -0.256351, -0.301625, -0.0958488, 0.186958, 0.318123}},
  Sinusoidal3_28 → {{0.00310167, 0.0689741, 0.992718, 0.0876263, 0.034195, 0.0196758, 0.00853432,
    0.00290803, 0.0206745, 0.00105018}, {0.183978, -0.0950358, -0.299192, -0.260119,
    -0.000174982, 0.255967, 0.300098, 0.100886, -0.192182, -0.310824, -0.184952, 0.0970852,
    0.295253, 0.257438, -0.00404045, -0.260552, -0.296205, -0.0967662, 0.186213, 0.322303}},
  Sinusoidal3_29 → {{0.00339205, 0.0760608, 0.992175, 0.0873783, 0.0356741, 0.0196286, 0.00880032,
    0.00231682, 0.0203832, 0.000740272}, {0.183876, -0.0988627, -0.305307, -0.256632,
    0.00317018, 0.260468, 0.302123, 0.0941186, -0.189588, -0.314868, -0.188801, 0.0964832,
    0.299184, 0.258037, -0.00594326, -0.253268, -0.300207, -0.0989009, 0.182234, 0.309715}},
  Sinusoidal3_30 → {{0.00257934, 0.0703805, 0.992874, 0.0841042, 0.0366041, 0.0177808,
    0.00934542, 0.00250325, 0.0204279, 0.000840241}, {0.182257, -0.0957033, -0.29856, -0.253459,
    -0.00492149, 0.25668, 0.295021, 0.099548, -0.187781, -0.319687, -0.189178, 0.101658,
    0.294904, 0.259763, -0.00602302, -0.254876, -0.301508, -0.0936902, 0.190601, 0.319915}}|>,
f5 → <|Sinusoidal2_11 → {{0.00241244, 0.0108583, 0.0319534, 0.0900548, 0.92982, 0.352639,
    0.0295216, 0.00448882, 0.0305453, 0.00145385}, {-0.092927, -0.260068, 0.253389, 0.100114,
    -0.314248, 0.0989384, 0.258441, -0.257756, -0.0941434, 0.315974, -0.0938249, -0.25948,
    0.256596, 0.0984101, -0.309957, 0.102006, 0.25199, -0.256067, -0.0966279, 0.320131}},
  Sinusoidal2_12 → {{0.00184654, 0.0113923, 0.0325092, 0.0946632, 0.930596, 0.3497, 0.028118,
    0.00489768, 0.0270365, 0.00178509}, {-0.103115, -0.259001, 0.252023, 0.100059,
    -0.317129, 0.092352, 0.253862, -0.253402, -0.0983022, 0.309318, -0.101194, -0.260919,
    0.260867, 0.0993181, -0.313013, 0.100475, 0.256178, -0.257678, -0.0969183, 0.316125}},
  Sinusoidal2_13 → {{0.00288343, 0.0111803, 0.0287065, 0.0912949, 0.933873, 0.341924,
    0.0260984, 0.00417784, 0.031244, 0.0013222}, {-0.098589, -0.257244, 0.258529, 0.0928432,
    -0.314366, 0.0939327, 0.25229, -0.260971, -0.103742, 0.320322, -0.103219, -0.253222,
    0.250536, 0.0920645, -0.323164, 0.0924493, 0.250811, -0.252493, -0.0967247, 0.317583}},
  Sinusoidal2_14 → {{0.00198207, 0.0114037, 0.0291772, 0.094748, 0.936452, 0.333919, 0.0268577,
    0.00394309, 0.0292408, 0.001227}, {-0.102727, -0.255283, 0.2623, 0.0920847,
    -0.321543, 0.100162, 0.253064, -0.262894, -0.103798, 0.318601, -0.0967554, -0.250968,
    0.251305, 0.0962062, -0.317671, 0.099466, 0.250622, -0.250444, -0.096221, 0.312701}},
  Sinusoidal2_15 → {{0.0020196, 0.00914319, 0.0305227, 0.0923031, 0.932904, 0.344117, 0.0282797,
    0.00552996, 0.0299864, 0.00203984}, {-0.0924726, -0.259481, 0.259208, 0.0950326,
    -0.320222, 0.103496, 0.252345, -0.257681, -0.100041, 0.318423, -0.096857, -0.257714,
    0.251383, 0.0926155, -0.310931, 0.103668, 0.25622, -0.250175, -0.0939588, 0.317973}},
  Sinusoidal2_16 → {{0.00228059, 0.0121483, 0.0339243, 0.0931457, 0.933486, 0.342001, 0.0278291,
    0.00483708, 0.0292861, 0.00169552}, {-0.0968592, -0.255287, 0.258061, 0.0986334,
    -0.312039, 0.0979214, 0.250773, -0.251639, -0.100906, 0.31409, -0.103165, -0.259206,
    0.254963, 0.103754, -0.314072, 0.102577, 0.256527, -0.260381, -0.102237, 0.316702}},
  Sinusoidal2_17 → {{0.00223609, 0.00860612, 0.0324592, 0.0934626, 0.932672, 0.344328,
    0.0291301, 0.00476875, 0.0286287, 0.0016605}, {-0.0911505, -0.250839, 0.255402, 0.0968908,
    -0.318414, 0.0972986, 0.259291, -0.252825, -0.0930127, 0.318065, -0.0964218, -0.259798,
    0.25422, 0.0979786, -0.312004, 0.101968, 0.260906, -0.254261, -0.0993867, 0.317754}},
  Sinusoidal2_18 → {{0.00290576, 0.0109007, 0.0321424, 0.0923504, 0.935635, 0.336336, 0.0307074,
    0.00451803, 0.0284682, 0.00157259}, {-0.0931505, -0.251535, 0.26009, 0.0976534,
    -0.311801, 0.0977955, 0.259946, -0.255825, -0.0915653, 0.321261, -0.0988258, -0.250485,
    0.252442, 0.101948, -0.313353, 0.0941893, 0.261621, -0.259934, -0.0996626, 0.315974}},
  Sinusoidal2_19 → {{0.00232623, 0.00970849, 0.027958, 0.0877828, 0.931319, 0.349775, 0.0287472,
    0.00419364, 0.0294773, 0.00134371}, {-0.0932553, -0.255583, 0.249059, 0.0978514,
    -0.316559, 0.101213, 0.25875, -0.254813, -0.0954245, 0.318124, -0.0944705, -0.258544,
    0.259558, 0.10213, -0.318333, 0.100434, 0.253212, -0.249302, -0.0959377, 0.318224}},
  Sinusoidal2_20 → {{0.00280659, 0.008674, 0.0295166, 0.0914764, 0.931428, 0.348598, 0.0291602,
    0.0050628, 0.0268288, 0.0019045}, {-0.0964046, -0.258443, 0.25169, 0.0935817, -0.313023,
    0.102589, 0.257181, -0.253734, -0.0974887, 0.320425, -0.0932952, -0.259485, 0.252389,
    0.0946759, -0.318053, 0.102364, 0.260771, -0.258778, -0.0950262, 0.310269}}|>,
f6 → <|Sinusoidal1_1 → {{0.00138545, 0.00155189, 0.0194479, 0.0361265, 0.0848665, 0.988756,
    0.112804, 0.00335445, 0.0271175, 0.00101966}, {-0.15664, -0.0920462, 0.291364, -0.275097,
    0.00231271, 0.241192, -0.282403, 0.110324, 0.19428, -0.321663, 0.197405, 0.0738606,
    -0.327218, 0.268895, -0.00388081, -0.239563, 0.317029, -0.0967765, -0.198135, 0.291153}},
  Sinusoidal1_2 → {{0.00627294, 0.00652985, 0.0189025, 0.0298589, 0.0738444, 0.989418,
    0.117018, 0.00984466, 0.0212781, 0.00504255}, {-0.157567, -0.113427, 0.276055, -0.235834,
    0.00233926, 0.235413, -0.331344, 0.11718, 0.218288, -0.293372, 0.182491, 0.127064,
    -0.318987, 0.233817, -0.0292775, -0.282748, 0.302566, -0.109604, -0.207253, 0.290918}},
  Sinusoidal1_3 → {{0.0055664, 0.00338223, 0.00949819, 0.0334988, 0.0797439, 0.989209,
```

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```
    0.114295, 0.0116455, 0.0249271, 0.00561498}, {-0.154502, -0.123067, 0.288704, -0.236689,
    -0.00375509, 0.279226, -0.300292, 0.0966414, 0.154841, -0.332208, 0.16948, 0.082772,
    -0.3275, 0.236577, 0.00406874, -0.258805, 0.32178, -0.0682032, -0.179221, 0.321974}},
Sinusoidal1_4 → {{0.00161611, 0.00845996, 0.013847, 0.0467698, 0.0908765, 0.98863, 0.106434,
    0.00965605, 0.0212751, 0.00501748}, {-0.203679, -0.128913, 0.319241, -0.258629,
    -0.0300659, 0.239889, -0.283192, 0.0926256, 0.15776, -0.301553, 0.188644, 0.120872,
    -0.315778, 0.252436, -0.00424931, -0.279741, 0.298634, -0.0941358, -0.16321, 0.305697}},
Sinusoidal1_5 → {{0.00457019, 0.00897303, 0.015286, 0.0489678, 0.102307, 0.987884, 0.101596,
    0.00544106, 0.0230101, 0.00200679}, {-0.19996, -0.106985, 0.292365, -0.262762,
    -0.0286363, 0.258772, -0.276, 0.0689393, 0.166193, -0.311867, 0.196236, 0.0878438,
    -0.318055, 0.229615, -0.00703813, -0.282803, 0.279672, -0.110983, -0.189635, 0.337382}},
Sinusoidal1_6 → {{0.0025459, 0.0023835, 0.0146334, 0.0334823, 0.0815841, 0.992695, 0.0774203,
    0.00597841, 0.0227646, 0.00218137}, {-0.203534, -0.108972, 0.269652, -0.265655,
    -0.0106712, 0.229755, -0.294554, 0.117949, 0.156957, -0.326942, 0.162023, 0.0728134,
    -0.320105, 0.245531, -0.00370382, -0.285289, 0.301362, -0.0679255, -0.186559, 0.335209}},
Sinusoidal1_7 → {{0.00440709, 0.00892625, 0.0128676, 0.0364823, 0.0929571, 0.982288,
    0.156199, 0.0114847, 0.017535, 0.0060619}, {-0.151071, -0.104299, 0.286906, -0.225005,
    -0.013005, 0.27131, -0.294784, 0.069568, 0.197732, -0.325434, 0.166092, 0.116314,
    -0.310118, 0.240848, -0.0105551, -0.272839, 0.322182, -0.124614, -0.160812, 0.328324}},
Sinusoidal1_8 → {{0.00192698, 0.0118864, 0.0249909, 0.0482262, 0.0820076, 0.990741, 0.0855474,
    0.000886269, 0.0359527, 0.0000957809}, {-0.183053, -0.0834166, 0.321535, -0.258072,
    -0.00078264, 0.221253, -0.30469, 0.081755, 0.18673, -0.315959, 0.191914, 0.11702,
    -0.32363, 0.239925, -0.00568014, -0.244783, 0.272365, -0.0912619, -0.210587, 0.326712}},
Sinusoidal1_9 → {{0.00172519, 0.00934475, 0.0140919, 0.0341051, 0.0979647, 0.989123, 0.097078,
    0.0018856, 0.0340337, 0.000622205}, {-0.180289, -0.0969378, 0.319032, -0.257932,
    0.0292389, 0.252354, -0.314051, 0.0983665, 0.187617, -0.335047, 0.161423, 0.102384,
    -0.276672, 0.274644, -0.0245465, -0.223007, 0.303841, -0.0651648, -0.176566, 0.320778}},
Sinusoidal1_10 → {{0.00210985, 0.00788555, 0.0164501, 0.0392419, 0.103095, 0.989679,
    0.0868089, 0.00581571, 0.0213286, 0.00242337}, {-0.1752, -0.0679374, 0.277381, -0.272639,
    0.000942946, 0.270425, -0.290537, 0.110502, 0.169061, -0.300817, 0.212401, 0.0816266,
    -0.285937, 0.272625, 0.00168945, -0.25475, 0.293687, -0.105191, -0.206154, 0.334683}}|>|>
```

We can now perform the clustering for all these classes of data:

In[3]:=
```
clusters1 = TimeSeriesClusters[classification1]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
<|SpikeMax → <|Cluster → Cluster[Cluster[ ··· 1 ··· ],
    {-0.0840441, 0.0147189, 0.962498, ··· 14 ···, 0.00673175, 0.0155535, -0.0950476} → ... ,
    0.575193, 19, 1], ··· 4 ···, ··· 1 ···|>, ··· 5 ···|>
```

large output | show less | show more | show all | set size limit...

We see that each class has different data associated with it:

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In[4]:=
```
Query[All, Keys]@clusters1
```

Out[4]=
```
<|SpikeMax →
  {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
 SpikeMin → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
 f1 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
 f3 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
 f5 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
 f6 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations}|>
```

For example, we look at the "f1" class clustering group associations:

In[5]:=
```
clusters1["f1", "GroupAssociations"]
```

Out[5]=
```
<|G1S1 → {LinearPositive_1, LinearPositive_3, LinearPositive_2, LinearPositive_10, LinearPositive_7,
   LinearPositive_8, LinearPositive_5, LinearPositive_4, LinearPositive_6, LinearPositive_9,
   LinearPositive_14, LinearPositive_18, LinearPositive_19, LinearPositive_13, LinearPositive_17,
   LinearPositive_15, LinearPositive_12, LinearPositive_11, LinearPositive_16, LinearPositive_20},
 G1S2 → {LinearNegative_10, LinearNegative_5, LinearNegative_7, LinearNegative_1,
   LinearNegative_6, LinearNegative_16, LinearNegative_12, LinearNegative_13,
   LinearNegative_17, LinearNegative_14, LinearNegative_15, LinearNegative_11,
   LinearNegative_18, LinearNegative_20, LinearNegative_19, LinearNegative_4, LinearNegative_9},
 G2S1 → {LinearNegative_8}, G2S2 → {LinearNegative_2, LinearNegative_3}|>
```

We can also obtain the "Data" rules for this class:

In[6]:=
```
clusters1["f1", "Data"]
```

Out[6]=
```
{{0.0199347, 0.0377555, 0.0562581, 0.0762601, 0.0947102, 0.111123, 0.131223, 0.150282, 0.166841, 0.185508,
   0.204115, 0.224124, 0.243998, 0.259847, 0.280103, 0.299076, 0.318333, 0.334809, 0.353249, 0.37517} →
  LinearPositive_1, {0.0173387, 0.037753, 0.0563274, 0.0759195, 0.0949854, 0.11182,
   0.129869, 0.149212, 0.16669, 0.185245, 0.205328, 0.222943, 0.241539, 0.25998,
   0.278714, 0.298384, 0.318275, 0.335333, 0.356683, 0.375635} → LinearPositive_3,
 {0.0172887, 0.0356868, 0.0552573, 0.0753153, 0.091731, 0.111321, 0.132215, 0.149934, 0.16912, 0.186614,
   0.205516, 0.222653, 0.240711, 0.261552, 0.280634, 0.29786, 0.318635, 0.336406, 0.35532, 0.372719} →
  LinearPositive_2, {0.0186558, 0.0376621, 0.0542485, 0.0753188, 0.0924002, 0.111122,
   0.129979, 0.150942, 0.166325, 0.187476, 0.205398, 0.223344, 0.241245, 0.261036,
   0.279755, 0.298906, 0.318436, 0.335665, 0.355968, 0.373417} → LinearPositive_10,
 {0.0193356, 0.039019, 0.0561566, 0.0731888, 0.0946615, 0.113026, 0.131002, 0.1485, 0.168802, 0.18575,
   0.205175, 0.225308, 0.241, 0.260953, 0.280043, 0.297827, 0.318318, 0.336522, 0.354446, 0.373199} →
  LinearPositive_7, {0.019302, 0.0375021, 0.054308, 0.0744515, 0.0946946, 0.110671,
   0.132267, 0.147428, 0.169424, 0.188172, 0.206256, 0.224286, 0.241937, 0.259699,
   0.278689, 0.297803, 0.3185, 0.334906, 0.355493, 0.374184} → LinearPositive_8,
 {0.0174462, 0.035586, 0.0561062, 0.0765267, 0.0920633, 0.112459, 0.129088, 0.150988, 0.167165, 0.187087,
   0.205875, 0.225352, 0.243463, 0.261553, 0.280539, 0.298242, 0.315651, 0.337885, 0.353986, 0.371866} →
  LinearPositive_5, {0.0185007, 0.035699, 0.0560113, 0.0743005, 0.0933379, 0.113211,
   0.130236, 0.151141, 0.166766, 0.187495, 0.206708, 0.222911, 0.243388, 0.260066,
   0.281462, 0.298943, 0.316714, 0.335842, 0.353704, 0.373289} → LinearPositive_4,
 {0.0188982, 0.0355953, 0.0563873, 0.0751591, 0.0932027, 0.113357, 0.132038, 0.150239, 0.168779, 0.187559,
   0.204709, 0.224196, 0.241598, 0.261833, 0.280855, 0.297735, 0.315718, 0.335204, 0.354982, 0.37372} →
  LinearPositive_6, {0.020375, 0.0381747, 0.0559756, 0.0742268, 0.092251, 0.111477,
   0.128786, 0.148566, 0.168262, 0.187704, 0.206227, 0.225012, 0.244183, 0.261007,
   0.280163, 0.299075, 0.315359, 0.336919, 0.35463, 0.372518} → LinearPositive_9,
 {0.0194809, 0.0457256, 0.0547346, 0.0794687, 0.0984364, 0.113827, 0.121604, 0.152472, 0.174322, 0.187285,
   0.209739, 0.229522, 0.243646, 0.257273, 0.284009, 0.300222, 0.316751, 0.32877, 0.351938, 0.369829} →
  LinearPositive_14, {0.0173101, 0.0405106, 0.062782, 0.0721944, 0.0902813, 0.116595,
   0.126082, 0.156066, 0.163147, 0.184891, 0.212374, 0.222758, 0.241299, 0.262615,
   0.275421, 0.305107, 0.318407, 0.331622, 0.347488, 0.378336} → LinearPositive_18,
 {0.0116046, 0.0409172, 0.0523513, 0.0696728, 0.0925748, 0.113611, 0.121585, 0.153742, 0.170072, 0.178235,
   0.202862, 0.22378, 0.247884, 0.258784, 0.279358, 0.307902, 0.313699, 0.332465, 0.361206, 0.371625} →
  LinearPositive_19, {0.021584, 0.0438283, 0.0466596, 0.0721454, 0.0927721, 0.117865,
   0.128274, 0.155776, 0.16681, 0.188215, 0.20633, 0.222772, 0.246899, 0.265878,
   0.279984, 0.287852, 0.318746, 0.332179, 0.359938, 0.370359} → LinearPositive_13,
 {0.0200818, 0.030321, 0.0600411, 0.0773368, 0.101962, 0.120458, 0.127589, 0.153403, 0.161296, 0.190393,
```

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```
  0.209961, 0.232065, 0.238544, 0.257888, 0.278956, 0.288243, 0.318614, 0.340761, 0.347047, 0.376545} →
 LinearPositive_17, {0.0162181, 0.0316563, 0.0613068, 0.0810228, 0.0874705, 0.109058,
  0.139262, 0.144095, 0.168543, 0.178105, 0.202327, 0.229253, 0.244029, 0.255307,
  0.281193, 0.294484, 0.321311, 0.338241, 0.351078, 0.379029} → LinearPositive_15,
{0.0196723, 0.0346545, 0.052271, 0.068526, 0.089011, 0.113453, 0.136979, 0.14991, 0.163486, 0.181103,
  0.202123, 0.230066, 0.248511, 0.264547, 0.272409, 0.306416, 0.31448, 0.340502, 0.354335, 0.367982} →
 LinearPositive_12, {0.0207479, 0.0283344, 0.0503468, 0.0733055, 0.0962158, 0.11681,
  0.129278, 0.147994, 0.161915, 0.184985, 0.195832, 0.229499, 0.250278, 0.254524,
  0.282982, 0.301868, 0.312857, 0.33831, 0.34914, 0.380826} → LinearPositive_11,
{0.0251266, 0.0287683, 0.0590565, 0.0781781, 0.0915877, 0.107255, 0.138039, 0.151186, 0.165702, 0.193785,
  0.199725, 0.219438, 0.235221, 0.262453, 0.285348, 0.303253, 0.313079, 0.33767, 0.350957, 0.375868} →
 LinearPositive_16, {0.0266735, 0.0390625, 0.0552967, 0.0771651, 0.0899947, 0.102376,
  0.125499, 0.144002, 0.169283, 0.181864, 0.197032, 0.21408, 0.248219, 0.269307,
  0.280916, 0.301233, 0.325388, 0.335119, 0.352261, 0.375815} → LinearPositive_20,
{-0.0141057, -0.0482497, -0.0376457, -0.0683769, -0.105011, -0.101699, -0.126482,
  -0.155368, -0.173431, -0.192801, -0.20327, -0.230179, -0.255774, -0.273372,
  -0.290241, -0.287415, -0.315625, -0.335273, -0.330474, -0.374275} → LinearNegative_10,
{-0.0110001, -0.0266517, -0.0559391, -0.0569901, -0.0937053, -0.114597, -0.118418,
  -0.130878, -0.178584, -0.183458, -0.208687, -0.21371, -0.258828, -0.27396,
  -0.288827, -0.29844, -0.317274, -0.325736, -0.361159, -0.364992} → LinearNegative_5,
{-0.0303484, -0.0533533, -0.0688604, -0.0851485, -0.106279, -0.115428, -0.116318,
  -0.151679, -0.175441, -0.179975, -0.215334, -0.210439, -0.256749, -0.249175,
  -0.278395, -0.294201, -0.327057, -0.337756, -0.35105, -0.364572} → LinearNegative_7,
{-0.0233745, -0.0376096, -0.0655662, -0.0825605, -0.103712, -0.124319, -0.130353,
  -0.152813, -0.172286, -0.181171, -0.210675, -0.235593, -0.251833, -0.257499,
  -0.280622, -0.279765, -0.307176, -0.338766, -0.366484, -0.357495} → LinearNegative_1,
{-0.0094452, -0.0245806, -0.048997, -0.0806322, -0.0841408, -0.126284, -0.125037,
  -0.146317, -0.168193, -0.182007, -0.216846, -0.231955, -0.247073, -0.250674,
  -0.281763, -0.3093, -0.310001, -0.343094, -0.361652, -0.352914} → LinearNegative_6,
{-0.0169409, -0.0378766, -0.0637393, -0.0789792, -0.096412, -0.110829, -0.134565,
  -0.154913, -0.176555, -0.178773, -0.201738, -0.22632, -0.249968, -0.256785,
  -0.283061, -0.291758, -0.312766, -0.341087, -0.347204, -0.375314} → LinearNegative_16,
{-0.00974557, -0.0433051, -0.0640029, -0.0780177, -0.101196, -0.105474, -0.123304,
  -0.148127, -0.169987, -0.181957, -0.199533, -0.230858, -0.239774, -0.260086,
  -0.286615, -0.292159, -0.313097, -0.343353, -0.347462, -0.380697} → LinearNegative_12,
{-0.0146271, -0.0422678, -0.0489597, -0.0817574, -0.0945617, -0.118945, -0.125021,
  -0.153468, -0.177466, -0.181607, -0.198867, -0.227021, -0.234617, -0.266365,
  -0.274371, -0.295576, -0.317404, -0.333515, -0.360874, -0.37448} → LinearNegative_13,
{-0.0223082, -0.0385322, -0.0640439, -0.0743739, -0.08446, -0.108322, -0.129556, -0.154037,
  -0.174605, -0.190325, -0.196689, -0.225239, -0.235193, -0.254259, -0.283464,
  -0.293308, -0.325079, -0.335208, -0.357971, -0.374627} → LinearNegative_17,
{-0.0271006, -0.0449866, -0.0589612, -0.0793313, -0.0986461, -0.110084, -0.130338,
  -0.156805, -0.166049, -0.180873, -0.211349, -0.219027, -0.239818, -0.262671,
  -0.274266, -0.293846, -0.328912, -0.333076, -0.353427, -0.372838} → LinearNegative_14,
{-0.0170231, -0.0309271, -0.0627263, -0.0796228, -0.100154, -0.1126, -0.125679, -0.157209,
  -0.162764, -0.186542, -0.208024, -0.226347, -0.235315, -0.258272, -0.284822,
  -0.298344, -0.325242, -0.337329, -0.352753, -0.365028} → LinearNegative_15,
{-0.0103102, -0.0302862, -0.0640276, -0.0790854, -0.0937109, -0.104306, -0.137082,
  -0.155288, -0.166331, -0.187829, -0.213326, -0.22378, -0.235462, -0.258738,
  -0.274955, -0.302968, -0.321077, -0.342999, -0.348412, -0.368261} → LinearNegative_11,
{-0.0219264, -0.0277344, -0.0477879, -0.0745452, -0.0964386, -0.115016, -0.137336,
  -0.150157, -0.167244, -0.192682, -0.197555, -0.219566, -0.24682, -0.265439,
  -0.279353, -0.301121, -0.315384, -0.333562, -0.351403, -0.374612} → LinearNegative_18,
{-0.0268322, -0.0299946, -0.0551747, -0.0714832, -0.0866237, -0.118598, -0.134838,
  -0.154978, -0.167431, -0.192744, -0.211158, -0.229616, -0.240512, -0.268104,
  -0.281693, -0.291355, -0.320036, -0.335781, -0.346191, -0.367394} → LinearNegative_20,
{-0.0146473, -0.0462727, -0.06027, -0.0750068, -0.101207, -0.117554, -0.137214, -0.142087,
  -0.1612, -0.190043, -0.208851, -0.215854, -0.235111, -0.252768, -0.284368,
  -0.307504, -0.319681, -0.338197, -0.354863, -0.368648} → LinearNegative_19,
{-0.00888579, -0.0237712, -0.0687079, -0.087675, -0.104314, -0.1223, -0.13566, -0.163767,
  -0.167979, -0.189628, -0.203732, -0.228004, -0.252329, -0.26505, -0.265497,
  -0.300217, -0.314195, -0.316063, -0.347814, -0.37959} → LinearNegative_4,
{-0.0118212, -0.0550686, -0.0673657, -0.066653, -0.0833839, -0.0993535, -0.121359,
  -0.144163, -0.170895, -0.172507, -0.202349, -0.23621, -0.228994, -0.272116,
  -0.277318, -0.311833, -0.331709, -0.322649, -0.364956, -0.363114} → LinearNegative_9,
{-0.00199578, -0.028114, -0.0586748, -0.0610859, -0.0763692, -0.119466, -0.122014,
```

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```
  -0.16666, -0.183601, -0.177851, -0.219529, -0.21767, -0.253901, -0.24662, -0.268059,
  -0.282575, -0.338406, -0.326166, -0.358247, -0.376982} → LinearNegative_8,
{-0.0297306, -0.0542285, -0.0428703, -0.0643093, -0.0793575, -0.107697, -0.140303,
  -0.137461, -0.174402, -0.185418, -0.224726, -0.214074, -0.237051, -0.253051,
  -0.26573, -0.290747, -0.332244, -0.353058, -0.34347, -0.37976} → LinearNegative_2,
{-0.0304623, -0.0495827, -0.038645, -0.0730843, -0.110634, -0.122647, -0.134941, -0.157957,
  -0.184759, -0.183027, -0.207671, -0.21835, -0.23962, -0.246301, -0.286548,
  -0.281659, -0.330628, -0.335724, -0.345895, -0.373772} → LinearNegative_3}
```

The data can be provided as a list of associations for each class (i.e. without class labels):

```
In[7]:= clusters1AssociationList = TimeSeriesClusters[Values@classification1];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

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Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

The classes are automatically enumerated in order of appearance:

```
In[8]:= Keys[clusters1AssociationList]
Out[8]= {1, 2, 3, 4, 5, 6}

In[9]:= Query[All, Keys]@clusters1AssociationList
Out[9]= <|1 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
  2 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
  3 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
  4 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
  5 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations},
  6 → {Cluster, InitialSplitCluster, IntermediateClusters, SubsplitClusters, Data, GroupAssociations}|>
```

We can also obtain the "GroupAssociations" or other information for any class as before. For example, for class 3 (which corresponds to "f1" in our fully labeled example above):

```
In[10]:= clusters1AssociationList[3, "GroupAssociations"]
Out[10]= <|G1S1 → {LinearPositive_1, LinearPositive_3, LinearPositive_2, LinearPositive_10, LinearPositive_7,
    LinearPositive_8, LinearPositive_5, LinearPositive_4, LinearPositive_6, LinearPositive_9,
    LinearPositive_14, LinearPositive_18, LinearPositive_19, LinearPositive_13, LinearPositive_17,
    LinearPositive_15, LinearPositive_12, LinearPositive_11, LinearPositive_16, LinearPositive_20},
  G1S2 → {LinearNegative_10, LinearNegative_5, LinearNegative_7, LinearNegative_1,
    LinearNegative_6, LinearNegative_16, LinearNegative_12, LinearNegative_13,
    LinearNegative_17, LinearNegative_14, LinearNegative_15, LinearNegative_11,
    LinearNegative_18, LinearNegative_20, LinearNegative_19, LinearNegative_4, LinearNegative_9},
  G2S1 → {LinearNegative_8}, G2S2 → {LinearNegative_2, LinearNegative_3}|>
```

The TimeSeriesClusters function can also work with data from a single class presented as an association:

```
In[11]:= clusters1Association = TimeSeriesClusters[classification1["f1"]];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

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The class is by default labeled as "1":

In[12]:=
```
Keys[clusters1Association]
```
Out[12]=
```
{1}
```

In[13]:=
```
clusters1Association["1", "GroupAssociations"]
```
Out[13]=
```
<|G1S1 → {LinearPositive_1, LinearPositive_3, LinearPositive_2, LinearPositive_10, LinearPositive_7,
   LinearPositive_8, LinearPositive_5, LinearPositive_4, LinearPositive_6, LinearPositive_9,
   LinearPositive_14, LinearPositive_18, LinearPositive_19, LinearPositive_13, LinearPositive_17,
   LinearPositive_15, LinearPositive_12, LinearPositive_11, LinearPositive_16, LinearPositive_20},
 G1S2 → {LinearNegative_10, LinearNegative_5, LinearNegative_7, LinearNegative_1,
   LinearNegative_6, LinearNegative_16, LinearNegative_12, LinearNegative_13,
   LinearNegative_17, LinearNegative_14, LinearNegative_15, LinearNegative_11,
   LinearNegative_18, LinearNegative_20, LinearNegative_19, LinearNegative_4, LinearNegative_9},
 G2S1 → {LinearNegative_8}, G2S2 → {LinearNegative_2, LinearNegative_3}|>
```

In addition, TimeSeriesClusters can also work with data from a single class presented as a list:

In[14]:=
```
clusters1List = TimeSeriesClusters[Values@classification1["f1"]];
```
Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

In[15]:=
```
Keys[clusters1List]
```
Out[15]=
```
{1}
```

The labeling for each time series is an index position corresponding to the position of the series in the initial input list:

In[16]:=
```
clusters1List["1", "GroupAssociations"]
```
Out[16]=
```
<|G1S1 → {1, 3, 2, 10, 7, 8, 5, 4, 6, 9, 14, 18, 19, 13, 17, 15, 12, 11, 16, 20},
 G1S2 → {30, 25, 27, 21, 26, 36, 32, 33, 37, 34, 35, 31, 38, 40, 39, 24, 29}, G2S1 → {28}, G2S2 → {22, 23}|>
```

Options (9)

ClusterLabeling (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ClusterLabeling provides a way to add a prepend text to all the cluster groups named.

We generate some data for classification:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

Method → "LombScargle"

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.407211, 0.338428, 0.213162, 0.387473, 0.0939036, 0.308636, 0.20045, 0.187288,
      0.555472, 0.190244}, {0.973063, 0.0668789, 0.0350421, 0.0489344, 0.0219513, 0.051431,
      0.0469277, -0.0606149, 0.00188526, 0.0868288, -0.0289949, -0.088536, -0.0499041,
      -0.0197416, -0.0596169, -0.050931, 0.00655394, 0.0342565, -0.0446175, 0.0871352}},
   SpikePositive_2 → {{0.241119, 0.450505, 0.254842, 0.233013, 0.276493, 0.388843, 0.0742593,
      0.240104, 0.507447, 0.267119}, {0.96954, 0.0967805, 0.0217178, -0.0305673, 0.0323016,
      -0.106684, 0.00320054, -0.00464251, -0.064266, 0.106396, -0.00441326, 0.0391446, 0.0364912,
      -0.0718369, -0.0630732, 0.0208595, -0.0720164, 0.0576052, 0.0169857, 0.00788644}},
   SpikePositive_3 → {{0.338955, 0.121869, 0.303907, 0.313147, 0.239729, 0.430686, 0.256372,
      0.169832, 0.554903, 0.185443}, {0.96819, 0.0596546, -0.0946777, -0.0500928, 0.0339764,
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      0.046449, 0.0788983, 0.00191789, 0.0894474, 0.0615317, -0.0750102, -0.0387326, 0.043984}},
   SpikePositive_4 → {{0.309256, 0.263652, 0.19671, 0.238244, 0.42427, 0.224292, 0.16929,
      0.344117, 0.498702, 0.336604}, {0.973478, -0.0369144, -0.0403579, 0.0478153, 0.0281915,
      -0.0807053, -0.0305573, 0.0487087, -0.0290685, -0.0358159, -0.0773708, -0.0314868, -0.0751744,
      -0.0796871, 0.0182986, -0.0818525, 0.0276266, 0.0479904, -0.0528151, -0.0495048}},
   SpikePositive_5 → {{0.238692, 0.233758, 0.18295, 0.152198, 0.240248, 0.366057, 0.329237,
      0.240399, 0.630089, 0.277183}, {0.977194, -0.0763145, 0.0067985, 0.0555749, -0.0392617,
      -0.0162453, 0.00236641, -0.050457, 0.0566709, 0.0126708, -0.0597736, 0.0881124, 0.00938194,
      0.00531787, -0.0408731, 0.0782521, 0.0447933, 0.0661329, -0.0507799, 0.0140935}},
   SpikePositive_6 → {{0.288543, 0.319625, 0.218683, 0.266543, 0.351941, 0.241489, 0.286531,
      0.0624725, 0.650771, 0.0634839}, {0.961911, 0.0753518, 0.0221363, 0.0112267, -0.0586292,
      -0.0682288, 0.056412, -0.0159392, 0.0397763, -0.0950589, 0.0834966, -0.0841665, -0.0860357,
      -0.0709811, 0.023512, 0.0313613, -0.0766983, -0.0619186, -0.0676395, 0.0629358}},
   SpikePositive_7 → {{0.229382, 0.219684, 0.211173, 0.404878, 0.23791, 0.398242, 0.286073,
      0.267403, 0.494693, 0.278101}, {0.975621, 0.0239748, -0.0579121, -0.0201652, 0.0431728,
      -0.0433259, -0.00179967, -0.0446675, 0.0831657, 0.0483274, -0.0333051, -0.0463799,
      0.0828898, 0.0628769, 0.0222459, 0.0394558, 0.0697797, -0.00992043, 0.0658079, -0.0583291}},
   SpikePositive_8 → {{0.383606, 0.358264, 0.217327, 0.379363, 0.175515, 0.227651, 0.356036,
      0.293604, 0.394861, 0.286068}, {0.969023, 0.089913, 0.0479439, 0.0805194, -0.0627074,
      0.0167534, -0.0220018, -0.0283969, 0.0908734, 0.0417541, -0.0855805, -0.0594202, -0.0825787,
      0.0101709, 0.0418229, -0.0884569, 0.0200922, 0.0134549, -0.0261571, 0.00194283}},
   SpikePositive_9 → {{0.394258, 0.391392, 0.224391, 0.148041, 0.291994, 0.15277, 0.225243,
      0.22667, 0.602604, 0.212746}, {0.958143, 0.0312918, 0.0913287, -0.0666888, 0.0399481,
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      -0.0886199, -0.0525311, -0.0290718, 0.0822623, -0.0186269, 0.0866361, 0.0853089}},
   SpikePositive_10 → {{0.124518, 0.128275, 0.354718, 0.388867, 0.399236, 0.227112, 0.224961,
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      0.0236732, 0.070547, -0.0515144, -0.0922468, -0.101101, 0.0518603, 0.0142614}},
   SpikePositive_11 → {{0.293263, 0.357688, 0.404607, 0.288842, 0.36091, 0.355571, 0.366368,
      0.211483, 0.239055, 0.214789}, {-0.0800053, -0.0123797, 0.970222, 0.0579382, 0.00132203,
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    0.0213753, 0.0344674, -0.0509426, -0.0323269, 0.0605242, 0.0762473, 0.0937488}},
  SpikePositive_12 → {{0.244651, 0.298213, 0.331382, 0.405188, 0.303145, 0.459361, 0.291097,
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    0.0892024, -0.060382, 0.0243007, 0.0446921, -0.049782, -0.0537847, 0.0795963, -0.0371689,
    0.0564376, -0.0585075, 0.0251873, 0.0113425, -0.0403116, 0.0626532, 0.0223764}},
  SpikePositive_13 → {{0.0836615, 0.334436, 0.452205, 0.259958, 0.331998, 0.39839, 0.175046,
    0.245157, 0.425594, 0.261295}, {0.0108041, -0.0691782, 0.976879, 0.0444929, -0.0417872,
    -0.0574481, 0.0216296, -0.0528086, 0.0636243, 0.00792628, 0.000800613, 0.0393167, 0.0159994,
    0.0793734, 0.0961075, -0.0106075, -0.0474616, -0.0368798, -0.0722662, 0.0111365}},
  SpikePositive_14 → {{0.306936, 0.262411, 0.27951, 0.116307, 0.198783, 0.303622, 0.370141,
    0.381691, 0.426034, 0.386497}, {0.0773519, 0.00720035, 0.979105, -0.055302, 0.0863504,
    0.0198403, -0.059639, -0.0344146, -0.0373628, -0.023534, -0.0643196, -0.0374436, 0.0064881,
    0.0543497, 0.0721109, 0.0286048, -0.0124239, -0.00220161, 0.0548176, -0.00132979}},
  SpikePositive_15 → {{0.166294, 0.291473, 0.341267, 0.377099, 0.487757, 0.333311, 0.152911,
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    0.0616552, 0.00156268, -0.0122607, 0.0395789, -0.0172082, -0.0146456, 0.0527748}},
  SpikePositive_16 → {{0.184068, 0.356906, 0.4061, 0.376049, 0.29383, 0.318231, 0.318779,
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    -0.0386989, 0.0559237, -0.0671605, -0.0100493, -0.0396152, 0.0562702, -0.0284125}},
  SpikePositive_17 → {{0.300751, 0.328444, 0.31927, 0.217947, 0.43016, 0.209588, 0.42072,
    0.277901, 0.265435, 0.313982}, {0.0538745, 0.0707395, 0.959679, 0.0917394, -0.0395649,
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    -0.0916805, 0.0915345, -0.0800205, 0.0313799, -0.0976998, 0.0754445, -0.0327061, -0.091}},
  SpikePositive_18 → {{0.197736, 0.340171, 0.508609, 0.176901, 0.412351, 0.266185, 0.37353,
    0.166715, 0.334258, 0.187812}, {0.00719197, 0.0536138, 0.975705, -0.000970522, -0.0400105,
    -0.0423578, -0.0589477, 0.0236487, 0.0487098, 0.0712863, 0.0384574, -0.0734255,
    0.0306517, 0.0886704, 0.0168889, 0.00315968, -0.033025, 0.0708798, 0.0100314, 0.0894783}},
  SpikePositive_19 → {{0.316692, 0.226013, 0.400815, 0.190191, 0.266784, 0.362937, 0.316844,
    0.327715, 0.368059, 0.325034}, {0.0836181, -0.00362699, 0.980834, 0.0488478, -0.000471711,
    0.010629, 0.0352269, 0.0181966, 0.0271106, 0.0493311, -0.0864674, -0.0605759, 0.0220444,
    -0.0301163, 0.0429017, -0.0174906, -0.0590721, -0.0395434, 0.0227323, -0.0588523}},
  SpikePositive_20 → {{0.106438, 0.381942, 0.249433, 0.540863, 0.346227, 0.216234, 0.372161,
    0.256667, 0.227174, 0.255777}, {-0.0624376, 0.0879868, 0.962452, -0.0746326, -0.0320742,
    -0.078217, -0.072243, 0.0267722, -0.0948669, -0.0411904, 0.0949676, 0.0381751, 0.0199289,
    0.0215877, -0.0794902, 0.00411162, 0.0589596, -0.058335, -0.0624999, -0.0650877}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.29252, 0.21911, 0.360887, 0.152706, 0.409652, 0.304814,
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    -0.0389164, 0.0600879, -0.0381734, -0.0824943, -0.0806781, -0.0730806, -0.0425366, 0.0157573}},
  SpikeNegative_2 → {{0.177333, 0.0988351, 0.225577, 0.267115, 0.46621, 0.209233, 0.431781,
    0.39374, 0.275453, 0.397591}, {-0.964604, 0.0814153, 0.0798189, -0.092252, 0.0320513,
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    -0.0853307, -0.0814281, 0.0728153, -0.0290694, 0.0322018, -0.0494282, 0.0910736}},
  SpikeNegative_3 → {{0.170813, 0.254949, 0.252319, 0.242357, 0.337943, 0.169633, 0.232149,
    0.215673, 0.693342, 0.243535}, {-0.962039, 0.0999422, 0.0611295, 0.0954904, -0.0611293,
    0.0378916, 0.077426, -0.0167049, 0.0538768, 0.050528, -0.023957, 0.0278296, 0.0548129,
    0.0739048, 0.0985978, 0.00467595, 0.0571292, -0.0557859, 0.0877574, 0.0331603}},
  SpikeNegative_4 → {{0.2229, 0.382175, 0.209388, 0.532587, 0.264318, 0.124764, 0.169799,
    0.249309, 0.472497, 0.277661}, {-0.963957, -0.0741631, 0.067615, 0.102532, -0.0857513,
    -0.0331507, 0.0761831, 0.0232988, -0.100159, -0.0794778, 0.0724793, 0.0118163, 0.0735413,
    -0.00237507, 0.0250968, 0.0159553, -0.00373792, -0.0831291, 0.0126699, 0.0167008}},
  SpikeNegative_5 → {{0.131096, 0.183449, 0.278157, 0.194923, 0.542817, 0.232764, 0.313611,
    0.308978, 0.440582, 0.311501}, {-0.968511, 0.0928466, 0.0141136, -0.00651305, 0.018801,
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    0.0752862, -0.0427115, 0.0528622, 0.0861445, 0.0337466, -0.0751606, 0.0624704}},
  SpikeNegative_6 → {{0.248568, 0.233072, 0.254016, 0.417572, 0.314118, 0.355463, 0.171099,
    0.27679, 0.493505, 0.265596}, {-0.978047, -0.0332419, 0.0303521, -0.0651224, -0.0465165,
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    -0.00930083, -0.0855746, 0.0703095, 0.0207484, 0.00666123, -0.00728521, -0.0312276}},
  SpikeNegative_7 → {{0.341687, 0.25988, 0.289041, 0.33953, 0.299289, 0.29574, 0.204129,
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    -0.0576134, 0.0436987, 0.0683446, 0.0195361, 0.0760997, 0.0105957, 0.0726752, 0.0340575,
    0.0115111, 0.01731, 0.0759675, 0.0788127, 0.0660923, -0.0154495, -0.0238947, 0.0513946}},
  SpikeNegative_8 → {{0.208087, 0.352004, 0.241774, 0.253647, 0.232474, 0.202157, 0.247727,
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  SpikeNegative_9 → {{0.374376, 0.302828, 0.30906, 0.335347, 0.109517, 0.239529, 0.291105,
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    0.0189354, 0.00124109, 0.0360564, -0.00905212, -0.0118028, -0.054426, -0.0418416}},
  SpikeNegative_10 → {{0.140093, 0.161708, 0.184732, 0.292737, 0.271779, 0.278676, 0.326186,
    0.389775, 0.532804, 0.375069}, {-0.976103, 0.0806034, -0.0398708, -0.0525933, 0.0510921,
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  SpikeNegative_11 → {{0.235827, 0.235934, 0.357431, 0.264144, 0.202442, 0.32094, 0.299828,
    0.40039, 0.355586, 0.412985}, {-0.0490831, -0.0660368, -0.966072, 0.0941932, -0.0955169,
    -0.0261413, 0.0579334, -0.0664286, 0.0191739, 0.0588881, 0.0564822, -0.0165072, 0.0559891,
    -0.101277, -0.0204163, -0.0371052, -0.026025, 0.0719098, 0.0693819, -0.0184742}},
  SpikeNegative_12 → {{0.22224, 0.420825, 0.333295, 0.350225, 0.483145, 0.318598, 0.23882,
    0.182945, 0.270304, 0.203153}, {0.0755239, -0.0541449, -0.976309, -0.0544376, 0.0517493,
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  SpikeNegative_13 → {{0.26124, 0.242446, 0.214404, 0.465445, 0.292756, 0.194202, 0.0949198,
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    0.0904187, 0.0393928, 0.0340747, 0.0433122, -0.0786861, 0.0566027, 0.0998084, 0.0185904}},
  SpikeNegative_14 → {{0.194123, 0.259899, 0.250803, 0.542213, 0.250009, 0.299026, 0.329889,
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    -0.0232812, 0.0627739, -0.0370129, -0.076054, -0.06419, 0.00642746, -0.067034, 0.0722189}},
  SpikeNegative_15 → {{0.325014, 0.234589, 0.221901, 0.271556, 0.424944, 0.280457, 0.298792,
    0.32877, 0.398585, 0.317617}, {0.0850719, -0.0671027, -0.975166, 0.0896091, -0.0733207,
    0.0259155, -0.0282413, 0.061389, 0.0173916, 0.0279494, 0.00722381, 0.0648886, 0.0143824,
    0.0127013, 0.0415862, 0.0451781, -0.0622385, -0.0103459, -0.0601388, 0.039811}},
  SpikeNegative_16 → {{0.187629, 0.337647, 0.266805, 0.482489, 0.368889, 0.261866, 0.404055,
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    -0.00562779, 0.0332805, -0.00836766, 0.0124755, 0.00537126, 0.0670755, 0.0696052}},
  SpikeNegative_17 → {{0.367563, 0.354704, 0.19463, 0.305454, 0.23978, 0.454638, 0.437356,
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    0.039987, 0.0313676, 0.0475839, 0.0694066, -0.0536307, -0.0128486, -0.0478261}},
  SpikeNegative_18 → {{0.267538, 0.392872, 0.180042, 0.304377, 0.202369, 0.360255, 0.412194,
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    -0.0483941, 0.0260276, -0.0475307, 0.0833831, -0.0579972, 0.00874375, -0.0914445,
    -0.000205053, 0.062488, 0.0208471, 0.0127887, 0.0872109, -0.0144463, -0.06954, -0.0153915}},
  SpikeNegative_19 → {{0.340586, 0.409916, 0.47351, 0.331272, 0.204043, 0.156616, 0.428282,
    0.123545, 0.319545, 0.122711}, {-0.084288, -0.0522977, -0.959922, -0.090222, 0.0361392,
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    0.0873225, 0.0593224, -0.0123378, 0.0496233, 0.0737566, -0.0217174, -0.0659173}},
  SpikeNegative_20 → {{0.260074, 0.196378, 0.490879, 0.290801, 0.275578, 0.351099, 0.326745,
    0.237914, 0.374504, 0.255806}, {-0.016141, -0.0692693, -0.976896, -0.00367995, -0.047481,
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    0.0633643, -0.00896643, -0.0819901, -0.0332209, -0.0353003, 0.0565215, 0.0320106}}|>,
f1 → <|LinearPositive_1 → {{0.983672, 0.169326, 0.0314105, 0.00267887, 0.00190434, 0.0108017,
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  LinearPositive_2 → {{0.984694, 0.163056, 0.0308958, 0.00205748, 0.00190645,
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  LinearPositive_4 → {{0.98374, 0.167807, 0.0328253, 0.00231803, 0.00216444, 0.0113949,
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    0.241518, 0.261297, 0.278277, 0.298051, 0.318106, 0.336483, 0.35596, 0.374173}},
LinearPositive_5 → {{0.984511, 0.164307, 0.0335286, 0.00292254, 0.00197451, 0.0100298,
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LinearPositive_6 → {{0.984566, 0.164035, 0.0323077, 0.00234967, 0.00148263, 0.0105919,
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LinearPositive_7 → {{0.984572, 0.163477, 0.0302117, 0.00233154, 0.00156194, 0.0103041,
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    0.22415, 0.24209, 0.263057, 0.281443, 0.299025, 0.315895, 0.335373, 0.355091, 0.373406}},
LinearPositive_8 → {{0.982841, 0.173451, 0.0333779, 0.00226192, 0.00136371,
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LinearPositive_9 → {{0.984661, 0.162795, 0.0316132, 0.00214793, 0.00185132,
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LinearPositive_10 → {{0.984861, 0.162294, 0.030833, 0.00183728, 0.00224482, 0.0104987,
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LinearPositive_11 → {{0.983393, 0.167782, 0.0292182, 0.000385851, 0.0000528885, 0.0113373,
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    0.222604, 0.236117, 0.257118, 0.282994, 0.305378, 0.308466, 0.334086, 0.363211, 0.37051}},
LinearPositive_12 → {{0.984159, 0.164681, 0.0317692, 0.00248665, 0.0022517,
    0.0106353, 0.0196048, 0.0327998, 0.0175516, 0.0375269},
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LinearPositive_13 → {{0.982966, 0.167059, 0.0328847, 0.000478335, 0.00637953, 0.0192068,
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LinearPositive_14 → {{0.982977, 0.172587, 0.032307, 0.00263269, 0.000590059, 0.00876953,
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    0.239661, 0.267053, 0.284561, 0.303036, 0.310259, 0.334857, 0.349682, 0.374646}},
LinearPositive_15 → {{0.98523, 0.155509, 0.0236856, 0.00338378, 0.00392608, 0.0118227,
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    0.246894, 0.264244, 0.284765, 0.300137, 0.31192, 0.344302, 0.349398, 0.371693}},
LinearPositive_16 → {{0.982801, 0.171808, 0.031669, 0.00281848, 0.00268818,
    0.0155727, 0.0223669, 0.0325738, 0.0194048, 0.0372261},
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LinearPositive_17 → {{0.98654, 0.151625, 0.0435896, 0.00340091, 0.00186494, 0.0110126,
    0.0171841, 0.021931, 0.016492, 0.0257661}, {0.0248409, 0.0401199, 0.0508438, 0.0701558,
    0.0920593, 0.115426, 0.122311, 0.152805, 0.165175, 0.178693, 0.201473, 0.232725,
    0.250701, 0.260636, 0.282678, 0.292798, 0.319188, 0.335557, 0.360772, 0.36761}},
LinearPositive_18 → {{0.981178, 0.184105, 0.0246265, 0.00236313, 0.00224582, 0.0103266,
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    0.242161, 0.262029, 0.283402, 0.302076, 0.32409, 0.333188, 0.352849, 0.370321}},
LinearPositive_19 → {{0.986463, 0.15065, 0.041459, 0.00230052, 0.00228119, 0.0124778,
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    0.0751444, 0.091858, 0.111725, 0.120914, 0.141435, 0.173519, 0.177153, 0.212243, 0.230448,
    0.246177, 0.252616, 0.27663, 0.290343, 0.324569, 0.334763, 0.359503, 0.376664}},
LinearPositive_20 → {{0.984196, 0.165894, 0.0294524, 0.0030751, 0.000551178, 0.017638,
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LinearNegative_1 → {{0.988959, 0.110016, 0.0382408, 0.00306028, 0.00139905, 0.030162, 0.029033,
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LinearNegative_2 → {{0.981888, 0.16728, 0.0618293, 0.0039215, 0.000595054, 0.0203611,
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LinearNegative_3 → {{0.980984, 0.181376, 0.0503096, 0.00221754, 0.00803793, 0.00892184,
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LinearNegative_4 → {{0.985112, 0.153787, 0.0381289, 0.00308668, 0.00287103, 0.00998517,
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LinearNegative_5 → {{0.98552, 0.14901, 0.0405635, 0.00296337, 0.0115265, 0.00427138, 0.0107115,
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LinearNegative_6 → {{0.98798, 0.135998, 0.0192298, 0.0130451, 0.00226894, 0.00591289,
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LinearNegative_7 → {{0.984025, 0.169785, 0.0173407, 0.00905289, 0.000244387, 0.0120177,
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LinearNegative_8 → {{0.986632, 0.157332, 0.0199848, 0.0032422, 0.00166003, 0.00852781,
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LinearNegative_9 → {{0.982988, 0.174997, 0.0338868, 0.00336878, 0.00196628, 0.00175594,
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LinearNegative_10 → {{0.973865, 0.211276, 0.0542253, 0.0023032, 0.000935343, 0.00653802,
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LinearNegative_12 → {{0.985026, 0.160038, 0.0276185, 0.0021179, 0.00238252, 0.0189999,
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LinearNegative_13 → {{0.986714, 0.146213, 0.0446107, 0.00704498, 0.0013134, 0.00957483,
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LinearNegative_14 → {{0.981165, 0.177134, 0.0355507, 0.00330449, 0.00131865, 0.00632342,
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LinearNegative_15 → {{0.985727, 0.158522, 0.029664, 0.00209005, 0.00612787, 0.0159006,
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LinearNegative_16 → {{0.986561, 0.151696, 0.0303596, 0.0000851195, 0.00192303, 0.0110902,
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LinearNegative_17 → {{0.983707, 0.166711, 0.0330781, 0.00241957, 0.00269761, 0.00564217,
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f3 → <|Sinusoidal3_21 → {{0.00289705, 0.0729544, 0.9924, 0.0872077, 0.0358703, 0.0194183,
    0.0089969, 0.00241979, 0.0213547, 0.000764174}, {0.187716, -0.10229, -0.304609, -0.260373,
    0.00429839, 0.252613, 0.303808, 0.0932497, -0.182499, -0.316294, -0.186185, 0.0932199,
    0.302975, 0.256965, 0.00105686, -0.257302, -0.295214, -0.0975683, 0.183742, 0.312614}},
  Sinusoidal3_22 → {{0.00392522, 0.071929, 0.992467, 0.0872754, 0.0359052, 0.0200076, 0.00790176,
    0.00255198, 0.021087, 0.000834182}, {0.191632, -0.0917535, -0.299478, -0.25703,
    0.00229855, 0.254343, 0.302449, 0.100612, -0.183979, -0.312102, -0.183482, 0.094369,
    0.303929, 0.257726, -0.00329508, -0.258547, -0.305694, -0.100611, 0.179952, 0.312057}},
  Sinusoidal3_23 → {{0.00376664, 0.0700889, 0.992619, 0.0872908, 0.0344602, 0.0203832, 0.0101009,
    0.00244514, 0.0212036, 0.000786078}, {0.184957, -0.100766, -0.299641, -0.251922,
    -0.00357137, 0.252197, 0.303781, 0.098131, -0.181923, -0.310302, -0.182096, 0.0968751,
    0.297672, 0.261304, -0.00471296, -0.259539, -0.302206, -0.101134, 0.188059, 0.322085}},
  Sinusoidal3_24 → {{0.00363122, 0.0708938, 0.993062, 0.0816517, 0.0355442, 0.0183355, 0.00903365,
    0.00252861, 0.0208307, 0.000837819}, {0.181075, -0.0978763, -0.300806, -0.250914,
    -0.00463757, 0.251365, 0.30491, 0.100461, -0.188355, -0.316296, -0.187126, 0.103394,
    0.297736, 0.252199, -0.00399759, -0.259242, -0.30508, -0.0942798, 0.183712, 0.318602}},
  Sinusoidal3_25 → {{0.00356595, 0.0757557, 0.992217, 0.0872877, 0.035939, 0.0188888, 0.0105026,
    0.00252152, 0.0192031, 0.000910416}, {0.180766, -0.0928548, -0.304743, -0.253073,
    -0.000184297, 0.258138, 0.307922, 0.0965344, -0.180946, -0.315939, -0.182821, 0.0999905,
    0.299044, 0.260558, 0.00375689, -0.253481, -0.298269, -0.101029, 0.182863, 0.317557}},
  Sinusoidal3_26 → {{0.00282931, 0.0699863, 0.992773, 0.0860701, 0.0342013, 0.0212853,
    0.00935453, 0.0035769, 0.0190358, 0.00148905}, {0.191202, -0.092627, -0.299742, -0.251546,
    -0.00556717, 0.257067, 0.298651, 0.102291, -0.19042, -0.314248, -0.184469, 0.0924161,
    0.300034, 0.261133, -0.00463991, -0.258514, -0.29606, -0.099826, 0.186883, 0.317467}},
  Sinusoidal3_27 → {{0.00203971, 0.0700795, 0.992874, 0.0841236, 0.0370345, 0.0189994,
    0.00942639, 0.00275239, 0.0194894, 0.000996943}, {0.18585, -0.0938925, -0.301297, -0.259417,
    -0.0022569, 0.252259, 0.298859, 0.092233, -0.18788, -0.318059, -0.189633, 0.100688,
    0.303827, 0.254465, -0.00235613, -0.256364, -0.293479, -0.0973833, 0.189117, 0.316821}},
  Sinusoidal3_28 → {{0.00258296, 0.067354, 0.992849, 0.0851535, 0.0383414, 0.020101, 0.00956762,
    0.0029778, 0.0219101, 0.00105151}, {0.191776, -0.103638, -0.305834, -0.253599,
    -0.00472603, 0.250456, 0.298135, 0.103548, -0.181403, -0.312972, -0.190017, 0.0970366,
    0.298705, 0.257329, -0.000725259, -0.252809, -0.297343, -0.0952631, 0.187097, 0.322564}},
  Sinusoidal3_29 → {{0.00375883, 0.0737185, 0.992813, 0.0830417, 0.0334417, 0.0182338, 0.0092164,
    0.00240194, 0.0208694, 0.000779821}, {0.181928, -0.0981269, -0.294761, -0.256667,
    -0.00286798, 0.256408, 0.30305, 0.0983723, -0.18714, -0.313129, -0.186055, 0.102964,
    0.299785, 0.260721, -0.00593152, -0.260196, -0.300112, -0.101189, 0.182335, 0.315936}},
  Sinusoidal3_30 → {{0.00311269, 0.0712876, 0.992515, 0.0888279, 0.0331414, 0.0192412,
    0.0074318, 0.00342224, 0.0198554, 0.0013507}, {0.182669, -0.0986421, -0.299713, -0.253993,
    -0.00458184, 0.258601, 0.297118, 0.0953051, -0.190527, -0.309796, -0.182495, 0.0918019,
    0.305329, 0.255522, -0.00298964, -0.259894, -0.305453, -0.0933083, 0.187839, 0.317703}}|>,
f5 → <|Sinusoidal2_11 → {{0.00292484, 0.0132394, 0.0326119, 0.0953118, 0.934539, 0.33861,
    0.0290285, 0.00412045, 0.0280552, 0.00133952}, {-0.103367, -0.256267, 0.257963, 0.101527,
    -0.312226, 0.0998183, 0.252794, -0.260021, -0.100836, 0.317518, -0.0938471, -0.252536,
    0.25015, 0.098281, -0.317663, 0.0998892, 0.253834, -0.260767, -0.102384, 0.313404}},
  Sinusoidal2_12 → {{0.00183504, 0.0119916, 0.0326696, 0.0975357, 0.932386, 0.344157, 0.0249385,
    0.00532331, 0.0288149, 0.00194065}, {-0.103857, -0.260409, 0.257706, 0.0946389,
    -0.316554, 0.0918059, 0.2503, -0.249964, -0.103343, 0.319126, -0.0943112, -0.252455,
    0.259479, 0.0974584, -0.312031, 0.0996498, 0.254011, -0.257838, -0.0970586, 0.320269}},
  Sinusoidal2_13 → {{0.00270099, 0.00914063, 0.02884, 0.0938903, 0.930211, 0.351282, 0.0305273,
    0.00543846, 0.0245929, 0.00219989}, {-0.0984187, -0.2547, 0.251691, 0.0973669,
    -0.319503, 0.0983912, 0.257596, -0.254095, -0.101925, 0.317549, -0.0924383, -0.259342,
    0.251098, 0.0947802, -0.320274, 0.0968225, 0.26008, -0.258776, -0.0919487, 0.309605}},
  Sinusoidal2_14 → {{0.0024293, 0.0109142, 0.0335061, 0.0920126, 0.932381, 0.345275, 0.0284252,
```

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```
    0.00380931, 0.0302279, 0.00114317}, {-0.0997478, -0.255768, 0.258546, 0.0984593,
    -0.31601, 0.0937737, 0.250607, -0.254097, -0.0930966, 0.32044, -0.101589, -0.252841,
    0.254073, 0.100412, -0.319967, 0.101791, 0.251283, -0.254859, -0.0941758, 0.319574}},
  Sinusoidal2_15 → {{0.00204469, 0.00977053, 0.0312587, 0.0898124, 0.935639, 0.337336,
    0.0281693, 0.00471865, 0.0286887, 0.00168765}, {-0.101812, -0.26041, 0.255812, 0.0922967,
    -0.312342, 0.0969426, 0.252802, -0.254679, -0.095903, 0.322384, -0.100374, -0.252481,
    0.252133, 0.101285, -0.313752, 0.0979861, 0.26063, -0.254813, -0.0922236, 0.319301}},
  Sinusoidal2_16 → {{0.00255982, 0.0110919, 0.0315011, 0.0940941, 0.933502, 0.342003,
    0.0281494, 0.00549837, 0.0283968, 0.002069}, {-0.0934156, -0.25087, 0.259655, 0.100645,
    -0.314598, 0.101613, 0.253036, -0.25543, -0.0963781, 0.312023, -0.101223, -0.25848,
    0.259144, 0.0945074, -0.312182, 0.100978, 0.258815, -0.254055, -0.0965166, 0.322378}},
  Sinusoidal2_17 → {{0.00403847, 0.0118757, 0.02998, 0.0941942, 0.926583, 0.36043, 0.0277905,
    0.00455855, 0.0284719, 0.00155085}, {-0.0952518, -0.254817, 0.258115, 0.102236,
    -0.309864, 0.0973808, 0.261089, -0.251489, -0.103854, 0.315327, -0.0922664, -0.261468,
    0.255248, 0.0949683, -0.320908, 0.0981, 0.249815, -0.26028, -0.0923576, 0.315361}},
  Sinusoidal2_18 → {{0.00292978, 0.0106882, 0.0285559, 0.0914598, 0.934351, 0.340745, 0.0257113,
    0.00464483, 0.0298848, 0.0015395}, {-0.0939179, -0.254163, 0.259198, 0.0925132,
    -0.317669, 0.102113, 0.257713, -0.254657, -0.101532, 0.315944, -0.0971187, -0.261216,
    0.258217, 0.0963304, -0.318174, 0.095807, 0.249471, -0.252701, -0.10117, 0.312631}},
  Sinusoidal2_19 → {{0.00256045, 0.00993971, 0.0336066, 0.0918107, 0.93314, 0.343498, 0.0282621,
    0.00397081, 0.0278985, 0.00124787}, {-0.101042, -0.254049, 0.259601, 0.095112,
    -0.31819, 0.0920673, 0.258793, -0.258168, -0.0948327, 0.316553, -0.096847, -0.262667,
    0.251779, 0.0973536, -0.313489, 0.0964551, 0.253199, -0.256812, -0.0935104, 0.314065}},
  Sinusoidal2_20 → {{0.00205627, 0.0101991, 0.0311658, 0.0890436, 0.934048, 0.341916, 0.0291925,
    0.00444993, 0.027672, 0.00154522}, {-0.0983715, -0.253301, 0.252147, 0.0999389,
    -0.313979, 0.10263, 0.251707, -0.255821, -0.0945993, 0.321123, -0.103072, -0.25372,
    0.255224, 0.102595, -0.316347, 0.104758, 0.259143, -0.252371, -0.0960358, 0.317537}}|>,
f6 → <|Sinusoidal1_1 → {{0.00216829, 0.00873713, 0.00912162, 0.0359007, 0.088363, 0.988522,
    0.11513, 0.00782549, 0.01523, 0.00376101}, {-0.19347, -0.119377, 0.270131, -0.270814,
    0.00835586, 0.273011, -0.275887, 0.0745423, 0.165631, -0.320623, 0.194594, 0.106474,
    -0.316526, 0.259778, 0.0137064, -0.269206, 0.317717, -0.117243, -0.183836, 0.278348}},
  Sinusoidal1_2 → {{0.00199877, 0.0120768, 0.0213572, 0.0437027, 0.0877056, 0.991521, 0.0738005,
    0.00302795, 0.0349429, 0.00112073}, {-0.207533, -0.127558, 0.313805, -0.279565,
    0.0207908, 0.231845, -0.297943, 0.0940323, 0.175035, -0.302801, 0.190931, 0.121914,
    -0.29017, 0.259555, 0.0168838, -0.233685, 0.284152, -0.0976249, -0.209025, 0.313311}},
  Sinusoidal1_3 → {{0.00112918, 0.00137279, 0.020753, 0.0294453, 0.0639655, 0.99304, 0.0895038,
    0.0062943, 0.0205483, 0.00259377}, {-0.193128, -0.115092, 0.275747, -0.275724,
    -0.0111377, 0.229744, -0.319211, 0.124171, 0.199151, -0.33483, 0.19798, 0.0655124,
    -0.312158, 0.229973, 0.0185966, -0.262384, 0.282947, -0.0778297, -0.178574, 0.307224}},
  Sinusoidal1_4 → {{0.00914452, 0.00574905, 0.0173818, 0.0462881, 0.106772, 0.988488, 0.0915365,
    0.0082875, 0.0216698, 0.00348385}, {-0.178351, -0.080248, 0.320235, -0.257804,
    0.00439244, 0.25737, -0.283428, 0.10804, 0.159937, -0.323601, 0.159019, 0.0693427,
    -0.307116, 0.233193, -0.0201619, -0.270295, 0.316823, -0.104007, -0.183813, 0.32701}},
  Sinusoidal1_5 → {{0.000373969, 0.00787813, 0.018975, 0.0347715, 0.101055, 0.988813, 0.099477,
    0.00898929, 0.0203229, 0.00399605}, {-0.167976, -0.0922527, 0.310619, -0.274482,
    -0.0217339, 0.256172, -0.311421, 0.0790414, 0.204452, -0.297862, 0.186294, 0.117114,
    -0.275685, 0.252075, 0.0311576, -0.261881, 0.310101, -0.0942426, -0.186668, 0.306908}},
  Sinusoidal1_6 → {{0.00247841, 0.00534246, 0.0251439, 0.0353695, 0.0851441, 0.990398,
    0.0973465, 0.0133855, 0.0148337, 0.00831042}, {-0.211424, -0.115422, 0.281303, -0.237174,
    -0.0276731, 0.268454, -0.310848, 0.117736, 0.204663, -0.334516, 0.167066, 0.0731,
    -0.280853, 0.231826, 0.0258847, -0.258481, 0.282695, -0.0911318, -0.172233, 0.34386}},
  Sinusoidal1_7 → {{0.00292614, 0.00608782, 0.0170427, 0.0373516, 0.0930212, 0.987529,
    0.118217, 0.00532233, 0.0198559, 0.00200473}, {-0.193556, -0.118013, 0.274275, -0.228202,
    -0.0100687, 0.273757, -0.277752, 0.0939747, 0.209297, -0.31171, 0.160368, 0.120761,
    -0.310184, 0.259656, 0.0107351, -0.253855, 0.31612, -0.0929852, -0.19499, 0.322835}},
  Sinusoidal1_8 → {{0.0080355, 0.005742, 0.0207383, 0.0245925, 0.0888876, 0.988422, 0.112786,
    0.00282627, 0.0354941, 0.000624551}, {-0.163519, -0.109924, 0.322252, -0.260299,
    0.015561, 0.272818, -0.307991, 0.0838052, 0.2105, -0.336612, 0.153441, 0.0674437,
    -0.318402, 0.242358, -0.00990765, -0.251047, 0.265419, -0.08467, -0.181298, 0.305919}},
  Sinusoidal1_9 → {{0.00146369, 0.00722457, 0.018879, 0.0421983, 0.1011, 0.987252, 0.110648,
    0.00522092, 0.025402, 0.00221449}, {-0.181475, -0.115518, 0.283714, -0.258694,
    0.0104247, 0.229982, -0.319361, 0.100388, 0.19431, -0.305159, 0.182497, 0.120114,
    -0.285408, 0.266143, -0.0316384, -0.230863, 0.331051, -0.115384, -0.209672, 0.298609}},
  Sinusoidal1_10 → {{0.0016534, 0.00483398, 0.0186694, 0.0304497, 0.107364, 0.985864, 0.12172,
    0.00765708, 0.0188452, 0.00382339}, {-0.19203, -0.1149, 0.270158, -0.266699, 0.00421191,
    0.258731, -0.315319, 0.0848923, 0.167249, -0.282647, 0.196691, 0.077445, -0.32497,
```

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In[3]:=
```
clusters1 = TimeSeriesClusters[classification1]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
<|SpikeMax → <|Cluster → Cluster[ ··· 1 ··· ], ··· 4 ···,
   GroupAssociations → <|G1S1 → {SpikePositive_1, SpikePositive_8, SpikePositive_6, SpikePositive_3,
       SpikePositive_7, SpikePositive_5, SpikePositive_9}, ··· 2 ···, ··· 1 ···|>|>, ··· 4 ···, f6 → ··· 1 ···|>
```

large output | show less | show more | show all | set size limit...

We can obtain the keys for this classification, which by default follow G#S# for groups and subgroups within each class:

In[4]:=
```
Query[All, "GroupAssociations" /* Keys]@clusters1
```

Out[4]=
```
<|SpikeMax → {G1S1, G1S2, G2S1, G2S2}, SpikeMin → {G1S1, G1S2, G2S1, G2S2}, f1 → {G1S1, G1S2, G2S1},
 f3 → {G1S1, G1S2, G2S1, G2S2, G3S1}, f5 → {G1S1, G1S2, G2S1}, f6 → {G1S1, G1S2, G2S1, G3S1}|>
```

Now let's say we want to prepend a text labeling to each of these:

In[5]:=
```
clusters1Labels = TimeSeriesClusters[classification1, ClusterLabeling → "LabelPrepend_"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[5]=
```
<|SpikeMax → <|Cluster → Cluster[ ··· 1 ··· ], ··· 4 ···,
   GroupAssociations → <|LabelPrepend_G1S1 → {SpikePositive_1, SpikePositive_8, SpikePositive_6, ... 3,
       SpikePositive_7, SpikePositive_5, SpikePositive_9}, ··· 2 ···, ··· 1 ···|>|>, ··· 4 ···, f6 → ··· 1 ···|>
```

large output | show less | show more | show all | set size limit...

In[6]:=
```
Query[All, "GroupAssociations" /* Keys]@clusters1Labels
```

Out[6]=
```
<|SpikeMax → {LabelPrepend_G1S1, LabelPrepend_G1S2, LabelPrepend_G2S1, LabelPrepend_G2S2},
 SpikeMin → {LabelPrepend_G1S1, LabelPrepend_G1S2, LabelPrepend_G2S1, LabelPrepend_G2S2},
 f1 → {LabelPrepend_G1S1, LabelPrepend_G1S2, LabelPrepend_G2S1},
 f3 → {LabelPrepend_G1S1, LabelPrepend_G1S2, LabelPrepend_G2S1, LabelPrepend_G2S2, LabelPrepend_G3S1},
 f5 → {LabelPrepend_G1S1, LabelPrepend_G1S2, LabelPrepend_G2S1},
 f6 → {LabelPrepend_G1S1, LabelPrepend_G1S2, LabelPrepend_G2S1, LabelPrepend_G3S1}|>
```

DendrogramPlotOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

DendrogramPlotOptions provides options for an internal DendrogramPlot in the case where either the PrintDendrograms or ReturnDendrograms option values are set to True.

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We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.213783, 0.168444, 0.484229, 0.240975, 0.270193, 0.293093, 0.330973, 0.352221,
      0.331288, 0.362098}, {0.967984, -0.0429778, -0.0589361, 0.0750241, -0.0230239, 0.0595448,
      -0.0071158, 0.0725743, -0.00872096, -0.0221838, -0.0907499, 0.0888766, 0.0824949,
      0.0720427, -0.0505117, -0.0417249, 0.0500206, 0.07888, 0.0291731, 0.00996556}},
   SpikePositive_2 → {{0.233792, 0.145552, 0.195881, 0.376439, 0.296819, 0.322055, 0.445195,
      0.373442, 0.29717, 0.355376}, {0.972427, -0.0599077, -0.0707029, 0.074777, -0.0731269,
      0.0741514, -0.0642417, -0.0442257, -0.0341503, -0.0284905, -0.0367281, -0.0580197, -0.055694,
      -0.020903, 0.0367026, -0.053511, -0.0234776, -0.0846419, 0.000324038, -0.0334542}},
   SpikePositive_3 → {{0.258698, 0.183018, 0.261826, 0.409449, 0.341968, 0.410366, 0.315992,
      0.249709, 0.392227, 0.248975}, {0.972792, -0.0010746, -0.0889475, -0.0112206, -0.0385214,
      -0.0321228, -0.0755673, -0.0803103, 0.0486883, -0.0134193, -0.0652984, -0.026472,
      0.0947927, 0.0179233, 0.054554, 0.0172848, -0.0291442, -0.0433038, 0.0647353, -0.0628323}},
   SpikePositive_4 → {{0.29437, 0.129609, 0.223886, 0.296584, 0.323857, 0.402532, 0.249787,
      0.321627, 0.4635, 0.33298}, {0.967392, 0.00257885, 0.0133562, 0.0817446, 0.0908455,
      0.0144253, 0.065505, -0.0968013, 0.000576385, 0.0252768, -0.0895913, 0.0851433, 0.0177477,
      -0.00105228, 0.0527154, 0.0179439, 0.00902835, -0.0582027, 0.0931067, 0.0607753}},
   SpikePositive_5 → {{0.183167, 0.274005, 0.277207, 0.202059, 0.310715, 0.227133, 0.13307,
      0.382913, 0.544332, 0.406127}, {0.960744, -0.0782077, 0.092051, -0.0853084, -0.0224272,
      -0.0453462, 0.0365633, 0.0771938, -0.0589659, 0.0519403, -0.0352063, 0.0782266,
      -0.0497206, -0.0261332, 0.0460718, 0.0147212, -0.0852603, 0.0351841, 0.10087, 0.0868251}},
   SpikePositive_6 → {{0.2556, 0.228288, 0.178301, 0.282552, 0.291184, 0.392235, 0.185204,
      0.35575, 0.49034, 0.361937}, {0.979679, -0.0574127, 0.00158988, 0.00426108, -0.0323984,
      -0.0389789, 0.0452444, -0.0617339, -0.023104, 0.0640805, -0.0731606, 0.0371364, -0.0468713,
      -0.0506978, 0.0938207, 0.0191671, 0.000963784, -0.00343512, 0.0523043, 0.0207085}},
   SpikePositive_7 → {{0.201323, 0.110955, 0.210988, 0.176318, 0.22315, 0.381581, 0.244381,
      0.202542, 0.714115, 0.255829}, {0.973246, -0.0664963, 0.039929, 0.0139051, 0.0558499,
      -0.0122793, 0.0866892, -0.042254, -0.013579, -0.0358098, -0.0474198, -0.0297231, -0.00105855,
      -0.0120395, -0.0836563, 0.0750076, -0.0848729, 0.0448614, -0.0557659, -0.0657099}},
   SpikePositive_8 → {{0.567119, 0.26409, 0.215053, 0.24805, 0.197071, 0.121806, 0.211775,
      0.352879, 0.395313, 0.348621}, {0.941687, 0.068748, 0.0591347, -0.0925454, -0.0886031,
      -0.0906255, -0.0956655, -0.0993911, -0.0868205, -0.0814433, -0.0772542, -0.0466982,
      -0.0921235, -0.00931198, 0.0953904, -0.0640835, 0.0764235, 0.0338616, 0.0503178, -0.0878948}},
   SpikePositive_9 → {{0.14294, 0.327096, 0.219374, 0.372389, 0.352763, 0.323011, 0.335957,
      0.35237, 0.304692, 0.356555}, {0.97311, 0.0329984, -0.0707812, -0.00303738, -0.0199943,
      -0.0693019, -0.0620472, 0.0717509, -0.017212, 0.0504435, 0.0901265, -0.0431663, -0.0120381,
      0.0592344, 0.00569179, -0.0469688, 0.00103468, -0.0466361, 0.0790835, -0.0748236}},
   SpikePositive_10 → {{0.272524, 0.160447, 0.193239, 0.198608, 0.226745, 0.314921, 0.406806,
      0.173883, 0.668615, 0.172745}, {0.959498, -0.0821399, 0.0890774, 0.0336759, 0.0168766,
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      -0.0678707, -0.0464139, 0.0248752, -0.05929, 0.0619767, -0.041175, -0.0795133}},
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    SpikePositive_11 → {{0.330284, 0.265492, 0.351496, 0.335383, 0.498386, 0.23636, 0.384584,
       0.210387, 0.217589, 0.201564}, {-0.0830891, 0.098987, 0.97305, -0.0355069, -0.000359874,
       0.0116444, -0.0472242, -0.00792772, -0.0778748, -0.0392069, -0.0031967, -0.0986818,
       0.0235708, 0.0612368, 0.00628692, 0.0217989, 0.0951219, -0.00175372, 0.039476, -0.00115852}},
    SpikePositive_12 → {{0.217459, 0.436259, 0.342834, 0.242627, 0.444462, 0.358594, 0.305157,
       0.221123, 0.268581, 0.21377}, {-0.0876844, -0.0438638, 0.972684, 0.0312374, -0.0826565,
       -0.037783, -0.0135587, -0.0626026, -0.0805988, 0.00131581, -0.0180512, -0.0442365, 0.0264628,
       -0.00130949, 0.0418532, -0.0846981, -0.0866556, -0.0195016, 0.0674845, -0.00912872}},
    SpikePositive_13 → {{0.352732, 0.37523, 0.281026, 0.218355, 0.327051, 0.389606, 0.178606,
       0.372885, 0.239863, 0.3477}, {0.0541955, 0.0292652, 0.966467, 0.0837629, -0.0324534,
       -0.0299348, -0.0401222, -0.0321118, -0.0721163, 0.0833579, -0.015429, 0.0352537, -0.0578242,
       -0.0820272, 0.0884969, -0.0871106, 0.0421387, 0.0397587, 0.0856837, -0.026862}},
    SpikePositive_14 → {{0.19377, 0.202186, 0.25181, 0.251805, 0.247281, 0.558826, 0.26275,
       0.312371, 0.375952, 0.336708}, {0.0237821, -0.0844225, 0.97379, 0.0227262, -0.0546951,
       -0.0363309, -0.00397665, 0.00643908, 0.0751576, 0.0106886, -0.0242552, 0.063893, -0.0853735,
       -0.053318, -0.00230533, -0.0255702, -0.0789177, 0.0967884, 0.0130634, -0.0465171}},
    SpikePositive_15 → {{0.142115, 0.40694, 0.276588, 0.381224, 0.335294, 0.133865, 0.247054,
       0.310002, 0.442006, 0.330941}, {0.058202, 0.0399306, 0.976981, -0.0325438, -0.00510491,
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       0.0794225, -0.0594883, 0.0188758, -0.0154565, -0.0823316, -0.0528555, 0.049578}},
    SpikePositive_16 → {{0.17973, 0.218074, 0.25685, 0.179096, 0.483426, 0.322126, 0.281411,
       0.38256, 0.317333, 0.397974}, {-0.0236405, 0.0408948, 0.970486, -0.0683315, 0.0304807,
       0.00422584, 0.0870583, 0.0467658, -0.00172452, 0.0963009, 0.0466116, 0.0133626, -0.0719194,
       0.0953414, -0.0028021, -0.0762428, -0.0663357, 0.0549682, -0.0125167, -0.0353995}},
    SpikePositive_17 → {{0.146685, 0.459498, 0.214314, 0.352931, 0.399121, 0.190846, 0.196055,
       0.33982, 0.345399, 0.357659}, {-0.00164197, 0.0933565, 0.962061, -0.0920806, -0.0372911,
       -0.0776571, 0.0614583, -0.0913452, -0.0962784, 0.0396093, -0.0233116, 0.0666904, 0.0340492,
       0.0333335, -0.085042, -0.0389236, -0.0655038, -0.0438903, -0.0677591, 0.00658222}},
    SpikePositive_18 → {{0.255533, 0.311069, 0.373349, 0.334428, 0.327493, 0.173503, 0.268382,
       0.338433, 0.404783, 0.314544}, {0.0672971, 0.0813997, 0.973907, -0.0530922, -0.0213661,
       -0.0330492, 0.0417079, 0.0694981, 0.0238005, 0.0410479, 0.0224757, -0.0167561, 0.0537835,
       0.00683968, 0.00126465, -0.0498872, 0.0809027, -0.0629684, 0.0876461, 0.052479}},
    SpikePositive_19 → {{0.376462, 0.306593, 0.248669, 0.197525, 0.362933, 0.331527, 0.277919,
       0.282831, 0.410411, 0.310042}, {0.0714679, 0.0879751, 0.973491, -0.034828, 0.018378,
       0.00217121, 0.00991538, -0.0687117, -0.0284202, -0.0150465, -0.0444654, -0.0506248, -0.0589797,
       -0.00720789, -0.0572042, -0.0568561, -0.0742238, 0.0341948, -0.0879561, -0.0553914}},
    SpikePositive_20 → {{0.24299, 0.284869, 0.240217, 0.259741, 0.274676, 0.518639, 0.427771,
       0.210014, 0.347071, 0.206521}, {-0.0610678, 0.0260464, 0.979264, -0.0529729, 0.0775095,
       0.0537994, -0.0499337, 0.0490917, 0.0798091, -0.0307619, 0.02734, 0.00326355, 0.0481343,
       -0.0290764, 0.00452071, -0.0774808, -0.00820722, 0.0389221, 0.0290946, -0.0182632}}|>,
  SpikeMin → <|SpikeNegative_1 → {{0.308919, 0.345824, 0.286937, 0.370492, 0.175729, 0.284947,
       0.252496, 0.24473, 0.521682, 0.239797}, {-0.970394, -0.0460279, 0.0411061, 0.0366332,
       -0.00708342, -0.0160594, 0.081672, -0.0775558, 0.0499397, -0.0588105, -0.0466276, 0.0755782,
       -0.0389149, -0.0780147, 0.0400975, -0.031179, -0.0460134, -0.0809221, 0.0497002, -0.0709664}},
    SpikeNegative_2 → {{0.234543, 0.254114, 0.16664, 0.169245, 0.105151, 0.424581, 0.298918,
       0.390706, 0.469858, 0.412199}, {-0.9746, 0.0383814, -0.0878553, -0.0358953, 0.0787378,
       0.0765708, 0.00870288, 0.0336251, 0.0225328, -0.0757956, 0.0609446, 0.0235776, -0.039571,
       -0.0480905, 0.0670231, 0.00403291, -0.0563127, 0.00804953, -0.00219025, 0.065235}},
    SpikeNegative_3 → {{0.124025, 0.220986, 0.244753, 0.417284, 0.408318, 0.270468, 0.214368,
       0.240791, 0.530185, 0.277211}, {-0.970381, 0.0768, 0.0798816, 0.0185707, -0.06064,
       0.0632462, -0.0430102, 0.033738, 0.0123344, -0.0368022, -0.0665638, -0.0317741, 0.0638574,
       -0.0480809, -0.020065, 0.018085, 0.0878113, -0.0767773, -0.0724668, 0.0463473}},
    SpikeNegative_4 → {{0.213588, 0.196803, 0.200641, 0.246759, 0.248845, 0.136405, 0.465043,
       0.113951, 0.703456, 0.099358}, {-0.964089, 0.0505211, -0.0700959, -0.0242415, -0.0152793,
       -0.0988989, 0.0341947, -0.0416477, -0.0897023, 0.0990235, -0.0972136, 0.0990263, -0.0107728,
       0.0309565, 0.0183618, 0.00930295, 0.0612632, -0.0477844, 0.0654077, -0.0252868}},
    SpikeNegative_5 → {{0.276265, 0.182057, 0.409072, 0.309189, 0.316692, 0.530268, 0.2448,
       0.180629, 0.344724, 0.186356}, {-0.966399, -0.0549246, 0.102071, 0.00719007, 0.0964048,
       0.0414593, -0.0624187, -0.0327445, 0.0852149, 0.0138136, 0.0209997, 0.0529835, -0.0341781,
       -0.0577319, -0.037152, -0.096376, 0.0558724, 0.0626648, -0.028101, -0.0538162}},
    SpikeNegative_6 → {{0.257912, 0.0725823, 0.208482, 0.188771, 0.187196, 0.324453, 0.278387,
       0.350595, 0.608028, 0.372409}, {-0.9696, 0.0852352, -0.0736289, -0.053348, -0.0864406,
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       -0.0527093, 0.000524712, -0.0373756, -0.0625223, 0.0286072, -0.026695, -0.0406509}},
    SpikeNegative_7 → {{0.207336, 0.118141, 0.213566, 0.22435, 0.443543, 0.289808, 0.281235,
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  SpikeNegative_8 → {{0.196991, 0.122041, 0.172109, 0.101104, 0.487064, 0.223962, 0.254023,
    0.435307, 0.413921, 0.440133}, {-0.960272, 0.069934, -0.016654, -0.0849796, -0.0493099,
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    0.036757, -0.0426407, 0.0604134, -0.0531445, 0.0587033, -0.0383372, 0.0858122}},
  SpikeNegative_9 → {{0.260798, 0.156128, 0.378326, 0.290086, 0.384392, 0.310995, 0.233795,
    0.250871, 0.517572, 0.224446}, {-0.97214, 0.0191721, 0.0836015, -0.0365419, 0.0129569,
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    0.00119272, 0.0750182, -0.0519595, 0.0653255, 0.0135596, -0.0539989, 0.0809802, 0.0834502}},
  SpikeNegative_10 → {{0.187865, 0.280521, 0.167666, 0.194284, 0.514669, 0.278423, 0.225155,
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    0.0928125, 0.018675, -0.0147335, -0.0148751, -0.0079587, 0.0396553, -0.089288, 0.0522704,
    0.0648879, -0.0533551, -0.0394514, -0.0336766, 0.0785741, 0.0672268, 0.0195378}},
  SpikeNegative_11 → {{0.238281, 0.17682, 0.322407, 0.359246, 0.355793, 0.522124, 0.252704,
    0.201356, 0.357029, 0.21881}, {0.0109802, -0.0184943, -0.982219, 0.0776608, 0.0841305,
    -0.0338096, 0.0220946, 0.0612914, -0.0238312, 0.0394322, 0.0499216, 0.00319927, 0.0462672,
    0.0341703, -0.0309623, -0.0390896, -0.0164572, -0.0358933, 0.0591501, -0.0284227}},
  SpikeNegative_12 → {{0.21882, 0.272457, 0.137057, 0.584451, 0.288805, 0.313426, 0.512363,
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    0.0720749, 0.0813909, -0.0598944, 0.0771004, -0.0494407, 0.0874585, -0.00158707}},
  SpikeNegative_13 → {{0.122891, 0.126414, 0.134321, 0.271836, 0.149471, 0.655934, 0.335639,
    0.243309, 0.429908, 0.260222}, {-0.0982731, 0.0848884, -0.96196, 0.0758061, 0.0626816,
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    0.0258236, 0.0794621, -0.0776833, -0.0423463, 0.0380306, -0.061175, 0.0188579, 0.0445505}},
  SpikeNegative_14 → {{0.168548, 0.28573, 0.19186, 0.154402, 0.254892, 0.570091, 0.371538,
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    -0.0480653, -0.006222, -0.065381, -0.0101373, 0.0846189, -0.0597597, -0.0622644, 0.0387389}},
  SpikeNegative_15 → {{0.270327, 0.332576, 0.213244, 0.293332, 0.188424, 0.28275, 0.317966,
    0.269361, 0.555257, 0.295601}, {-0.0684678, 0.00163073, -0.984171, 0.0151192, -0.0359712,
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    0.0371087, 0.0592896, -0.0286222, 0.0429108, -0.00283483, -0.0214072, -0.0338992}},
  SpikeNegative_16 → {{0.206492, 0.281637, 0.238351, 0.457049, 0.468682, 0.180205, 0.35596,
    0.265909, 0.296654, 0.273462}, {0.0702752, 0.0245346, -0.970042, 0.044003, 0.0397228,
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    -0.0802492, 0.0694406, -0.066287, -0.0503832, 0.0664645, -0.039692, -0.0877904}},
  SpikeNegative_17 → {{0.176372, 0.323686, 0.173258, 0.332032, 0.434904, 0.301099, 0.374372,
    0.327799, 0.282134, 0.341832}, {-0.00716288, -0.0659571, -0.975344, 0.0419934, -0.0458457,
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  SpikeNegative_18 → {{0.134197, 0.470455, 0.335392, 0.260266, 0.291946, 0.350592, 0.185295,
    0.299892, 0.400554, 0.295936}, {-0.0187718, -0.0598362, -0.977564, 0.0396097, -0.0151647,
    0.0134726, -0.021198, 0.0397173, -0.0669308, -0.0301432, -0.0843302, -0.0798061, -0.00671947,
    -0.0460581, -0.0355382, 0.0733061, 0.0282104, 0.0882172, -0.00476239, -0.012444}},
  SpikeNegative_19 → {{0.255659, 0.385035, 0.345797, 0.361291, 0.322421, 0.373808, 0.367754,
    0.159256, 0.324067, 0.164218}, {0.0792551, 0.00610192, -0.974334, -0.0144928, 0.00991565,
    0.0223759, 0.0714463, 0.0909331, 0.0596916, 0.00762243, -0.0713428, -0.00126643, -0.0183805,
    0.048681, -0.0704264, -0.0696318, -0.027174, -0.0463947, -0.0453522, -0.0632056}},
  SpikeNegative_20 → {{0.17803, 0.426613, 0.286171, 0.359723, 0.316372, 0.548758, 0.335014,
    0.128689, 0.165966, 0.132082}, {0.0588079, -0.0920445, -0.964901, -0.0138333, 0.0727882,
    -0.0176159, 0.0611537, -0.0233295, -0.0797593, -0.0612105, -0.0173368, -0.0681204,
    -0.0638019, 0.0924787, 0.0374556, 0.0717738, 0.0745809, -0.0592612, 0.0265041, 0.0542992}}|>,
f1 → <|LinearPositive_1 → {{0.983985, 0.167424, 0.0328055, 0.00193734, 0.00182301, 0.0114572,
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    0.0934276, 0.112129, 0.131756, 0.148618, 0.167088, 0.186222, 0.204508, 0.224776,
    0.240882, 0.262167, 0.280937, 0.298145, 0.319043, 0.336074, 0.35567, 0.371842}},
  LinearPositive_2 → {{0.984282, 0.165991, 0.0334999, 0.00196835, 0.00116231, 0.010039,
    0.0200007, 0.0264511, 0.0188956, 0.0308255}, {0.018615, 0.0360453, 0.0557215, 0.0760094,
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    0.240871, 0.259825, 0.280668, 0.299327, 0.317106, 0.334244, 0.35651, 0.371986}},
  LinearPositive_3 → {{0.983607, 0.169262, 0.0315293, 0.00221263, 0.00249517, 0.00989564,
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    0.0929049, 0.112367, 0.130101, 0.149254, 0.169073, 0.187226, 0.204331, 0.222253,
    0.244126, 0.25983, 0.278655, 0.299854, 0.317308, 0.335246, 0.354885, 0.375094}},
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LinearPositive_4 → {{0.983629, 0.168872, 0.0324502, 0.00204758, 0.00160901, 0.0102593,
   0.0227993, 0.0285666, 0.0188714, 0.0331647}, {0.0197516, 0.0390665, 0.0562414, 0.0731375,
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   0.241599, 0.260575, 0.280125, 0.299551, 0.316329, 0.337881, 0.354618, 0.372663}},
LinearPositive_5 → {{0.984207, 0.165115, 0.031745, 0.00249073, 0.00158526,
   0.0112917, 0.0201167, 0.0303561, 0.0194849, 0.0349785},
  {0.0182988, 0.0382, 0.0559839, 0.0763377, 0.0927184, 0.111758, 0.129626, 0.148014, 0.169441, 0.186455,
   0.206566, 0.224342, 0.24044, 0.262327, 0.278911, 0.297962, 0.316954, 0.336907, 0.355551, 0.37335}},
LinearPositive_6 → {{0.983629, 0.168679, 0.0315039, 0.00226836, 0.00204493, 0.0104391,
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   0.244101, 0.261064, 0.279959, 0.299765, 0.317069, 0.336123, 0.354359, 0.372947}},
LinearPositive_7 → {{0.984351, 0.164554, 0.0302749, 0.00205466, 0.00255111, 0.0118097,
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   0.242217, 0.261965, 0.279621, 0.300363, 0.319225, 0.335529, 0.353327, 0.374295}},
LinearPositive_8 → {{0.984307, 0.165362, 0.0310805, 0.00277722, 0.00218824, 0.00979115,
   0.0217635, 0.0284905, 0.0184458, 0.0330869}, {0.0204915, 0.0385519, 0.0560731,
   0.0739424, 0.0934021, 0.112217, 0.131048, 0.147668, 0.168778, 0.188175, 0.203381,
   0.22321, 0.243065, 0.262425, 0.280493, 0.298469, 0.316367, 0.33607, 0.354773, 0.3735}},
LinearPositive_9 → {{0.983958, 0.167148, 0.031743, 0.00197109, 0.00179572, 0.00968964,
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LinearPositive_10 → {{0.984436, 0.163975, 0.0303378, 0.00224573, 0.00295764, 0.0120854,
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   0.243469, 0.262942, 0.278988, 0.299204, 0.317848, 0.335594, 0.352881, 0.373413}},
LinearPositive_11 → {{0.984388, 0.160719, 0.0328405, 0.00154722, 0.00169637,
   0.0123178, 0.0342136, 0.031931, 0.0174446, 0.0376712},
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LinearPositive_12 → {{0.984562, 0.16473, 0.0300582, 0.00651438, 0.00235281,
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   0.197975, 0.216493, 0.248525, 0.257958, 0.281759, 0.293327, 0.326213, 0.333709, 0.361607, 0.373165}},
LinearPositive_13 → {{0.985513, 0.159761, 0.0341128, 0.00353816, 0.000357952, 0.00914269,
   0.0145061, 0.0264076, 0.0097258, 0.0312885}, {0.0204799, 0.0305035, 0.0560878, 0.0791727,
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   0.252906, 0.257208, 0.28108, 0.294416, 0.322921, 0.329406, 0.358252, 0.366401}},
LinearPositive_14 → {{0.982768, 0.169542, 0.0318772, 0.00233186, 0.0029839, 0.0113864,
   0.0203159, 0.039123, 0.0192173, 0.0441531}, {0.0160805, 0.0450352, 0.0509483, 0.0765866,
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   0.245068, 0.265152, 0.278463, 0.303651, 0.316227, 0.33331, 0.351897, 0.367061}},
LinearPositive_15 → {{0.984506, 0.166965, 0.0233032, 0.00297519, 0.00419559,
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LinearPositive_16 → {{0.985808, 0.15906, 0.0307398, 0.000565111, 0.00179831, 0.0126147,
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   0.238338, 0.26333, 0.283332, 0.297848, 0.319454, 0.332352, 0.359095, 0.379522}},
LinearPositive_17 → {{0.984754, 0.15969, 0.02804, 0.00613785, 0.00269728,
   0.0110532, 0.0225532, 0.0364692, 0.0136022, 0.0422139},
  {0.0103368, 0.0402019, 0.0585081, 0.0759572, 0.100563, 0.115795, 0.13624, 0.143016, 0.173651, 0.180089,
   0.198964, 0.215108, 0.246096, 0.269529, 0.287112, 0.295232, 0.312339, 0.337328, 0.358947, 0.367574}},
LinearPositive_18 → {{0.979216, 0.190991, 0.0336549, 0.00130096, 0.000221687, 0.012133,
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   0.236199, 0.252685, 0.280862, 0.298448, 0.314177, 0.334641, 0.362308, 0.378868}},
LinearPositive_19 → {{0.981997, 0.176036, 0.0338037, 0.00267923, 0.00167445, 0.0206933,
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LinearPositive_20 → {{0.981453, 0.175264, 0.0382493, 0.00118975, 0.00521065, 0.0148119,
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  LinearNegative_1 → {{0.982654, 0.157522, 0.068966, 0.00781972, 0.000278269, 0.00950426,
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    -0.256985, -0.268419, -0.271934, -0.288482, -0.303103, -0.349133, -0.348596, -0.371614}},
  LinearNegative_2 → {{0.980699, 0.188877, 0.0305299, 0.00847553, 0.00168516, 0.00611453,
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  LinearNegative_3 → {{0.980239, 0.188172, 0.0270281, 0.00290176, 0.0158093, 0.00922239,
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  LinearNegative_4 → {{0.974542, 0.201289, 0.0390513, 0.00277157, 0.00221901, 0.0205234,
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  LinearNegative_5 → {{0.986768, 0.140542, 0.0233124, 0.0016182, 0.000686887, 0.0189287,
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  LinearNegative_6 → {{0.988643, 0.135137, 0.0249375, 0.00222662, 0.00180561, 0.00174085,
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  LinearNegative_7 → {{0.984113, 0.154526, 0.0367736, 0.000270206, 0.00424096, 0.0149114,
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  LinearNegative_8 → {{0.990182, 0.130169, 0.0252611, 0.00105159, 0.00162709, 0.00878773,
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  LinearNegative_9 → {{0.982623, 0.167266, 0.0203323, 0.0107643, 0.00812261, 0.0246007,
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  LinearNegative_11 → {{0.98511, 0.162152, 0.0359095, 0.00317666, 0.000463496, 0.0107606,
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  LinearNegative_15 → {{0.981776, 0.172042, 0.0345481, 0.00462935, 0.00173467, 0.00671893,
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  LinearNegative_16 → {{0.984571, 0.162209, 0.0337627, 0.00558202, 0.000572966, 0.00977281,
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  LinearNegative_18 → {{0.986261, 0.14967, 0.0349958, 0.00105222, 0.00143069, 0.0139558,
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      -0.240347, -0.257017, -0.281286, -0.299696, -0.318082, -0.339022, -0.353786, -0.369423}}|>,
f3 → <|Sinusoidal3_21 → {{0.00327884, 0.0714666, 0.992531, 0.086525, 0.0366168, 0.0188517,
      0.00818245, 0.00240002, 0.0225522, 0.000720536}, {0.187317, -0.103582, -0.297752, -0.253711,
      0.00406616, 0.253472, 0.297682, 0.1006, -0.181155, -0.315134, -0.189176, 0.0924202,
      0.300003, 0.259375, -0.0029073, -0.257366, -0.303322, -0.0939211, 0.18858, 0.319049}},
  Sinusoidal3_22 → {{0.00296026, 0.0748904, 0.992822, 0.0818001, 0.0340676, 0.0185746,
      0.00742669, 0.00250117, 0.0206799, 0.00082306}, {0.180533, -0.0987908, -0.296541, -0.254,
      -0.00240605, 0.251916, 0.30509, 0.103233, -0.188193, -0.32089, -0.183825, 0.0945416,
      0.303386, 0.258976, 0.0024458, -0.253646, -0.303174, -0.0932446, 0.184853, 0.314072}},
  Sinusoidal3_23 → {{0.0029962, 0.0746351, 0.992723, 0.0826832, 0.0347817, 0.0170952, 0.00747628,
      0.00225519, 0.0228343, 0.000644194}, {0.185819, -0.103061, -0.295995, -0.256311,
      -0.00111215, 0.251519, 0.300571, 0.0981714, -0.183982, -0.323358, -0.183478, 0.0948836,
      0.303956, 0.258296, 0.000573503, -0.256897, -0.306626, -0.0921739, 0.180481, 0.311497}},
  Sinusoidal3_24 → {{0.00240106, 0.0745234, 0.992304, 0.0868039, 0.0363455, 0.0203682,
      0.00816668, 0.00208349, 0.0207565, 0.000606924}, {0.18816, -0.0936882, -0.298485, -0.253631,
      0.00110945, 0.250908, 0.301222, 0.0933487, -0.190983, -0.315924, -0.179701, 0.101762,
      0.306163, 0.261006, -0.00121493, -0.251026, -0.305063, -0.0970976, 0.189197, 0.312887}},
  Sinusoidal3_25 → {{0.00320492, 0.0687534, 0.992967, 0.0838631, 0.0377674, 0.0184346,
      0.00899442, 0.00291417, 0.0197119, 0.00109722}, {0.181563, -0.0943124, -0.304125, -0.254249,
      -0.00521637, 0.250927, 0.301487, 0.100431, -0.183947, -0.317106, -0.185739, 0.100806,
      0.300001, 0.250636, -0.000672658, -0.257497, -0.303949, -0.0955863, 0.186406, 0.320292}},
  Sinusoidal3_26 → {{0.00345224, 0.0788068, 0.991936, 0.088463, 0.0359257, 0.0186921,
      0.00791449, 0.003795, 0.0171593, 0.00168281}, {0.179826, -0.096652, -0.301112, -0.254047,
      0.00323079, 0.260842, 0.294419, 0.102283, -0.190944, -0.313991, -0.179008, 0.0993844,
      0.304523, 0.261275, 0.00595932, -0.259234, -0.301094, -0.102376, 0.187896, 0.310271}},
  Sinusoidal3_27 → {{0.00389344, 0.0756579, 0.992528, 0.0843747, 0.0351644, 0.0171838,
      0.00790357, 0.0028715, 0.0206216, 0.00101265}, {0.182564, -0.101947, -0.298174, -0.255669,
      0.00123932, 0.256282, 0.306811, 0.0994089, -0.183624, -0.314541, -0.190839, 0.0959313,
      0.303648, 0.251689, 0.00582231, -0.258624, -0.30323, -0.0966768, 0.181738, 0.311827}},
  Sinusoidal3_28 → {{0.00247586, 0.0708809, 0.992507, 0.0871917, 0.0376063, 0.0204758, 0.00916723,
      0.00259637, 0.0192707, 0.000926497}, {0.187471, -0.0937736, -0.303259, -0.256217,
      -0.00311804, 0.253588, 0.30123, 0.102503, -0.187074, -0.317321, -0.18684, 0.0957068,
      0.296946, 0.260693, 0.000714232, -0.249275, -0.299238, -0.0997791, 0.191281, 0.314265}},
  Sinusoidal3_29 → {{0.00403566, 0.0752563, 0.99237, 0.085419, 0.0385877, 0.0185081, 0.00825854,
      0.00328831, 0.0176775, 0.00137836}, {0.180983, -0.0932706, -0.303685, -0.25513,
      0.00368587, 0.256012, 0.298541, 0.101058, -0.180006, -0.321347, -0.183397, 0.0935285,
      0.305704, 0.253071, 0.00167295, -0.260473, -0.304103, -0.10323, 0.184952, 0.309186}},
  Sinusoidal3_30 → {{0.00296487, 0.068009, 0.992913, 0.085367, 0.0364234, 0.0193505, 0.008435,
      0.00276239, 0.020548, 0.00100654}, {0.191347, -0.0920654, -0.298299, -0.256266,
      -0.00417914, 0.250364, 0.298828, 0.103721, -0.190985, -0.312121, -0.188145, 0.101955,
      0.297076, 0.257164, -0.00325659, -0.259144, -0.304852, -0.0974504, 0.186927, 0.31446}}|>,
f5 → <|Sinusoidal2_11 → {{0.00181779, 0.00957387, 0.0318158, 0.0895246, 0.934626, 0.340371,
      0.0263298, 0.00470244, 0.0279551, 0.00163384}, {-0.102146, -0.25524, 0.254858, 0.0918994,
      -0.316819, 0.0934641, 0.253029, -0.256533, -0.0972243, 0.321624, -0.100887, -0.257539,
      0.255053, 0.0978558, -0.31217, 0.0969952, 0.256865, -0.252641, -0.0919434, 0.320829}},
  Sinusoidal2_12 → {{0.00224262, 0.0100748, 0.0350277, 0.0941632, 0.930129, 0.350987,
      0.0272973, 0.00441086, 0.0264708, 0.00154854}, {-0.102835, -0.255556, 0.25366, 0.103885,
      -0.319568, 0.0923809, 0.256785, -0.250309, -0.0919122, 0.316873, -0.10086, -0.261199,
      0.26068, 0.0993969, -0.313294, 0.104164, 0.254246, -0.253962, -0.0994046, 0.310837}},
  Sinusoidal2_13 → {{0.00308455, 0.0113633, 0.0308781, 0.0981732, 0.9285, 0.354217, 0.0307521,
      0.00423434, 0.0268938, 0.00143824}, {-0.102283, -0.257913, 0.254197, 0.101146,
```

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```
    -0.31792, 0.0990659, 0.263321, -0.252662, -0.0952994, 0.313427, -0.0997244, -0.251013,
    0.256261, 0.0976352, -0.315379, 0.101918, 0.251065, -0.261182, -0.0922397, 0.314686}},
  Sinusoidal2_14 → {{0.00272178, 0.0112166, 0.030211, 0.0965752, 0.935616, 0.335338, 0.0297195,
    0.00638971, 0.0294676, 0.00256919}, {-0.0943336, -0.261216, 0.259473, 0.0954593,
    -0.315733, 0.103159, 0.250721, -0.252605, -0.100392, 0.311754, -0.101455, -0.252873,
    0.252602, 0.0944352, -0.31419, 0.0947504, 0.260225, -0.260045, -0.100785, 0.319383}},
  Sinusoidal2_15 → {{0.00219132, 0.0096725, 0.0302119, 0.0942665, 0.93694, 0.332675, 0.0263432,
    0.0042484, 0.0293064, 0.00135499}, {-0.102346, -0.257031, 0.260755, 0.092903,
    -0.316279, 0.0998906, 0.254281, -0.252804, -0.100166, 0.311332, -0.102976, -0.260407,
    0.254208, 0.0995047, -0.316749, 0.101394, 0.258785, -0.248628, -0.0966761, 0.315618}},
  Sinusoidal2_16 → {{0.00272976, 0.0101144, 0.0311974, 0.0937662, 0.933187, 0.342895, 0.0284966,
    0.00445665, 0.0295787, 0.00146407}, {-0.0924687, -0.254662, 0.258726, 0.0937955,
    -0.314401, 0.0954146, 0.258823, -0.259848, -0.0958138, 0.319627, -0.0937956, -0.256277,
    0.252609, 0.0926329, -0.315137, 0.0964877, 0.258083, -0.258967, -0.10148, 0.312406}},
  Sinusoidal2_17 → {{0.00237785, 0.010703, 0.0279469, 0.0913897, 0.931997, 0.347087, 0.0266903,
    0.00450181, 0.0304053, 0.00147689}, {-0.0921019, -0.256927, 0.259888, 0.0940753,
    -0.31405, 0.0975934, 0.258978, -0.253024, -0.0991143, 0.314163, -0.101765, -0.257361,
    0.262657, 0.0997098, -0.317532, 0.0969668, 0.25464, -0.251483, -0.0952186, 0.313763}},
  Sinusoidal2_18 → {{0.00324295, 0.0116709, 0.0275198, 0.0934798, 0.932732, 0.344509, 0.0299234,
    0.00559555, 0.0273779, 0.00218217}, {-0.0953021, -0.255808, 0.254663, 0.101432,
    -0.311579, 0.102577, 0.25803, -0.253088, -0.0980007, 0.316, -0.101885, -0.249242,
    0.258356, 0.0966583, -0.317759, 0.092371, 0.259596, -0.256838, -0.0949933, 0.319633}},
  Sinusoidal2_19 → {{0.00226919, 0.0106161, 0.0305182, 0.0938892, 0.930958, 0.348975, 0.0292464,
    0.00619168, 0.0277433, 0.00249124}, {-0.0912385, -0.258743, 0.257111, 0.102916,
    -0.321512, 0.0985333, 0.253611, -0.255808, -0.101557, 0.314227, -0.0961898, -0.259972,
    0.256371, 0.0935846, -0.313604, 0.0965954, 0.257454, -0.253799, -0.101251, 0.310152}},
  Sinusoidal2_20 → {{0.00287168, 0.0118206, 0.0299209, 0.0917174, 0.9342, 0.340788, 0.0271472,
    0.00439872, 0.0303247, 0.00140647}, {-0.0986387, -0.25875, 0.260625, 0.0966721,
    -0.313379, 0.102063, 0.251999, -0.26234, -0.103724, 0.312401, -0.100986, -0.260099,
    0.251798, 0.0932326, -0.317372, 0.0993944, 0.251239, -0.253421, -0.0976202, 0.315158}}|>,
f6 → <|Sinusoidal1_1 → {{0.00298875, 0.00870514, 0.0180078, 0.0326069, 0.0838575, 0.985927,
    0.13722, 0.00209855, 0.0247028, 0.000283552}, {-0.169844, -0.0999165, 0.312054, -0.226886,
    0.0082717, 0.251345, -0.287438, 0.0664941, 0.193204, -0.335016, 0.210701, 0.0817488,
    -0.317357, 0.271274, -0.00113056, -0.244695, 0.309459, -0.0890122, -0.155717, 0.315073}},
  Sinusoidal1_2 → {{0.00211248, 0.0111664, 0.0172166, 0.0250448, 0.0864492, 0.990354, 0.101858,
    0.0054511, 0.0162135, 0.00210037}, {-0.183135, -0.085849, 0.283297, -0.250114,
    0.0294515, 0.248326, -0.303014, 0.0802454, 0.170615, -0.333638, 0.179995, 0.0703624,
    -0.308341, 0.273284, 0.0125912, -0.274737, 0.311395, -0.110928, -0.185182, 0.297915}},
  Sinusoidal1_3 → {{0.00972567, 0.00708023, 0.0102732, 0.0314505, 0.090621, 0.991643, 0.0817988,
    0.00727088, 0.0209412, 0.00304041}, {-0.192621, -0.0894681, 0.314766, -0.274315,
    0.0222813, 0.278389, -0.298989, 0.105314, 0.158085, -0.323686, 0.162816, 0.0795048,
    -0.313, 0.230264, -0.0165754, -0.285575, 0.278321, -0.0816075, -0.16731, 0.307501}},
  Sinusoidal1_4 → {{0.00298852, 0.00633496, 0.0232794, 0.0360283, 0.105603, 0.988108,
    0.0967453, 0.00128584, 0.0352106, 0.000280295}, {-0.162976, -0.0736948, 0.332062,
    -0.258, 0.0118881, 0.241068, -0.28338, 0.0973393, 0.214487, -0.304707, 0.1806, 0.093946,
    -0.296116, 0.270298, -0.015565, -0.243918, 0.304523, -0.0754175, -0.188427, 0.329302}},
  Sinusoidal1_5 → {{0.00395033, 0.001741, 0.0231724, 0.0359091, 0.0838233, 0.98672, 0.131135,
    0.00991729, 0.0138138, 0.00517776}, {-0.171288, -0.0959572, 0.293953, -0.232923,
    -0.0142033, 0.259195, -0.29767, 0.118843, 0.200119, -0.302733, 0.209081, 0.070545,
    -0.328474, 0.24689, -0.00363711, -0.250612, 0.325536, -0.102637, -0.158616, 0.311373}},
  Sinusoidal1_6 → {{0.0044267, 0.00569231, 0.0189772, 0.0359945, 0.0764742, 0.988445, 0.12138,
    0.00106881, 0.0261797, 0.0000952612}, {-0.20199, -0.124427, 0.280519, -0.254657,
    -0.00953567, 0.246464, -0.304336, 0.104359, 0.210008, -0.323168, 0.204747, 0.108497,
    -0.316332, 0.266735, -0.0235157, -0.23696, 0.271156, -0.0972847, -0.192537, 0.292607}},
  Sinusoidal1_7 → {{0.00466062, 0.00196003, 0.0216546, 0.0332104, 0.0918312, 0.989277,
    0.102347, 0.00439162, 0.0283679, 0.00123122}, {-0.173523, -0.106035, 0.286107, -0.245677,
    -0.00117433, 0.272415, -0.276545, 0.116136, 0.211283, -0.285594, 0.179688, 0.0980431,
    -0.324888, 0.260458, 0.00911654, -0.245803, 0.303289, -0.0815159, -0.194957, 0.337077}},
  Sinusoidal1_8 → {{0.000958251, 0.00251062, 0.0131592, 0.0340965, 0.0908623, 0.992562,
    0.0699721, 0.0107832, 0.0133077, 0.00562073}, {-0.206527, -0.0887062, 0.277052, -0.279736,
    -0.00907299, 0.250919, -0.301022, 0.124887, 0.157029, -0.29684, 0.177643, 0.0902014,
    -0.305533, 0.248704, 0.0160817, -0.282923, 0.3186, -0.0735031, -0.185805, 0.309529}},
  Sinusoidal1_9 → {{0.00156818, 0.00961423, 0.0234583, 0.0339226, 0.0673208, 0.990997,
    0.105032, 0.00480591, 0.0232082, 0.00165578}, {-0.192049, -0.118401, 0.276005, -0.230238,
    -0.0153502, 0.225065, -0.317269, 0.103329, 0.178562, -0.32432, 0.176281, 0.110867,
    -0.328631, 0.26729, 0.00611968, -0.270639, 0.280024, -0.100157, -0.214758, 0.29993}},
```

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```
Sinusoidal1_10 → {{0.00986012, 0.00938438, 0.0179365, 0.037415, 0.100151, 0.990128, 0.085156,
   0.00347194, 0.0210926, 0.000851912}, {-0.208486, -0.0817182, 0.319824, -0.269535,
   0.0100686, 0.264246, -0.303073, 0.095196, 0.189285, -0.296793, 0.194346, 0.0857397,
   -0.314905, 0.222057, -0.0295158, -0.274562, 0.266782, -0.0978667, -0.175764, 0.314112}} |> |⟩
```

Let's print the dendrograms, with a left orientation and in blue:

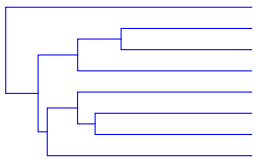
```
In[3]:= clusters1DendrogramOptions = TimeSeriesClusters[classification1,
   PrintDendrograms → True, DendrogramPlotOptions → {PlotStyle → Blue, Orientation → Left}];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

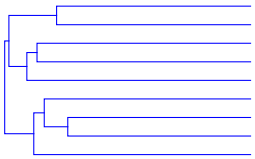
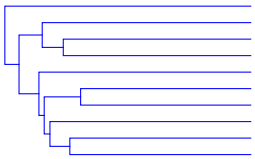
Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

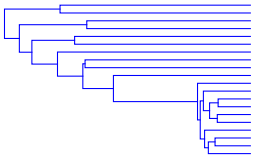
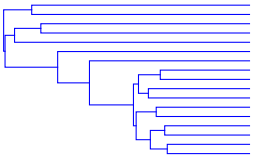
General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

⟨| SpikeMax → ⟨| G1 → ⟨| {G1S1} →  , {G1S2} → |⟩ ,

G2 → ⟨| {G2S1} → |⟩ |⟩ ,

SpikeMin → ⟨| G1 → ⟨| {G1S1} →  , {G1S2} →  |⟩ ,

G2 → ⟨| {G2S1} → {{-0.964089, 0.0505211, -0.0700959, -0.0242415, -0.0152793,
-0.0988989, 0.0341947, -0.0416477, -0.0897023, 0.0990235, -0.0972136,
0.0990263, -0.0107728, 0.0309565, 0.0183618, 0.00930295, 0.0612632,
-0.0477844, 0.0654077, -0.0252868} → SpikeNegative_4} |⟩ |⟩ ,

f1 → ⟨| G1 → ⟨| {G1S1} →  , {G1S2} →  |⟩ ,

G2 → ⟨| {G2S1} → {{-0.0110301, -0.0374316, -0.0679157, -0.0590307,
-0.100358, -0.118107, -0.145138, -0.151847, -0.166683,
-0.195226, -0.21855, -0.2331, -0.223109, -0.248773, -0.276709,
-0.308414, -0.300835, -0.346339, -0.33939, -0.381116} →

LinearNegative_4}, {G2S2} → |⟩ |⟩ ,

f3 → ⟨| G1 → ⟨| {G1S1} → {{0.187317, -0.103582, -0.297752, -0.253711,

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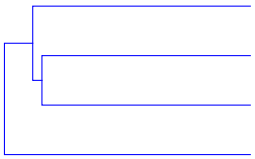
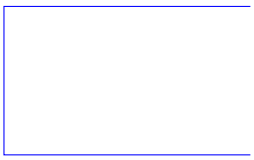
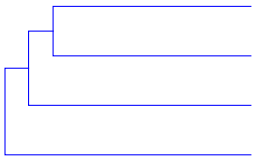
```
    0.00406616, 0.253472, 0.297682, 0.1006, -0.181155, -0.315134,
    -0.189176, 0.0924202, 0.300003, 0.259375, -0.0029073, -0.257366,
    -0.303322, -0.0939211, 0.18858, 0.319049} → Sinusoidal3_21},
```

{G1S2} →  |⟩, G2 → ⟨| {G2S1} → ,

```
{G2S2} → {{0.182564, -0.101947, -0.298174, -0.255669, 0.00123932,
    0.256282, 0.306811, 0.0994089, -0.183624, -0.314541, -0.190839,
    0.0959313, 0.303648, 0.251689, 0.00582231, -0.258624,
    -0.30323, -0.0966768, 0.181738, 0.311827} → Sinusoidal3_27} |⟩,
```

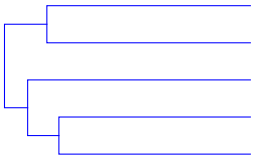
G3 → ⟨| {G3S1} →  |⟩ |⟩, f5 →

⟨| G1 → ⟨| {G1S1} →  ,

```
{G1S2} → {{-0.0924687, -0.254662, 0.258726, 0.0937955, -0.314401,
    0.0954146, 0.258823, -0.259848, -0.0958138, 0.319627, -0.0937956,
    -0.256277, 0.252609, 0.0926329, -0.315137, 0.0964877,
    0.258083, -0.258967, -0.10148, 0.312406} → Sinusoidal2_16},
```

{G1S3} → |⟩, G2 → ⟨| {G2S1} → ,

```
{G2S2} → {{-0.0912385, -0.258743, 0.257111, 0.102916, -0.321512,
    0.0985333, 0.253611, -0.255808, -0.101557, 0.314227, -0.0961898,
    -0.259972, 0.256371, 0.0935846, -0.313604, 0.0965954, 0.257454,
    -0.253799, -0.101251, 0.310152} → Sinusoidal2_19} |⟩ |⟩,
```

f6 → ⟨| G1 → ⟨| {G1S1} →  , {G1S2} → |⟩,

G2 → ⟨| {G2S1} → ,

```
{G2S2} → {{-0.206527, -0.0887062, 0.277052, -0.279736, -0.00907299,
    0.250919, -0.301022, 0.124887, 0.157029, -0.29684, 0.177643,
    0.0902014, -0.305533, 0.248704, 0.0160817, -0.282923, 0.3186,
    -0.0735031, -0.185805, 0.309529} → Sinusoidal1_8} |⟩ |⟩ |⟩
```

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DistanceFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

DistanceFunction provides options for which DistanceFunction to use in the first tier clustering.

We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.324409, 0.170114, 0.165824, 0.123258, 0.296411, 0.168117, 0.113074, 0.338552,
      0.684644, 0.332967}, {0.961598, -0.0784818, 0.0810648, 0.00311141, 0.0587387, -0.0958059,
      -0.049226, -0.0684896, -0.0610883, -0.0440209, -0.0191229, 0.0976175, 0.023173,
      -0.0669337, 0.0841547, -0.0357017, 0.079293, 0.0713104, -0.0457205, -0.0210911}},
   SpikePositive_2 → {{0.334467, 0.153398, 0.110432, 0.323538, 0.266019, 0.424313, 0.318101,
      0.305017, 0.452943, 0.312315}, {0.96344, -0.0652302, -0.0609021, 0.102723, 0.0572351,
      0.0667109, -0.025624, -0.0576658, -0.00950837, 0.026989, -0.0986821, -0.0758774, -0.0772708,
      -0.0816285, -0.0474007, 0.0410352, 0.0384367, -0.027473, -0.0715449, -0.0364503}},
   SpikePositive_3 → {{0.237775, 0.251808, 0.365905, 0.328654, 0.256463, 0.230115, 0.189401,
      0.316748, 0.518767, 0.337799}, {0.980425, 0.0628899, -0.00578454, -0.050829, 0.0382936,
      0.0195252, 0.0662929, -0.0263428, -0.0025991, 0.00223482, -0.0592579, 0.0193684, -0.0560032,
      -0.035472, -0.00588783, -0.0817247, -0.027714, 0.0388076, -0.0121693, -0.0884821}},
   SpikePositive_4 → {{0.0766058, 0.177007, 0.187344, 0.274591, 0.30402, 0.40651, 0.323552,
      0.312303, 0.509701, 0.364157}, {0.974075, -0.0836186, -0.0576299, 0.0175985, 0.045611,
      0.00957002, 0.0860471, 0.0352185, 0.0528924, 0.0699089, -0.0261313, 0.0314563, -0.0515711,
      0.0494964, -0.0635652, 0.0774129, -0.0538926, -0.03402, 0.0149701, -0.0308797}},
   SpikePositive_5 → {{0.356249, 0.362821, 0.169696, 0.32207, 0.205216, 0.422436, 0.0933727,
      0.140038, 0.586208, 0.128008}, {0.96115, 0.0915494, 0.0510295, -0.0200335, -0.0265268,
      -0.0803989, -0.0420036, -0.0746378, -0.0615318, 0.0778489, 0.0189356, -0.0828489,
      0.0861323, -0.0884553, 0.045092, 0.0653972, -0.0813578, 0.0244817, -0.0450231, 0.0493382}},
   SpikePositive_6 → {{0.223601, 0.173281, 0.327951, 0.262359, 0.139409, 0.504536, 0.231769,
      0.243409, 0.540111, 0.254785}, {0.964113, 0.0392403, 0.0748115, 0.0935003, 0.0306903,
      -0.0287454, 0.093744, -0.00149223, 0.00297592, 0.0500414, -0.0588538, -0.0707234, 0.0824526,
      0.0756554, -0.0482946, -0.0531639, -0.0664139, -0.0972533, -0.0103852, 0.037575}},
   SpikePositive_7 → {{0.319523, 0.296405, 0.157895, 0.431088, 0.0852705, 0.249883, 0.22182,
      0.222771, 0.601288, 0.263042}, {0.952834, 0.0945743, 0.030454, -0.0452833, 0.0491966,
      -0.0344369, -0.0362046, -0.0918258, -0.0790606, 0.0850141, 0.079548, -0.0939621, -0.0400184,
      0.0854323, -0.0627653, 0.003358, 0.0281629, 0.0935197, -0.0860753, -0.0916674}},
   SpikePositive_8 → {{0.25955, 0.193723, 0.347494, 0.341775, 0.304991, 0.278284, 0.124688,
      0.349916, 0.483867, 0.339067}, {0.958091, -0.0314661, -0.0677753, 0.0941882, 0.0953837,
      0.0613179, -0.0569369, 0.0587116, -0.0579202, 0.0495027, -0.0941885, 0.0363477, 0.0404173,
```

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```
    -0.0382393, -0.0735132, -0.0835398, -0.0143758, 0.0739196, -0.0945755, 0.044349}},
  SpikePositive_9 → {{0.402032, 0.314144, 0.0849046, 0.216271, 0.261497, 0.229649, 0.23392,
    0.276437, 0.583299, 0.305301}, {0.961595, 0.0601491, 0.0611236, -0.0171698, -0.0647952,
    -0.0543573, -0.0755457, -0.0821092, 0.0554399, 0.0386217, -0.0526821, 0.0802057, -0.062859,
    -0.00571523, 0.0931794, 0.0936427, 0.0400029, 0.0514697, -0.0885209, -0.0280979}},
  SpikePositive_10 → {{0.191051, 0.181014, 0.385388, 0.265829, 0.107359, 0.443934, 0.507368,
    0.205606, 0.399869, 0.208204}, {0.966831, 0.00607185, -0.0804752, 0.0265999, -0.0870397,
    0.0690163, 0.0795389, -0.0321288, 0.0196556, -0.0267794, -0.0517151, -0.0937161, 0.0189925,
    0.0540714, -0.102079, -0.0365956, 0.0321433, -0.0818259, -0.0526239, -0.0147425}},
  SpikePositive_11 → {{0.148919, 0.390472, 0.254307, 0.320998, 0.297897, 0.397987, 0.332789,
    0.242302, 0.418196, 0.257214}, {0.0401193, -0.0910461, 0.964525, 0.0365123, -0.0885476,
    0.0268375, 0.0414704, -0.0193192, 0.0747423, -0.0661318, 0.0775741, 0.0626327, 0.0105756,
    0.0385886, -0.0413832, -0.0663581, -0.0969631, -0.0952763, -0.0242641, -0.0334632}},
  SpikePositive_12 → {{0.265742, 0.117546, 0.403624, 0.479129, 0.167669, 0.325997, 0.244961,
    0.27459, 0.414912, 0.284855}, {-0.0454271, -0.0167973, 0.967797, -0.0771211, -0.00968068,
    -0.0687945, -0.00183506, 0.0312344, 0.0891281, -0.0782193, -0.0972396, -0.00889991,
    -0.0385532, -0.0982314, -0.0288761, 0.0802374, 0.0409004, -0.0487324, -0.0031135, 0.0566374}},
  SpikePositive_13 → {{0.173279, 0.245618, 0.294944, 0.345844, 0.427337, 0.278339, 0.355834,
    0.335467, 0.298559, 0.33862}, {0.00189091, 0.0221816, 0.984424, -0.0100288, 0.0132018,
    0.00594962, -0.019277, -0.0212296, -0.0791649, 0.0230189, 0.0415584, 0.00594445, -0.00937534,
    0.0506408, 0.0334736, 0.0646462, 0.0857078, 0.0128384, -0.0327356, -0.0647042}},
  SpikePositive_14 → {{0.365713, 0.131486, 0.384639, 0.293238, 0.30674, 0.254335, 0.410016,
    0.317627, 0.280831, 0.329222}, {0.100438, -0.000524075, 0.965334, 0.0401153, -0.0842799,
    0.0237028, -0.0330817, 0.0359796, 0.039724, 0.0492155, -0.0980652, -0.0981046, -0.017342,
    -0.0368979, -0.0925996, 0.0899983, 0.0531406, -0.0161144, 0.0254894, -0.0326757}},
  SpikePositive_15 → {{0.168642, 0.180759, 0.374248, 0.28054, 0.398254, 0.27873, 0.28357,
    0.365957, 0.365981, 0.368166}, {0.0273659, -0.0756866, 0.971883, -0.00316362, -0.0391962,
    -0.0436402, 0.00898363, 0.0549797, 0.0809708, 0.078566, -0.0559259, -0.0443052, 0.00758892,
    0.0254679, -0.0625557, -0.0825764, -0.000688716, -0.0509654, -0.0590314, -0.0840962}},
  SpikePositive_16 → {{0.113839, 0.276447, 0.254759, 0.354632, 0.198091, 0.552714, 0.420095,
    0.198242, 0.337488, 0.213403}, {0.0333572, -0.0338306, 0.967753, 0.0468255, -0.0161832,
    0.0930872, 0.0260943, 0.00974097, 0.0635434, -0.0773527, 0.05261, 0.074454, 0.0515434,
    0.00122569, 0.0771992, 0.0848385, -0.0705351, -0.0163253, -0.0338837, -0.0936158}},
  SpikePositive_17 → {{0.261061, 0.374045, 0.400207, 0.314758, 0.493563, 0.210457, 0.181021,
    0.205828, 0.357744, 0.204177}, {-0.0431428, 0.0148359, 0.97353, 0.0272582, 0.0470465,
    -0.0582541, -0.03756, -0.0318125, 0.0340365, 0.0414851, -0.0305859, -0.0551946, 0.0432195,
    0.0275345, -0.0590031, -0.0898656, 0.0915828, -0.0364591, -0.0684289, 0.0770827}},
  SpikePositive_18 → {{0.0572751, 0.460842, 0.402336, 0.223204, 0.294133, 0.473247, 0.307829,
    0.17048, 0.323254, 0.184007}, {-0.0753792, 0.0177089, 0.968826, -0.0818318, -0.0142227,
    -0.0294494, -0.0967815, -0.0326495, 0.0475555, 0.0283284, 0.062302, 0.0522249, 0.0418503,
    0.0422576, 0.0665184, -0.0512926, -0.0976195, -0.0207886, -0.0705533, 0.0444513}},
  SpikePositive_19 → {{0.131783, 0.102578, 0.241117, 0.136871, 0.502546, 0.303553, 0.277353,
    0.326786, 0.490963, 0.354662}, {0.0675407, -0.0776988, 0.967758, -0.0893773, -0.0288154,
    0.0364147, 0.0737268, -0.000694568, 0.0851939, 0.094056, 0.0128182, -0.0569573, -0.0330189,
    0.0945116, -0.0311605, -0.0307327, 0.0159362, 0.0572427, -0.0472124, 0.00735099}},
  SpikePositive_20 → {{0.297366, 0.43718, 0.447243, 0.1796, 0.410744, 0.340269, 0.233486,
    0.163875, 0.305527, 0.170156}, {0.0242373, 0.0691, 0.975304, 0.0747793, 0.0394068,
    0.00824561, -0.0538148, -0.0839856, -0.038557, 0.0335737, 0.0415809, -0.0517749, -0.0461063,
    0.0250425, 0.0865305, -0.0400083, -0.0177558, 0.0071326, -0.0837924, 0.00219165}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.179003, 0.204896, 0.297333, 0.237381, 0.265238, 0.256171,
    0.123157, 0.445015, 0.493314, 0.434372}, {-0.981318, -0.0100425, 0.0380315, 0.0197688,
    -0.0270245, -0.00672693, -0.0282116, -0.0679478, 0.0423293, -0.0710326, 0.0456178, -0.0605604,
    -0.0314144, -0.00325147, -0.0648475, 0.0226442, -0.0680108, -0.0203878, 0.0741272, -0.00722323}},
  SpikeNegative_2 → {{0.245872, 0.225012, 0.377768, 0.328454, 0.259723, 0.38181, 0.19233,
    0.174591, 0.577199, 0.156398}, {-0.956162, 0.017739, 0.077512, -0.0113142, 0.00307949,
    0.0773279, -0.101818, 0.0280849, -0.0926582, 0.0488129, 0.0898659, 0.0974435, -0.099591,
    0.0234161, -0.0779867, 0.0841428, -0.0411222, -0.033115, -0.0847825, 0.00395747}},
  SpikeNegative_3 → {{0.262819, 0.346714, 0.276141, 0.450925, 0.32582, 0.214813, 0.2329,
    0.311464, 0.364247, 0.308054}, {-0.974911, -0.0449396, 0.0591886, 0.0171312, 0.0220633,
    -0.0315871, -0.00483449, 0.0358151, 0.0389408, -0.0682913, -0.0512576, -0.087228, 0.0687409,
    0.00786763, -0.091478, 0.0151002, -0.0243068, -0.0282888, -0.0634719, -0.0756436}},
  SpikeNegative_4 → {{0.223617, 0.335725, 0.181144, 0.288271, 0.321971, 0.398915, 0.230377,
    0.356142, 0.398328, 0.346406}, {-0.975909, 0.0559513, 0.0518219, -0.0690764, -0.0262965,
    0.0396372, -0.0107718, -0.0224228, -0.0293667, -0.0835916, 0.045471, 0.0102257, 0.0225189,
    0.0671045, 0.0104705, 0.0385565, -0.0516468, 0.0284054, -0.0947395, -0.0710906}},
  SpikeNegative_5 → {{0.145001, 0.157052, 0.222327, 0.125408, 0.173933, 0.259836, 0.214589,
```

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```
    0.345517, 0.692238, 0.383096}, {-0.964327, 0.0667145, -0.00810299, 0.0670594, -0.0101228,
    0.0552289, -0.0753919, -0.0285311, 0.0770709, -0.0189331, -0.0114068, -0.0783523, 0.0368964,
    -0.0752661, 0.0496075, -0.0550931, -0.0672168, 0.0714993, 0.0952962, -0.0872166}},
  SpikeNegative_6 → {{0.344097, 0.375351, 0.212451, 0.399676, 0.143612, 0.216183, 0.349564,
    0.335704, 0.357275, 0.325477}, {-0.970591, -0.0363973, -0.0119474, -0.041528, 0.0775416,
    -0.0824483, 0.071797, -0.0114515, -0.0539497, -0.054287, 0.0867971, 0.0884819, 0.0808983,
    0.00484463, 0.0219777, 0.0702502, -0.0140336, -0.0424424, 0.0381083, -0.00276115}},
  SpikeNegative_7 → {{0.132039, 0.340113, 0.380128, 0.30797, 0.209748, 0.382568, 0.173156,
    0.355862, 0.414887, 0.329305}, {-0.970257, -0.0505386, 0.061682, 0.0161627, 0.000952396,
    -0.0285682, 0.00116972, -0.0693475, -0.0304483, -0.0897618, 0.057097, 0.0423872, -0.0928625,
    0.0455007, 0.0752469, 0.0944997, -0.00214996, 0.0485326, 0.0678758, -0.00769229}},
  SpikeNegative_8 → {{0.131093, 0.314882, 0.125857, 0.204973, 0.359241, 0.306417, 0.268164,
    0.313116, 0.585163, 0.300825}, {-0.981694, -0.00558128, 0.0162387, 0.00466025, 0.0248748,
    0.0725767, -0.0137947, -0.00926848, -0.047714, -0.0307545, -0.065042, -0.0143445,
    0.013626, 0.070069, -0.0633442, -0.00517626, -0.0474797, 0.0740414, 0.051339, 0.0513052}},
  SpikeNegative_9 → {{0.32923, 0.185845, 0.167432, 0.145041, 0.330696, 0.275704, 0.292255,
    0.377789, 0.491631, 0.390881}, {-0.976962, 0.0475481, -0.0936904, -0.0818149, -0.0225711,
    0.047689, 0.0763995, -0.0600423, 0.0416753, 0.0494156, 0.0792433, 0.0124057, 0.00739354,
    0.0309667, 0.0510013, 0.00169237, 0.00614644, 0.00336503, 0.00673845, 0.035534}},
  SpikeNegative_10 → {{0.187411, 0.0930663, 0.215966, 0.321665, 0.270455, 0.262331, 0.345698,
    0.281244, 0.624969, 0.273772}, {-0.975516, 0.0298507, -0.0437535, -0.0783597, -0.0605997,
    -0.0455421, 0.0115917, -0.0321885, 0.0296251, 0.029112, -0.0326921, 0.0594723, -0.0283263,
    -0.0677324, -0.0220843, 0.0450488, 0.0618429, 0.0708626, 0.0970465, -0.0018368}},
  SpikeNegative_11 → {{0.176128, 0.343758, 0.289346, 0.161823, 0.3588, 0.14812, 0.435386,
    0.325134, 0.437189, 0.322207}, {-0.00163858, 0.0323919, -0.97892, 0.0600375, -0.0320745,
    0.0525876, 0.00249879, 0.00306832, 0.0689435, -0.0415393, -0.0640893, 0.0817419, -0.0411028,
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  SpikeNegative_17 → {{0.166684, 0.393327, 0.385405, 0.316463, 0.322372, 0.380084, 0.429402,
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  SpikeNegative_18 → {{0.186337, 0.279965, 0.301089, 0.295955, 0.347575, 0.346384, 0.393757,
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  SpikeNegative_19 → {{0.372109, 0.253615, 0.22408, 0.218012, 0.21274, 0.299365, 0.493739,
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    0.0213689, 0.0488518, 0.0831079, 0.0467081, -0.0328894, 0.0581781, -0.078336, 0.0854451}},
  SpikeNegative_20 → {{0.144877, 0.19337, 0.175026, 0.142599, 0.207976, 0.282338, 0.379352,
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  LinearPositive_2 → {{0.984679, 0.161762, 0.0333001, 0.00167776, 0.00140789, 0.0109205,
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  LinearPositive_3 → {{0.98466, 0.163983, 0.0322273, 0.00176189, 0.00124205, 0.0103367,
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 LinearNegative_6 → {{0.978655, 0.19112, 0.040888, 0.00389164, 0.0186442, 0.030439, 0.0177513,
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 LinearNegative_12 → {{0.988495, 0.136003, 0.030744, 0.00593072, 0.000702021, 0.0125464,
    0.0145338, 0.0343565, 0.0180293, 0.0390509}, {-0.0263679, -0.0342002, -0.059017, -0.078281,
    -0.0989404, -0.114876, -0.121597, -0.143242, -0.170009, -0.181484, -0.212152, -0.222524,
    -0.243861, -0.267845, -0.283372, -0.297594, -0.307468, -0.338588, -0.351279, -0.375796}},
 LinearNegative_13 → {{0.98146, 0.178187, 0.0295216, 0.00301151, 0.00341845, 0.0137251,
    0.0237685, 0.0325506, 0.0302352, 0.036969}, {-0.0222552, -0.0402555, -0.052707, -0.0743782,
    -0.0955371, -0.116884, -0.132659, -0.156057, -0.171436, -0.195362, -0.205455, -0.223429,
    -0.24011, -0.26533, -0.274309, -0.298982, -0.310427, -0.332618, -0.348174, -0.379776}},
 LinearNegative_14 → {{0.981774, 0.180332, 0.0256042, 0.00353723, 0.00430883, 0.0133722,
    0.0250272, 0.0276591, 0.0153707, 0.0332874}, {-0.0168089, -0.0403072, -0.0651172, -0.0827957,
    -0.101917, -0.117166, -0.135523, -0.154009, -0.173065, -0.193206, -0.203322, -0.214752,
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    -0.241889, -0.260099, -0.280266, -0.291651, -0.322339, -0.327147, -0.355588, -0.372716}},
  LinearNegative_15 → {{0.987724, 0.145566, 0.0319869, 0.0033068, 0.00147833, 0.0129642,
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    -0.250936, -0.267161, -0.278694, -0.291986, -0.313951, -0.334619, -0.360808, -0.373007}},
  LinearNegative_16 → {{0.982027, 0.175165, 0.0219579, 0.00381154, 0.00409042, 0.0116753,
    0.0281979, 0.0369909, 0.0171225, 0.0428136}, {-0.0142174, -0.0429482, -0.0589244, -0.0702076,
    -0.0952233, -0.106899, -0.122869, -0.154016, -0.175891, -0.195111, -0.2074, -0.214991,
    -0.249602, -0.252965, -0.279622, -0.29724, -0.310579, -0.336733, -0.356544, -0.377085}},
  LinearNegative_17 → {{0.984102, 0.163069, 0.0387436, 0.00513678, 0.00142559, 0.00779368,
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    -0.0907055, -0.105676, -0.138321, -0.142613, -0.17695, -0.177534, -0.203353, -0.229492,
    -0.246658, -0.261704, -0.274307, -0.293598, -0.321743, -0.343219, -0.34796, -0.373367}},
  LinearNegative_18 → {{0.984242, 0.169052, 0.0229009, 0.000673742, 0.00272595, 0.015397,
    0.0197784, 0.0214214, 0.0206599, 0.0253512}, {-0.0193951, -0.0431264, -0.0641145, -0.0671858,
    -0.0881164, -0.104892, -0.125881, -0.159399, -0.172231, -0.188223, -0.2052, -0.232901,
    -0.240471, -0.261562, -0.276641, -0.30191, -0.320334, -0.330985, -0.350964, -0.372042}},
  LinearNegative_19 → {{0.984044, 0.166389, 0.0327706, 0.00107319, 0.000598246, 0.0115866,
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    -0.0950467, -0.110606, -0.134401, -0.148067, -0.161132, -0.183664, -0.208669, -0.22302,
    -0.234051, -0.260674, -0.28512, -0.300344, -0.3204, -0.336652, -0.352431, -0.374348}},
  LinearNegative_20 → {{0.983161, 0.174933, 0.0199582, 0.00357246, 0.00109791, 0.0151254,
    0.0218184, 0.0244129, 0.0154511, 0.0290027}, {-0.0275468, -0.0454451, -0.0642388, -0.0785529,
    -0.10047, -0.10405, -0.126503, -0.152971, -0.170625, -0.186359, -0.201706, -0.216099,
    -0.23451, -0.262821, -0.28293, -0.299345, -0.321704, -0.335315, -0.355355, -0.373356}}|>,
f3 → <|Sinusoidal3_21 → {{0.00292282, 0.0723861, 0.992282, 0.0889114, 0.0375414, 0.0192376,
    0.00972046, 0.00361142, 0.0182714, 0.00154167}, {0.190591, -0.0926574, -0.301805, -0.254497,
    -0.000763073, 0.259747, 0.299262, 0.102098, -0.187901, -0.319228, -0.183668, 0.0960092,
    0.295408, 0.257006, 0.00431851, -0.25659, -0.296404, -0.102617, 0.188094, 0.314132}},
  Sinusoidal3_22 → {{0.00266195, 0.0698983, 0.992446, 0.0875486, 0.0402319, 0.0195484,
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    0.298948, 0.251349, 0.000100679, -0.256482, -0.303455, -0.103322, 0.189479, 0.312861}},
  Sinusoidal3_23 → {{0.00296313, 0.0743051, 0.992748, 0.0808714, 0.0378805, 0.0211109,
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    0.000851559, 0.253095, 0.303028, 0.0966111, -0.191306, -0.315011, -0.190683, 0.102086,
    0.306645, 0.250558, -0.00620057, -0.252019, -0.295407, -0.0997793, 0.180645, 0.32236}},
  Sinusoidal3_24 → {{0.00309097, 0.0741291, 0.992734, 0.0815613, 0.0377608, 0.0212423,
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    0.307909, 0.257171, -0.00208093, -0.257156, -0.295621, -0.102821, 0.189089, 0.312455}},
  Sinusoidal3_25 → {{0.00312159, 0.0678554, 0.993, 0.0852891, 0.034079, 0.0195727, 0.00735691,
    0.00248309, 0.0213736, 0.000802607}, {0.191433, -0.0959741, -0.29472, -0.259209,
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    0.303403, 0.256909, -0.00346767, -0.261734, -0.30204, -0.09341, 0.189078, 0.312377}},
  Sinusoidal3_26 → {{0.00381225, 0.0715025, 0.992152, 0.0910767, 0.0355622, 0.0202016,
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    0.00449844, 0.259616, 0.304268, 0.0921556, -0.187659, -0.309002, -0.181644, 0.0923256,
    0.304272, 0.248776, -0.00341994, -0.256989, -0.304514, -0.0943228, 0.184616, 0.315025}},
  Sinusoidal3_27 → {{0.00370384, 0.0737267, 0.992206, 0.0899309, 0.0342931, 0.018897,
    0.0094179, 0.00323772, 0.0188814, 0.0012882}, {0.181827, -0.1008, -0.303489, -0.256921,
    -0.00476018, 0.260279, 0.304828, 0.0954533, -0.18826, -0.311594, -0.180371, 0.0977238,
    0.298238, 0.25499, 0.00284382, -0.257486, -0.30033, -0.102966, 0.185703, 0.31415}},
  Sinusoidal3_28 → {{0.00349335, 0.0721722, 0.992041, 0.0914769, 0.039105, 0.016348, 0.00866276,
    0.00269504, 0.0196495, 0.000955532}, {0.179858, -0.0962786, -0.306235, -0.260317,
    0.00595141, 0.261357, 0.301205, 0.0951823, -0.181077, -0.31138, -0.189045, 0.10143,
    0.297761, 0.249857, 0.0062538, -0.255561, -0.302114, -0.0938207, 0.188719, 0.3175}},
  Sinusoidal3_29 → {{0.00319757, 0.0694313, 0.992568, 0.0880905, 0.0365624, 0.0192917,
    0.00865748, 0.00295183, 0.0205694, 0.00108579}, {0.188347, -0.0945985, -0.305483, -0.25378,
    0.000474935, 0.258684, 0.302223, 0.0998503, -0.181676, -0.313183, -0.184518, 0.0938802,
    0.301256, 0.25557, -0.000714167, -0.2543, -0.299826, -0.0914277, 0.185698, 0.319683}},
  Sinusoidal3_30 → {{0.00391618, 0.0720855, 0.992435, 0.0870535, 0.0383196, 0.0197234,
    0.00892488, 0.00335903, 0.018234, 0.00138539}, {0.184949, -0.0961161, -0.301489, -0.25239,
    0.00376141, 0.257597, 0.299398, 0.0964897, -0.182432, -0.311126, -0.191358, 0.095487,
    0.305482, 0.250194, -0.0032087, -0.261025, -0.301213, -0.102868, 0.191264, 0.314435}}|>,
f5 → <|Sinusoidal2_11 → {{0.00284077, 0.0111087, 0.0307626, 0.0842076, 0.934763, 0.340999,
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    0.0298089, 0.00470431, 0.0292555, 0.00162558}, {-0.092165, -0.255592, 0.252404, 0.0944007,
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    0.250399, 0.102954, -0.318791, 0.0942407, 0.252872, -0.260342, -0.101261, 0.31474}},
  Sinusoidal2_12 → {{0.00253192, 0.0124714, 0.0321723, 0.0947591, 0.933458, 0.341499, 0.029373,
    0.0041148, 0.0312637, 0.00127359}, {-0.093155, -0.251626, 0.260382, 0.103878,
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    0.256951, 0.0970855, -0.312997, 0.101574, 0.250648, -0.251864, -0.101645, 0.322261}},
  Sinusoidal2_13 → {{0.00252106, 0.0110662, 0.0319376, 0.0994105, 0.930918, 0.347382, 0.0269242,
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    0.2576, 0.092321, -0.312074, 0.101037, 0.256851, -0.256058, -0.097411, 0.321325}},
  Sinusoidal2_14 → {{0.00305731, 0.0105643, 0.0304245, 0.0893043, 0.933417, 0.343514, 0.029246,
    0.00456226, 0.0288209, 0.00155637}, {-0.0926531, -0.25113, 0.251693, 0.0998038,
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  Sinusoidal2_15 → {{0.00212629, 0.0124322, 0.0317973, 0.0942015, 0.933435, 0.342055, 0.0265463,
    0.00432159, 0.0304744, 0.00135159}, {-0.0976646, -0.257094, 0.258788, 0.0962843,
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  Sinusoidal2_16 → {{0.00284976, 0.00972103, 0.0316066, 0.0933518, 0.932793, 0.34423, 0.0284229,
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    0.251573, 0.0949102, -0.31882, 0.0999403, 0.257066, -0.256946, -0.0969964, 0.317199}},
  Sinusoidal2_17 → {{0.00294637, 0.0137297, 0.0301856, 0.0942431, 0.935611, 0.336232, 0.029257,
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  Sinusoidal2_18 → {{0.00215495, 0.0115957, 0.0330484, 0.092051, 0.935392, 0.337103, 0.0278206,
    0.00494438, 0.0299459, 0.00173322}, {-0.0954901, -0.25317, 0.259506, 0.097923,
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    0.251446, 0.101907, -0.312945, 0.0984158, 0.25376, -0.254797, -0.100368, 0.320998}},
  Sinusoidal2_19 → {{0.00292591, 0.0109045, 0.0308532, 0.0953816, 0.937546, 0.330331,
    0.0285929, 0.00385343, 0.0296513, 0.0011513}, {-0.103513, -0.25616, 0.259637, 0.0995757,
    -0.314906, 0.0982229, 0.255955, -0.255446, -0.0925275, 0.313311, -0.097782, -0.25305,
    0.253755, 0.0980591, -0.318604, 0.095522, 0.257173, -0.250112, -0.0985996, 0.321534}},
  Sinusoidal2_20 → {{0.00229292, 0.0111321, 0.0297504, 0.0976859, 0.930556, 0.348844, 0.0308141,
    0.00487638, 0.0289877, 0.00172975}, {-0.0964554, -0.25827, 0.250986, 0.101907,
    -0.320886, 0.0968102, 0.25908, -0.25407, -0.103569, 0.312573, -0.100316, -0.25181,
    0.251522, 0.099567, -0.315348, 0.0980275, 0.25585, -0.256402, -0.101144, 0.317865}}|>,
f6 → <|Sinusoidal1_1 → {{0.00429964, 0.0124488, 0.0146388, 0.038082, 0.112685, 0.985554,
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  Sinusoidal1_2 → {{0.0048946, 0.00686714, 0.0323743, 0.0296123, 0.0929603, 0.991707, 0.0727256,
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  Sinusoidal1_3 → {{0.0020732, 0.00790223, 0.0217488, 0.0391645, 0.109589, 0.987627, 0.0984774,
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    -0.290008, 0.238611, 0.00395618, -0.253256, 0.320151, -0.0987232, -0.185447, 0.324157}},
  Sinusoidal1_4 → {{0.00129307, 0.00514324, 0.0201373, 0.0363008, 0.0931888, 0.990024,
    0.0930243, 0.012798, 0.0236757, 0.00630453}, {-0.159802, -0.117588, 0.290612, -0.26891,
    0.00449458, 0.25747, -0.315099, 0.118402, 0.203053, -0.30526, 0.16267, 0.109941,
    -0.274445, 0.241485, 0.0250239, -0.246895, 0.322745, -0.109316, -0.212678, 0.307772}},
  Sinusoidal1_5 → {{0.00428916, 0.00798887, 0.00841959, 0.0306058, 0.0810507, 0.991345,
    0.096711, 0.00360773, 0.0144464, 0.00120236}, {-0.213237, -0.0884702, 0.276059, -0.27168,
    0.0298997, 0.269128, -0.319434, 0.097692, 0.185151, -0.336828, 0.176184, 0.112197,
    -0.306885, 0.236025, -0.0279022, -0.2615, 0.281624, -0.0979225, -0.158926, 0.295315}},
  Sinusoidal1_6 → {{0.0012906, 0.00529952, 0.0246016, 0.048774, 0.0930448, 0.991126, 0.0720239,
    0.00234908, 0.0283626, 0.000245433}, {-0.185055, -0.0742135, 0.326284, -0.290171,
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    -0.299467, 0.230226, 0.0204371, -0.231715, 0.300248, -0.0955051, -0.210378, 0.304217}},
  Sinusoidal1_7 → {{0.00237765, 0.00912731, 0.0207385, 0.0478056, 0.102713, 0.989166, 0.0868789,
    0.00432749, 0.0250609, 0.00115304}, {-0.188149, -0.0954195, 0.324817, -0.268983,
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    -0.273687, 0.252698, 0.0195018, -0.238251, 0.299492, -0.0962879, -0.204687, 0.309552}},
  Sinusoidal1_8 → {{0.00632634, 0.00297285, 0.0230942, 0.027816, 0.0959568, 0.990317, 0.089321,
    0.0031466, 0.0268455, 0.000798393}, {-0.184681, -0.0675504, 0.279701, -0.272229,
    0.0206599, 0.270953, -0.319563, 0.126323, 0.199255, -0.30184, 0.154078, 0.0792755,
    -0.324575, 0.255526, -0.0238053, -0.235483, 0.274648, -0.0957902, -0.178475, 0.336321}},
  Sinusoidal1_9 → {{0.000945797, 0.0170578, 0.0170628, 0.0423125, 0.103314, 0.988527, 0.0941891,
    0.00382555, 0.0296784, 0.00105013}, {-0.166893, -0.0660021, 0.309722, -0.269759,
    0.00753992, 0.262709, -0.31926, 0.0723509, 0.159835, -0.312553, 0.177214, 0.119819,
    -0.288854, 0.271561, 0.00174154, -0.229631, 0.286327, -0.103739, -0.18458, 0.342242}},
  Sinusoidal1_10 → {{0.00578135, 0.0115757, 0.0224454, 0.0405197, 0.0843891, 0.990723,
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Let's use correlation as a distance function for the first clustering:

```
In[3]:= clusters1CorrelationDistance = TimeSeriesClusters[classification1, DistanceFunction → CorrelationDistance];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

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Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

```
In[4]:= Query[All, "GroupAssociations"]@clusters1CorrelationDistance

Out[4]= <|SpikeMax → <|G1S1 →
      {SpikePositive_1, SpikePositive_9, SpikePositive_5, SpikePositive_7, SpikePositive_3, SpikePositive_8},
    G1S2 → {SpikePositive_12}, G2S1 → {SpikePositive_2, SpikePositive_4, SpikePositive_6, SpikePositive_10},
    G2S2 → {SpikePositive_11, SpikePositive_16, SpikePositive_18},
    G3S1 → {SpikePositive_17, SpikePositive_20}, G4S1 → {SpikePositive_19, SpikePositive_15},
    G4S2 → {SpikePositive_14}, G4S3 → {SpikePositive_13}|>,
  SpikeMin → <|G1S1 → {SpikeNegative_1, SpikeNegative_8, SpikeNegative_7, SpikeNegative_4,
      SpikeNegative_10, SpikeNegative_9, SpikeNegative_5, SpikeNegative_2},
    G1S2 → {SpikeNegative_20, SpikeNegative_15, SpikeNegative_14},
    G2S1 → {SpikeNegative_12, SpikeNegative_13, SpikeNegative_17, SpikeNegative_18, SpikeNegative_11},
    G2S2 → {SpikeNegative_16, SpikeNegative_19}, G3S1 → {SpikeNegative_3, SpikeNegative_6}|>,
  f1 → <|G1S1 → {LinearPositive_1, LinearPositive_2, LinearPositive_10, LinearPositive_3,
      LinearPositive_5, LinearPositive_4, LinearPositive_7, LinearPositive_6, LinearPositive_9,
      LinearPositive_8, LinearPositive_15, LinearPositive_13, LinearPositive_14, LinearPositive_12,
      LinearPositive_17, LinearPositive_20, LinearPositive_18, LinearPositive_19, LinearPositive_11},
    G1S2 → {LinearNegative_17, LinearNegative_14, LinearNegative_20, LinearNegative_19,
      LinearNegative_11, LinearNegative_15, LinearNegative_12, LinearNegative_18, LinearNegative_16,
      LinearNegative_13, LinearNegative_9, LinearNegative_3, LinearNegative_10, LinearNegative_1},
    G2S1 → {LinearPositive_16}, G2S2 → {LinearNegative_5, LinearNegative_2, LinearNegative_7,
      LinearNegative_4, LinearNegative_8, LinearNegative_6}|>,
  f3 → <|G1S1 → {Sinusoidal3_21, Sinusoidal3_27, Sinusoidal3_30, Sinusoidal3_22,
      Sinusoidal3_25, Sinusoidal3_29, Sinusoidal3_26}, G1S2 → {Sinusoidal3_28},
    G2S1 → {Sinusoidal3_24, Sinusoidal3_23}|>, f5 → <|G1S1 → {Sinusoidal2_11},
    G1S2 → {Sinusoidal2_12, Sinusoidal2_14, Sinusoidal2_15, Sinusoidal2_13, Sinusoidal2_20, Sinusoidal2_16},
    G2S1 → {Sinusoidal2_17}, G2S2 → {Sinusoidal2_18, Sinusoidal2_19}|>,
  f6 → <|G1S1 → {Sinusoidal1_1}, G2S1 → {Sinusoidal1_2, Sinusoidal1_8, Sinusoidal1_5},
    G2S2 → {Sinusoidal1_10, Sinusoidal1_6, Sinusoidal1_7, Sinusoidal1_3, Sinusoidal1_4, Sinusoidal1_9}|>|>
```

Let's use Euclidean distance (default) for the first clustering:

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In[5]:=
```
clusters1EuclideanDistance = TimeSeriesClusters[classification1, DistanceFunction → EuclideanDistance]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[5]=
```
<|SpikeMax → <|Cluster → Cluster[ ··· 1 ··· ], ··· 4 ···, GroupAssociations →
    <|G1S1 → {SpikePositive_1, SpikePositive_9, SpikePositive_5, ··· 4 ···, SpikePositive_3,
       SpikePositive_6, SpikePositive_10}, G1S2 → ··· 1 ··· |> |>, ··· 4 ···, f6 → <| ··· 1 ··· |> |>
```

large output | show less | show more | show all | set size limit...

We can see that the groupings are now different:

In[6]:=
```
Query[All, "GroupAssociations"]@clusters1EuclideanDistance
```

Out[6]=
```
<|SpikeMax → <|G1S1 → {SpikePositive_1, SpikePositive_9, SpikePositive_5, SpikePositive_7, SpikePositive_2,
      SpikePositive_8, SpikePositive_4, SpikePositive_3, SpikePositive_6, SpikePositive_10},
    G1S2 → {SpikePositive_17, SpikePositive_13, SpikePositive_20, SpikePositive_18, SpikePositive_11,
      SpikePositive_16, SpikePositive_12, SpikePositive_15, SpikePositive_19, SpikePositive_14}|>,
  SpikeMin → <|G1S1 → {SpikeNegative_1, SpikeNegative_8, SpikeNegative_5, SpikeNegative_9, SpikeNegative_10,
      SpikeNegative_2}, G1S2 → {SpikeNegative_11, SpikeNegative_15, SpikeNegative_20, SpikeNegative_19},
    G2S1 → {SpikeNegative_12, SpikeNegative_13, SpikeNegative_17, SpikeNegative_18, SpikeNegative_16,
      SpikeNegative_14}, G2S2 → {SpikeNegative_4, SpikeNegative_3, SpikeNegative_7, SpikeNegative_6}|>,
  f1 → <|G1S1 → {LinearPositive_1, LinearPositive_2, LinearPositive_10, LinearPositive_4, LinearPositive_3,
      LinearPositive_5, LinearPositive_7, LinearPositive_8, LinearPositive_9, LinearPositive_6,
      LinearPositive_15, LinearPositive_13, LinearPositive_12, LinearPositive_14, LinearPositive_17,
      LinearPositive_16, LinearPositive_20, LinearPositive_19, LinearPositive_18, LinearPositive_11},
    G1S2 → {LinearNegative_4, LinearNegative_19, LinearNegative_11, LinearNegative_14, LinearNegative_20,
      LinearNegative_15, LinearNegative_12, LinearNegative_16, LinearNegative_13, LinearNegative_18,
      LinearNegative_17, LinearNegative_8, LinearNegative_1, LinearNegative_10, LinearNegative_7,
      LinearNegative_6, LinearNegative_2, LinearNegative_3, LinearNegative_5, LinearNegative_9}|>,
  f3 → <|G1S1 → {Sinusoidal3_21, Sinusoidal3_27, Sinusoidal3_30, Sinusoidal3_22,
      Sinusoidal3_25, Sinusoidal3_29, Sinusoidal3_26}, G1S2 → {Sinusoidal3_28},
    G2S1 → {Sinusoidal3_24, Sinusoidal3_23}|>, f5 → <|G1S1 → {Sinusoidal2_11},
    G1S2 → {Sinusoidal2_12, Sinusoidal2_14, Sinusoidal2_15, Sinusoidal2_13, Sinusoidal2_20, Sinusoidal2_16},
    G2S1 → {Sinusoidal2_17}, G2S2 → {Sinusoidal2_18, Sinusoidal2_19}|>,
  f6 → <|G1S1 → {Sinusoidal1_1}, G1S2 → {Sinusoidal1_3, Sinusoidal1_9, Sinusoidal1_7},
    G2S1 → {Sinusoidal1_2, Sinusoidal1_8}, G2S2 → {Sinusoidal1_6},
    G3S1 → {Sinusoidal1_4, Sinusoidal1_10}, G3S2 → {Sinusoidal1_5}|>|>
```

LinkageMeasure (1)

In[1]:=
```
Needs["MathIOmica`"]
```

LinkageMeasure provides options for which Linkage to use in the hierarchical clustering.

We generate some data for classification:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
  Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.324409, 0.170114, 0.165824, 0.123258, 0.296411, 0.168117, 0.113074, 0.338552,
      0.684644, 0.332967}, {0.961598, -0.0784818, 0.0810648, 0.00311141, 0.0587387, -0.0958059,
      -0.049226, -0.0684896, -0.0610883, -0.0440209, -0.0191229, 0.0976175, 0.023173,
      -0.0669337, 0.0841547, -0.0357017, 0.079293, 0.0713104, -0.0457205, -0.0210911}},
   SpikePositive_2 → {{0.334467, 0.153398, 0.110432, 0.323538, 0.266019, 0.424313, 0.318101,
      0.305017, 0.452943, 0.312315}, {0.96344, -0.0652302, -0.0609021, 0.102723, 0.0572351,
      0.0667109, -0.025624, -0.0576658, -0.00950837, 0.026989, -0.0986821, -0.0758774, -0.0772708,
      -0.0816285, -0.0474007, 0.0410352, 0.0384367, -0.027473, -0.0715449, -0.0364503}},
   SpikePositive_3 → {{0.237775, 0.251808, 0.365905, 0.328654, 0.256463, 0.230115, 0.189401,
      0.316748, 0.518767, 0.337799}, {0.980425, 0.0628899, -0.00578454, -0.050829, 0.0382936,
      0.0195252, 0.0662929, -0.0263428, -0.0025991, 0.00223482, -0.0592579, 0.0193684, -0.0560032,
      -0.035472, -0.00588783, -0.0817247, -0.027714, 0.0388076, -0.0121693, -0.0884821}},
   SpikePositive_4 → {{0.0766058, 0.177007, 0.187344, 0.274591, 0.30402, 0.40651, 0.323552,
      0.312303, 0.509701, 0.364157}, {0.974075, -0.0836186, -0.0576299, 0.0175985, 0.045611,
      0.00957002, 0.0860471, 0.0352185, 0.0528924, 0.0699089, -0.0261313, 0.0314563, -0.0515711,
      0.0494964, -0.0635652, 0.0774129, -0.0538926, -0.03402, 0.0149701, -0.0308797}},
   SpikePositive_5 → {{0.356249, 0.362821, 0.169696, 0.32207, 0.205216, 0.422436, 0.0933727,
      0.140038, 0.586208, 0.128008}, {0.96115, 0.0915494, 0.0510295, -0.0200335, -0.0265268,
      -0.0803989, -0.0420036, -0.0746378, -0.0615318, 0.0778489, 0.0189356, -0.0828489,
      0.0861323, -0.0884553, 0.045092, 0.0653972, -0.0813578, 0.0244817, -0.0450231, 0.0493382}},
   SpikePositive_6 → {{0.223601, 0.173281, 0.327951, 0.262359, 0.139409, 0.504536, 0.231769,
      0.243409, 0.540111, 0.254785}, {0.964113, 0.0392403, 0.0748115, 0.0935003, 0.0306903,
      -0.0287454, 0.093744, -0.00149223, 0.00297592, 0.0500414, -0.0588538, -0.0707234, 0.0824526,
      0.0756554, -0.0482946, -0.0531639, -0.0664139, -0.0972533, -0.0103852, 0.037575}},
   SpikePositive_7 → {{0.319523, 0.296405, 0.157895, 0.431088, 0.0852705, 0.249883, 0.22182,
      0.222771, 0.601288, 0.263042}, {0.952834, 0.0945743, 0.030454, -0.0452833, 0.0491966,
      -0.0344369, -0.0362046, -0.0918258, -0.0790606, 0.0850141, 0.079548, -0.0939621, -0.0400184,
      0.0854323, -0.0627653, 0.003358, 0.0281629, 0.0935197, -0.0860753, -0.0916674}},
   SpikePositive_8 → {{0.25955, 0.193723, 0.347494, 0.341775, 0.304991, 0.278284, 0.124688,
      0.349916, 0.483867, 0.339067}, {0.958091, -0.0314661, -0.0677753, 0.0941882, 0.0953837,
      0.0613179, -0.0569369, 0.0587116, -0.0579202, 0.0495027, -0.0941885, 0.0363477, 0.0404173,
      -0.0382393, -0.0735132, -0.0835398, -0.0143758, 0.0739196, -0.0945755, 0.044349}},
   SpikePositive_9 → {{0.402032, 0.314144, 0.0849046, 0.216271, 0.261497, 0.229649, 0.23392,
      0.276437, 0.583299, 0.305301}, {0.961595, 0.0601491, 0.0611236, -0.0171698, -0.0647952,
      -0.0543573, -0.0755457, -0.0821092, 0.0554399, 0.0386217, -0.0526821, 0.0802057, -0.062859,
      -0.00571523, 0.0931794, 0.0936427, 0.0400029, 0.0514697, -0.0885209, -0.0280979}},
   SpikePositive_10 → {{0.191051, 0.181014, 0.385388, 0.265829, 0.107359, 0.443934, 0.507368,
      0.205606, 0.399869, 0.208204}, {0.966831, 0.00607185, -0.0804752, 0.0265999, -0.0870397,
      0.0690163, 0.0795389, -0.0321288, 0.0196556, -0.0267794, -0.0517151, -0.0937161, 0.0189925,
      0.0540714, -0.102079, -0.0365956, 0.0321433, -0.0818259, -0.0526239, -0.0147425}},
   SpikePositive_11 → {{0.148919, 0.390472, 0.254307, 0.320998, 0.297897, 0.397987, 0.332789,
      0.242302, 0.418196, 0.257214}, {0.0401193, -0.0910461, 0.964525, 0.0365123, -0.0885476,
      0.0268375, 0.0414704, -0.0193192, 0.0747423, -0.0661318, 0.0775741, 0.0626327, 0.0105756,
```

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```
    0.0385886, -0.0413832, -0.0663581, -0.0969631, -0.0952763, -0.0242641, -0.0334632}},
  SpikePositive_12 → {{0.265742, 0.117546, 0.403624, 0.479129, 0.167669, 0.325997, 0.244961,
    0.27459, 0.414912, 0.284855}, {-0.0454271, -0.0167973, 0.967797, -0.0771211, -0.00968068,
    -0.0687945, -0.00183506, 0.0312344, 0.0891281, -0.0782193, -0.0972396, -0.00889991,
    -0.0385532, -0.0982314, -0.0288761, 0.0802374, 0.0409004, -0.0487324, -0.0031135, 0.0566374}},
  SpikePositive_13 → {{0.173279, 0.245618, 0.294944, 0.345844, 0.427337, 0.278339, 0.355834,
    0.335467, 0.298559, 0.33862}, {0.00189091, 0.0221816, 0.984424, -0.0100288, 0.0132018,
    0.00594962, -0.019277, -0.0212296, -0.0791649, 0.0230189, 0.0415584, 0.00594445, -0.00937534,
    0.0506408, 0.0334736, 0.0646462, 0.0857078, 0.0128384, -0.0327356, -0.0647042}},
  SpikePositive_14 → {{0.365713, 0.131486, 0.384639, 0.293238, 0.30674, 0.254335, 0.410016,
    0.317627, 0.280831, 0.329222}, {0.100438, -0.000524075, 0.965334, 0.0401153, -0.0842799,
    0.0237028, -0.0330817, 0.0359796, 0.039724, 0.0492155, -0.0980652, -0.0981046, -0.017342,
    -0.0368979, -0.0925996, 0.0899983, 0.0531406, -0.0161144, 0.0254894, -0.0326757}},
  SpikePositive_15 → {{0.168642, 0.180759, 0.374248, 0.28054, 0.398254, 0.27873, 0.28357,
    0.365957, 0.365981, 0.368166}, {0.0273659, -0.0756866, 0.971883, -0.00316362, -0.0391962,
    -0.0436402, 0.00898363, 0.0549797, 0.0809708, 0.078566, -0.0559259, -0.0443052, 0.00758892,
    0.0254679, -0.0625557, -0.0825764, -0.000688716, -0.0509654, -0.0590314, -0.0840962}},
  SpikePositive_16 → {{0.113839, 0.276447, 0.254759, 0.354632, 0.198091, 0.552714, 0.420095,
    0.198242, 0.337488, 0.213403}, {0.0333572, -0.0338306, 0.967753, 0.0468255, -0.0161832,
    0.0930872, 0.0260943, 0.00974097, 0.0635434, -0.0773527, 0.05261, 0.074454, 0.0515434,
    0.00122569, 0.0771992, 0.0848385, -0.0705351, -0.0163253, -0.0338837, -0.0936158}},
  SpikePositive_17 → {{0.261061, 0.374045, 0.400207, 0.314758, 0.493563, 0.210457, 0.181021,
    0.205828, 0.357744, 0.204177}, {-0.0431428, 0.0148359, 0.97353, 0.0272582, 0.0470465,
    -0.0582541, -0.03756, -0.0318125, 0.0340365, 0.0414851, -0.0305859, -0.0551946, 0.0432195,
    0.0275345, -0.0590031, -0.0898656, 0.0915828, -0.0364591, -0.0684289, 0.0770827}},
  SpikePositive_18 → {{0.0572751, 0.460842, 0.402336, 0.223204, 0.294133, 0.473247, 0.307829,
    0.17048, 0.323254, 0.184007}, {-0.0753792, 0.0177089, 0.968826, -0.0818318, -0.0142227,
    -0.0294494, -0.0967815, -0.0326495, 0.0475555, 0.0283284, 0.062302, 0.0522249, 0.0418503,
    0.0422576, 0.0665184, -0.0512926, -0.0976195, -0.0207886, -0.0705533, 0.0444513}},
  SpikePositive_19 → {{0.131783, 0.102578, 0.241117, 0.136871, 0.502546, 0.303553, 0.277353,
    0.326786, 0.490963, 0.354662}, {0.0675407, -0.0776988, 0.967758, -0.0893773, -0.0288154,
    0.0364147, 0.0737268, -0.000694568, 0.0851939, 0.094056, 0.0128182, -0.0569573, -0.0330189,
    0.0945116, -0.0311605, -0.0307327, 0.0159362, 0.0572427, -0.0472124, 0.00735099}},
  SpikePositive_20 → {{0.297366, 0.43718, 0.447243, 0.1796, 0.410744, 0.340269, 0.233486,
    0.163875, 0.305527, 0.170156}, {0.0242373, 0.0691, 0.975304, 0.0747793, 0.0394068,
    0.00824561, -0.0538148, -0.0839856, -0.038557, 0.0335737, 0.0415809, -0.0517749, -0.0461063,
    0.0250425, 0.0865305, -0.0400083, -0.0177558, 0.0071326, -0.0837924, 0.00219165}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.179003, 0.204896, 0.297333, 0.237381, 0.265238, 0.256171,
    0.123157, 0.445015, 0.493314, 0.434372}, {-0.981318, -0.0100425, 0.0380315, 0.0197688,
    -0.0270245, -0.00672693, -0.0282116, -0.0679478, 0.0423293, -0.0710326, 0.0456178, -0.0605604,
    -0.0314144, -0.00325147, -0.0648475, 0.0226442, -0.0680108, -0.0203878, 0.0741272, -0.00722323}},
  SpikeNegative_2 → {{0.245872, 0.225012, 0.377768, 0.328454, 0.259723, 0.38181, 0.19233,
    0.174591, 0.577199, 0.156398}, {-0.956162, 0.017739, 0.077512, -0.0113142, 0.00307949,
    0.0773279, -0.101818, 0.0280849, -0.0926582, 0.0488129, 0.0898659, 0.0974435, -0.099591,
    0.0234161, -0.0779867, 0.0841428, -0.0411222, -0.033115, -0.0847825, 0.00395747}},
  SpikeNegative_3 → {{0.262819, 0.346714, 0.276141, 0.450925, 0.32582, 0.214813, 0.2329,
    0.311464, 0.364247, 0.308054}, {-0.974911, -0.0449396, 0.0591886, 0.0171312, 0.0220633,
    -0.0315871, -0.00483449, 0.0358151, 0.0389408, -0.0682913, -0.0512576, -0.087228, 0.0687409,
    0.00786763, -0.091478, 0.0151002, -0.0243068, -0.0282888, -0.0634719, -0.0756436}},
  SpikeNegative_4 → {{0.223617, 0.335725, 0.181144, 0.288271, 0.321971, 0.398915, 0.230377,
    0.356142, 0.398328, 0.346406}, {-0.975909, 0.0559513, 0.0518219, -0.0690764, -0.0262965,
    0.0396372, -0.0107718, -0.0224228, -0.0293667, -0.0835916, 0.045471, 0.0102257, 0.0225189,
    0.0671045, 0.0104705, 0.0385565, -0.0516468, 0.0284054, -0.0947395, -0.0710906}},
  SpikeNegative_5 → {{0.145001, 0.157052, 0.222327, 0.125408, 0.173933, 0.259836, 0.214589,
    0.345517, 0.692238, 0.383096}, {-0.964327, 0.0667145, -0.00810299, 0.0670594, -0.0101228,
    0.0552289, -0.0753919, -0.0285311, 0.0770709, -0.0189331, -0.0114068, -0.0783523, 0.0368964,
    -0.0752661, 0.0496075, -0.0550931, -0.0672168, 0.0714993, 0.0952962, -0.0872166}},
  SpikeNegative_6 → {{0.344097, 0.375351, 0.212451, 0.399676, 0.143612, 0.216183, 0.349564,
    0.335704, 0.357275, 0.325477}, {-0.970591, -0.0363973, -0.0119474, -0.041528, 0.0775416,
    -0.0824483, 0.071797, -0.0114515, -0.0539497, -0.054287, 0.0867971, 0.0884819, 0.0808983,
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  SpikeNegative_7 → {{0.132039, 0.340113, 0.380128, 0.30797, 0.209748, 0.382568, 0.173156,
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    0.0455007, 0.0752469, 0.0944997, -0.00214996, 0.0485326, 0.0678758, -0.00769229}},
  SpikeNegative_8 → {{0.131093, 0.314882, 0.125857, 0.204973, 0.359241, 0.306417, 0.268164,
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    0.313116, 0.585163, 0.300825}, {-0.981694, -0.00558128, 0.0162387, 0.00466025, 0.0248748,
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    0.013626, 0.070069, -0.0633442, -0.00517626, -0.0474797, 0.0740414, 0.051339, 0.0513052}},
  SpikeNegative_9 → {{0.32923, 0.185845, 0.167432, 0.145041, 0.330696, 0.275704, 0.292255,
    0.377789, 0.491631, 0.390881}, {-0.976962, 0.0475481, -0.0936904, -0.0818149, -0.0225711,
    0.047689, 0.0763995, -0.0600423, 0.0416753, 0.0494156, 0.0792433, 0.0124057, 0.00739354,
    0.0309667, 0.0510013, 0.00169237, 0.00614644, 0.00336503, 0.00673845, 0.035534}},
  SpikeNegative_10 → {{0.187411, 0.0930663, 0.215966, 0.321665, 0.270455, 0.262331, 0.345698,
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  SpikeNegative_11 → {{0.176128, 0.343758, 0.289346, 0.161823, 0.3588, 0.14812, 0.435386,
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    -0.0526344, -0.00350307, 0.0436464, 0.0420949, 0.0475216, -0.073602, -0.0125228}},
  SpikeNegative_12 → {{0.272616, 0.240016, 0.414269, 0.345708, 0.258061, 0.468833, 0.358079,
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  SpikeNegative_13 → {{0.274462, 0.302742, 0.398966, 0.330174, 0.172799, 0.348522, 0.404711,
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    0.087111, -0.0437711, -0.0545356, 0.0798857, 0.00943981, -0.068422, 0.0489834}},
  SpikeNegative_14 → {{0.384863, 0.27341, 0.228036, 0.322194, 0.243925, 0.489082, 0.228304,
    0.227893, 0.388388, 0.260219}, {-0.0479572, 0.0374899, -0.966048, -0.0912153, 0.0709753,
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    0.0769182, 0.022607, 0.0225365, -0.038849, 0.0754123, -0.0535594, -0.0612562, -0.0857435}},
  SpikeNegative_15 → {{0.230687, 0.269172, 0.373866, 0.273987, 0.264156, 0.253968, 0.268366,
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    -0.0640884, -0.0318087, -0.0231045, -0.0347508, 0.00437704, -0.0669236, -0.0426882}},
  SpikeNegative_16 → {{0.229082, 0.0799973, 0.409866, 0.423687, 0.239709, 0.234286, 0.385261,
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    0.0199986, -0.0414975, -0.0992975, -0.0984926, 0.0510657, -0.0754586, 0.0339435}},
  SpikeNegative_17 → {{0.166684, 0.393327, 0.385405, 0.316463, 0.322372, 0.380084, 0.429402,
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  SpikeNegative_18 → {{0.186337, 0.279965, 0.301089, 0.295955, 0.347575, 0.346384, 0.393757,
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  SpikeNegative_19 → {{0.372109, 0.253615, 0.22408, 0.218012, 0.21274, 0.299365, 0.493739,
    0.26954, 0.425025, 0.259843}, {-0.0520982, -0.0710526, -0.963523, 0.0614959, -0.0403345,
    -0.0503211, 0.0626594, -0.0136963, -0.0780811, 0.0838425, -0.0564514, 0.0752164,
    0.0213689, 0.0488518, 0.0831079, 0.0467081, -0.0328894, 0.0581781, -0.078336, 0.0854451}},
  SpikeNegative_20 → {{0.144877, 0.19337, 0.175026, 0.142599, 0.207976, 0.282338, 0.379352,
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f1 → <|LinearPositive_1 → {{0.983935, 0.166507, 0.0339889, 0.00233813, 0.00163589, 0.00880631,
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  LinearPositive_2 → {{0.984679, 0.161762, 0.0333001, 0.00167776, 0.00140789, 0.0109205,
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  LinearPositive_3 → {{0.98466, 0.163983, 0.0322273, 0.00176189, 0.00124205, 0.0103367,
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  LinearPositive_4 → {{0.983725, 0.16791, 0.033991, 0.00186403, 0.00159822, 0.0108547,
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LinearPositive_5 → {{0.984486, 0.164113, 0.0326301, 0.0020634, 0.00160084, 0.0104488,
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LinearPositive_6 → {{0.984637, 0.163387, 0.0317204, 0.00214223, 0.00172703, 0.0120002,
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LinearPositive_7 → {{0.983774, 0.16856, 0.0331076, 0.001263, 0.00200541, 0.011145, 0.0211818,
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LinearPositive_8 → {{0.983361, 0.170755, 0.0322405, 0.00229647, 0.00154357,
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LinearPositive_9 → {{0.984281, 0.164714, 0.0315442, 0.0024577, 0.00207134, 0.0112388,
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LinearPositive_10 → {{0.984764, 0.16126, 0.0317102, 0.00229469, 0.00139603, 0.0102961,
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LinearPositive_11 → {{0.987118, 0.144523, 0.0366661, 0.00393286, 0.00483524,
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LinearPositive_12 → {{0.986719, 0.151113, 0.0352971, 0.00296734, 0.00301888, 0.00992348,
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    0.246162, 0.263628, 0.275081, 0.288028, 0.316328, 0.339994, 0.360727, 0.37308}},
LinearPositive_13 → {{0.98278, 0.17513, 0.031048, 0.00229001, 0.000887874, 0.00702331,
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LinearPositive_14 → {{0.981309, 0.179364, 0.0425146, 0.0023647, 0.000666643, 0.00950443,
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LinearPositive_15 → {{0.98502, 0.156961, 0.0311612, 0.00298664, 0.00374908, 0.0119586,
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LinearPositive_16 → {{0.978469, 0.194014, 0.0293632, 0.0015612, 0.00214793, 0.0102621,
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LinearPositive_17 → {{0.981775, 0.174633, 0.034803, 0.000923569, 0.00218341, 0.0109267,
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    0.235246, 0.259728, 0.277804, 0.305222, 0.318375, 0.342636, 0.352692, 0.383145}},
LinearPositive_18 → {{0.984191, 0.163589, 0.0189233, 0.00150159, 0.00600921,
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LinearPositive_19 → {{0.984084, 0.166032, 0.0222184, 0.00323771, 0.00232831, 0.0109216,
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LinearPositive_20 → {{0.98221, 0.173127, 0.0301068, 0.00172851, 0.000910722, 0.00703237,
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LinearNegative_1 → {{0.987368, 0.147014, 0.0219869, 0.00941451, 0.0084185, 0.0103108,
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LinearNegative_2 → {{0.970518, 0.228564, 0.0410945, 0.00133246, 0.00228022, 0.0212103,
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LinearNegative_3 → {{0.98841, 0.131066, 0.0592048, 0.00861195, 0.00310801, 0.0117901,
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LinearNegative_4 → {{0.977804, 0.194424, 0.0563161, 0.00661649, 0.00747073, 0.00225223,
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LinearNegative_5 → {{0.977667, 0.197968, 0.0398888, 0.00807205, 0.00186104, 0.0196089,
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LinearNegative_6 → {{0.978655, 0.19112, 0.040888, 0.00389164, 0.0186442, 0.030439, 0.0177513,
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LinearNegative_7 → {{0.978623, 0.198349, 0.0450803, 0.00174271, 0.00248991, 0.00787426,
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LinearNegative_8 → {{0.97731, 0.201519, 0.0484284, 0.00342077, 0.00288628, 0.0054388,
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LinearNegative_9 → {{0.980316, 0.181855, 0.0265032, 0.00270405, 0.00750296, 0.0300809,
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LinearNegative_10 → {{0.99182, 0.116106, 0.0183764, 0.000307791, 0.0108507, 0.0185854,
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LinearNegative_11 → {{0.981933, 0.179097, 0.0266438, 0.00172494, 0.00343522, 0.0180727,
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LinearNegative_12 → {{0.988495, 0.136003, 0.030744, 0.00593072, 0.000702021, 0.0125464,
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LinearNegative_13 → {{0.98146, 0.178187, 0.0295216, 0.00301151, 0.00341845, 0.0137251,
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LinearNegative_14 → {{0.981774, 0.180332, 0.0256042, 0.00353723, 0.00430883, 0.0133722,
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LinearNegative_15 → {{0.987724, 0.145566, 0.0319869, 0.0033068, 0.00147833, 0.0129642,
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LinearNegative_16 → {{0.982027, 0.175165, 0.0219579, 0.00381154, 0.00409042, 0.0116753,
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f3 → <|Sinusoidal3_21 → {{0.00292282, 0.0723861, 0.992282, 0.0889114, 0.0375414, 0.0192376,
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  Sinusoidal3_28 → {{0.00349335, 0.0721722, 0.992041, 0.0914769, 0.039105, 0.016348, 0.00866276,
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  Sinusoidal3_29 → {{0.00319757, 0.0694313, 0.992568, 0.0880905, 0.0365624, 0.0192917,
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  Sinusoidal3_30 → {{0.00391618, 0.0720855, 0.992435, 0.0870535, 0.0383196, 0.0197234,
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  Sinusoidal2_12 → {{0.00253192, 0.0124714, 0.0321723, 0.0947591, 0.933458, 0.341499, 0.029373,
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  Sinusoidal2_13 → {{0.00252106, 0.0110662, 0.0319376, 0.0994105, 0.930918, 0.347382, 0.0269242,
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f6 → <|Sinusoidal1_1 → {{0.00429964, 0.0124488, 0.0146388, 0.038082, 0.112685, 0.985554,
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    0.0930243, 0.012798, 0.0236757, 0.00630453}, {-0.159802, -0.117588, 0.290612, -0.26891,
    0.00449458, 0.25747, -0.315099, 0.118402, 0.203053, -0.30526, 0.16267, 0.109941,
    -0.274445, 0.241485, 0.0250239, -0.246895, 0.322745, -0.109316, -0.212678, 0.307772}},
  Sinusoidal1_5 → {{0.00428916, 0.00798887, 0.00841959, 0.0306058, 0.0810507, 0.991345,
    0.096711, 0.00360773, 0.0144464, 0.00120236}, {-0.213237, -0.0884702, 0.276059, -0.27168,
    0.0298997, 0.269128, -0.319434, 0.097692, 0.185151, -0.336828, 0.176184, 0.112197,
    -0.306885, 0.236025, -0.0279022, -0.2615, 0.281624, -0.0979225, -0.158926, 0.295315}},
  Sinusoidal1_6 → {{0.0012906, 0.00529952, 0.0246016, 0.048774, 0.0930448, 0.991126, 0.0720239,
    0.00234908, 0.0283626, 0.000245433}, {-0.185055, -0.0742135, 0.326284, -0.290171,
    0.0163459, 0.238313, -0.294571, 0.0979962, 0.187897, -0.323299, 0.191414, 0.0825405,
    -0.299467, 0.230226, 0.0204371, -0.231715, 0.300248, -0.0955051, -0.210378, 0.304217}},
  Sinusoidal1_7 → {{0.00237765, 0.00912731, 0.0207385, 0.0478056, 0.102713, 0.989166, 0.0868789,
    0.00432749, 0.0250609, 0.00115304}, {-0.188149, -0.0954195, 0.324817, -0.268983,
    -0.00271577, 0.263017, -0.288029, 0.100362, 0.201479, -0.299525, 0.194192, 0.121691,
    -0.273687, 0.252698, 0.0195018, -0.238251, 0.299492, -0.0962879, -0.204687, 0.309552}},
  Sinusoidal1_8 → {{0.00632634, 0.00297285, 0.0230942, 0.027816, 0.0959568, 0.990317, 0.089321,
    0.0031466, 0.0268455, 0.000798393}, {-0.184681, -0.0675504, 0.279701, -0.272229,
    0.0206599, 0.270953, -0.319563, 0.126323, 0.199255, -0.30184, 0.154078, 0.0792755,
    -0.324575, 0.255526, -0.0238053, -0.235483, 0.274648, -0.0957902, -0.178475, 0.336321}},
  Sinusoidal1_9 → {{0.000945797, 0.0170578, 0.0170628, 0.0423125, 0.103314, 0.988527, 0.0941891,
    0.00382555, 0.0296784, 0.00105013}, {-0.166893, -0.0660021, 0.309722, -0.269759,
    0.00753992, 0.262709, -0.31926, 0.0723509, 0.159835, -0.312553, 0.177214, 0.119819,
    -0.288854, 0.271561, 0.00174154, -0.229631, 0.286327, -0.103739, -0.18458, 0.342242}},
  Sinusoidal1_10 → {{0.00578135, 0.0115757, 0.0224454, 0.0405197, 0.0843891, 0.990723,
    0.0920894, 0.0139274, 0.0171826, 0.0079934}, {-0.176786, -0.0890543, 0.304733, -0.244822,
    0.00224419, 0.269678, -0.317232, 0.111837, 0.163631, -0.292167, 0.171464, 0.115597,
```

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The default linkage is "Average" as a distance function for the first clustering:

In[3]:=
```
clusters1 = TimeSeriesClusters[classification1, LinkageMeasure → "Average"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
⟨|SpikeMax → ⟨|Cluster → Cluster[ ··· 1 ··· ], ··· 4 ···, GroupAssociations →
    ⟨|G1S1 → {SpikePositive_1, SpikePositive_9, SpikePositive_5, ··· 4 ···, SpikePositive_3,
       SpikePositive_6, SpikePositive_10}, G1S2 → ··· 1 ··· |⟩ |⟩, ··· 4 ···, f6 → ⟨| ··· 1 ··· |⟩ |⟩
```

large output | show less | show more | show all | set size limit...

In[4]:=
```
Query[All, "GroupAssociations"]@clusters1
```

Out[4]=
```
⟨|SpikeMax → ⟨|G1S1 → {SpikePositive_1, SpikePositive_9, SpikePositive_5, SpikePositive_7, SpikePositive_2,
      SpikePositive_8, SpikePositive_4, SpikePositive_3, SpikePositive_6, SpikePositive_10},
    G1S2 → {SpikePositive_17, SpikePositive_13, SpikePositive_20, SpikePositive_18, SpikePositive_11,
      SpikePositive_16, SpikePositive_12, SpikePositive_15, SpikePositive_19, SpikePositive_14}|⟩,
  SpikeMin → ⟨|G1S1 → {SpikeNegative_1, SpikeNegative_8, SpikeNegative_5, SpikeNegative_9, SpikeNegative_10,
      SpikeNegative_2}, G1S2 → {SpikeNegative_11, SpikeNegative_15, SpikeNegative_20, SpikeNegative_19},
    G2S1 → {SpikeNegative_12, SpikeNegative_13, SpikeNegative_17, SpikeNegative_18, SpikeNegative_16,
      SpikeNegative_14}, G2S2 → {SpikeNegative_4, SpikeNegative_3, SpikeNegative_7, SpikeNegative_6}|⟩,
  f1 → ⟨|G1S1 → {LinearPositive_1, LinearPositive_2, LinearPositive_10, LinearPositive_4, LinearPositive_3,
      LinearPositive_5, LinearPositive_7, LinearPositive_8, LinearPositive_9, LinearPositive_6,
      LinearPositive_15, LinearPositive_13, LinearPositive_12, LinearPositive_14, LinearPositive_17,
      LinearPositive_16, LinearPositive_20, LinearPositive_19, LinearPositive_18, LinearPositive_11},
    G1S2 → {LinearNegative_4, LinearNegative_19, LinearNegative_11, LinearNegative_14, LinearNegative_20,
      LinearNegative_15, LinearNegative_12, LinearNegative_16, LinearNegative_13, LinearNegative_18,
      LinearNegative_17, LinearNegative_8, LinearNegative_1, LinearNegative_10, LinearNegative_7,
      LinearNegative_6, LinearNegative_2, LinearNegative_3, LinearNegative_5, LinearNegative_9}|⟩,
  f3 → ⟨|G1S1 → {Sinusoidal3_21, Sinusoidal3_27, Sinusoidal3_30, Sinusoidal3_22,
      Sinusoidal3_25, Sinusoidal3_29, Sinusoidal3_26}, G1S2 → {Sinusoidal3_28},
    G2S1 → {Sinusoidal3_24, Sinusoidal3_23}|⟩, f5 → ⟨|G1S1 → {Sinusoidal2_11},
    G1S2 → {Sinusoidal2_12, Sinusoidal2_14, Sinusoidal2_15, Sinusoidal2_13, Sinusoidal2_20, Sinusoidal2_16},
    G2S1 → {Sinusoidal2_17}, G2S2 → {Sinusoidal2_18, Sinusoidal2_19}|⟩,
  f6 → ⟨|G1S1 → {Sinusoidal1_1}, G1S2 → {Sinusoidal1_3, Sinusoidal1_9, Sinusoidal1_7},
    G2S1 → {Sinusoidal1_2, Sinusoidal1_8}, G2S2 → {Sinusoidal1_6},
    G3S1 → {Sinusoidal1_4, Sinusoidal1_10}, G3S2 → {Sinusoidal1_5}|⟩ |⟩
```

In[5]:=
```
clusters1LinkageSingle = TimeSeriesClusters[classification1, LinkageMeasure → "Single"]
```

Out[5]=
```
⟨|SpikeMax → ⟨|Cluster → Cluster[Cluster[ ··· 1 ··· ], ··· 1 ···, 0.324687, 4, 16],
    ··· 4 ···, GroupAssociations → ··· 1 ··· |⟩, ··· 4 ···,
  f6 → ⟨|Cluster → ··· 1 ···, ··· 4 ···, GroupAssociations → ⟨|G1S1 → { ... }, ··· 1 ···, G2S2 → ··· 1 ··· |⟩ |⟩ |⟩
```

large output | show less | show more | show all | set size limit...

We can see that the groupings are now different:

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In[6]:=
```
Query[All, "GroupAssociations"]@clusters1LinkageSingle
```

Out[6]=
```
<|SpikeMax → <|G1S1 → {SpikePositive_1, SpikePositive_9, SpikePositive_5},
    G1S2 → {SpikePositive_7}, G2S1 → {SpikePositive_2, SpikePositive_8,
      SpikePositive_4, SpikePositive_3, SpikePositive_10, SpikePositive_6},
    G2S2 → {SpikePositive_14, SpikePositive_15, SpikePositive_19, SpikePositive_17, SpikePositive_20,
      SpikePositive_13, SpikePositive_11, SpikePositive_16, SpikePositive_18, SpikePositive_12}|>,
  SpikeMin → <|G1S1 → {SpikeNegative_1, SpikeNegative_8, SpikeNegative_7, SpikeNegative_3,
      SpikeNegative_4, SpikeNegative_6, SpikeNegative_9, SpikeNegative_10, SpikeNegative_2},
    G1S2 → {SpikeNegative_19, SpikeNegative_20, SpikeNegative_12, SpikeNegative_13,
      SpikeNegative_17, SpikeNegative_18, SpikeNegative_15, SpikeNegative_11,
      SpikeNegative_16, SpikeNegative_14}, G2S1 → {SpikeNegative_5}|>,
  f1 → <|G1S1 → {LinearPositive_1, LinearPositive_5, LinearPositive_3, LinearPositive_4, LinearPositive_9,
      LinearPositive_8, LinearPositive_7, LinearPositive_10, LinearPositive_2, LinearPositive_6,
      LinearPositive_15, LinearPositive_13, LinearPositive_14, LinearPositive_12, LinearPositive_17,
      LinearPositive_16, LinearPositive_18, LinearPositive_20, LinearPositive_19, LinearPositive_11},
    G1S2 → {LinearNegative_6, LinearNegative_11, LinearNegative_14, LinearNegative_20, LinearNegative_19,
      LinearNegative_12, LinearNegative_15, LinearNegative_13, LinearNegative_16, LinearNegative_18,
      LinearNegative_17, LinearNegative_8, LinearNegative_9, LinearNegative_3, LinearNegative_1,
      LinearNegative_5, LinearNegative_4, LinearNegative_10, LinearNegative_7}, G2S1 → {LinearNegative_2}|>,
  f3 → <|G1S1 → {Sinusoidal3_21, Sinusoidal3_27, Sinusoidal3_29, Sinusoidal3_26, Sinusoidal3_22,
      Sinusoidal3_30, Sinusoidal3_28}, G1S2 → {Sinusoidal3_25}, G2S1 → {Sinusoidal3_24, Sinusoidal3_23}|>,
  f5 → <|G1S1 → {Sinusoidal2_11, Sinusoidal2_18, Sinusoidal2_15, Sinusoidal2_12,
      Sinusoidal2_14, Sinusoidal2_19, Sinusoidal2_17}, G1S2 → {Sinusoidal2_16},
    G2S1 → {Sinusoidal2_20, Sinusoidal2_13}|>, f6 → <|G1S1 → {Sinusoidal1_1},
    G2S1 → {Sinusoidal1_3, Sinusoidal1_4, Sinusoidal1_7, Sinusoidal1_6, Sinusoidal1_9, Sinusoidal1_10},
    G2S2 → {Sinusoidal1_2, Sinusoidal1_8, Sinusoidal1_5}|>|>
```

PrintDendrograms (1)

In[1]:=
```
Needs["MathIOmica`"]
```

PrintDendrograms provides the option to print the associated dendrograms for the groupings (if the cluster contains more than 2 members).

We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.198711, 0.238588, 0.236158, 0.112496, 0.136744, 0.209157, 0.183886, 0.34481,
      0.675053, 0.405356}, {0.96752, -0.04298, 0.0614263, -0.0816569, 0.00308498, -0.0260664,
      0.0474652, 0.0292474, 0.0079997, 0.0462686, -0.0925788, 0.0786909, -0.0251367,
```

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```
    0.0619508, -0.0902928, 0.0857098, 0.0466183, 0.0671261, -0.0388714, 0.0518957}},
  SpikePositive_2 → {{0.402192, 0.255827, 0.289398, 0.225312, 0.300567, 0.0763128, 0.148608,
    0.279096, 0.593595, 0.299632}, {0.968293, 0.0756875, 0.0266752, -0.0798795, 0.0115426,
    0.00535745, -0.0478362, -0.000445416, -0.0792457, -0.0481242, -0.0479775, 0.0994404,
    -0.0915178, -0.0101904, 0.0172022, 0.0184486, 0.0205991, 0.0326286, -0.0845006, 0.0927723}},
  SpikePositive_3 → {{0.179049, 0.261365, 0.189412, 0.0990876, 0.243085, 0.128907, 0.314066,
    0.235587, 0.749938, 0.248358}, {0.969189, -0.0877407, 0.0238794, -0.0713174, -0.0146809,
    -0.0413045, 0.0272029, -0.0480138, 0.0763518, -0.0922883, 0.00865572, 0.0607548, -0.0694363,
    -0.0687661, -0.0177777, -0.0153042, 0.094417, -0.00523972, -0.0720572, -0.0018927}},
  SpikePositive_4 → {{0.223693, 0.105929, 0.224306, 0.401169, 0.353977, 0.288704, 0.381271,
    0.257694, 0.482749, 0.272068}, {0.970594, -0.0548076, -0.0576759, 0.0842618, 0.0534897,
    0.0444216, -0.00531463, 0.0400087, 0.0399054, -0.0118515, -0.0712027, -0.0429042, -0.0615165,
    0.0868642, 0.00771808, 0.0040817, -0.048735, -0.0837642, -0.0158043, 0.0914444}},
  SpikePositive_5 → {{0.379709, 0.340229, 0.100664, 0.235147, 0.318119, 0.317575, 0.273015,
    0.341932, 0.403668, 0.343775}, {0.964745, -0.060518, -0.0228997, 0.0655166, -0.0712967,
    -0.0872572, -0.0404702, 0.00423473, 0.0363451, 0.048454, -0.0954839, -0.0165661,
    -0.0898891, -0.0110913, 0.0860843, 0.0557988, 0.0964505, 0.0363048, 0.0424818, 0.0471479}},
  SpikePositive_6 → {{0.233873, 0.267706, 0.448133, 0.31623, 0.315953, 0.22086, 0.289433,
    0.227468, 0.490015, 0.220408}, {0.98238, 0.0497022, -0.0545117, 0.0182343, -0.0121798,
    -0.0189355, 0.0342949, 0.0425863, 0.0836861, -0.0430681, -0.0654343, -0.00646828,
    0.0216702, 0.0385758, 0.029481, -0.0915793, 0.0130284, 0.0183182, -0.0128371, 0.0243396}},
  SpikePositive_7 → {{0.181285, 0.262293, 0.114856, 0.173447, 0.309949, 0.296347, 0.371129,
    0.153108, 0.69399, 0.168437}, {0.973604, -0.0762028, 0.0523743, -0.0284875, -0.0367637,
    -0.0364233, -0.0489934, -0.021529, 0.0732682, -0.0520838, 0.0419523, -0.05548, 0.00150504,
    -0.091493, -0.0170929, 0.0886587, -0.0615582, 0.0118487, -0.0363984, -0.0499323}},
  SpikePositive_8 → {{0.220634, 0.129171, 0.176884, 0.264386, 0.206572, 0.24891, 0.18753,
    0.350511, 0.670241, 0.348672}, {0.977611, -0.0333592, 0.0372189, -0.0469115, 0.0881891,
    -0.00512532, -0.0331052, 0.00256644, 0.0434426, 0.015669, -0.0936398, -0.0470202, 0.0855585,
    0.00640515, 0.022561, 0.0166483, 0.0707158, -0.0200505, -0.0583302, -0.0246218}},
  SpikePositive_9 → {{0.299818, 0.383322, 0.162786, 0.240146, 0.18115, 0.402783, 0.210323,
    0.240508, 0.568864, 0.241389}, {0.970922, -0.0517079, -0.0671596, -0.000838028, -0.0445366,
    -0.0104706, -0.0147278, -0.0140633, -0.00194644, 0.0776549, -0.0746261, -0.0654341,
    -0.0285246, -0.0565457, -0.0638889, 0.0642625, 0.075029, 0.0284601, -0.0722146, 0.0886323}},
  SpikePositive_10 → {{0.341986, 0.332978, 0.303091, 0.297606, 0.290113, 0.438653, 0.307132,
    0.188584, 0.374612, 0.211959}, {0.969908, 0.0546415, -0.0313082, 0.0475371, -0.0614424,
    -0.0242772, -0.0832884, -0.028195, 0.00658888, 0.0399821, -0.0631371, 0.0233191,
    0.0737397, 0.0656838, -0.0682482, 0.0839882, -0.0490473, 0.0179504, 0.0643197, 0.0803421}},
  SpikePositive_11 → {{0.18063, 0.236395, 0.182873, 0.32281, 0.38471, 0.345253, 0.498071,
    0.183088, 0.432703, 0.194453}, {0.00996215, -0.0730526, 0.962564, -0.103499, -0.0625982,
    0.0866284, -0.030968, -0.0875077, -0.0713025, -0.0738482, -0.0195337, -0.0774558, 0.0787542,
    -0.045251, -0.0248307, 0.0539273, -0.019131, -0.0499068, -0.0727359, -0.0210531}},
  SpikePositive_12 → {{0.2042, 0.24174, 0.178551, 0.395169, 0.299683, 0.510199, 0.358711,
    0.224166, 0.35722, 0.234912}, {-0.0115302, -0.0782834, 0.967461, 0.0691733, -0.0561193,
    -0.0157316, 0.0411108, -0.0638878, -0.0596408, -0.0787224, 0.0251837, 0.0446026, 0.0198667,
    -0.0699181, 0.0647505, 0.0731721, -0.0319153, 0.0777739, 0.0561946, -0.0798251}},
  SpikePositive_13 → {{0.340183, 0.446777, 0.436689, 0.430316, 0.189248, 0.329075, 0.174578,
    0.194122, 0.243801, 0.192593}, {-0.00145091, 0.0644135, 0.975114, 0.0761793, -0.0567073,
    -0.0849239, -0.0517795, -0.0103859, -0.0515892, -0.0378542, -0.00809739, 0.0589365, -0.0444679,
    -0.0483628, 0.0787702, 0.00695102, -0.00783521, -0.00707345, 0.0317465, 0.0815993}},
  SpikePositive_14 → {{0.356671, 0.306316, 0.509416, 0.294035, 0.291115, 0.259806, 0.342153,
    0.252788, 0.211621, 0.23451}, {-0.059732, 0.0152682, 0.9638, 0.0718152, 0.0919261,
    0.0238416, -0.0926492, 0.0835076, -0.0256737, 0.059905, 0.0904863, -0.0444059, -0.082571,
    -0.0268602, 0.0279079, -0.0117649, 0.0825615, -0.0451036, 0.0308774, 0.0699046}},
  SpikePositive_15 → {{0.182568, 0.315615, 0.231987, 0.175374, 0.326629, 0.39334, 0.395121,
    0.344998, 0.326449, 0.373317}, {0.0982988, 0.0919042, 0.966707, -0.00526106, 0.0346742,
    0.0465304, 0.00257918, -0.0140614, -0.0499928, 0.0314697, 0.0360261, 0.0477057, -0.0116447,
    0.0948392, 0.066198, 0.0500865, -0.072966, 0.0830116, -0.0255568, -0.0884158}},
  SpikePositive_16 → {{0.259297, 0.226271, 0.333259, 0.439115, 0.416219, 0.311216, 0.356898,
    0.270953, 0.181262, 0.27192}, {-0.0797085, -0.0183359, 0.974888, 0.0324648, -0.0544431,
    0.0939498, 0.0126086, 0.0373316, 0.0209754, 0.0371803, 0.0656784, 0.00817884, -0.0754308,
    -0.0153092, -0.0852506, 0.0175932, 0.0200066, -0.0853546, 0.00368693, -0.0332149}},
  SpikePositive_17 → {{0.306053, 0.270427, 0.282077, 0.170656, 0.367222, 0.393102, 0.198555,
    0.286216, 0.473714, 0.298966}, {0.0523427, -0.0721619, 0.971566, 0.0620521, 0.0222904,
    -0.0336901, 0.0358117, -0.088266, -0.0324773, 0.0753113, 0.0145382, -0.000526489, -0.0795619,
    -0.0518939, 0.0811517, -0.0259833, -0.0143682, 0.0859592, 0.0211517, 0.0478777}},
  SpikePositive_18 → {{0.176411, 0.459024, 0.258404, 0.376825, 0.267208, 0.290119, 0.213718,
```

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```
    0.297255, 0.393929, 0.323452}, {0.0789177, 0.0233231, 0.948247, 0.0959564, 0.0312196,
    -0.0422357, 0.102192, -0.0318246, -0.0612569, -0.0990578, -0.0837751, 0.0646432, 0.0975633,
    0.103161, 0.0507488, 0.0451485, -0.0676083, -0.00570149, -0.102033, -0.0779884}},
  SpikePositive_19 → {{0.26039, 0.425361, 0.423755, 0.447421, 0.207986, 0.348286, 0.196533,
    0.160007, 0.338735, 0.167274}, {0.0319079, 0.0605523, 0.977781, 0.080539, -0.00618243,
    -0.0266514, -0.0585408, -0.0223829, 0.0756325, -0.0818774, 0.0196063, 0.0560734,
    0.0251256, 0.0088971, 0.0180352, 0.0280578, 0.0585291, -0.0393765, -0.0343217, 0.0645572}},
  SpikePositive_20 → {{0.143992, 0.191429, 0.215202, 0.228018, 0.466852, 0.364189, 0.230938,
    0.357607, 0.431009, 0.356017}, {0.0539091, 0.00518876, 0.973335, -0.0575574, -0.0738336,
    -0.0319849, 0.0826118, -0.023439, 0.0722221, 0.0353774, 0.0524822, 0.00449832, -0.0399622,
    0.0342783, -0.00731633, -0.0782255, 0.0452537, 0.0451656, 0.0489638, -0.0886151}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.241473, 0.245039, 0.439444, 0.324696, 0.0975897, 0.409425,
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    -0.00864736, -0.0345756, -0.0809619, 0.0337372, 0.0842658, -0.0755802, 0.0723328, 0.074779,
    -0.0818944, 0.0470061, 0.0340188, 0.0825058, -0.0612466, -0.0824694, -0.0201691, 0.0182585}},
  SpikeNegative_2 → {{0.200584, 0.17181, 0.242494, 0.434529, 0.388311, 0.29649, 0.226694,
    0.2162, 0.542745, 0.226346}, {-0.969552, 0.0782814, 0.0671222, -0.0633742, -0.0872104,
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    -0.0610372, -0.0435924, 0.0766818, 0.0134915, -0.0657816, -0.0834564, 0.0219212}},
  SpikeNegative_3 → {{0.338556, 0.201239, 0.238586, 0.229114, 0.163399, 0.340562, 0.259666,
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    -0.0298171, 0.0295418, 0.0832932, -0.072606, 0.0360522, -0.0508585, 0.0596861, 0.0419706}},
  SpikeNegative_4 → {{0.306202, 0.307718, 0.30571, 0.16287, 0.30152, 0.23546, 0.313669, 0.262032,
    0.564204, 0.24461}, {-0.973247, -0.0409237, 0.00403878, 0.0125439, 0.0679249, 0.0826774,
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    -0.054748, -0.0412854, -0.000567288, -0.0659441, 0.0712405, 0.0608743, -0.0917343}},
  SpikeNegative_5 → {{0.332491, 0.270219, 0.322832, 0.382085, 0.270124, 0.18713, 0.248114,
    0.207694, 0.549248, 0.227741}, {-0.972798, 0.0479328, 0.0303153, 0.00730474, -0.0174714,
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  SpikeNegative_6 → {{0.165132, 0.203107, 0.264264, 0.144021, 0.388361, 0.494588, 0.481417,
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  SpikeNegative_7 → {{0.254246, 0.34022, 0.146837, 0.175817, 0.289341, 0.280403, 0.360155,
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    0.0341849, 0.0642336, -0.0239553, -0.0659233, 0.00698249, 0.0908422, 0.00460205}},
  SpikeNegative_8 → {{0.275958, 0.185945, 0.315164, 0.418591, 0.127652, 0.197036, 0.27154,
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  SpikeNegative_9 → {{0.264483, 0.196641, 0.388135, 0.214638, 0.457892, 0.3717, 0.201973,
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  SpikeNegative_10 → {{0.259446, 0.175198, 0.445185, 0.424121, 0.189817, 0.36046, 0.237509,
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  SpikeNegative_11 → {{0.233992, 0.187656, 0.330971, 0.364944, 0.297602, 0.361746, 0.347988,
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  SpikeNegative_12 → {{0.26418, 0.224084, 0.163715, 0.427088, 0.198595, 0.238035, 0.19663,
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  SpikeNegative_13 → {{0.195538, 0.291384, 0.451622, 0.395576, 0.279848, 0.213091, 0.4546,
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  SpikeNegative_14 → {{0.234298, 0.254402, 0.237306, 0.438149, 0.350998, 0.383004, 0.310876,
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  SpikeNegative_18 → {{0.218086, 0.362401, 0.405945, 0.227387, 0.246725, 0.304077, 0.185362,
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  SpikeNegative_19 → {{0.213938, 0.314186, 0.282571, 0.344314, 0.171467, 0.43948, 0.355962,
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  SpikeNegative_20 → {{0.33985, 0.410606, 0.209342, 0.228937, 0.487645, 0.299744, 0.438526,
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  LinearPositive_3 → {{0.984032, 0.165725, 0.0335368, 0.00224807, 0.00170631, 0.0108862,
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  LinearPositive_4 → {{0.983946, 0.1674, 0.0323711, 0.00217931, 0.00168684, 0.00972767,
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  LinearPositive_6 → {{0.983395, 0.170467, 0.03063, 0.00193096, 0.00173954,
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  LinearPositive_7 → {{0.983808, 0.169101, 0.0320381, 0.00204249, 0.00154798,
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  LinearPositive_8 → {{0.984795, 0.16124, 0.0333497, 0.00241186, 0.00179385, 0.00945372,
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      0.244036, 0.260629, 0.279419, 0.298253, 0.315804, 0.337168, 0.355249, 0.37356}},
  LinearPositive_9 → {{0.984327, 0.165449, 0.0338275, 0.00236504, 0.00196581,
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  LinearPositive_10 → {{0.98418, 0.166035, 0.0322447, 0.00224316, 0.00229779,
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  LinearPositive_11 → {{0.982446, 0.171936, 0.0291037, 0.00530476, 0.00942929,
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LinearPositive_12 → {{0.98342, 0.167285, 0.0370091, 0.00486094, 0.00219401, 0.0160332,
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LinearPositive_14 → {{0.983225, 0.170542, 0.0310959, 0.00135042, 0.0039724, 0.00323519,
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LinearPositive_15 → {{0.984696, 0.160862, 0.0368671, 0.00219256, 0.000225512, 0.0097909,
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LinearPositive_16 → {{0.984389, 0.163045, 0.0380854, 0.00535364, 0.00222127,
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LinearPositive_17 → {{0.985213, 0.162216, 0.0266663, 0.00317086, 0.000929652, 0.0117921,
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LinearPositive_18 → {{0.985169, 0.158389, 0.0275371, 0.00283566, 0.00572869, 0.00655639,
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LinearPositive_19 → {{0.98673, 0.153099, 0.0298463, 0.00263217, 0.00233725, 0.00739195,
    0.0244542, 0.0218236, 0.014705, 0.0260075}, {0.0190805, 0.0332992, 0.0595253,
    0.0760281, 0.101431, 0.104726, 0.138991, 0.143084, 0.164383, 0.193361, 0.201403,
    0.225116, 0.243699, 0.268394, 0.27949, 0.30329, 0.31934, 0.330491, 0.352743, 0.367901}},
LinearPositive_20 → {{0.981261, 0.182007, 0.0362608, 0.00271341, 0.00108858, 0.00845965,
    0.0196049, 0.0274779, 0.0221232, 0.0312623}, {0.0178482, 0.0340831, 0.0507481, 0.0769936,
    0.0851739, 0.116434, 0.127264, 0.144522, 0.175817, 0.183333, 0.197346, 0.233899,
    0.236079, 0.255218, 0.283474, 0.301883, 0.319018, 0.343212, 0.357052, 0.366786}},
LinearNegative_1 → {{0.988496, 0.145776, 0.0117444, 0.00267918, 0.00130722, 0.0114949,
    0.00815591, 0.0199039, 0.0185596, 0.0232347}, {-0.0157059, -0.0247912, -0.0726773, -0.0930051,
    -0.0792835, -0.103557, -0.114836, -0.144554, -0.158428, -0.169724, -0.194874, -0.20734,
    -0.224953, -0.274662, -0.284148, -0.302655, -0.328826, -0.332102, -0.368213, -0.383223}},
LinearNegative_2 → {{0.986143, 0.150497, 0.0281292, 0.00603283, 0.00311333, 0.0219996,
    0.0341439, 0.0267259, 0.0264154, 0.0311956}, {-0.00539556, -0.0357518, -0.0585193, -0.0647483,
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    -0.25242, -0.271503, -0.289167, -0.299301, -0.315997, -0.347633, -0.342106, -0.370586}},
LinearNegative_3 → {{0.986531, 0.155054, 0.0287734, 0.00242953, 0.000408675, 0.0122485,
    0.0108357, 0.0238165, 0.0173523, 0.0272799}, {-0.0344366, -0.030307, -0.0646148, -0.0666878,
    -0.0889836, -0.0939543, -0.117189, -0.165357, -0.15735, -0.173567, -0.218392, -0.214776,
    -0.248679, -0.267632, -0.270675, -0.310529, -0.30496, -0.343143, -0.361238, -0.371943}},
LinearNegative_4 → {{0.984648, 0.15547, 0.0586382, 0.00254949, 0.00205017, 0.0219796,
    0.0140505, 0.0293358, 0.0133463, 0.0336076}, {-0.0272079, -0.0422236, -0.0500477, -0.0619922,
    -0.0867024, -0.111678, -0.117181, -0.144698, -0.166476, -0.175673, -0.221058, -0.235913,
    -0.247514, -0.26041, -0.271694, -0.287432, -0.332741, -0.350687, -0.34783, -0.364937}},
LinearNegative_5 → {{0.981598, 0.181554, 0.0297068, 0.00627522, 0.00360327, 0.0102472,
    0.0113371, 0.0312486, 0.0108834, 0.0352017}, {-0.0365993, -0.0239178, -0.0498282, -0.09036,
    -0.0808088, -0.0957927, -0.125529, -0.148298, -0.179828, -0.171369, -0.219969, -0.225298,
    -0.225783, -0.264844, -0.284562, -0.292741, -0.321906, -0.346554, -0.355791, -0.367465}},
LinearNegative_6 → {{0.981802, 0.152725, 0.0300897, 0.000074544, 0.00425414, 0.01539, 0.0544862,
    0.0418385, 0.0686557, 0.0463335}, {-0.000874318, -0.051438, -0.0422079, -0.0896784,
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    -0.234556, -0.261554, -0.271422, -0.292373, -0.307517, -0.325, -0.345718, -0.386583}},
LinearNegative_7 → {{0.979907, 0.185388, 0.0311121, 0.000268708, 0.0156931, 0.0149683,
    0.0209261, 0.0317311, 0.0348341, 0.0362927}, {-0.0069468, -0.0457908, -0.0589881, -0.075218,
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    -0.234406, -0.256661, -0.268519, -0.306489, -0.334323, -0.323966, -0.34772, -0.378174}},
  LinearNegative_8 → {{0.986447, 0.152277, 0.0212915, 0.00185118, 0.0129931, 0.0061893,
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    -0.249309, -0.271636, -0.265575, -0.310418, -0.326966, -0.314266, -0.355731, -0.376937}},
  LinearNegative_9 → {{0.990457, 0.129814, 0.0196149, 0.00951074, 0.00346493, 0.0157535,
    0.0271298, 0.0148025, 0.00920826, 0.0191702}, {-0.0162153, -0.0227382, -0.0591005, -0.0804256,
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  LinearNegative_10 → {{0.984277, 0.158342, 0.0530111, 0.000644043, 0.00318717, 0.00829247,
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    -0.0853941, -0.117786, -0.141244, -0.138758, -0.151951, -0.178192, -0.210465, -0.223354,
    -0.246257, -0.247626, -0.282309, -0.291469, -0.319713, -0.346474, -0.367028, -0.366602}},
  LinearNegative_11 → {{0.985619, 0.157452, 0.0276958, 0.000591314, 0.00112605, 0.0146555,
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  LinearNegative_12 → {{0.987049, 0.148053, 0.0374698, 0.00403896, 0.000610038, 0.0140053,
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    -0.247205, -0.266602, -0.283167, -0.296702, -0.313921, -0.330752, -0.357791, -0.367176}},
  LinearNegative_13 → {{0.98051, 0.183334, 0.0280933, 0.000320921, 0.0027564, 0.00828044,
    0.0266658, 0.0361625, 0.0186756, 0.041906}, {-0.0164881, -0.0308429, -0.0609165, -0.0720012,
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  LinearNegative_14 → {{0.98083, 0.182982, 0.043175, 0.00245185, 0.00113761, 0.0118315, 0.0252734,
    0.0265178, 0.00986035, 0.0322503}, {-0.0236688, -0.0287583, -0.0525818, -0.0686153,
    -0.102637, -0.1042, -0.1395, -0.144922, -0.169947, -0.189437, -0.212602, -0.224887,
    -0.239091, -0.254876, -0.274798, -0.294199, -0.320803, -0.332619, -0.357247, -0.378649}},
  LinearNegative_15 → {{0.982957, 0.172862, 0.0335347, 0.0021123, 0.000742396, 0.0112426,
    0.0253124, 0.0256454, 0.0219156, 0.0296625}, {-0.0252036, -0.0447859, -0.0556758, -0.0727306,
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  LinearNegative_16 → {{0.988119, 0.139049, 0.0326459, 0.00184671, 0.00271135, 0.0160685,
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  LinearNegative_17 → {{0.980308, 0.188317, 0.0296766, 0.00292428, 0.00271784, 0.0103199,
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  LinearNegative_18 → {{0.987725, 0.142605, 0.0298175, 0.000732303, 0.00477249, 0.0123864,
    0.0173457, 0.0280202, 0.029759, 0.0320164}, {-0.0190967, -0.0373048, -0.0634991, -0.0692248,
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  LinearNegative_19 → {{0.984459, 0.164995, 0.0314156, 0.00234875, 0.00305665, 0.0107167,
    0.0228484, 0.0248446, 0.0227299, 0.0290768}, {-0.019676, -0.0374824, -0.0549533, -0.0669165,
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    -0.237064, -0.264003, -0.284082, -0.306199, -0.311909, -0.328707, -0.352815, -0.377137}},
  LinearNegative_20 → {{0.98731, 0.146656, 0.0348533, 0.00133293, 0.00297714, 0.00799105,
    0.0160928, 0.0267527, 0.022606, 0.0305911}, {-0.0259145, -0.0394168, -0.0569783, -0.0667939,
    -0.0841575, -0.105409, -0.127144, -0.141154, -0.166594, -0.181127, -0.200389, -0.232862,
    -0.243302, -0.266917, -0.270782, -0.302586, -0.311777, -0.336889, -0.359802, -0.381267}}|>,
f3 → <|Sinusoidal3_21 → {{0.00255585, 0.0744366, 0.992216, 0.0879348, 0.0365614, 0.0195526,
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    0.297001, 0.256057, 0.00152654, -0.253034, -0.297739, -0.0966719, 0.180304, 0.316838}},
  Sinusoidal3_22 → {{0.0024942, 0.0738207, 0.992905, 0.0805357, 0.0363402, 0.020321, 0.00888886,
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  Sinusoidal3_23 → {{0.00270461, 0.0763328, 0.992558, 0.0818167, 0.0383166, 0.0189116,
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    Sinusoidal3_25 → {{0.00291858, 0.0714892, 0.992711, 0.0852029, 0.0366904, 0.0192424,
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    Sinusoidal3_26 → {{0.0027997, 0.071484, 0.992095, 0.090835, 0.0371734, 0.0210539, 0.00860022,
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    Sinusoidal3_27 → {{0.00227716, 0.0727259, 0.992363, 0.088267, 0.0358297, 0.0187322, 0.007205,
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    Sinusoidal3_28 → {{0.00312878, 0.0715934, 0.992516, 0.0882315, 0.0345117, 0.0178514,
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    Sinusoidal3_29 → {{0.0034786, 0.0716267, 0.992235, 0.0895934, 0.0379123, 0.0200901,
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    Sinusoidal3_30 → {{0.00329621, 0.0734579, 0.992191, 0.0884629, 0.0369744, 0.0205368,
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f5 → ‹|Sinusoidal2_11 → {{0.00214142, 0.0113461, 0.0271614, 0.093491, 0.929864, 0.352021,
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    Sinusoidal2_12 → {{0.00265779, 0.0124429, 0.0280191, 0.0882136, 0.93458, 0.340768, 0.0279562,
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    Sinusoidal2_13 → {{0.00205643, 0.00837221, 0.0286961, 0.100046, 0.932188, 0.34422, 0.0282881,
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    Sinusoidal2_14 → {{0.0021733, 0.0120582, 0.030852, 0.0887924, 0.929571, 0.35393, 0.0293392,
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    Sinusoidal2_15 → {{0.003211, 0.0125322, 0.0291146, 0.0917017, 0.932214, 0.346446, 0.0288529,
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    Sinusoidal2_16 → {{0.00329807, 0.0106659, 0.0298396, 0.0894634, 0.936594, 0.334858, 0.0285978,
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    Sinusoidal2_17 → {{0.00323921, 0.0104267, 0.0310995, 0.0937253, 0.937717, 0.330232, 0.028827,
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        -0.312122, 0.103194, 0.257906, -0.257355, -0.0921103, 0.319936, -0.094276, -0.250974,
        0.251413, 0.0924457, -0.309199, 0.0930346, 0.259247, -0.258655, -0.102927, 0.321497}},
    Sinusoidal2_18 → {{0.00261862, 0.0117595, 0.0294173, 0.0928994, 0.935446, 0.337253, 0.0284566,
        0.00439605, 0.0269919, 0.00153599}, {-0.102305, -0.25133, 0.250327, 0.0986084,
        -0.314055, 0.0963326, 0.255742, -0.254077, -0.0950258, 0.314974, -0.0968378, -0.253655,
        0.260833, 0.101781, -0.320021, 0.0929391, 0.257739, -0.256152, -0.100764, 0.320176}},
    Sinusoidal2_19 → {{0.00238335, 0.00977215, 0.0264627, 0.0937981, 0.931964, 0.346374, 0.0297822,
        0.00311707, 0.0311639, 0.000768734}, {-0.0966753, -0.258399, 0.250503, 0.0925838,
        -0.311387, 0.0994216, 0.262851, -0.257669, -0.0960513, 0.3147, -0.0940436, -0.250804,
        0.255071, 0.0999753, -0.321173, 0.103028, 0.257795, -0.252902, -0.0949492, 0.319319}},
    Sinusoidal2_20 → {{0.00194052, 0.0094224, 0.0312386, 0.0951129, 0.932341, 0.345053, 0.0238456,
```

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```
    0.00521261, 0.0310552, 0.00178866}, {-0.0953611, -0.259725, 0.255227, 0.0950605,
    -0.313494, 0.0928888, 0.256859, -0.250327, -0.0995728, 0.320633, -0.0948312, -0.257297,
    0.260059, 0.0930896, -0.309578, 0.100408, 0.259907, -0.249571, -0.102064, 0.321463}}|>,
f6 → <|Sinusoidal1_1 → {{0.00076993, 0.00712448, 0.0251898, 0.026261, 0.102449, 0.989062,
    0.0977837, 0.00882471, 0.0150545, 0.00445633}, {-0.186555, -0.0780429, 0.268567, -0.272305,
    -0.0179468, 0.272494, -0.324032, 0.0975626, 0.187757, -0.308072, 0.152418, 0.0791627,
    -0.301182, 0.275013, 0.021472, -0.260505, 0.287795, -0.114582, -0.205246, 0.30221}},
  Sinusoidal1_2 → {{0.0028637, 0.0136851, 0.0255902, 0.054506, 0.088803, 0.988769, 0.0992801,
    0.00306564, 0.027597, 0.000892624}, {-0.199404, -0.0863746, 0.323603, -0.246948,
    -0.00415995, 0.242694, -0.291487, 0.0795271, 0.156959, -0.321973, 0.168725, 0.111965,
    -0.326103, 0.260471, 0.00731065, -0.230901, 0.283581, -0.110767, -0.172209, 0.343016}},
  Sinusoidal1_3 → {{0.00465902, 0.0101013, 0.0240866, 0.040161, 0.0921357, 0.988627, 0.10482,
    0.00434695, 0.028321, 0.00142201}, {-0.167216, -0.0815467, 0.314595, -0.276177,
    0.0160765, 0.268161, -0.288515, 0.090746, 0.169194, -0.33973, 0.158121, 0.0738147,
    -0.311772, 0.267603, 0.0140794, -0.233775, 0.278188, -0.120874, -0.170643, 0.327455}},
  Sinusoidal1_4 → {{0.00563062, 0.00427494, 0.0148009, 0.0375169, 0.0809494, 0.989713,
    0.108194, 0.00712603, 0.0217556, 0.00288291}, {-0.178259, -0.118887, 0.29746, -0.223064,
    0.00271644, 0.259369, -0.304819, 0.109425, 0.197609, -0.33292, 0.17321, 0.0928643,
    -0.310265, 0.226957, -0.0166977, -0.26868, 0.314921, -0.0737973, -0.198664, 0.301398}},
  Sinusoidal1_5 → {{0.0032709, 0.00661173, 0.0172819, 0.0226644, 0.0680941, 0.989408, 0.123209,
    0.00938287, 0.0167023, 0.00464881}, {-0.177352, -0.12701, 0.276012, -0.228738,
    0.0252745, 0.271529, -0.319621, 0.112552, 0.203298, -0.341653, 0.15704, 0.086575,
    -0.310518, 0.25289, 0.0142425, -0.249179, 0.307321, -0.0970257, -0.161375, 0.303209}},
  Sinusoidal1_6 → {{0.00175287, 0.00750089, 0.0132294, 0.0346023, 0.0895818, 0.990514,
    0.093313, 0.00717444, 0.025661, 0.00283061}, {-0.192589, -0.123766, 0.274563, -0.240822,
    0.00953682, 0.276125, -0.323419, 0.105639, 0.183886, -0.30809, 0.176856, 0.118127,
    -0.28931, 0.24103, -0.00660842, -0.240824, 0.302609, -0.0787592, -0.197625, 0.333891}},
  Sinusoidal1_7 → {{0.00242459, 0.00493401, 0.0259745, 0.051773, 0.0939762, 0.987965, 0.106174,
    0.00627447, 0.0197723, 0.00240998}, {-0.195373, -0.10111, 0.322406, -0.269841,
    -0.0300188, 0.223407, -0.308059, 0.103372, 0.191433, -0.309555, 0.206984, 0.0811364,
    -0.312975, 0.22185, -0.0192448, -0.256687, 0.305149, -0.112948, -0.189084, 0.285476}},
  Sinusoidal1_8 → {{0.00351956, 0.00421323, 0.0239072, 0.0416013, 0.0931106, 0.987394, 0.114556,
    0.00241431, 0.0303787, 0.000408254}, {-0.164502, -0.0992274, 0.290275, -0.255909,
    -0.00020463, 0.250563, -0.290844, 0.0685403, 0.199769, -0.329359, 0.190177, 0.0703945,
    -0.332473, 0.232381, -0.00209005, -0.240212, 0.30216, -0.112529, -0.21771, 0.313304}},
  Sinusoidal1_9 → {{0.00241787, 0.013584, 0.0177839, 0.0316483, 0.0800176, 0.987803, 0.12562,
    0.0155341, 0.0152456, 0.00888645}, {-0.173419, -0.114721, 0.301098, -0.227489,
    -0.0211782, 0.281089, -0.31624, 0.103717, 0.183186, -0.337743, 0.176722, 0.0952649,
    -0.275198, 0.252482, 0.018304, -0.273947, 0.280302, -0.10734, -0.156423, 0.326763}},
  Sinusoidal1_10 → {{0.00339793, 0.0137885, 0.0238913, 0.0392441, 0.12013, 0.98551, 0.104272,
    0.0019218, 0.0339003, 0.000867092}, {-0.189225, -0.102829, 0.325754, -0.269566,
    0.00297632, 0.260635, -0.288521, 0.0750669, 0.195864, -0.28915, 0.195195, 0.103992,
    -0.28847, 0.285843, -0.0133318, -0.234752, 0.278846, -0.111982, -0.210869, 0.303587}}|>|>
```

We now cluster the data and also print the dendrograms in the notebook:

```
In[3]:= clusters1DendrogramPrint = TimeSeriesClusters[classification1, PrintDendrograms → True]
```

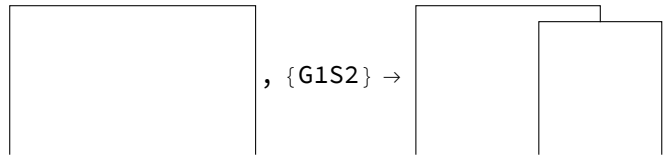
Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

```
<|SpikeMax → <|G1 → <|{G1S1} → ,{G1S2} → |>,
```



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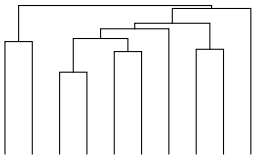
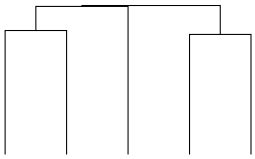
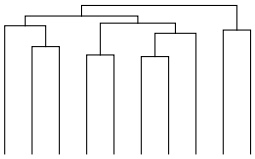
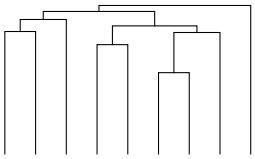
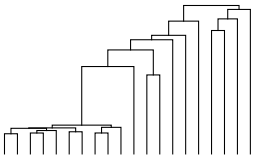
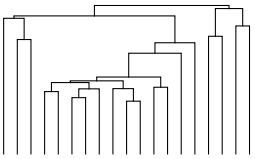
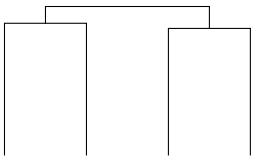
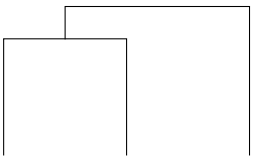
G2 → ⟨| {G2S1} →  , {G2S2} →  |⟩ |⟩ ,

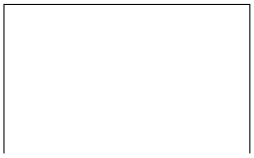
SpikeMin → ⟨| G1 → ⟨| {G1S1} →  , {G1S2} →  |⟩ ,

G2 → ⟨| {G2S1} → {{0.0174219, -0.0488439, -0.965113, 0.020763, 0.0748517, -0.0511357, 0.0880155, 0.0773812, 0.0741427, 0.0093807, -0.0455673, 0.0982058, -0.0329699, 0.0259155, 0.0745446, 0.0294527, 0.0456798, -0.0955923, 0.0254361, -0.0782614} → SpikeNegative_20} |⟩ |⟩ ,

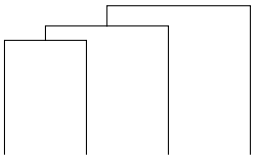
f1 → ⟨| G1 → ⟨| {G1S1} →  , {G1S2} →  |⟩ ,

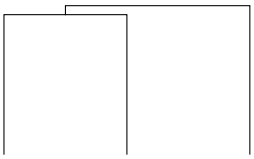
G2 → ⟨| {G2S1} → {{-0.000874318, -0.051438, -0.0422079, -0.0896784, -0.0860793, -0.116874, -0.137804, -0.155811, -0.165569, -0.206009, -0.20299, -0.245759, -0.234556, -0.261554, -0.271422, -0.292373, -0.307517, -0.325, -0.345718, -0.386583} → LinearNegative_6} |⟩ |⟩ ,

f3 → ⟨| G1 → ⟨| {G1S1} →  , {G1S2} →  |⟩ ,

G2 → ⟨| {G2S1} →  ,

{G2S2} → {{0.190381, -0.0917509, -0.294444, -0.250554, -0.00338723, 0.259708, 0.2969, 0.101933, -0.187752, -0.318593, -0.187298, 0.0927863, 0.304214, 0.254346, -0.000731432, -0.256545, -0.300469, -0.0991535, 0.190884, 0.315939} → Sinusoidal3_25} |⟩ |⟩ ,

f5 → ⟨| G1 → ⟨| {G1S1} →  , {G1S2} → |⟩ ,

G2 → ⟨| {G2S1} →  ,

{G2S2} → {{-0.0973995, -0.261294, 0.256682, 0.0934788, -0.312122,

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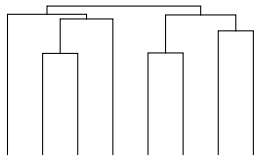
```
0.103194, 0.257906, -0.257355, -0.0921103, 0.319936, -0.094276,
-0.250974, 0.251413, 0.0924457, -0.309199, 0.0930346, 0.259247,
-0.258655, -0.102927, 0.321497} → Sinusoidal2_17} |⟩ |⟩,
```

f6 → ⟨| G1 → ⟨| {G1S1} →



|⟩,

G2 → ⟨| {G2S1} →

|⟩ |⟩ |⟩

Out[3]=

```
⟨|SpikeMax → ⟨|Cluster → Cluster[Cluster[ ··· 1 ··· ],
    Cluster[Cluster[ ··· 1 ··· ], Cluster[ ··· 1 ··· ], 0.420465, 6, 9], 0.524699, 5, 15],
  ··· 4 ···, GroupAssociations → ⟨|G1S1 → { ··· 1 ··· }, ··· 3 ··· |⟩ |⟩, ··· 4 ···, f6 → ⟨| ··· 1 ··· |⟩ |⟩
```

large output | show less | show more | show all | set size limit...

ReturnDendrograms (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ReturnDendrograms provides the option to return the dendrograms instead of the clustering information (if the cluster contains more than 2 members).

We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → ⟨|20 → {0.42, -0.42}|⟩]
```

```
Method → "LombScargle"
```

Out[2]=
```
⟨|SpikeMax →
  ⟨|SpikePositive_1 → {{0.198711, 0.238588, 0.236158, 0.112496, 0.136744, 0.209157, 0.183886, 0.34481,
      0.675053, 0.405356}, {0.96752, -0.04298, 0.0614263, -0.0816569, 0.00308498, -0.0260664,
      0.0474652, 0.0292474, 0.0079997, 0.0462686, -0.0925788, 0.0786909, -0.0251367,
      0.0619508, -0.0902928, 0.0857098, 0.0466183, 0.0671261, -0.0388714, 0.0518957}},
   SpikePositive_2 → {{0.402192, 0.255827, 0.289398, 0.225312, 0.300567, 0.0763128, 0.148608,
```

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```
    0.279096, 0.593595, 0.299632}, {0.968293, 0.0756875, 0.0266752, -0.0798795, 0.0115426,
    0.00535745, -0.0478362, -0.000445416, -0.0792457, -0.0481242, -0.0479775, 0.0994404,
    -0.0915178, -0.0101904, 0.0172022, 0.0184486, 0.0205991, 0.0326286, -0.0845006, 0.0927723}},
  SpikePositive_3 → {{0.179049, 0.261365, 0.189412, 0.0990876, 0.243085, 0.128907, 0.314066,
    0.235587, 0.749938, 0.248358}, {0.969189, -0.0877407, 0.0238794, -0.0713174, -0.0146809,
    -0.0413045, 0.0272029, -0.0480138, 0.0763518, -0.0922883, 0.00865572, 0.0607548, -0.0694363,
    -0.0687661, -0.0177777, -0.0153042, 0.094417, -0.00523972, -0.0720572, -0.0018927}},
  SpikePositive_4 → {{0.223693, 0.105929, 0.224306, 0.401169, 0.353977, 0.288704, 0.381271,
    0.257694, 0.482749, 0.272068}, {0.970594, -0.0548076, -0.0576759, 0.0842618, 0.0534897,
    0.0444216, -0.00531463, 0.0400087, 0.0399054, -0.0118515, -0.0712027, -0.0429042, -0.0615165,
    0.0868642, 0.00771808, 0.0040817, -0.048735, -0.0837642, -0.0158043, 0.0914444}},
  SpikePositive_5 → {{0.379709, 0.340229, 0.100664, 0.235147, 0.318119, 0.317575, 0.273015,
    0.341932, 0.403668, 0.343775}, {0.964745, -0.060518, -0.0228997, 0.0655166, -0.0712967,
    -0.0872572, -0.0404702, 0.00423473, 0.0363451, 0.048454, -0.0954839, -0.0165661,
    -0.0898891, -0.0110913, 0.0860843, 0.0557988, 0.0964505, 0.0363048, 0.0424818, 0.0471479}},
  SpikePositive_6 → {{0.233873, 0.267706, 0.448133, 0.31623, 0.315953, 0.22086, 0.289433,
    0.227468, 0.490015, 0.220408}, {0.98238, 0.0497022, -0.0545117, 0.0182343, -0.0121798,
    -0.0189355, 0.0342949, 0.0425863, 0.0836861, -0.0430681, -0.0654343, -0.00646828,
    0.0216702, 0.0385758, 0.029481, -0.0915793, 0.0130284, 0.0183182, -0.0128371, 0.0243396}},
  SpikePositive_7 → {{0.181285, 0.262293, 0.114856, 0.173447, 0.309949, 0.296347, 0.371129,
    0.153108, 0.69399, 0.168437}, {0.973604, -0.0762028, 0.0523743, -0.0284875, -0.0367637,
    -0.0364233, -0.0489934, -0.021529, 0.0732682, -0.0520838, 0.0419523, -0.05548, 0.00150504,
    -0.091493, -0.0170929, 0.0886587, -0.0615582, 0.0118487, -0.0363984, -0.0499323}},
  SpikePositive_8 → {{0.220634, 0.129171, 0.176884, 0.264386, 0.206572, 0.24891, 0.18753,
    0.350511, 0.670241, 0.348672}, {0.977611, -0.0333592, 0.0372189, -0.0469115, 0.0881891,
    -0.00512532, -0.0331052, 0.00256644, 0.0434426, 0.015669, -0.0936398, -0.0470202, 0.0855585,
    0.00640515, 0.022561, 0.0166483, 0.0707158, -0.0200505, -0.0583302, -0.0246218}},
  SpikePositive_9 → {{0.299818, 0.383322, 0.162786, 0.240146, 0.18115, 0.402783, 0.210323,
    0.240508, 0.568864, 0.241389}, {0.970922, -0.0517079, -0.0671596, -0.000838028, -0.0445366,
    -0.0104706, -0.0147278, -0.0140633, -0.00194644, 0.0776549, -0.0746261, -0.0654341,
    -0.0285246, -0.0565457, -0.0638889, 0.0642625, 0.075029, 0.0284601, -0.0722146, 0.0886323}},
  SpikePositive_10 → {{0.341986, 0.332978, 0.303091, 0.297606, 0.290113, 0.438653, 0.307132,
    0.188584, 0.374612, 0.211959}, {0.969908, 0.0546415, -0.0313082, 0.0475371, -0.0614424,
    -0.0242772, -0.0832884, -0.028195, 0.00658888, 0.0399821, -0.0631371, 0.0233191,
    0.0737397, 0.0656838, -0.0682482, 0.0839882, -0.0490473, 0.0179504, 0.0643197, 0.0803421}},
  SpikePositive_11 → {{0.18063, 0.236395, 0.182873, 0.32281, 0.38471, 0.345253, 0.498071,
    0.183088, 0.432703, 0.194453}, {0.00996215, -0.0730526, 0.962564, -0.103499, -0.0625982,
    0.0866284, -0.030968, -0.0875077, -0.0713025, -0.0738482, -0.0195337, -0.0774558, 0.0787542,
    -0.045251, -0.0248307, 0.0539273, -0.019131, -0.0499068, -0.0727359, -0.0210531}},
  SpikePositive_12 → {{0.2042, 0.24174, 0.178551, 0.395169, 0.299683, 0.510199, 0.358711,
    0.224166, 0.35722, 0.234912}, {-0.0115302, -0.0782834, 0.967461, 0.0691733, -0.0561193,
    -0.0157316, 0.0411108, -0.0638878, -0.0596408, -0.0787224, 0.0251837, 0.0446026, 0.0198667,
    -0.0699181, 0.0647505, 0.0731721, -0.0319153, 0.0777739, 0.0561946, -0.0798251}},
  SpikePositive_13 → {{0.340183, 0.446777, 0.436689, 0.430316, 0.189248, 0.329075, 0.174578,
    0.194122, 0.243801, 0.192593}, {-0.00145091, 0.0644135, 0.975114, 0.0761793, -0.0567073,
    -0.0849239, -0.0517795, -0.0103859, -0.0515892, -0.0378542, -0.00809739, 0.0589365, -0.0444679,
    -0.0483628, 0.0787702, 0.00695102, -0.00783521, -0.00707345, 0.0317465, 0.0815993}},
  SpikePositive_14 → {{0.356671, 0.306316, 0.509416, 0.294035, 0.291115, 0.259806, 0.342153,
    0.252788, 0.211621, 0.23451}, {-0.059732, 0.0152682, 0.9638, 0.0718152, 0.0919261,
    0.0238416, -0.0926492, 0.0835076, -0.0256737, 0.059905, 0.0904863, -0.0444059, -0.082571,
    -0.0268602, 0.0279079, -0.0117649, 0.0825615, -0.0451036, 0.0308774, 0.0699046}},
  SpikePositive_15 → {{0.182568, 0.315615, 0.231987, 0.175374, 0.326629, 0.39334, 0.395121,
    0.344998, 0.326449, 0.373317}, {0.0982988, 0.0919042, 0.966707, -0.00526106, 0.0346742,
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    0.0948392, 0.066198, 0.0500865, -0.072966, 0.0830116, -0.0255568, -0.0884158}},
  SpikePositive_16 → {{0.259297, 0.226271, 0.333259, 0.439115, 0.416219, 0.311216, 0.356898,
    0.270953, 0.181262, 0.27192}, {-0.0797085, -0.0183359, 0.974888, 0.0324648, -0.0544431,
    0.0939498, 0.0126086, 0.0373316, 0.0209754, 0.0371803, 0.0656784, 0.00817884, -0.0754308,
    -0.0153092, -0.0852506, 0.0175932, 0.0200066, -0.0853546, 0.00368693, -0.0332149}},
  SpikePositive_17 → {{0.306053, 0.270427, 0.282077, 0.170656, 0.367222, 0.393102, 0.198555,
    0.286216, 0.473714, 0.298966}, {0.0523427, -0.0721619, 0.971566, 0.0620521, 0.0222904,
    -0.0336901, 0.0358117, -0.088266, -0.0324773, 0.0753113, 0.0145382, -0.000526489, -0.0795619,
    -0.0518939, 0.0811517, -0.0259833, -0.0143682, 0.0859592, 0.0211517, 0.0478777}},
  SpikePositive_18 → {{0.176411, 0.459024, 0.258404, 0.376825, 0.267208, 0.290119, 0.213718,
    0.297255, 0.393929, 0.323452}, {0.0789177, 0.0233231, 0.948247, 0.0959564, 0.0312196,
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    0.103161, 0.0507488, 0.0451485, -0.0676083, -0.00570149, -0.102033, -0.0779884}},
  SpikePositive_19 → {{0.26039, 0.425361, 0.423755, 0.447421, 0.207986, 0.348286, 0.196533,
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    -0.0266514, -0.0585408, -0.0223829, 0.0756325, -0.0818774, 0.0196063, 0.0560734,
    0.0251256, 0.0088971, 0.0180352, 0.0280578, 0.0585291, -0.0393765, -0.0343217, 0.0645572}},
  SpikePositive_20 → {{0.143992, 0.191429, 0.215202, 0.228018, 0.466852, 0.364189, 0.230938,
    0.357607, 0.431009, 0.356017}, {0.0539091, 0.00518876, 0.973335, -0.0575574, -0.0738336,
    -0.0319849, 0.0826118, -0.023439, 0.0722221, 0.0353774, 0.0524822, 0.00449832, -0.0399622,
    0.0342783, -0.00731633, -0.0782255, 0.0452537, 0.0451656, 0.0489638, -0.0886151}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.241473, 0.245039, 0.439444, 0.324696, 0.0975897, 0.409425,
    0.108516, 0.313648, 0.454004, 0.299475}, {-0.965691, 0.0227016, 0.0624193, 0.0475031,
    -0.00864736, -0.0345756, -0.0809619, 0.0337372, 0.0842658, -0.0755802, 0.0723328, 0.074779,
    -0.0818944, 0.0470061, 0.0340188, 0.0825058, -0.0612466, -0.0824694, -0.0201691, 0.0182585}},
  SpikeNegative_2 → {{0.200584, 0.17181, 0.242494, 0.434529, 0.388311, 0.29649, 0.226694,
    0.2162, 0.542745, 0.226346}, {-0.969552, 0.0782814, 0.0671222, -0.0633742, -0.0872104,
    0.08333, -0.0475134, -0.00238939, -0.0298965, 0.0175015, 0.00179001, 0.0616872, 0.00606212,
    -0.0610372, -0.0435924, 0.0766818, 0.0134915, -0.0657816, -0.0834564, 0.0219212}},
  SpikeNegative_3 → {{0.338556, 0.201239, 0.238586, 0.229114, 0.163399, 0.340562, 0.259666,
    0.220023, 0.642862, 0.252344}, {-0.977698, -0.000975266, -0.0462191, 0.0504633,
    -0.0016264, -0.0105188, 0.0334855, 0.0584616, 0.0561494, 0.0111377, 0.0639992, 0.0649414,
    -0.0298171, 0.0295418, 0.0832932, -0.072606, 0.0360522, -0.0508585, 0.0596861, 0.0419706}},
  SpikeNegative_4 → {{0.306202, 0.307718, 0.30571, 0.16287, 0.30152, 0.23546, 0.313669, 0.262032,
    0.564204, 0.24461}, {-0.973247, -0.0409237, 0.00403878, 0.0125439, 0.0679249, 0.0826774,
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    -0.054748, -0.0412854, -0.000567288, -0.0659441, 0.0712405, 0.0608743, -0.0917343}},
  SpikeNegative_5 → {{0.332491, 0.270219, 0.322832, 0.382085, 0.270124, 0.18713, 0.248114,
    0.207694, 0.549248, 0.227741}, {-0.972798, 0.0479328, 0.0303153, 0.00730474, -0.0174714,
    0.0474301, 0.081522, 0.0880914, 0.0647898, 0.047476, 0.0116883, -0.0125373, 0.0286463,
    -0.0648917, 0.039654, 0.0782456, 0.0605819, -0.0537992, -0.0363133, -0.0779596}},
  SpikeNegative_6 → {{0.165132, 0.203107, 0.264264, 0.144021, 0.388361, 0.494588, 0.481417,
    0.222279, 0.312879, 0.257674}, {-0.963126, -0.0123264, 0.056581, -0.0826042, 0.0910013,
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    -0.0337829, 0.0437509, -0.0807794, 0.0312579, 0.0526726, -0.0716147, 0.0969001}},
  SpikeNegative_7 → {{0.254246, 0.34022, 0.146837, 0.175817, 0.289341, 0.280403, 0.360155,
    0.315737, 0.51942, 0.324951}, {-0.984161, 0.00532845, 0.0106652, -0.0477899, 0.0290876,
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    0.0341849, 0.0642336, -0.0239553, -0.0659233, 0.00698249, 0.0908422, 0.00460205}},
  SpikeNegative_8 → {{0.275958, 0.185945, 0.315164, 0.418591, 0.127652, 0.197036, 0.27154,
    0.42717, 0.346554, 0.428133}, {-0.962778, -0.0936947, -0.0418349, 0.0754703, 0.0777766,
    -0.0296368, 0.0829871, 0.00863079, 0.0908133, -0.0370441, 0.0284427, 0.0592091,
    -0.00766309, -0.0994385, -0.0622661, 0.0513787, 0.0328932, 0.0365931, 0.047829, 0.088541}},
  SpikeNegative_9 → {{0.264483, 0.196641, 0.388135, 0.214638, 0.457892, 0.3717, 0.201973,
    0.087267, 0.535731, 0.106866}, {-0.957567, -0.0733498, 0.0586849, -0.101275, -0.101539,
    0.0915064, -0.0846168, -0.0424881, -0.0628782, 0.0938677, 0.0505544, 0.0120833, -0.0465535,
    -0.00226864, 0.0810739, 0.039705, 0.0896697, 0.0192788, 0.00777766, -0.0455578}},
  SpikeNegative_10 → {{0.259446, 0.175198, 0.445185, 0.424121, 0.189817, 0.36046, 0.237509,
    0.224118, 0.449998, 0.220963}, {-0.960432, -0.0978924, 0.0532751, 0.065266, 0.00633453,
    -0.0119909, -0.0009645, 0.0874828, 0.0919893, 0.0475701, 0.0311544, 0.0948259, -0.0524222,
    -0.000315951, 0.0381869, 0.0807451, 0.0788538, 0.0911934, 0.0395078, 0.0744451}},
  SpikeNegative_11 → {{0.233992, 0.187656, 0.330971, 0.364944, 0.297602, 0.361746, 0.347988,
    0.227811, 0.471073, 0.230167}, {0.091615, 0.0115478, -0.978927, 0.0355429, -0.0743778,
    0.0598753, -0.0215184, -0.00660695, -0.0834167, 0.00255393, -0.0165301, 0.0349156, -0.0316354,
    0.0814727, -0.00937909, 0.00141352, -0.0514843, -0.0478664, -0.0311358, -0.0138555}},
  SpikeNegative_12 → {{0.26418, 0.224084, 0.163715, 0.427088, 0.198595, 0.238035, 0.19663,
    0.384503, 0.47596, 0.40205}, {-0.0911697, -0.0181831, -0.961637, 0.0359735, -0.0962873,
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    -0.036433, 0.00444899, -0.0668625, -0.0956182, 0.0448592, 0.0476885, -0.0569854}},
  SpikeNegative_13 → {{0.195538, 0.291384, 0.451622, 0.395576, 0.279848, 0.213091, 0.4546,
    0.261139, 0.21789, 0.265262}, {0.0224315, -0.0765291, -0.974943, -0.0240935, 0.060617,
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    -0.0152643, 0.0919373, -0.0818753, 0.00277175, 0.0711326, -0.0568905, 0.061579}},
  SpikeNegative_14 → {{0.234298, 0.254402, 0.237306, 0.438149, 0.350998, 0.383004, 0.310876,
    0.340279, 0.203685, 0.329064}, {0.0774416, 0.0223855, -0.967546, 0.0390332, 0.018816,
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    0.0504978, 0.00876055, -0.00697817, -0.0876137, -0.00494352, -0.0660763, -0.0842408}},
  SpikeNegative_15 → {{0.149324, 0.34373, 0.29466, 0.386012, 0.339379, 0.224253, 0.280897,
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    0.331029, 0.403819, 0.326651}, {-0.0384312, -0.0386873, -0.969613, 0.0951184, 0.0509129,
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  SpikeNegative_16 → {{0.216285, 0.15187, 0.327253, 0.28973, 0.344432, 0.312534, 0.189311,
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  SpikeNegative_17 → {{0.221635, 0.0704837, 0.45918, 0.14583, 0.341457, 0.420454, 0.412896,
    0.323002, 0.202249, 0.323581}, {0.00922877, -0.0170242, -0.961043, 0.0459152, 0.0168643,
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    -0.068361, -0.0539719, -0.0601639, -0.0624707, -0.0550696, -0.0807418, 0.00443171}},
  SpikeNegative_18 → {{0.218086, 0.362401, 0.405945, 0.227387, 0.246725, 0.304077, 0.185362,
    0.426144, 0.239416, 0.421893}, {-0.0806195, -0.0657376, -0.970725, -0.0613415, -0.013095,
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    -0.0690963, -0.0942681, -0.00369563, 0.0381293, 0.0628074, -0.0256343, 0.0166454}},
  SpikeNegative_19 → {{0.213938, 0.314186, 0.282571, 0.344314, 0.171467, 0.43948, 0.355962,
    0.303768, 0.349299, 0.305912}, {0.0216304, -0.0504347, -0.981502, 0.0252397, -0.085584,
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    0.0694586, -0.00917151, -0.0188791, -0.0295949, -0.0477707, -0.0189333, 0.033256}},
  SpikeNegative_20 → {{0.33985, 0.410606, 0.209342, 0.228937, 0.487645, 0.299744, 0.438526,
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    -0.0511357, 0.0880155, 0.0773812, 0.0741427, 0.0093807, -0.0455673, 0.0982058, -0.0329699,
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f1 → <|LinearPositive_1 → {{0.983907, 0.167469, 0.0322329, 0.00228634, 0.00217574, 0.00969369,
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  LinearPositive_2 → {{0.984602, 0.163566, 0.0309586, 0.0018432, 0.00171738, 0.0107595,
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  LinearPositive_3 → {{0.984032, 0.165725, 0.0335368, 0.00224807, 0.00170631, 0.0108862,
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  LinearPositive_4 → {{0.983946, 0.1674, 0.0323711, 0.00217931, 0.00168684, 0.00972767,
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    0.224756, 0.24159, 0.26041, 0.279381, 0.300041, 0.317795, 0.336305, 0.355463, 0.372044}},
  LinearPositive_5 → {{0.984079, 0.165516, 0.0314355, 0.00243925, 0.00160657, 0.0119993,
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    0.241648, 0.261496, 0.280684, 0.298451, 0.318451, 0.336979, 0.353634, 0.374053}},
  LinearPositive_6 → {{0.983395, 0.170467, 0.03063, 0.00193096, 0.00173954,
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   {0.01973, 0.0386025, 0.0566479, 0.0732625, 0.0922229, 0.110285, 0.132158, 0.150655, 0.169772, 0.186386,
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  LinearPositive_7 → {{0.983808, 0.169101, 0.0320381, 0.00204249, 0.00154798,
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  LinearPositive_8 → {{0.984795, 0.16124, 0.0333497, 0.00241186, 0.00179385, 0.00945372,
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  LinearPositive_10 → {{0.98418, 0.166035, 0.0322447, 0.00224316, 0.00229779,
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LinearNegative_2 → {{0.986143, 0.150497, 0.0281292, 0.00603283, 0.00311333, 0.0219996,
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LinearNegative_3 → {{0.986531, 0.155054, 0.0287734, 0.00242953, 0.000408675, 0.0122485,
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LinearNegative_4 → {{0.984648, 0.15547, 0.0586382, 0.00254949, 0.00205017, 0.0219796,
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LinearNegative_5 → {{0.981598, 0.181554, 0.0297068, 0.00627522, 0.00360327, 0.0102472,
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LinearNegative_6 → {{0.981802, 0.152725, 0.0300897, 0.000074544, 0.00425414, 0.01539, 0.0544862,
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LinearNegative_7 → {{0.979907, 0.185388, 0.0311121, 0.000268708, 0.0156931, 0.0149683,
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  Sinusoidal3_27 → {{0.00227716, 0.0727259, 0.992363, 0.088267, 0.0358297, 0.0187322, 0.007205,
    0.00255293, 0.0208825, 0.000837324}, {0.185737, -0.0940815, -0.298896, -0.259089,
    1.48483×10^-6, 0.255884, 0.301234, 0.0995285, -0.190573, -0.31724, -0.183169, 0.0947753,
    0.301282, 0.258249, 0.00469396, -0.249273, -0.302099, -0.0921134, 0.187734, 0.316153}},
  Sinusoidal3_28 → {{0.00312878, 0.0715934, 0.992516, 0.0882315, 0.0345117, 0.0178514,
    0.00911218, 0.0024579, 0.0197939, 0.000826678}, {0.180591, -0.0986181, -0.303211, -0.258065,
    -0.00631027, 0.2612, 0.305786, 0.0934377, -0.187952, -0.313163, -0.1887, 0.0984031,
    0.29601, 0.254151, -0.00147889, -0.252403, -0.302232, -0.0950268, 0.188054, 0.313489}},
  Sinusoidal3_29 → {{0.0034786, 0.0716267, 0.992235, 0.0895934, 0.0379123, 0.0200901,
    0.00999492, 0.00349348, 0.018588, 0.00145429}, {0.18664, -0.100951, -0.305994, -0.250885,
    -0.00327161, 0.259902, 0.302736, 0.0955416, -0.185528, -0.313439, -0.182792, 0.0975035,
    0.29928, 0.250164, 0.000425761, -0.254352, -0.300503, -0.102794, 0.191301, 0.316491}},
  Sinusoidal3_30 → {{0.00329621, 0.0734579, 0.992191, 0.0884629, 0.0369744, 0.0205368,
    0.00905924, 0.00260226, 0.0211301, 0.000896112}, {0.190937, -0.0963179, -0.3023, -0.252635,
    0.0000459842, 0.252126, 0.297713, 0.0968727, -0.191639, -0.312982, -0.191119, 0.0969279,
    0.296136, 0.258115, -0.0046907, -0.258354, -0.30735, -0.102885, 0.182149, 0.31233}}|〉,
f5 → ‹| Sinusoidal2_11 → {{0.00214142, 0.0113461, 0.0271614, 0.093491, 0.929864, 0.352021,
    0.0294497, 0.00363199, 0.0306765, 0.00106862}, {-0.0947556, -0.259637, 0.257984, 0.0957323,
    -0.313241, 0.0922049, 0.259663, -0.256906, -0.0985306, 0.311251, -0.100334, -0.252273,
    0.260489, 0.101385, -0.322236, 0.0974091, 0.255828, -0.25368, -0.0920393, 0.31276}},
  Sinusoidal2_12 → {{0.00265779, 0.0124429, 0.0280191, 0.0882136, 0.93458, 0.340768, 0.0279562,
    0.0039104, 0.0301583, 0.00122412}, {-0.0939315, -0.251018, 0.254883, 0.0993814,
    -0.310031, 0.0973845, 0.256326, -0.261378, -0.103688, 0.321841, -0.103581, -0.250768,
    0.253248, 0.102955, -0.321167, 0.092882, 0.255606, -0.252249, -0.101904, 0.316063}},
  Sinusoidal2_13 → {{0.00205643, 0.00837221, 0.0286961, 0.100046, 0.932188, 0.34422, 0.0282881,
    0.00387921, 0.0285525, 0.00120728}, {-0.097927, -0.252787, 0.253756, 0.0933291,
    -0.323071, 0.0963587, 0.262142, -0.254623, -0.0930537, 0.313322, -0.0955838, -0.253481,
    0.258614, 0.0924675, -0.318639, 0.104289, 0.258467, -0.250475, -0.0985705, 0.31445}},
  Sinusoidal2_14 → {{0.0021733, 0.0120582, 0.030852, 0.0887924, 0.929571, 0.35393, 0.0293392,
    0.00559766, 0.0273594, 0.00218191}, {-0.092202, -0.251605, 0.253068, 0.100315,
    -0.318514, 0.101419, 0.250751, -0.25588, -0.101558, 0.316974, -0.0978413, -0.259361,
    0.258987, 0.101105, -0.314885, 0.100336, 0.250073, -0.258619, -0.0936094, 0.318862}},
  Sinusoidal2_15 → {{0.003211, 0.0125322, 0.0291146, 0.0917017, 0.932214, 0.346446, 0.0288529,
    0.00433386, 0.0259633, 0.00150534}, {-0.0993523, -0.250937, 0.260037, 0.100623,
    -0.311858, 0.0997025, 0.257719, -0.258159, -0.100377, 0.313261, -0.0926861, -0.260429,
    0.258213, 0.0987456, -0.320926, 0.0953376, 0.254054, -0.258088, -0.0922069, 0.310434}},
  Sinusoidal2_16 → {{0.00329807, 0.0106659, 0.0298396, 0.0894634, 0.936594, 0.334858, 0.0285978,
    0.00480122, 0.028259, 0.00177199}, {-0.0971945, -0.257413, 0.259233, 0.0910695,
    -0.313817, 0.101752, 0.255769, -0.253944, -0.0981209, 0.320672, -0.096714, -0.256765,
    0.251619, 0.101657, -0.319794, 0.0921172, 0.255016, -0.260049, -0.0994702, 0.308809}},
  Sinusoidal2_17 → {{0.00323921, 0.0104267, 0.0310995, 0.0937253, 0.937717, 0.330232, 0.028827,
    0.00523682, 0.0300115, 0.00184944}, {-0.0973995, -0.261294, 0.256682, 0.0934788,
    -0.312122, 0.103194, 0.257906, -0.257355, -0.0921103, 0.319936, -0.094276, -0.250974,
    0.251413, 0.0924457, -0.309199, 0.0930346, 0.259247, -0.258655, -0.102927, 0.321497}},
  Sinusoidal2_18 → {{0.00261862, 0.0117595, 0.0294173, 0.0928994, 0.935446, 0.337253, 0.0284566,
    0.00439605, 0.0269919, 0.00153599}, {-0.102305, -0.25133, 0.250327, 0.0986084,
    -0.314055, 0.0963326, 0.255742, -0.254077, -0.0950258, 0.314974, -0.0968378, -0.253655,
    0.260833, 0.101781, -0.320021, 0.0929391, 0.257739, -0.256152, -0.100764, 0.320176}},
  Sinusoidal2_19 → {{0.00238335, 0.00977215, 0.0264627, 0.0937981, 0.931964, 0.346374, 0.0297822,
    0.00311707, 0.0311639, 0.000768734}, {-0.0966753, -0.258399, 0.250503, 0.0925838,
    -0.311387, 0.0994216, 0.262851, -0.257669, -0.0960513, 0.3147, -0.0940436, -0.250804,
    0.255071, 0.0999753, -0.321173, 0.103028, 0.257795, -0.252902, -0.0949492, 0.319319}},
  Sinusoidal2_20 → {{0.00194052, 0.0094224, 0.0312386, 0.0951129, 0.932341, 0.345053, 0.0238456,
    0.00521261, 0.0310552, 0.00178866}, {-0.0953611, -0.259725, 0.255227, 0.0950605,
    -0.313494, 0.0928888, 0.256859, -0.250327, -0.0995728, 0.320633, -0.0948312, -0.257297,
```

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```
      0.260059, 0.0930896, -0.309578, 0.100408, 0.259907, -0.249571, -0.102064, 0.321463}}|>,
f6 → <|Sinusoidal1_1 → {{0.00076993, 0.00712448, 0.0251898, 0.026261, 0.102449, 0.989062,
      0.0977837, 0.00882471, 0.0150545, 0.00445633}, {-0.186555, -0.0780429, 0.268567, -0.272305,
      -0.0179468, 0.272494, -0.324032, 0.0975626, 0.187757, -0.308072, 0.152418, 0.0791627,
      -0.301182, 0.275013, 0.021472, -0.260505, 0.287795, -0.114582, -0.205246, 0.30221}},
  Sinusoidal1_2 → {{0.0028637, 0.0136851, 0.0255902, 0.054506, 0.088803, 0.988769, 0.0992801,
      0.00306564, 0.027597, 0.000892624}, {-0.199404, -0.0863746, 0.323603, -0.246948,
      -0.00415995, 0.242694, -0.291487, 0.0795271, 0.156959, -0.321973, 0.168725, 0.111965,
      -0.326103, 0.260471, 0.00731065, -0.230901, 0.283581, -0.110767, -0.172209, 0.343016}},
  Sinusoidal1_3 → {{0.00465902, 0.0101013, 0.0240866, 0.040161, 0.0921357, 0.988627, 0.10482,
      0.00434695, 0.028321, 0.00142201}, {-0.167216, -0.0815467, 0.314595, -0.276177,
      0.0160765, 0.268161, -0.288515, 0.090746, 0.169194, -0.33973, 0.158121, 0.0738147,
      -0.311772, 0.267603, 0.0140794, -0.233775, 0.278188, -0.120874, -0.170643, 0.327455}},
  Sinusoidal1_4 → {{0.00563062, 0.00427494, 0.0148009, 0.0375169, 0.0809494, 0.989713,
      0.108194, 0.00712603, 0.0217556, 0.00288291}, {-0.178259, -0.118887, 0.29746, -0.223064,
      0.00271644, 0.259369, -0.304819, 0.109425, 0.197609, -0.33292, 0.17321, 0.0928643,
      -0.310265, 0.226957, -0.0166977, -0.26868, 0.314921, -0.0737973, -0.198664, 0.301398}},
  Sinusoidal1_5 → {{0.0032709, 0.00661173, 0.0172819, 0.0226644, 0.0680941, 0.989408, 0.123209,
      0.00938287, 0.0167023, 0.00464881}, {-0.177352, -0.12701, 0.276012, -0.228738,
      0.0252745, 0.271529, -0.319621, 0.112552, 0.203298, -0.341653, 0.15704, 0.086575,
      -0.310518, 0.25289, 0.0142425, -0.249179, 0.307321, -0.0970257, -0.161375, 0.303209}},
  Sinusoidal1_6 → {{0.00175287, 0.00750089, 0.0132294, 0.0346023, 0.0895818, 0.990514,
      0.093313, 0.00717444, 0.025661, 0.00283061}, {-0.192589, -0.123766, 0.274563, -0.240822,
      0.00953682, 0.276125, -0.323419, 0.105639, 0.183886, -0.30809, 0.176856, 0.118127,
      -0.28931, 0.24103, -0.00660842, -0.240824, 0.302609, -0.0787592, -0.197625, 0.333891}},
  Sinusoidal1_7 → {{0.00242459, 0.00493401, 0.0259745, 0.051773, 0.0939762, 0.987965, 0.106174,
      0.00627447, 0.0197723, 0.00240998}, {-0.195373, -0.10111, 0.322406, -0.269841,
      -0.0300188, 0.223407, -0.308059, 0.103372, 0.191433, -0.309555, 0.206984, 0.0811364,
      -0.312975, 0.22185, -0.0192448, -0.256687, 0.305149, -0.112948, -0.189084, 0.285476}},
  Sinusoidal1_8 → {{0.00351956, 0.00421323, 0.0239072, 0.0416013, 0.0931106, 0.987394, 0.114556,
      0.00241431, 0.0303787, 0.000408254}, {-0.164502, -0.0992274, 0.290275, -0.255909,
      -0.00020463, 0.250563, -0.290844, 0.0685403, 0.199769, -0.329359, 0.190177, 0.0703945,
      -0.332473, 0.232381, -0.00209005, -0.240212, 0.30216, -0.112529, -0.21771, 0.313304}},
  Sinusoidal1_9 → {{0.00241787, 0.013584, 0.0177839, 0.0316483, 0.0800176, 0.987803, 0.12562,
      0.0155341, 0.0152456, 0.00888645}, {-0.173419, -0.114721, 0.301098, -0.227489,
      -0.0211782, 0.281089, -0.31624, 0.103717, 0.183186, -0.337743, 0.176722, 0.0952649,
      -0.275198, 0.252482, 0.018304, -0.273947, 0.280302, -0.10734, -0.156423, 0.326763}},
  Sinusoidal1_10 → {{0.00339793, 0.0137885, 0.0238913, 0.0392441, 0.12013, 0.98551, 0.104272,
      0.0019218, 0.0339003, 0.000867092}, {-0.189225, -0.102829, 0.325754, -0.269566,
      0.00297632, 0.260635, -0.288521, 0.0750669, 0.195864, -0.28915, 0.195195, 0.103992,
      -0.28847, 0.285843, -0.0133318, -0.234752, 0.278846, -0.111982, -0.210869, 0.303587}}|>|>
```

We now cluster and return the dendrograms as output

In[3]:=
```
clusters1DendrogramsReturn = TimeSeriesClusters[classification1, ReturnDendrograms → True]
```

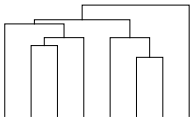
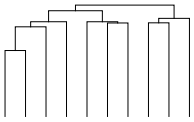
Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]= ⟨|SpikeMax →

⟨|G1 → ⟨|{G1S1} →  , {G1S2} →  |⟩, G2 → ⟨|{G2S1} → |⟩|⟩,

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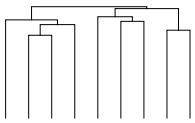
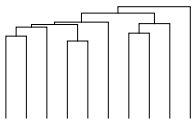
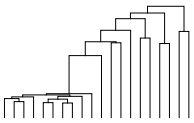
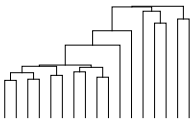
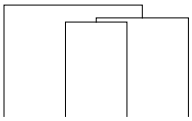
SpikeMin → ⟨|G1 → ⟨|{G1S1} →  , {G1S2} →  |⟩,

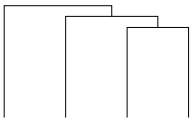
G2 → <|{G2S1} → {{-0.964089, 0.0505211, -0.0700959, -0.0242415, -0.0152793, -0.0988989, 0.0341947, -0.0416477, -0.0897023, 0.0990235, -0.0972136, 0.0990263, -0.0107728, 0.0309565, 0.0183618, 0.00930295, 0.0612632, -0.0477844, 0.0654077, -0.0252868} → SpikeNegative_4}|>|⟩,

f1 → ⟨|G1 → ⟨|{G1S1} →  , {G1S2} →  |⟩,

G2 → ⟨|{G2S1} → {{-0.0110301, -0.0374316, -0.0679157, -0.0590307, -0.100358, -0.118107, -0.145138, -0.151847, -0.166683, -0.195226, -0.21855, -0.2331, -0.223109, -0.248773, -0.276709, -0.308414, -0.300835, -0.346339, -0.33939, -0.381116} → LinearNegative_4}, {G2S2} → |⟩|⟩,

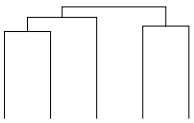
f3 → ⟨|G1 → ⟨|{G1S1} → {{0.187317, -0.103582, -0.297752, -0.253711, 0.00406616, 0.253472, 0.297682, 0.1006, -0.181155, -0.315134, -0.189176, 0.0924202, 0.300003, 0.259375, -0.0029073, -0.257366, -0.303322, -0.0939211, 0.18858, 0.319049} → Sinusoidal3_21}, {G1S2} →  |⟩,

G2 → ⟨|{G2S1} → , {G2S2} → {{0.182564, -0.101947, -0.298174, -0.255669, 0.00123932, 0.256282, 0.306811, 0.0994089, -0.183624, -0.314541, -0.190839, 0.0959313, 0.303648, 0.251689, 0.00582231, -0.258624, -0.30323, -0.0966768, 0.181738, 0.311827} → Sinusoidal3_27}|⟩,

G3 → ⟨|{G3S1} → |⟩|⟩, f5 → ⟨|G1 → ⟨|{G1S1} →  ,

{G1S2} → {{-0.0924687, -0.254662, 0.258726, 0.0937955, -0.314401, 0.0954146, 0.258823, -0.259848, -0.0958138, 0.319627, -0.0937956, -0.256277, 0.252609, 0.0926329, -0.315137, 0.0964877, 0.258083, -0.258967, -0.10148, 0.312406} → Sinusoidal2_16}, {G1S3} → |⟩,

G2 → ⟨|{G2S1} → , {G2S2} → {{-0.0912385, -0.258743, 0.257111, 0.102916, -0.321512, 0.0985333, 0.253611, -0.255808, -0.101557, 0.314227, -0.0961898, -0.259972, 0.256371, 0.0935846, -0.313604, 0.0965954, 0.257454, -0.253799, -0.101251, 0.310152} → Sinusoidal2_19}|⟩|⟩,

f6 → ⟨|G1 → ⟨|{G1S1} →  , {G1S2} → |⟩,

G2 → ⟨|{G2S1} → , {G2S2} → {{-0.206527, -0.0887062, 0.277052, -0.279736, -0.00907299, 0.250919, -0.301022, 0.124887, 0.157029, -0.29684, 0.177643, 0.0902014, -0.305533, 0.248704,

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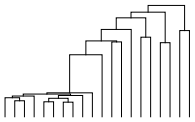
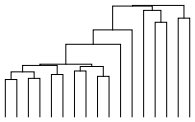
```
0.0160817, -0.282923, 0.3186, -0.0735031, -0.185805, 0.309529} → Sinusoidal1_8} |⟩ |⟩ |⟩
```

For example for class "f1" we have for each group and subgroup the following dendrograms:

```
In[4]:= clusters1DendrogramsReturn["f1"]
```

Out[4]= ⟨|G1 → ⟨|{G1S1} →  , {G1S2} →  |⟩,

```
G2 → ⟨|{G2S1} → {{-0.0110301, -0.0374316, -0.0679157, -0.0590307, -0.100358, -0.118107, -0.145138, -0.151847,
    -0.166683, -0.195226, -0.21855, -0.2331, -0.223109, -0.248773, -0.276709, -0.308414,
    -0.300835, -0.346339, -0.33939, -0.381116} → LinearNegative_4}, {G2S2} → |⟩ |⟩
```

We note that group {G2S1} is only one datapoint so no dendrogram plot was generated:

```
In[5]:= clusters1DendrogramsReturn["f1", "G2", {"G2S1"}]

Out[5]= {{-0.0110301, -0.0374316, -0.0679157, -0.0590307, -0.100358, -0.118107,
    -0.145138, -0.151847, -0.166683, -0.195226, -0.21855, -0.2331, -0.223109, -0.248773,
    -0.276709, -0.308414, -0.300835, -0.346339, -0.33939, -0.381116} → LinearNegative_4}
```

We note also that dendrogram plots are referenced by curly brackets around text indexes.

SignificanceCriterion (1)

```
In[1]:= Needs["MathIOmica`"]
```

SignificanceCriterion provides an option for which method to use for determining the number of clusters in the groupings and sub-groupings.

We generate some data for classification:

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]

  Method → "LombScargle"
```

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```
Out[2]= <|SpikeMax →
    <|SpikePositive_1 → {{0.201759, 0.196539, 0.230503, 0.171206, 0.377219, 0.357123, 0.533871, 0.141722,
        0.491418, 0.147634}, {0.967292, 0.0629204, -0.0715822, 0.0653913, -0.0081952, 0.00144367,
        0.0575822, -0.00121645, 0.0890683, -0.0816886, 0.0786827, 0.0109882, 0.0418998,
        0.0219192, 0.0143353, 0.0828812, 0.0941044, -0.0165709, -0.0269993, -0.0866778}},
     SpikePositive_2 → {{0.264775, 0.188196, 0.383117, 0.265475, 0.415081, 0.278634, 0.160439,
        0.126855, 0.606281, 0.133727}, {0.977143, 0.0134075, -0.0665249, -0.0607794, 0.0683479,
        0.0107078, 0.0337247, -0.0528388, 0.00460127, -0.0802131, -0.00648356, 0.0326366,
        0.0708358, -0.0835274, 0.0201592, 0.0542655, -0.0335379, 0.0463918, 0.0260266, 0.0362403}},
     SpikePositive_3 → {{0.183177, 0.202594, 0.154959, 0.263218, 0.412774, 0.49841, 0.320652,
        0.309414, 0.363048, 0.288014}, {0.967207, -0.0115834, -0.0847565, 0.0868217, -0.00943518,
        0.0703426, -0.0732179, 0.0557774, 0.0384005, 0.0447944, -0.065689, -0.0379917, 0.0598646,
        -0.0736211, -0.0348829, 0.0857963, -0.0111896, -0.0556474, -0.077816, 0.00689867}},
     SpikePositive_4 → {{0.109415, 0.338329, 0.148212, 0.462844, 0.259883, 0.326623, 0.349119,
        0.16417, 0.528618, 0.186753}, {0.957266, -0.0735263, -0.0515449, -0.0362485, 0.0469006,
        -0.0309814, -0.0858215, -0.103155, 0.0865938, 0.0740841, 0.0952425, -0.0333467, 0.0239657,
        0.0164038, -0.090649, 0.0225104, -0.0863222, -0.0412894, 0.0985047, 0.0387593}},
     SpikePositive_5 → {{0.283261, 0.513489, 0.164798, 0.29791, 0.311394, 0.29137, 0.174418,
        0.280732, 0.415061, 0.277151}, {0.972209, 0.063114, 0.0397555, -0.0173676, -0.0132597,
        -0.08296, -0.0916129, -0.0196715, -0.0519485, 0.0795628, 0.0809273, -0.00235602, 0.000239206,
        -0.0926891, 0.00211707, -0.00617592, -0.0311999, 0.0373609, 0.0805025, -0.00627514}},
     SpikePositive_6 → {{0.284983, 0.167964, 0.177082, 0.323414, 0.137448, 0.374906, 0.263161,
        0.265342, 0.616278, 0.275159}, {0.979301, -0.0389222, 0.043035, 0.049011, -0.0210267,
        0.0398196, 0.0776162, -0.0629274, -0.0267408, 0.0551603, -0.0506827, -0.0642708, -0.0626465,
        0.00602565, 0.0116781, -0.00263877, -0.015781, -0.0361078, -0.0596493, 0.0593054}},
     SpikePositive_7 → {{0.23776, 0.452074, 0.230493, 0.287079, 0.24021, 0.204795, 0.124917,
        0.176658, 0.655334, 0.166257}, {0.971345, 0.0634984, -0.030585, -0.0311872, 0.0084132,
        -0.0579878, -0.00417612, -0.0801568, 0.00177414, 0.0652683, 0.0798505, 0.0775081,
        0.0216686, -0.0591078, 0.0381308, -0.0349853, 0.0470049, 0.05251, -0.0869295, 0.0697253}},
     SpikePositive_8 → {{0.200705, 0.154851, 0.199666, 0.355056, 0.278127, 0.18434, 0.38739,
        0.276642, 0.575874, 0.316607}, {0.98133, -0.0348701, 0.0113131, -0.00429828, 0.0887592,
        0.0383563, -0.0544019, -0.0329966, -0.00976035, -0.00367161, 0.0782656, 0.0309334, -0.0256644,
        0.0876472, -0.0182329, 0.0458584, -0.00427474, 0.0463326, 0.00203625, -0.0457717}},
     SpikePositive_9 → {{0.135273, 0.213014, 0.0889129, 0.171319, 0.185172, 0.296753, 0.422941,
        0.397826, 0.494908, 0.441181}, {0.964332, 0.0375694, 0.072847, -0.00720115, -0.0497045,
        -0.0291429, -0.0420508, 0.0224369, -0.00159217, 0.0788818, 0.0634889, 0.0414699, -0.0115687,
        0.0893151, -0.0152608, 0.0982934, 0.0219318, -0.0799857, -0.100317, -0.103827}},
     SpikePositive_10 → {{0.217896, 0.181692, 0.197216, 0.174667, 0.331005, 0.266111, 0.298542,
        0.291248, 0.63267, 0.309037}, {0.97809, -0.0680239, 0.00432598, -0.034574, 0.0334114,
        -0.0245722, 0.0289941, -0.0790163, -0.022506, -0.0426455, 0.0480137, 0.0909841, -0.0323564,
        -0.0549274, 0.00840333, 0.0750826, 0.0602474, -0.0467219, 0.0141469, 0.00054535}},
     SpikePositive_11 → {{0.245414, 0.392672, 0.429424, 0.364428, 0.403534, 0.147018, 0.273759,
        0.179703, 0.369543, 0.200288}, {0.042259, 0.058792, 0.977714, 0.0577118, -0.00817264,
        -0.0130239, 0.00600541, -0.0232701, 0.0412005, 0.0378355, 0.0573757, -0.0392803,
        0.0381802, 0.0336944, -0.0812568, 0.0465604, 0.0224865, -0.0671545, -0.071677, 0.072167}},
     SpikePositive_12 → {{0.123557, 0.162852, 0.260307, 0.280626, 0.275966, 0.382435, 0.201874,
        0.477823, 0.314505, 0.470433}, {-0.0477946, -0.00850869, 0.970231, -0.0607766, 0.0735852,
        0.0453051, 0.0882273, 0.00253046, 0.0511511, 0.00699008, -0.0795474, 0.0763966, -0.00593681,
        0.0829299, 0.0588371, 0.0600412, 0.0478022, -0.040942, 0.0296539, -0.0607842}},
     SpikePositive_13 → {{0.255588, 0.257787, 0.204362, 0.39127, 0.317167, 0.501531, 0.323223,
        0.278007, 0.258482, 0.26956}, {-0.0380298, 0.0469053, 0.980206, -0.0321468, 0.000863018,
        0.0508631, 0.0391162, 0.00479407, -0.0758963, -0.0346433, -0.0794287, 0.0448412, 0.0368863,
        -0.0527659, 0.0774253, -0.0182864, -0.00605453, 0.0329545, -0.0000157909, -0.0591596}},
     SpikePositive_14 → {{0.0955536, 0.292401, 0.303644, 0.443424, 0.4144, 0.413215, 0.221284,
        0.251707, 0.309165, 0.257228}, {-0.0688682, -0.0501315, 0.979081, 0.0528445, -0.0584674,
        -0.0641155, 0.0714302, -0.000734941, 0.00155179, 0.00853238, 0.0635481, 0.0838826, -0.0073822,
        -0.00124452, 0.053602, -0.0206682, -0.0284305, 0.0178328, -0.0205205, -0.0516438}},
     SpikePositive_15 → {{0.322909, 0.343535, 0.328839, 0.389644, 0.18419, 0.106376, 0.344999,
        0.381272, 0.27301, 0.365495}, {0.0812924, 0.0813536, 0.961474, 0.036724, 0.0863743,
        0.00473717, -0.0349055, 0.0976262, -0.0546211, 0.0731872, 0.0716415, 0.0274846, -0.00268746,
        -0.032298, -0.0183149, 0.0592103, 0.100661, -0.0876587, 0.0499396, 0.0577113}},
     SpikePositive_16 → {{0.270775, 0.185541, 0.251988, 0.481309, 0.279083, 0.565575, 0.218242,
        0.22263, 0.242537, 0.208133}, {-0.0636891, 0.018237, 0.974092, -0.0426707, -0.0424537,
        0.0693304, 0.0410023, 0.080947, 0.025573, -0.0644782, -0.0667701, 0.0610011, -0.00559627,
        -0.082226, 0.0408403, -0.0893563, 0.0177095, -0.0104953, -0.0151877, 0.0012764}},
```

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```
    SpikePositive_17 → {{0.57429, 0.273668, 0.23518, 0.225685, 0.244243, 0.424632, 0.184644,
        0.204148, 0.369246, 0.192287}, {-0.00199185, 0.0155031, 0.971245, 0.013609, 0.038642,
        0.0543859, -0.035312, -0.0641883, 0.0195306, -0.0854026, -0.0485967, -0.0433223, -0.0706579,
        -0.0883566, 0.0108185, -0.0873632, 0.0556143, 0.00615126, 0.0741441, 0.0731138}},
    SpikePositive_18 → {{0.204569, 0.259253, 0.282373, 0.177188, 0.256526, 0.531301, 0.295239,
        0.335777, 0.353939, 0.326401}, {0.0457244, -0.0708635, 0.967926, -0.069317, -0.0476454,
        0.0515303, -0.0736901, -0.0332735, -0.0183563, 0.0403951, -0.0812428, 0.000524366,
        -0.032734, -0.0873964, 0.0557448, -0.0877, -0.0737877, -0.0497431, -0.0515999, -0.032858}},
    SpikePositive_19 → {{0.46776, 0.303338, 0.280215, 0.275618, 0.342855, 0.282476, 0.483859,
        0.173911, 0.19298, 0.189085}, {-0.0983889, 0.0769339, 0.961785, 0.00948056, 0.0361624,
        0.0805696, 0.0053824, 0.0932285, -0.0532836, -0.0626666, -0.0313044, -0.0655813, 0.0176015,
        0.0491247, -0.0686173, -0.0206747, -0.0832945, 0.0684194, 0.0798427, 0.0697211}},
    SpikePositive_20 → {{0.119752, 0.312852, 0.49033, 0.148154, 0.328654, 0.216426, 0.30293,
        0.290035, 0.458611, 0.290424}, {-0.0362821, -0.0252786, 0.970951, -0.0541325, 0.0995157,
        -0.0698355, -0.0451651, -0.0178926, 0.0345133, 0.0809073, 0.0721659, -0.0614289, 0.00213694,
        0.0735961, 0.0641674, -0.0166105, 0.0130512, -0.0682154, -0.00989035, 0.0614251}}|>,
  SpikeMin → <|SpikeNegative_1 → {{0.151138, 0.21572, 0.187678, 0.191317, 0.135245, 0.326563,
        0.293833, 0.467678, 0.457784, 0.468227}, {-0.96497, 0.0969889, -0.0674345, -0.0396528,
        -0.02567, -0.04746, -0.0384615, 0.0729381, 0.0582529, -0.0979184, -0.0428482, -0.0498294,
        0.0314379, 0.0598809, 0.0559528, 0.0593186, -0.0927528, 0.0560542, -0.0450063, 0.0360613}},
    SpikeNegative_2 → {{0.183981, 0.270497, 0.344196, 0.170571, 0.406676, 0.215923, 0.312279,
        0.221429, 0.584304, 0.213187}, {-0.972048, 0.0396042, 0.0296197, 0.0577001, -0.0393503,
        -0.023819, -0.0276084, -0.0710069, -0.0485043, 0.0775126, -0.0877527, -0.0317322, -0.0654469,
        0.0568339, -0.0184644, -0.0528735, -0.0701643, -0.0349949, -0.0824581, -0.0276269}},
    SpikeNegative_3 → {{0.176879, 0.21545, 0.184047, 0.413192, 0.214764, 0.267328, 0.19233,
        0.181535, 0.695287, 0.216186}, {-0.956452, -0.0965723, -0.0216773, 0.0471958, -0.0712269,
        0.0961442, -0.0566218, 0.0827334, 0.0486591, -0.00621282, -0.0980497, 0.0539796,
        0.0677075, -0.0735231, 0.0032429, 0.0232168, 0.088513, 0.0865506, 0.0862725, 0.0238179}},
    SpikeNegative_4 → {{0.311433, 0.182113, 0.356226, 0.0979829, 0.324781, 0.320175, 0.287037,
        0.270073, 0.529904, 0.298704}, {-0.971121, -0.0648466, -0.0801351, -0.0650309, -0.0684539,
        0.0256867, -0.0345433, -0.0414595, 0.0302769, 0.0757547, 0.0355464, -0.0767821, -0.0710721,
        -0.0500954, 0.0814012, -0.0356922, -0.00298359, 0.0450974, -0.0197061, -0.0458598}},
    SpikeNegative_5 → {{0.160987, 0.104659, 0.338623, 0.142199, 0.169041, 0.165776, 0.243539,
        0.464434, 0.522413, 0.473562}, {-0.969355, 0.0208514, -0.065928, 0.0817897, -0.0871451,
        -0.0501728, 0.0050669, -0.0361181, 0.08267, 0.0405522, 0.0384029, -0.0448581, -0.0443621,
        -0.0177148, 0.07898, 0.0635287, -0.0496065, 0.0754305, 0.0414446, 0.0552129}},
    SpikeNegative_6 → {{0.433613, 0.197068, 0.323339, 0.360889, 0.186006, 0.22521, 0.297007,
        0.215858, 0.522864, 0.21176}, {-0.958731, -0.0698422, -0.0643256, 0.0672847, -0.00239053,
        -0.0640947, -0.0880477, 0.00856566, 0.0969507, 0.0909877, -0.0545927, 0.0942621, 0.0805709,
        0.0179675, -0.00573308, -0.024449, -0.0315376, 0.0720545, -0.0577023, -0.0940587}},
    SpikeNegative_7 → {{0.134301, 0.230667, 0.282328, 0.250085, 0.302289, 0.201324, 0.341598,
        0.295138, 0.594669, 0.311717}, {-0.978772, 0.00697048, -0.0583959, -0.0442459, -0.0193825,
        -0.0533425, 0.0522586, -0.0886402, -0.00901232, -0.017265, -0.0361036, -0.0545188,
        -0.0420767, -0.0579584, 0.0296534, 0.0187006, 0.078387, -0.0227852, 0.0697729, -0.0153111}},
    SpikeNegative_8 → {{0.278867, 0.339982, 0.228451, 0.202067, 0.41212, 0.176264, 0.390378,
        0.171601, 0.540854, 0.195825}, {-0.979544, -0.05172, -0.00249447, -0.0342192, -0.0191713,
        0.0554175, 0.0390009, -0.0374903, -0.0267527, 0.0801846, -0.0748227, -0.0356328, 0.0822322,
        -0.0399135, 0.0575752, -0.00868158, 0.0037138, 0.0119838, 0.00932664, -0.0653735}},
    SpikeNegative_9 → {{0.267486, 0.198862, 0.382987, 0.25002, 0.198216, 0.288668, 0.505444,
        0.299426, 0.329026, 0.32204}, {-0.966721, -0.064368, 0.0234431, 0.0691812, 0.0699065,
        -0.0442427, 0.0927974, 0.00620253, 0.00924091, 0.0434403, 0.0295029, 0.00795737, -0.0920634,
        -0.0973085, 0.085086, -0.0464308, -0.0266022, 0.0353508, -0.014584, 0.0897799}},
    SpikeNegative_10 → {{0.277699, 0.233061, 0.239886, 0.432809, 0.235675, 0.444763, 0.380043,
        0.260251, 0.291974, 0.270053}, {-0.972579, -0.0612529, 0.0759321, -0.0501211, 0.0956801,
        0.0228434, -0.0246887, 0.0861699, -0.00578279, -0.0670904, 0.0346431, 0.00219603, 0.0205669,
        -0.0796614, -0.0791708, -0.0175387, -0.00310285, 0.050835, -0.0516879, 0.000296412}},
    SpikeNegative_11 → {{0.175555, 0.377885, 0.366755, 0.282767, 0.320078, 0.371677, 0.207769,
        0.270087, 0.435683, 0.255712}, {-0.00147132, -0.0675502, -0.9775, 0.00924698, 0.00849405,
        0.0763115, -0.0568258, 0.053323, -0.0420257, -0.0440184, -0.0439577, -0.0189741,
        -0.0176092, 0.0532649, -0.0730485, 0.0730134, 0.0303473, 0.0419628, -0.0284756, 0.0676218}},
    SpikeNegative_12 → {{0.176819, 0.203465, 0.402282, 0.317055, 0.45858, 0.227409, 0.465663,
        0.208887, 0.302936, 0.225223}, {-0.0502025, -0.0146732, -0.970004, 0.0212483, 0.0578043,
        -0.0855987, 0.0378647, -0.0311633, 0.0511426, -0.0481868, -0.0809552, 0.0703906, 0.0276272,
        -0.0804496, -0.0207223, -0.101988, -0.0329304, 0.0251394, 0.0686864, -0.0434119}},
    SpikeNegative_13 → {{0.255604, 0.22054, 0.329416, 0.173743, 0.473974, 0.430419, 0.472116,
        0.131898, 0.28091, 0.134961}, {-0.0499908, -0.0939433, -0.966663, 0.0371538, 0.0482621,
```

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    -0.0921804, 0.0994415, 0.00438417, -0.0603879, 0.00574437, -0.0706249, 0.104324, -0.00519757,
    -0.0443769, -0.0163014, 0.0134511, -0.0590087, -0.0731483, 0.01356, 0.0333627}},
  SpikeNegative_14 → {{0.22898, 0.269146, 0.321571, 0.498244, 0.234442, 0.399898, 0.224602,
    0.300207, 0.29857, 0.280852}, {-0.0319822, -0.0613186, -0.969192, -0.00924069, 0.0695373,
    0.0330256, -0.0145088, -0.0929817, -0.0918269, -0.0139322, -0.0387085, -0.0698804,
    0.0310955, 0.10158, 0.00458151, 0.0631232, -0.0690113, 0.0279686, -0.0358071, 0.0623697}},
  SpikeNegative_15 → {{0.245545, 0.28563, 0.207043, 0.301009, 0.176745, 0.385285, 0.283792,
    0.39096, 0.387667, 0.401613}, {0.0125342, 0.03149, -0.97585, 0.0601685, -0.00370468,
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    0.0630741, -0.0287081, -0.0343994, 0.023026, -0.0494368, -0.0767467, -0.0154701}},
  SpikeNegative_16 → {{0.297324, 0.336412, 0.295526, 0.278759, 0.245056, 0.318937, 0.250643,
    0.388363, 0.303036, 0.407593}, {-0.0400702, 0.0546704, -0.972757, -0.0843888, -0.0448392,
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    0.0418384, -0.0520887, 0.0350102, 0.0363633, 0.0786127, 0.0614368, 0.0607404, 0.0042901}},
  SpikeNegative_17 → {{0.208954, 0.236332, 0.227303, 0.313061, 0.185284, 0.285081, 0.305249,
    0.445982, 0.382833, 0.443365}, {-0.0500567, 0.0615101, -0.964028, -0.0424776, -0.0608032,
    0.0484783, -0.0932164, 0.00675612, 0.0917275, -0.0513798, 0.0806272, -0.0292141,
    -0.0434281, 0.0802618, -0.028805, -0.0697576, 0.0412039, 0.0704427, -0.0210238, 0.090776}},
  SpikeNegative_18 → {{0.125661, 0.345671, 0.290321, 0.541012, 0.330576, 0.346989, 0.359568,
    0.183145, 0.252761, 0.17703}, {0.0637703, 0.0170482, -0.976772, 0.0310032, 0.0958129,
    0.0103727, 0.0549246, -0.0920391, -0.000171055, 0.0447182, -0.0655219, -0.0463124,
    -0.0505533, 0.0113488, 0.0376016, 0.0559696, -0.0298409, 0.0331692, 0.0138885, -0.0443797}},
  SpikeNegative_19 → {{0.278732, 0.233116, 0.436472, 0.284349, 0.322525, 0.299596, 0.283411,
    0.325436, 0.312102, 0.345232}, {0.029348, 0.0453181, -0.96819, -0.0136947, -0.00745223,
    -0.0359863, -0.0330837, -0.0632341, 0.0138135, 0.0662721, 0.0756972, 0.0493927, 0.0984751,
    -0.0988025, 0.00498469, 0.00803444, 0.0746088, 0.0877685, 0.0844884, 0.0187667}},
  SpikeNegative_20 → {{0.334271, 0.434111, 0.433495, 0.21859, 0.328219, 0.163239, 0.186898,
    0.337219, 0.255569, 0.340256}, {0.0197994, -0.0662971, -0.961564, -0.0685973, -0.0185152,
    0.0882361, 0.0352751, 0.0879639, 0.0430174, 0.0417512, 0.0807419, 0.0666948, 0.0608026,
    -0.0863153, 0.0682553, 0.0422124, 0.0413467, 0.0978466, 0.021418, 0.0699975}}|>,
f1 → <|LinearPositive_1 → {{0.984641, 0.162688, 0.0323981, 0.0023219, 0.0017005,
    0.0101525, 0.0219279, 0.0292455, 0.0192272, 0.0338803},
   {0.0186334, 0.0386214, 0.055949, 0.0759478, 0.0930578, 0.113214, 0.131531, 0.149052, 0.16728, 0.187061,
    0.204623, 0.224346, 0.24333, 0.261902, 0.28103, 0.297442, 0.316034, 0.335773, 0.355255, 0.372846}},
  LinearPositive_2 → {{0.983273, 0.169647, 0.032428, 0.00199873, 0.00227361, 0.0113103,
    0.0226311, 0.0316239, 0.0189014, 0.0365468}, {0.0171416, 0.0378118, 0.0549821, 0.0742681,
    0.0945316, 0.113659, 0.131239, 0.147572, 0.168249, 0.187366, 0.20603, 0.222512,
    0.241358, 0.259941, 0.280837, 0.300046, 0.318146, 0.336674, 0.352872, 0.373769}},
  LinearPositive_3 → {{0.984364, 0.165621, 0.0304344, 0.00224077, 0.00189177, 0.0100519,
    0.0205372, 0.027167, 0.0202331, 0.0314912}, {0.0194077, 0.0356278, 0.0561041, 0.0748831,
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    0.242314, 0.262404, 0.279456, 0.299678, 0.317489, 0.335801, 0.35375, 0.374253}},
  LinearPositive_4 → {{0.983752, 0.167837, 0.0315147, 0.00167351, 0.00225991, 0.0113587,
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    0.0926289, 0.113016, 0.131697, 0.149163, 0.169034, 0.186169, 0.204368, 0.224574,
    0.241896, 0.260581, 0.280059, 0.298191, 0.317043, 0.33613, 0.354034, 0.37496}},
  LinearPositive_5 → {{0.983531, 0.169262, 0.0325116, 0.00244512, 0.00212863, 0.0109489,
    0.0206202, 0.0298566, 0.0176222, 0.0346929}, {0.0183958, 0.0371673, 0.0569043, 0.0750446,
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  LinearPositive_6 → {{0.984324, 0.164395, 0.0320928, 0.00176118, 0.00202845, 0.0119897,
    0.019451, 0.0301279, 0.0202211, 0.0346986}, {0.0170423, 0.0375401, 0.0548801, 0.074606,
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    0.241824, 0.262584, 0.278865, 0.299586, 0.317977, 0.334906, 0.354399, 0.374077}},
  LinearPositive_7 → {{0.983252, 0.171028, 0.0314672, 0.00226886, 0.00160253, 0.0115778,
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    0.241219, 0.26265, 0.27924, 0.297512, 0.317437, 0.337241, 0.354078, 0.373111}},
  LinearPositive_8 → {{0.984882, 0.16197, 0.0321906, 0.00169601, 0.00218179,
    0.0120811, 0.0205674, 0.0271432, 0.0206928, 0.0315467},
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    0.204819, 0.225676, 0.241046, 0.263197, 0.278647, 0.297435, 0.318022, 0.334603, 0.354489, 0.375347}},
  LinearPositive_9 → {{0.98383, 0.167311, 0.0324696, 0.00159909, 0.00202386, 0.0105193,
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    0.0759273, 0.0929665, 0.113427, 0.132135, 0.149329, 0.168615, 0.185327, 0.20412,
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LinearPositive_10 → {{0.983707, 0.169048, 0.0303735, 0.00201493, 0.0018901, 0.0102194,
   0.0222369, 0.0280959, 0.0188277, 0.0327194}, {0.0182209, 0.0367355, 0.0560385,
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   0.224886, 0.241739, 0.26043, 0.281232, 0.299432, 0.317514, 0.334669, 0.3538, 0.37316}},
LinearPositive_11 → {{0.984628, 0.159881, 0.0269777, 0.00252542, 0.00106036, 0.00537479,
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   0.218785, 0.248346, 0.256388, 0.283841, 0.298, 0.311155, 0.337197, 0.363342, 0.371211}},
LinearPositive_12 → {{0.986522, 0.151708, 0.0215795, 0.00183589, 0.000418219, 0.00885534,
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   0.236743, 0.262671, 0.289152, 0.300124, 0.312046, 0.33376, 0.360346, 0.368283}},
LinearPositive_13 → {{0.982534, 0.171894, 0.0520577, 0.000742212, 0.000699524,
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LinearPositive_14 → {{0.984694, 0.163, 0.0387294, 0.00165471, 0.00410167,
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LinearPositive_15 → {{0.981362, 0.177946, 0.0283716, 0.00164422, 0.00184888,
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   0.200745, 0.222157, 0.241148, 0.255994, 0.276806, 0.306027, 0.319744, 0.33796, 0.356624, 0.374723}},
LinearPositive_16 → {{0.985891, 0.155656, 0.0271961, 0.000305768, 0.0023344, 0.0139841,
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   0.245277, 0.25929, 0.285593, 0.292005, 0.323421, 0.332657, 0.346832, 0.380021}},
LinearPositive_17 → {{0.983893, 0.166907, 0.024865, 0.00179595, 0.00126226,
   0.0107203, 0.0179333, 0.032141, 0.0260392, 0.0363981},
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LinearPositive_18 → {{0.98641, 0.15058, 0.0368809, 0.00174217, 0.00210634,
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   0.199806, 0.234584, 0.237284, 0.262995, 0.278161, 0.291875, 0.325344, 0.336179, 0.353754, 0.373691}},
LinearPositive_19 → {{0.98597, 0.14983, 0.0314963, 0.00289346, 0.00345308, 0.00986692,
   0.018777, 0.038736, 0.0240328, 0.0432842}, {0.0272029, 0.0460588, 0.0560888, 0.084535,
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   0.246625, 0.261101, 0.275823, 0.298173, 0.313536, 0.331269, 0.350886, 0.377439}},
LinearPositive_20 → {{0.982563, 0.176252, 0.0438063, 0.00257025, 0.000806196, 0.0116656,
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LinearNegative_1 → {{0.981231, 0.178878, 0.0437501, 0.000215405, 0.00018167, 0.0114352,
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LinearNegative_2 → {{0.980199, 0.18259, 0.0341631, 0.00813135, 0.000147234, 0.0108796,
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LinearNegative_3 → {{0.980226, 0.177529, 0.0296018, 0.00163609, 0.00438857, 0.0153958,
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LinearNegative_4 → {{0.979222, 0.176264, 0.0432781, 0.0127619, 0.00582446, 0.0110541,
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   -0.227111, -0.27171, -0.279835, -0.292592, -0.303367, -0.351405, -0.341255, -0.364393}},
LinearNegative_5 → {{0.985947, 0.15267, 0.0294985, 0.00236353, 0.000152379, 0.0127685,
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   -0.237416, -0.252796, -0.290151, -0.298084, -0.302964, -0.34267, -0.350928, -0.377758}},
LinearNegative_6 → {{0.981093, 0.187206, 0.0328321, 0.00544956, 0.00151147, 0.00845078,
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  LinearNegative_7 → {{0.987784, 0.137453, 0.0524734, 0.00172857, 0.00907878, 0.0222887,
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  LinearNegative_8 → {{0.981869, 0.176114, 0.0184722, 0.000897044, 0.00908914, 0.0126187,
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  LinearNegative_9 → {{0.977432, 0.193472, 0.0566997, 0.00894665, 0.00891502, 0.0042068,
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  LinearNegative_10 → {{0.988387, 0.13491, 0.0347655, 0.00600934, 0.00182395, 0.0127304,
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  LinearNegative_14 → {{0.981695, 0.179748, 0.0364798, 0.00475101, 0.00172876, 0.0127355,
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  LinearNegative_15 → {{0.976331, 0.206183, 0.02716, 0.00245466, 0.00112872, 0.0143514,
    0.0289664, 0.0289241, 0.0228639, 0.0334317}, {-0.0252422, -0.0440882, -0.053639, -0.0710578,
    -0.0870667, -0.107721, -0.132379, -0.157656, -0.1747, -0.191921, -0.20206, -0.224194,
    -0.233227, -0.258368, -0.282298, -0.292582, -0.319034, -0.343497, -0.350277, -0.37493}},
  LinearNegative_16 → {{0.987736, 0.143433, 0.0283328, 0.00446943, 0.00556613, 0.0119332,
    0.0149432, 0.0320117, 0.0133276, 0.0371846}, {-0.0250662, -0.0390993, -0.0653205, -0.0761738,
    -0.0939578, -0.112879, -0.126173, -0.140947, -0.173107, -0.187256, -0.210142, -0.217357,
    -0.249279, -0.268359, -0.274695, -0.293429, -0.318555, -0.333666, -0.352283, -0.375974}},
  LinearNegative_17 → {{0.982142, 0.177652, 0.0255142, 0.00494585, 0.0025063, 0.0110966,
    0.0236003, 0.0314129, 0.0115281, 0.0368004}, {-0.0167817, -0.0361715, -0.0479143, -0.0726877,
    -0.100812, -0.104149, -0.130289, -0.153099, -0.175409, -0.181922, -0.199906, -0.217333,
    -0.250916, -0.261323, -0.285784, -0.304936, -0.323431, -0.333305, -0.350126, -0.366266}},
  LinearNegative_18 → {{0.982498, 0.178886, 0.0298389, 0.00251013, 0.000273148, 0.0146888,
    0.0188368, 0.0203044, 0.0147745, 0.0244653}, {-0.0269009, -0.0404336, -0.0575823, -0.0746906,
    -0.100892, -0.106132, -0.134284, -0.158913, -0.160083, -0.187583, -0.207667, -0.21616,
    -0.237912, -0.262373, -0.278894, -0.300526, -0.31698, -0.328561, -0.363453, -0.373212}},
  LinearNegative_19 → {{0.980805, 0.178744, 0.0312507, 0.00385866, 0.000303263, 0.0141318,
    0.0153966, 0.0414289, 0.0285314, 0.0459753}, {-0.0103403, -0.0327523, -0.0486275, -0.0836464,
    -0.0848485, -0.12043, -0.122245, -0.156687, -0.170878, -0.178198, -0.206108, -0.21948,
    -0.237799, -0.260403, -0.283108, -0.294084, -0.313891, -0.340493, -0.35988, -0.376412}},
  LinearNegative_20 → {{0.985477, 0.151368, 0.0339708, 0.00203108, 0.00403423, 0.0117805,
    0.0255893, 0.0384737, 0.0239465, 0.043598}, {-0.011371, -0.0358959, -0.055762, -0.0831128,
    -0.0949378, -0.111166, -0.136444, -0.140029, -0.164687, -0.187045, -0.20637, -0.223236,
    -0.23979, -0.268208, -0.275346, -0.299109, -0.319079, -0.339089, -0.348505, -0.37613}}|>,
f3 → <|Sinusoidal3_21 → {{0.00324198, 0.0748274, 0.992348, 0.0876808, 0.0332557, 0.0198469,
    0.00905293, 0.0031642, 0.0188136, 0.00125146}, {0.18554, -0.0924734, -0.296734, -0.252516,
    -0.000102723, 0.260055, 0.303447, 0.0966792, -0.190365, -0.311489, -0.185935, 0.0950707,
    0.302149, 0.260465, -0.000163241, -0.25925, -0.297569, -0.100573, 0.186551, 0.315385}},
  Sinusoidal3_22 → {{0.00315632, 0.0724328, 0.992957, 0.0820758, 0.0364115, 0.0173491,
    0.00755488, 0.00271987, 0.0187405, 0.000989853}, {0.18084, -0.0923326, -0.296635, -0.258749,
    0.000134102, 0.256604, 0.294865, 0.100661, -0.187916, -0.320259, -0.180767, 0.103928,
    0.305742, 0.25651, -0.0056151, -0.259717, -0.302771, -0.0959814, 0.188423, 0.310488}},
```

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```
    Sinusoidal3_23 → {{0.0026894, 0.0704479, 0.992574, 0.0885695, 0.0342091, 0.0181111, 0.00866939,
        0.00304367, 0.0199329, 0.00116405}, {0.188573, -0.0998226, -0.298237, -0.255635,
        -0.00546735, 0.258297, 0.299475, 0.0997135, -0.190091, -0.316305, -0.18791, 0.0930397,
        0.294227, 0.258761, 0.00120523, -0.257376, -0.302185, -0.0940496, 0.191161, 0.31174}},
    Sinusoidal3_24 → {{0.00371315, 0.0729027, 0.991955, 0.0921778, 0.0365309, 0.017989, 0.00820268,
        0.00287529, 0.0215647, 0.000990405}, {0.182723, -0.104051, -0.300745, -0.261382,
        0.00275145, 0.25758, 0.295002, 0.0978765, -0.181605, -0.310806, -0.180761, 0.0950668,
        0.29895, 0.25873, 0.00254854, -0.259283, -0.303782, -0.101026, 0.185311, 0.319979}},
    Sinusoidal3_25 → {{0.00302973, 0.0706909, 0.992852, 0.0845145, 0.0353105, 0.0194166,
        0.00817535, 0.00249513, 0.0199474, 0.000836871}, {0.185691, -0.0960997, -0.303393, -0.25749,
        0.0000464661, 0.2529, 0.306505, 0.0977119, -0.189341, -0.316594, -0.188304, 0.0954075,
        0.300989, 0.252118, -0.00210792, -0.256743, -0.300064, -0.0934621, 0.186217, 0.310341}},
    Sinusoidal3_26 → {{0.00342175, 0.0749208, 0.992155, 0.0883842, 0.0373117, 0.0172917, 0.00948568,
        0.00251785, 0.0200828, 0.000851137}, {0.182881, -0.0942333, -0.298778, -0.257724,
        -0.00207845, 0.259442, 0.303135, 0.0978176, -0.179354, -0.31416, -0.186602, 0.101233,
        0.299649, 0.259499, 0.00576636, -0.251503, -0.30251, -0.102934, 0.184504, 0.317352}},
    Sinusoidal3_27 → {{0.00305362, 0.0728575, 0.992375, 0.0864532, 0.038425, 0.0208329, 0.00719554,
        0.00319627, 0.0206424, 0.0012056}, {0.188188, -0.0917327, -0.302671, -0.260487,
        0.0027039, 0.260647, 0.298295, 0.100066, -0.191313, -0.318308, -0.179481, 0.0947416,
        0.305672, 0.250722, -0.00555224, -0.248949, -0.297832, -0.100963, 0.179496, 0.318183}},
    Sinusoidal3_28 → {{0.00281647, 0.0749161, 0.992367, 0.0866, 0.0352125, 0.0182883, 0.00801821,
        0.00235301, 0.0210635, 0.000747503}, {0.181404, -0.100442, -0.300457, -0.255733,
        0.00116647, 0.255732, 0.300306, 0.0944678, -0.186001, -0.320043, -0.181673, 0.094748,
        0.302739, 0.258924, -0.000231987, -0.254045, -0.303375, -0.0931959, 0.186521, 0.314758}},
    Sinusoidal3_29 → {{0.00306988, 0.0746792, 0.99256, 0.0822924, 0.0391192, 0.0216471, 0.00845716,
        0.00292074, 0.0196492, 0.00108419}, {0.186559, -0.0963395, -0.300337, -0.250556,
        0.00192566, 0.252437, 0.298941, 0.10306, -0.189052, -0.319577, -0.188738, 0.0961246,
        0.304349, 0.255348, -0.00491883, -0.251368, -0.299971, -0.104178, 0.187058, 0.315624}},
    Sinusoidal3_30 → {{0.00353065, 0.0737251, 0.993156, 0.0786819, 0.0344431, 0.018833,
        0.00945567, 0.00317993, 0.0189805, 0.0012539}, {0.18306, -0.0992546, -0.304299, -0.249124,
        -0.00531719, 0.255262, 0.304405, 0.102393, -0.189806, -0.317633, -0.190988, 0.101534,
        0.301338, 0.254537, -0.00431822, -0.260187, -0.297591, -0.0956779, 0.180106, 0.31061}}|>,
f5 → <|Sinusoidal2_11 → {{0.00320854, 0.0107656, 0.0306431, 0.0950402, 0.926253, 0.360937,
        0.0286762, 0.00489602, 0.0288511, 0.00173079}, {-0.0929014, -0.258086, 0.254954, 0.101603,
        -0.311501, 0.092206, 0.256947, -0.252511, -0.0995599, 0.311181, -0.102879, -0.261263,
        0.257929, 0.0921587, -0.321472, 0.0986526, 0.256408, -0.260569, -0.0976118, 0.31187}},
    Sinusoidal2_12 → {{0.00293028, 0.0105296, 0.0285753, 0.0892427, 0.937002, 0.333884, 0.0286903,
        0.00468004, 0.0282929, 0.00162732}, {-0.0925216, -0.252292, 0.260838, 0.0979884,
        -0.310951, 0.104167, 0.254349, -0.257599, -0.0925887, 0.321367, -0.0939998, -0.253659,
        0.257542, 0.0977037, -0.320051, 0.0952882, 0.261675, -0.250955, -0.09826, 0.313106}},
    Sinusoidal2_13 → {{0.0025511, 0.00945565, 0.030427, 0.0942742, 0.933183, 0.34317, 0.0276828,
        0.00548426, 0.026349, 0.00211744}, {-0.10216, -0.259376, 0.254448, 0.0951553,
        -0.319037, 0.094629, 0.261667, -0.251941, -0.095753, 0.314986, -0.0980554, -0.258856,
        0.258224, 0.0945903, -0.310182, 0.091565, 0.258496, -0.255481, -0.0941314, 0.315632}},
    Sinusoidal2_14 → {{0.00305447, 0.0111124, 0.0293574, 0.0962215, 0.933188, 0.342122, 0.031813,
        0.00404923, 0.0287822, 0.00128701}, {-0.0979017, -0.252936, 0.249988, 0.100117,
        -0.311247, 0.0970162, 0.257962, -0.26072, -0.0968349, 0.311878, -0.103857, -0.250431,
        0.249939, 0.0944182, -0.32075, 0.0964221, 0.261477, -0.259709, -0.101391, 0.321415}},
    Sinusoidal2_15 → {{0.00244452, 0.0105101, 0.0295223, 0.0947383, 0.928476, 0.355292, 0.0311265,
        0.00405818, 0.0273577, 0.00136247}, {-0.0951454, -0.250939, 0.25223, 0.0961777,
        -0.316743, 0.0979217, 0.260293, -0.25574, -0.0977587, 0.314889, -0.102164, -0.252916,
        0.255277, 0.0998546, -0.319771, 0.103482, 0.254943, -0.261701, -0.0924755, 0.314304}},
    Sinusoidal2_16 → {{0.00276258, 0.0103437, 0.031391, 0.0938688, 0.931133, 0.348463, 0.0307315,
        0.00501319, 0.0260691, 0.00189284}, {-0.0984633, -0.253894, 0.253717, 0.100948,
        -0.318145, 0.0965037, 0.251932, -0.25218, -0.0978469, 0.312933, -0.0937753, -0.261787,
        0.25392, 0.0981599, -0.322789, 0.0982714, 0.257584, -0.259412, -0.0959231, 0.313136}},
    Sinusoidal2_17 → {{0.00197862, 0.010913, 0.0280379, 0.0912521, 0.931706, 0.347798, 0.0276642,
        0.00431498, 0.0306278, 0.00136957}, {-0.0923891, -0.256244, 0.250903, 0.0969061,
        -0.314844, 0.0986133, 0.250473, -0.261931, -0.103793, 0.31933, -0.0948321, -0.254593,
        0.25503, 0.0949468, -0.32242, 0.102177, 0.255675, -0.251946, -0.103508, 0.314164}},
    Sinusoidal2_18 → {{0.00206024, 0.0103922, 0.0326602, 0.0991964, 0.934473, 0.337777, 0.0281628,
        0.00485504, 0.0287966, 0.00169112}, {-0.0971245, -0.253392, 0.256933, 0.0934395,
        -0.317148, 0.0955048, 0.256129, -0.257923, -0.0974009, 0.313655, -0.0938798, -0.256202,
        0.253691, 0.0923778, -0.310673, 0.100713, 0.260773, -0.260128, -0.103594, 0.318607}},
    Sinusoidal2_19 → {{0.00224261, 0.0106745, 0.0296714, 0.0912405, 0.930989, 0.349307, 0.0281466,
        0.00359732, 0.0333762, 0.000940057}, {-0.0931969, -0.2614, 0.259674, 0.0959712,
```

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```
    -0.316093, 0.096965, 0.255063, -0.260104, -0.0996832, 0.312752, -0.0977896, -0.25906,
    0.254131, 0.0973563, -0.31823, 0.102857, 0.249461, -0.249419, -0.0952764, 0.316957}},
  Sinusoidal2_20 → {{0.00194758, 0.0084844, 0.0294208, 0.0955062, 0.934742, 0.338682, 0.0276307,
    0.00559975, 0.0262645, 0.00219874}, {-0.100077, -0.254286, 0.256418, 0.0921802,
    -0.323638, 0.0939406, 0.250776, -0.252093, -0.100208, 0.315398, -0.0963071, -0.259558,
    0.254584, 0.0931344, -0.32049, 0.094895, 0.262327, -0.251585, -0.0942254, 0.314184}}|>,
f6 → <|Sinusoidal1_1 → {{0.000107588, 0.00606525, 0.0255869, 0.0275349, 0.0875394, 0.990925,
    0.0918864, 0.00521119, 0.021933, 0.00187434}, {-0.169232, -0.0751922, 0.302906, -0.258644,
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    -0.287264, 0.269937, 0.0313625, -0.250125, 0.296736, -0.0673161, -0.194753, 0.311864}},
  Sinusoidal1_2 → {{0.00848391, 0.00962613, 0.0187187, 0.0202322, 0.100167, 0.988722, 0.102075,
    0.00331495, 0.0322103, 0.00176964}, {-0.177867, -0.0919027, 0.322273, -0.239902,
    0.02811, 0.270117, -0.288952, 0.0846549, 0.190342, -0.289089, 0.165817, 0.0882306,
    -0.331486, 0.286672, -0.0201759, -0.27358, 0.274728, -0.0726351, -0.176309, 0.316001}},
  Sinusoidal1_3 → {{0.00542461, 0.0117773, 0.0118991, 0.029902, 0.0851117, 0.990012, 0.103962,
    0.00584004, 0.0241044, 0.00219625}, {-0.162235, -0.0978008, 0.271419, -0.252535,
    0.0219523, 0.276397, -0.294568, 0.116449, 0.202602, -0.333291, 0.189176, 0.10859,
    -0.265244, 0.260423, -0.00833012, -0.270729, 0.278017, -0.11022, -0.194751, 0.332937}},
  Sinusoidal1_4 → {{0.00263351, 0.00853833, 0.0196326, 0.0482503, 0.093274, 0.989056, 0.0973599,
    0.00168151, 0.0281754, 0.000117746}, {-0.174826, -0.0757044, 0.315848, -0.281481,
    0.00984634, 0.235876, -0.292594, 0.120089, 0.203479, -0.328212, 0.208492, 0.101891,
    -0.271403, 0.256786, -0.0235251, -0.237232, 0.288568, -0.112357, -0.192304, 0.310905}},
  Sinusoidal1_5 → {{0.000478492, 0.0121874, 0.0106474, 0.036478, 0.0807532, 0.990072, 0.105802,
    0.00249257, 0.0210535, 0.000832323}, {-0.192051, -0.0900236, 0.302019, -0.240743,
    0.0293644, 0.238063, -0.294775, 0.0895113, 0.16114, -0.33048, 0.206464, 0.117452,
    -0.298853, 0.290384, -0.0125904, -0.242284, 0.321127, -0.076973, -0.160928, 0.307167}},
  Sinusoidal1_6 → {{0.00402383, 0.00811295, 0.0135754, 0.0452503, 0.100659, 0.988964, 0.0948149,
    0.0144005, 0.0155153, 0.00807697}, {-0.197888, -0.102824, 0.275285, -0.258221,
    -0.0148624, 0.259268, -0.319889, 0.104513, 0.149237, -0.283548, 0.196396, 0.0985562,
    -0.312068, 0.217932, -0.02992, -0.275309, 0.309098, -0.119934, -0.184399, 0.332655}},
  Sinusoidal1_7 → {{0.00344252, 0.00817737, 0.00889592, 0.025091, 0.0774686, 0.991008,
    0.103334, 0.0036944, 0.020504, 0.00132129}, {-0.172056, -0.0942098, 0.275791, -0.258363,
    0.022543, 0.279999, -0.274169, 0.0915495, 0.188152, -0.340698, 0.214004, 0.0795236,
    -0.29964, 0.269174, 0.0182049, -0.278523, 0.28708, -0.0807614, -0.18654, 0.29795}},
  Sinusoidal1_8 → {{0.00258313, 0.00683127, 0.017596, 0.0303859, 0.102555, 0.988987, 0.098363,
    0.0055604, 0.0197562, 0.00230464}, {-0.187887, -0.0885268, 0.27559, -0.278963,
    -0.0237702, 0.2573, -0.313546, 0.112125, 0.192519, -0.308527, 0.203677, 0.0815246,
    -0.272252, 0.275667, -0.0138681, -0.265923, 0.280434, -0.0967196, -0.200849, 0.309352}},
  Sinusoidal1_9 → {{0.000975477, 0.00633969, 0.013062, 0.0330435, 0.0760569, 0.987848,
    0.128574, 0.00610209, 0.0222002, 0.00252221}, {-0.161637, -0.107124, 0.276063, -0.258103,
    -0.0136662, 0.269028, -0.3021, 0.0704434, 0.169211, -0.342208, 0.169827, 0.10046,
    -0.333248, 0.267166, 0.0218251, -0.245357, 0.301393, -0.094524, -0.179398, 0.301734}},
  Sinusoidal1_10 → {{0.00681886, 0.00439285, 0.0183738, 0.0417539, 0.0853837, 0.986179,
    0.132158, 0.00222401, 0.0232963, 0.000396375}, {-0.18002, -0.0977941, 0.303294, -0.245654,
    -0.0165229, 0.273552, -0.286236, 0.0928426, 0.20958, -0.321812, 0.200039, 0.097673,
    -0.336743, 0.243711, -0.0239039, -0.245776, 0.278891, -0.0998256, -0.185554, 0.295051}}|>|>
```

The default SignificanceCriterion is "Silhouette":

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In[3]:=
```
clusters1 = TimeSeriesClusters[classification1, SignificanceCriterion → "Silhouette"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
⟨|SpikeMax → ⟨|Cluster → Cluster[ ··· 1 ··· ], ··· 4 ···,
   GroupAssociations → ⟨|G1S1 → {SpikePositive_1, SpikePositive_8, SpikePositive_10, ··· 3 ···,
       SpikePositive_5, SpikePositive_7, SpikePositive_4}, ··· 4 ··· |⟩ |⟩, ··· 4 ···, f6 → ⟨| ··· 1 ··· |⟩ |⟩
```

large output | show less | show more | show all | set size limit...

In[4]:=
```
Query[All, "GroupAssociations" /* Keys]@clusters1
```

Out[4]=
```
⟨|SpikeMax → {G1S1, G1S2, G2S1, G2S2, G3S1}, SpikeMin → {G1S1, G1S2}, f1 → {G1S1, G1S2, G2S1},
 f3 → {G1S1, G1S2, G2S1, G2S2}, f5 → {G1S1, G1S2, G2S1, G2S2, G2S3}, f6 → {G1S1, G1S2, G2S1} |⟩
```

In[5]:=
```
clusters1Gap = TimeSeriesClusters[classification1, SignificanceCriterion → "Gap"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[5]=
```
⟨|SpikeMax → ⟨|Cluster → Cluster[ ··· 1 ··· ], ··· 4 ···, GroupAssociations →
    ⟨|G1S1 → {SpikePositive_1, SpikePositive_8, SpikePositive_10, ··· 4 ···, SpikePositive_4,
       SpikePositive_5, SpikePositive_7}, G1S2 → ··· 1 ··· |⟩ |⟩, ··· 4 ···, f6 → ⟨| ··· 1 ··· |⟩ |⟩
```

large output | show less | show more | show all | set size limit...

We can see that the number of groups generated is different:

In[6]:=
```
Query[All, "GroupAssociations" /* Keys]@clusters1Gap
```

Out[6]=
```
⟨|SpikeMax → {G1S1, G1S2}, SpikeMin → {G1S1, G1S2},
 f1 → {G1S1, G1S2, G1S3, G1S4}, f3 → {G1S1}, f5 → {G1S1}, f6 → {G1S1, G1S2} |⟩
```

In[7]:=
```
(Query[All, "GroupAssociations" /* Keys]@clusters1Gap) ==
 (Query[All, "GroupAssociations" /* Keys]@clusters1)
```

Out[7]= False

SingleAssociationLabel (1)

In[1]:=
```
Needs["MathIOmica`"]
```

SingleAssociationLabel provides an option for what to label the class if a single class is provided as input in the form of a list. The default label is "1".

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

Method → "LombScargle"

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.426578, 0.240878, 0.279335, 0.170519, 0.281174, 0.24267, 0.309003, 0.358691,
      0.411439, 0.348615}, {0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564, -0.0362021,
      -0.0625238, 0.0341425, -0.0893761, -0.0883628, -0.017962, -0.0386128, -0.0180346,
      0.00287015, -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174}},
   SpikePositive_2 → {{0.177315, 0.286388, 0.273761, 0.425425, 0.295363, 0.311857, 0.311019,
      0.291322, 0.3924, 0.332471}, {0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821,
      0.0140267, 0.0130259, 0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081,
      0.0633006, -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478}},
   SpikePositive_3 → {{0.217843, 0.348982, 0.400833, 0.133907, 0.226083, 0.261081, 0.164317,
      0.396591, 0.471008, 0.356016}, {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406,
      -0.088789, 0.0161993, 0.0873614, 0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181,
      -0.0275224, 0.0821854, -0.0656115, 0.0495169, -0.0958318, -0.0295775, 0.0577959}},
   SpikePositive_4 → {{0.169769, 0.3444, 0.407241, 0.180462, 0.508351, 0.196951, 0.199545,
      0.262783, 0.417435, 0.271698}, {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915,
      -0.102642, -0.0491586, 0.0387547, -0.0805303, -0.0750145, 0.0435078, 0.096307, -0.0207842,
      -0.074725, -0.0219338, -0.0702263, -0.0708028, 0.0629065, 0.0539273, -0.0472406}},
   SpikePositive_5 → {{0.262958, 0.158095, 0.395484, 0.32363, 0.33396, 0.299747, 0.317155,
      0.241743, 0.471193, 0.249576}, {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513,
      0.0519281, 0.0476815, 0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776,
      -0.0145575, -0.0471635, -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704}},
   SpikePositive_6 → {{0.22831, 0.308065, 0.102432, 0.280228, 0.215963, 0.200512, 0.31406,
      0.202464, 0.701822, 0.211957}, {0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398,
      0.0300977, -0.0143248, -0.0347325, 0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375,
      -0.041878, -0.00608792, 0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065}},
   SpikePositive_7 → {{0.416316, 0.226461, 0.283807, 0.508477, 0.277805, 0.203989, 0.365412,
      0.180652, 0.348591, 0.172735}, {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331,
      0.0436824, -0.0808607, -0.0618148, -0.00363485, -0.0607952, -0.0266488, -0.0885909,
      -0.0604068, 0.0564238, 0.027816, -0.0300755, -0.00964389, 0.0219551, 0.0830947, 0.100236}},
   SpikePositive_8 → {{0.140741, 0.144032, 0.153469, 0.401912, 0.320464, 0.267291, 0.223201,
      0.404252, 0.472347, 0.404808}, {0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284,
      -0.0342585, -0.0327609, 0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291,
      0.0449639, 0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327}},
   SpikePositive_9 → {{0.108303, 0.215436, 0.305921, 0.520232, 0.230187, 0.207485, 0.344013,
      0.360486, 0.325724, 0.356654}, {0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074,
      0.0910254, 0.0377891, 0.0330553, -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855,
      0.0528972, 0.0722006, -0.0375273, -0.00701134, -0.0825865, -0.0268527, -0.0449685}},
   SpikePositive_10 → {{0.352345, 0.381423, 0.307933, 0.276346, 0.127597, 0.185925, 0.300244,
      0.34709, 0.412546, 0.357099}, {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085,
      -0.0290915, -0.0700719, 0.0187234, 0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485,
      0.0886753, -0.0765068, -0.0746426, 0.0807971, -0.0126166, -0.0042573, 0.0843061}},
   SpikePositive_11 → {{0.145425, 0.537688, 0.26197, 0.274584, 0.266036, 0.317601, 0.433018,
      0.232026, 0.26148, 0.253694}, {-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591,
      0.0800972, -0.0821497, -0.0789604, -0.0537447, 0.089175, 0.0760246, 0.0874422, 0.0627384,
```

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```
    -0.0346583, -0.0692825, 0.0851396, -0.0759865, -0.0253768, -0.0417439, -0.0104898}},
  SpikePositive_12 → {{0.149633, 0.564058, 0.380469, 0.209973, 0.290635, 0.427485, 0.243199,
    0.155, 0.29752, 0.178053}, {-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951,
    -0.0190127, -0.084559, -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588,
    0.076484, 0.0945541, 0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871}},
  SpikePositive_13 → {{0.261646, 0.351498, 0.187571, 0.312059, 0.486411, 0.371912, 0.355245,
    0.229646, 0.242729, 0.250316}, {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784,
    0.078485, -0.0941461, -0.0893966, -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524,
    0.00305398, -0.0753412, 0.0791486, 0.0322394, 0.080124, -0.000969041, 0.0870857}},
  SpikePositive_14 → {{0.0723294, 0.252403, 0.180185, 0.322985, 0.530444, 0.361662, 0.415142,
    0.2543, 0.281695, 0.256402}, {-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473,
    0.0140683, -0.0113637, -0.0208056, -0.0484049, 0.0489594, 0.0405395, 0.0157363, 0.0839891,
    0.030142, -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291}},
  SpikePositive_15 → {{0.265672, 0.158292, 0.353015, 0.431081, 0.309169, 0.361211, 0.266931,
    0.319575, 0.300486, 0.32277}, {0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004,
    -0.0231518, -0.00286655, 0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133,
    -0.00792171, 0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659}},
  SpikePositive_16 → {{0.410152, 0.230961, 0.170521, 0.24057, 0.184991, 0.426604, 0.332134,
    0.244615, 0.472127, 0.286731}, {0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881,
    0.0544409, -0.00693186, -0.0482937, 0.0280248, -0.0959175, -0.0672972, 0.00106747,
    -0.0451342, -0.0567082, -0.0918568, 0.0302632, -0.0902741, 0.0774122, 0.0136075, 0.0648783}},
  SpikePositive_17 → {{0.128807, 0.15667, 0.217053, 0.270196, 0.343886, 0.320885, 0.552592,
    0.351385, 0.236802, 0.364165}, {0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173,
    0.0441891, -0.0575291, 0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992,
    -0.0922154, 0.10018, -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815}},
  SpikePositive_18 → {{0.285634, 0.240484, 0.327196, 0.378566, 0.376518, 0.291937, 0.266319,
    0.32315, 0.325309, 0.319437}, {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976,
    -0.0189917, -0.041052, 0.00572256, -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528,
    0.00777195, -0.0217935, -0.0107251, 0.0930318, -0.0216511, -0.00863921, 0.0518108}},
  SpikePositive_19 → {{0.190492, 0.311333, 0.34998, 0.344232, 0.282691, 0.381625, 0.481425,
    0.209168, 0.274675, 0.221999}, {-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202,
    0.0586092, -0.0125386, 0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416,
    0.0121501, -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867}},
  SpikePositive_20 → {{0.294919, 0.264271, 0.417464, 0.211378, 0.407543, 0.270107, 0.388684,
    0.272428, 0.272163, 0.292938}, {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402,
    0.0541689, -0.0432748, 0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019,
    0.0728601, -0.0844032, -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.300918, 0.12577, 0.0865807, 0.17251, 0.298637, 0.263493,
    0.391376, 0.287362, 0.607797, 0.304291}, {-0.970907, 0.0401695, -0.088695, -0.0568028,
    -0.0460609, 0.0306784, -0.0368859, 0.0109469, 0.0490514, 0.0599829, -0.081578, 0.0645303,
    0.0850677, -0.0173421, -0.0290798, -0.0699666, -0.0704747, 0.0288648, -0.0052948, 0.0644987}},
  SpikeNegative_2 → {{0.265023, 0.244782, 0.254276, 0.269454, 0.178434, 0.231024, 0.494378,
    0.319675, 0.441578, 0.325238}, {-0.964559, 0.0614044, -0.0265329, 0.0785433, 0.0608998,
    -0.0886832, 0.074269, -0.0363919, 0.0976695, 0.0359249, -0.0547092, 0.0810664, 0.0550517,
    -0.00682936, 0.0926606, -0.0495218, -0.00586302, 0.049991, -0.0352768, -0.0477537}},
  SpikeNegative_3 → {{0.312113, 0.200244, 0.240998, 0.18669, 0.391052, 0.406419, 0.203221,
    0.387753, 0.356642, 0.364159}, {-0.970414, -0.0382255, -0.0398241, -0.0770396, 0.00948429,
    -0.0753827, 0.0404422, -0.0300602, 0.035445, -0.0310938, 0.0637881, -0.0767297, -0.0871087,
    0.079282, -0.0495086, -0.0744528, 0.00399949, 0.0306214, -0.0176352, -0.0754366}},
  SpikeNegative_4 → {{0.229903, 0.255279, 0.243387, 0.154931, 0.25739, 0.292411, 0.522188,
    0.239361, 0.510754, 0.236937}, {-0.985359, 0.0230187, -0.03218, -0.0552386, 0.0775039,
    -0.046887, 0.0425714, -0.0190925, -0.0281896, 0.0489385, -0.0522405, -0.0112681, -0.0428901,
    -0.00311955, 0.0401724, -0.0397719, -0.0261781, -0.0230012, 0.0381753, 0.0174853}},
  SpikeNegative_5 → {{0.143532, 0.142397, 0.227575, 0.182566, 0.333763, 0.285383, 0.218401,
    0.153445, 0.762155, 0.170396}, {-0.963065, -0.0193029, -0.0283241, -0.100441, -0.0914133,
    0.0856932, -0.0940453, 0.0260441, -0.0362625, 0.0542725, -0.0604653, -0.0318016, -0.06787,
    -0.0227999, -0.00694351, 0.0627985, 0.00247265, -0.0288134, 0.0971304, 0.0877639}},
  SpikeNegative_6 → {{0.137377, 0.238601, 0.215763, 0.235035, 0.148059, 0.306627, 0.159441,
    0.328172, 0.6679, 0.356725}, {-0.964556, 0.100594, 0.0574003, 0.0837961, -0.0610619,
    0.0705001, -0.0255353, -0.0544496, -0.00761041, -0.0753725, 0.0637942, 0.0354175, -0.0233298,
    -0.0682889, 0.0768609, -0.0215223, -0.0904352, -0.0122301, 0.0626204, -0.0446094}},
  SpikeNegative_7 → {{0.257688, 0.125144, 0.407165, 0.32608, 0.185928, 0.145625, 0.213335,
    0.253575, 0.647941, 0.24578}, {-0.967683, 0.0262048, 0.0316536, 0.0827514, -0.0895921,
    -0.0511321, 0.00358148, 0.0377385, 0.0964141, 0.061766, -0.0656343, 0.0435943, -0.0388761,
    -0.0134713, -0.0163893, 0.0597168, -0.0671195, -0.0832954, 0.0567659, 0.0588427}},
  SpikeNegative_8 → {{0.178598, 0.383484, 0.206112, 0.318472, 0.198925, 0.239426, 0.299646,
```

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```
    0.320915, 0.528343, 0.329121}, {-0.961371, 0.0481934, -0.0612303, 0.079868, 0.0688298,
    0.0820927, 0.0881741, 0.0788901, -0.00563582, -0.0628233, -0.099146, -0.0293345, -0.0510806,
    -0.0368136, -0.0159913, 0.0703926, 0.0348639, -0.0213314, -0.0817692, 0.0750901}},
  SpikeNegative_9 → {{0.0842676, 0.094976, 0.19394, 0.209134, 0.0775198, 0.319147, 0.313809,
    0.183172, 0.780142, 0.232413}, {-0.950364, 0.101242, -0.0837148, 0.0713045, -0.015486,
    0.0199376, -0.0898773, 0.0871573, 0.0144087, -0.0130525, -0.0734895, 0.082757, -0.0799732,
    -0.0984375, 0.086115, -0.0420311, 0.0757735, -0.0262399, 0.0718597, 0.0930855}},
  SpikeNegative_10 → {{0.235324, 0.304585, 0.307514, 0.239148, 0.369408, 0.166305, 0.353502,
    0.254179, 0.513906, 0.286888}, {-0.974856, -0.00610897, 0.044452, 0.0600431, 0.060705,
    0.0493209, 0.0650291, -0.0689887, 0.0431441, 0.0486794, -0.0448363, -0.0485303, 0.082492,
    -0.0886706, 0.0299378, -0.0297761, 0.0277851, 0.00211484, 0.0309282, -0.0463888}},
  SpikeNegative_11 → {{0.082834, 0.268038, 0.430241, 0.179543, 0.282023, 0.328048, 0.342915,
    0.382853, 0.317297, 0.389813}, {0.0659028, -0.0966074, -0.96013, 0.0437336, -0.071429,
    0.0906464, -0.00120639, 0.0435635, -0.0888938, -0.0898465, -0.0253244, -0.0197621,
    -0.0378295, -0.0748998, -0.051477, -0.083832, 0.0494364, -0.0509701, -0.0455586, 0.0806333}},
  SpikeNegative_12 → {{0.155052, 0.067039, 0.229633, 0.391266, 0.326956, 0.283062, 0.331374,
    0.400016, 0.402924, 0.382689}, {0.0423013, 0.0906316, -0.957717, 0.0981261, 0.0411838,
    0.050264, -0.0820196, 0.0246482, 0.0965743, -0.030318, 0.0434382, 0.0361146, 0.000211044,
    0.0855167, -0.0733807, -0.0939636, -0.0895242, 0.0198047, -0.0636511, 0.0645515}},
  SpikeNegative_13 → {{0.292648, 0.104288, 0.202432, 0.322947, 0.486015, 0.245852, 0.423411,
    0.303638, 0.308371, 0.308203}, {0.0755194, 0.0513576, -0.973209, 0.0366214, 0.0358723,
    -0.016093, -0.0592775, -0.0454328, 0.029529, 0.0331799, -0.0257214, 0.095823, 0.0671603,
    -0.0137473, 0.0828746, 0.00920408, -0.0436543, -0.0482728, -0.0828685, 0.0385433}},
  SpikeNegative_14 → {{0.337179, 0.133844, 0.213469, 0.270341, 0.320492, 0.466905, 0.174509,
    0.319904, 0.430457, 0.333081}, {-0.0197011, 0.0418739, -0.977336, 0.0226633, -0.0505248,
    -0.0779811, -0.0694652, 0.0337659, -0.000482683, 0.0160955, 0.0714615, -0.0247899, 0.0860662,
    0.0132762, -0.0587754, -0.00851111, -0.0564477, -0.0561142, 0.0225303, -0.0602181}},
  SpikeNegative_15 → {{0.316209, 0.210734, 0.348635, 0.209919, 0.312923, 0.324472, 0.275605,
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    0.0897559, 0.0473494, 0.0274418, 0.0876019, 0.0199764, 0.0584157, -0.0968252, -0.042633}},
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  SpikeNegative_17 → {{0.330143, 0.125304, 0.172668, 0.218275, 0.402059, 0.362982, 0.259277,
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  SpikeNegative_18 → {{0.252932, 0.246864, 0.273314, 0.30064, 0.242976, 0.309996, 0.361798,
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  SpikeNegative_19 → {{0.207615, 0.361604, 0.283699, 0.244474, 0.312918, 0.473886, 0.419185,
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  SpikeNegative_20 → {{0.215966, 0.397298, 0.185277, 0.162898, 0.346172, 0.272493, 0.251371,
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    -0.0572105, 0.0129034, 0.0873857, 0.0797024, -0.0170267, 0.00130268, -0.0179771}}|>,
f1 → <|LinearPositive_1 → {{0.984411, 0.164878, 0.0298154, 0.00231118, 0.00182363, 0.0101943,
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    0.242747, 0.26239, 0.279313, 0.300339, 0.316607, 0.336229, 0.35523, 0.372874}},
  LinearPositive_2 → {{0.984046, 0.166873, 0.0316066, 0.00237348, 0.00217535, 0.0105079,
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    0.243118, 0.261523, 0.278673, 0.296921, 0.318101, 0.337172, 0.355022, 0.37461}},
  LinearPositive_3 → {{0.98383, 0.168589, 0.0305552, 0.00247403, 0.00168266,
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  LinearPositive_4 → {{0.983513, 0.16988, 0.0328131, 0.0024759, 0.00191191, 0.0101673,
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LinearPositive_5 → {{0.983646, 0.168703, 0.03085, 0.00171956, 0.00266524, 0.011245, 0.0222365,
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LinearPositive_7 → {{0.983064, 0.172297, 0.0340516, 0.00273888, 0.00159961, 0.0118281,
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LinearPositive_8 → {{0.984412, 0.164716, 0.0324118, 0.00239043, 0.00202071, 0.0112605,
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LinearPositive_9 → {{0.983849, 0.167787, 0.030964, 0.00247469, 0.00163303, 0.0115522,
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LinearPositive_10 → {{0.983625, 0.169376, 0.029263, 0.00273574, 0.00169172, 0.0107992,
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LinearPositive_11 → {{0.980552, 0.185951, 0.0335077, 0.00414524, 0.00274833, 0.00638931,
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LinearPositive_12 → {{0.984098, 0.161767, 0.0237318, 0.00345236, 0.00211508, 0.0101286,
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LinearPositive_13 → {{0.987525, 0.144914, 0.0411227, 0.00209615, 0.00241117, 0.0107433,
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LinearPositive_14 → {{0.982671, 0.169305, 0.02931, 0.0016522, 0.000595208,
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LinearPositive_15 → {{0.986039, 0.148661, 0.0568496, 0.00344523, 0.00146566, 0.00790359,
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LinearPositive_16 → {{0.983702, 0.167453, 0.0376277, 0.00302881, 0.00346708, 0.00701049,
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LinearPositive_19 → {{0.983034, 0.167714, 0.0301624, 0.00250016, 0.00196756, 0.020049,
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LinearPositive_20 → {{0.980606, 0.183674, 0.0461222, 0.00186666, 0.00208756, 0.0158248,
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LinearNegative_1 → {{0.984238, 0.155065, 0.0305725, 0.00429355, 0.000907603, 0.0115932,
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LinearNegative_4 → {{0.981706, 0.17868, 0.0184274, 0.00108065, 0.00480526, 0.0104052,
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LinearNegative_5 → {{0.987284, 0.135479, 0.0328459, 0.00474419, 0.0108896, 0.0113128,
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LinearNegative_7 → {{0.983437, 0.168269, 0.0495285, 0.000828358, 0.00114834, 0.0134683,
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LinearNegative_8 → {{0.98945, 0.127627, 0.0266902, 0.000730683, 0.0052411, 0.0174906, 0.0343464,
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LinearNegative_9 → {{0.982316, 0.156906, 0.0360415, 0.00654635, 0.00114955, 0.0138536,
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LinearNegative_10 → {{0.983021, 0.176176, 0.0392573, 0.000273201, 0.000913773, 0.00909489,
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LinearNegative_13 → {{0.98505, 0.164803, 0.0270407, 0.001064, 0.0030468, 0.0114083, 0.0167547,
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LinearNegative_14 → {{0.985946, 0.148996, 0.0300907, 0.00379374, 0.0017371, 0.00904696,
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LinearNegative_15 → {{0.988286, 0.142216, 0.027642, 0.00190957, 0.00136283, 0.010732,
    0.0204206, 0.0231314, 0.0223637, 0.0269927}, {-0.0143673, -0.0384603, -0.059481, -0.0814686,
    -0.0998357, -0.11163, -0.121543, -0.148495, -0.164093, -0.184204, -0.200603, -0.230545,
    -0.239957, -0.261717, -0.285006, -0.306132, -0.31674, -0.331959, -0.356233, -0.369045}},
LinearNegative_16 → {{0.983537, 0.162043, 0.0379753, 0.000698808, 0.00175385, 0.010855,
    0.0235062, 0.0416472, 0.0161167, 0.0478248}, {-0.0170801, -0.0394996, -0.0522426, -0.0802166,
    -0.0999452, -0.109939, -0.136438, -0.155399, -0.168092, -0.176397, -0.211083, -0.226024,
    -0.246991, -0.251052, -0.279034, -0.299568, -0.307063, -0.330226, -0.361266, -0.379009}},
LinearNegative_17 → {{0.981928, 0.171959, 0.0362682, 0.00181571, 0.000735952, 0.00820844,
    0.0162851, 0.043629, 0.017204, 0.0489566}, {-0.0167061, -0.0417885, -0.0610393, -0.0811488,
    -0.0843311, -0.110818, -0.131706, -0.154061, -0.166461, -0.17863, -0.213542, -0.216073,
```

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```
    -0.248686, -0.253663, -0.275578, -0.295755, -0.311593, -0.345715, -0.362742, -0.370796}},
  LinearNegative_18 → {{0.987446, 0.142407, 0.0305043, 0.000608932, 0.00349367, 0.00916454,
    0.0190662, 0.0356901, 0.0188877, 0.0406225}, {-0.0182673, -0.0431502, -0.0583943, -0.0720847,
    -0.0908552, -0.116809, -0.130064, -0.140945, -0.169783, -0.17904, -0.206654, -0.232505,
    -0.244303, -0.257534, -0.28405, -0.307937, -0.30985, -0.330361, -0.353638, -0.375697}},
  LinearNegative_19 → {{0.98524, 0.154209, 0.0287085, 0.000623168, 0.0083283, 0.0116831,
    0.0342978, 0.0348556, 0.0211998, 0.0406379}, {-0.0118551, -0.0469184, -0.059877, -0.0726465,
    -0.0874648, -0.116257, -0.13931, -0.141859, -0.163578, -0.189816, -0.199394, -0.222064,
    -0.245791, -0.263162, -0.283581, -0.293518, -0.32017, -0.333319, -0.349831, -0.379486}},
  LinearNegative_20 → {{0.987813, 0.142329, 0.0300675, 0.00251521, 0.00274699, 0.00769738,
    0.0220686, 0.0276628, 0.0271988, 0.031592}, {-0.0175031, -0.0352515, -0.0633653, -0.0821156,
    -0.0860969, -0.108683, -0.130367, -0.144426, -0.165554, -0.189321, -0.200028, -0.231649,
    -0.243045, -0.26745, -0.274418, -0.29663, -0.313939, -0.340651, -0.352044, -0.375845}}|>,
f3 → <|Sinusoidal3_21 → {{0.00348941, 0.0709096, 0.99279, 0.0851529, 0.0355604, 0.0191222,
    0.00754121, 0.00313075, 0.0194696, 0.00122375}, {0.18438, -0.100687, -0.297126, -0.258636,
    0.000694858, 0.261391, 0.300471, 0.100998, -0.188208, -0.313126, -0.189847, 0.0932049,
    0.302746, 0.252189, -0.00622074, -0.255929, -0.298389, -0.0975506, 0.191825, 0.312314}},
  Sinusoidal3_22 → {{0.00272817, 0.0728436, 0.992452, 0.0873699, 0.036363, 0.0171011, 0.0102896,
    0.0023799, 0.019107, 0.000815788}, {0.184933, -0.0918857, -0.304918, -0.255817,
    0.00315255, 0.258918, 0.30475, 0.0909833, -0.178536, -0.315254, -0.18883, 0.101821,
    0.302605, 0.258799, 0.00392631, -0.256614, -0.295106, -0.0918552, 0.187734, 0.313486}},
  Sinusoidal3_23 → {{0.00362855, 0.071662, 0.992177, 0.0905986, 0.037022, 0.0183136, 0.00821167,
    0.00257538, 0.0211408, 0.000849481}, {0.185223, -0.100913, -0.301222, -0.261129,
    0.00254563, 0.258014, 0.302308, 0.0964885, -0.187302, -0.31206, -0.179547, 0.10098,
    0.297655, 0.252221, 0.000863572, -0.255607, -0.303352, -0.0994261, 0.187334, 0.316005}},
  Sinusoidal3_24 → {{0.00283278, 0.0719129, 0.992458, 0.0874699, 0.0374596, 0.017831, 0.00938514,
    0.00308867, 0.0194033, 0.00118872}, {0.183512, -0.0973849, -0.304518, -0.253233,
    -0.00500096, 0.259361, 0.295694, 0.10307, -0.18496, -0.317598, -0.183799, 0.100461,
    0.295293, 0.260485, 0.00230323, -0.252889, -0.301817, -0.0955436, 0.188539, 0.317648}},
  Sinusoidal3_25 → {{0.00251503, 0.0768544, 0.992133, 0.0861869, 0.0382631, 0.0192065,
    0.00972112, 0.00293141, 0.019851, 0.00109656}, {0.191859, -0.100412, -0.300195, -0.250473,
    0.00178675, 0.25849, 0.305002, 0.0931399, -0.187887, -0.321252, -0.191453, 0.0973687,
    0.3013, 0.252848, 0.00508386, -0.24962, -0.296694, -0.100465, 0.188761, 0.310308}},
  Sinusoidal3_26 → {{0.00314684, 0.0749982, 0.992479, 0.0832184, 0.0395602, 0.0197981,
    0.00903979, 0.00326275, 0.019324, 0.00132711}, {0.188305, -0.102527, -0.305393, -0.251599,
    0.00538523, 0.250672, 0.299012, 0.102564, -0.187994, -0.315224, -0.190392, 0.103607,
    0.303115, 0.254279, 0.00273218, -0.257886, -0.297519, -0.100912, 0.186634, 0.310478}},
  Sinusoidal3_27 → {{0.0024442, 0.070112, 0.992785, 0.0848049, 0.0372383, 0.0186978, 0.0090305,
    0.00291491, 0.020892, 0.00104149}, {0.190337, -0.0954242, -0.304036, -0.25673,
    -0.00513247, 0.256643, 0.302591, 0.0992802, -0.188617, -0.321443, -0.186284, 0.0979387,
    0.297381, 0.252296, 0.000116697, -0.250632, -0.297285, -0.0943158, 0.182359, 0.316827}},
  Sinusoidal3_28 → {{0.00220347, 0.0749496, 0.992212, 0.0869161, 0.0374307, 0.0205851,
    0.00965245, 0.00256939, 0.0203184, 0.000875737}, {0.190627, -0.092948, -0.304157, -0.255315,
    -0.000889438, 0.254881, 0.301083, 0.0924648, -0.188237, -0.317575, -0.185215, 0.0993937,
    0.304201, 0.260112, 0.000217846, -0.248874, -0.296425, -0.101368, 0.182555, 0.314777}},
  Sinusoidal3_29 → {{0.00287541, 0.070719, 0.993079, 0.0821473, 0.0356972, 0.0170157,
    0.00851218, 0.00354631, 0.0196262, 0.0014699}, {0.187086, -0.102576, -0.29395, -0.256212,
    -0.00544231, 0.255521, 0.299433, 0.100508, -0.184027, -0.312566, -0.191021, 0.102711,
    0.306475, 0.25373, 0.00304628, -0.259647, -0.297796, -0.0968863, 0.190614, 0.314016}},
  Sinusoidal3_30 → {{0.00286486, 0.0721879, 0.992638, 0.0846981, 0.0382608, 0.0177506,
    0.0087775, 0.0029062, 0.0202786, 0.00105452}, {0.186579, -0.0968586, -0.294824, -0.258765,
    -0.00468069, 0.257553, 0.300009, 0.094859, -0.184043, -0.316666, -0.189358, 0.101867,
    0.30487, 0.250847, -0.000277949, -0.25225, -0.300892, -0.103367, 0.18753, 0.316696}}|>,
f5 → <|Sinusoidal2_11 → {{0.00263247, 0.0105769, 0.0335125, 0.0978234, 0.932959, 0.342139,
    0.0291986, 0.00389591, 0.0291076, 0.00119476}, {-0.0999421, -0.253416, 0.255697, 0.0981876,
    -0.317896, 0.0917799, 0.254523, -0.253954, -0.0941007, 0.315378, -0.0920311, -0.25612,
    0.252578, 0.0971222, -0.320231, 0.100103, 0.255687, -0.25896, -0.102308, 0.317695}},
  Sinusoidal2_12 → {{0.00197373, 0.0120029, 0.0322146, 0.0921104, 0.931921, 0.346767,
    0.0279169, 0.00507157, 0.0282252, 0.00183848}, {-0.0938961, -0.250642, 0.254697, 0.1004,
    -0.317201, 0.092662, 0.252554, -0.262605, -0.0970329, 0.322361, -0.102724, -0.250771,
    0.258408, 0.0932395, -0.312044, 0.0960783, 0.255459, -0.256773, -0.101611, 0.317972}},
  Sinusoidal2_13 → {{0.00214852, 0.0107535, 0.0305386, 0.0888205, 0.933187, 0.344406, 0.0271851,
    0.00484505, 0.0289699, 0.00168381}, {-0.0938439, -0.255921, 0.255301, 0.100659,
    -0.311512, 0.0976074, 0.251098, -0.261076, -0.0959496, 0.317857, -0.0960171, -0.260156,
    0.259852, 0.0940569, -0.315712, 0.099422, 0.259646, -0.250499, -0.100253, 0.315158}},
  Sinusoidal2_14 → {{0.00238156, 0.0111312, 0.0310099, 0.0872852, 0.930051, 0.353023, 0.0272819,
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    0.00480849, 0.0299957, 0.00162975}, {-0.0941616, -0.261274, 0.250783, 0.102689,
    -0.310822, 0.0927825, 0.253423, -0.260853, -0.0939409, 0.319546, -0.100607, -0.258212,
    0.261294, 0.0930121, -0.314285, 0.0956176, 0.255177, -0.252537, -0.100668, 0.316778}},
  Sinusoidal2_15 → {{0.0026873, 0.00984343, 0.0331601, 0.0963617, 0.934898, 0.337252, 0.0260687,
    0.00391833, 0.0322709, 0.00112692}, {-0.0993597, -0.258551, 0.259899, 0.0914446,
    -0.320098, 0.0918606, 0.259981, -0.249571, -0.0986243, 0.319786, -0.0976853, -0.255051,
    0.249843, 0.100213, -0.314025, 0.0959927, 0.250294, -0.254331, -0.102658, 0.319138}},
  Sinusoidal2_16 → {{0.00244822, 0.0099122, 0.0291904, 0.0943838, 0.932308, 0.345774, 0.0240681,
    0.00505501, 0.027746, 0.00185541}, {-0.0995723, -0.252143, 0.254452, 0.0926543,
    -0.318145, 0.100423, 0.253532, -0.249277, -0.103077, 0.321637, -0.102407, -0.255729,
    0.260149, 0.0944323, -0.320047, 0.102512, 0.252391, -0.253155, -0.0984776, 0.313815}},
  Sinusoidal2_17 → {{0.0028358, 0.0111138, 0.0283478, 0.0932398, 0.937421, 0.331618, 0.031187,
    0.00458662, 0.025424, 0.00169039}, {-0.101451, -0.248566, 0.254308, 0.0983114,
    -0.320388, 0.103006, 0.256032, -0.260918, -0.093353, 0.316431, -0.0958187, -0.250287,
    0.254512, 0.0969772, -0.320292, 0.0918162, 0.257471, -0.254932, -0.0970362, 0.316435}},
  Sinusoidal2_18 → {{0.00170135, 0.0112262, 0.0312218, 0.0983246, 0.933712, 0.340297, 0.0288674,
    0.00460647, 0.0274089, 0.00161538}, {-0.100583, -0.252443, 0.253065, 0.0918012,
    -0.320384, 0.0977115, 0.252099, -0.251379, -0.10177, 0.311561, -0.0924259, -0.256167,
    0.256963, 0.103528, -0.317473, 0.104141, 0.256696, -0.26203, -0.100759, 0.316336}},
  Sinusoidal2_19 → {{0.0025962, 0.0108424, 0.0301405, 0.0898405, 0.932102, 0.347009, 0.0301982,
    0.00483464, 0.0269808, 0.00180353}, {-0.0980563, -0.251307, 0.249772, 0.103387,
    -0.321666, 0.099317, 0.258251, -0.256265, -0.0998176, 0.316164, -0.0949114, -0.259869,
    0.253237, 0.102275, -0.315745, 0.0947401, 0.251353, -0.252325, -0.0954722, 0.320582}},
  Sinusoidal2_20 → {{0.0026546, 0.010974, 0.0295707, 0.0946031, 0.934034, 0.340729, 0.0278109,
    0.00470173, 0.027103, 0.00166456}, {-0.101684, -0.25613, 0.250696, 0.095516, -0.309967,
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    0.101315, -0.316667, 0.0994236, 0.261172, -0.259414, -0.0999887, 0.317352}}|>,
f6 → <|Sinusoidal1_1 → {{0.00584669, 0.0018432, 0.0165107, 0.0456074, 0.0786607, 0.989228,
    0.109533, 0.00634386, 0.0284247, 0.0022031}, {-0.169977, -0.114178, 0.301652, -0.252384,
    -0.0156333, 0.257121, -0.269553, 0.123871, 0.167186, -0.342165, 0.166715, 0.0752933,
    -0.324991, 0.246258, 0.000336998, -0.247797, 0.306559, -0.0788041, -0.16496, 0.3398}},
  Sinusoidal1_2 → {{0.00472316, 0.00251647, 0.00472845, 0.0457108, 0.0782285, 0.989892,
    0.1066, 0.00768032, 0.0205201, 0.0032419}, {-0.16361, -0.0968838, 0.278859, -0.264114,
    -0.00380314, 0.260703, -0.267547, 0.126273, 0.172048, -0.332535, 0.208385, 0.103643,
    -0.303073, 0.228145, -0.0266305, -0.276794, 0.322967, -0.0783889, -0.160968, 0.329975}},
  Sinusoidal1_3 → {{0.00195981, 0.00852751, 0.0200966, 0.0531746, 0.0965187, 0.989253,
    0.0896005, 0.00267242, 0.026799, 0.000678245}, {-0.20748, -0.120194, 0.283976, -0.264574,
    -0.00611185, 0.247481, -0.278254, 0.0906812, 0.209363, -0.338459, 0.160025, 0.11704,
    -0.280126, 0.234616, 0.0180046, -0.236037, 0.302135, -0.107637, -0.221034, 0.32551}},
  Sinusoidal1_4 → {{0.000294432, 0.00818968, 0.0221495, 0.0351307, 0.07778, 0.990781, 0.0984074,
    0.00728208, 0.0277068, 0.00262703}, {-0.160395, -0.100144, 0.321803, -0.265021,
    -0.0143507, 0.232063, -0.331177, 0.104347, 0.187937, -0.302108, 0.223244, 0.0875224,
    -0.298214, 0.237872, 0.0107771, -0.248604, 0.293763, -0.075207, -0.171897, 0.320627}},
  Sinusoidal1_5 → {{0.00636643, 0.0100575, 0.0226145, 0.0401752, 0.0976424, 0.985354, 0.129111,
    0.0125789, 0.0201432, 0.00655941}, {-0.161423, -0.106118, 0.320667, -0.245495,
    -0.0324307, 0.253993, -0.286427, 0.117341, 0.178808, -0.310814, 0.192755, 0.0789337,
    -0.295604, 0.261321, -0.0190798, -0.293762, 0.287101, -0.129673, -0.182762, 0.302118}},
  Sinusoidal1_6 → {{0.0017307, 0.00540895, 0.0205001, 0.0342393, 0.111028, 0.986431, 0.10951,
    0.00215069, 0.0317012, 0.000285091}, {-0.154986, -0.0844171, 0.308176, -0.269886,
    -0.0164997, 0.264337, -0.272179, 0.084886, 0.207588, -0.30012, 0.212702, 0.0774819,
    -0.292459, 0.281252, 0.00454802, -0.253455, 0.292696, -0.0858567, -0.203266, 0.319287}},
  Sinusoidal1_7 → {{0.00118974, 0.00879923, 0.0188074, 0.0334476, 0.105215, 0.99026, 0.0799184,
    0.00518776, 0.0186085, 0.0020463}, {-0.214086, -0.0899446, 0.291531, -0.257297,
    -0.00638012, 0.271888, -0.323551, 0.115182, 0.187049, -0.302537, 0.174176, 0.102793,
    -0.270305, 0.279588, 0.00941545, -0.237702, 0.303023, -0.0663513, -0.21253, 0.293821}},
  Sinusoidal1_8 → {{0.00159773, 0.00623527, 0.0130573, 0.0357615, 0.0937595, 0.988133,
    0.113875, 0.00653731, 0.0171276, 0.00289253}, {-0.202442, -0.108809, 0.294202, -0.281594,
    0.00365581, 0.238604, -0.320211, 0.0850299, 0.198552, -0.330326, 0.173263, 0.103135,
    -0.294698, 0.230764, -0.0302892, -0.263496, 0.307019, -0.117154, -0.155078, 0.287995}},
  Sinusoidal1_9 → {{0.000786044, 0.00902277, 0.0244466, 0.0246116, 0.102665, 0.990242,
    0.082153, 0.00341011, 0.0288783, 0.000673848}, {-0.168798, -0.08007, 0.314639, -0.277953,
    0.0158685, 0.22463, -0.316077, 0.0786847, 0.206944, -0.311884, 0.166364, 0.0803937,
    -0.282805, 0.261564, 0.00792446, -0.27702, 0.298613, -0.0916065, -0.2067, 0.30383}},
  Sinusoidal1_10 → {{0.000579026, 0.00853774, 0.0113025, 0.0447869, 0.0839945, 0.987696,
    0.118163, 0.00188387, 0.0350523, 0.000698855}, {-0.175779, -0.118498, 0.308374, -0.288389,
    -0.0283508, 0.231767, -0.299123, 0.079629, 0.183548, -0.339664, 0.206563, 0.123931,
```

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Let's cluster only the "SpikeMax" class extracted from the data

In[3]:=
```
clusters1Class = TimeSeriesClusters[classification1["SpikeMax"]]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Out[3]=
```
<|1 → <|Cluster →
  Cluster[Cluster[Cluster[Cluster[Cluster[Cluster[{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564,
          -0.0362021, -0.0625238, 0.0341425, -0.0893761, -0.0883628, -0.017962, -0.0386128, -0.0180346,
          0.00287015, -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174} →
         SpikePositive_1, {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915, -0.0700719,
          0.0187234, 0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485, 0.0886753, -0.0765068,
          -0.0746426, 0.0807971, -0.0126166, -0.0042573, 0.0843061} → SpikePositive_10, 0.253714, 1, 1],
        {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789, 0.0161993, 0.0873614,
         0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181, -0.0275224, 0.0821854, -0.0656115,
         0.0495169, -0.0958318, -0.0295775, 0.0577959} → SpikePositive_3, 0.30679, 2, 1], Cluster[
        Cluster[Cluster[Cluster[{0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267,
             0.0130259, 0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081, 0.0633006,
             -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478} → SpikePositive_2,
           Cluster[{0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518, -0.00286655,
              0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133, -0.00792171,
              0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659} → SpikePositive_15,
            {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917, -0.041052,
              0.00572256, -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528,
              0.00777195, -0.0217935, -0.0107251, 0.0930318, -0.0216511, -0.00863921,
              0.0518108} → SpikePositive_18, 0.143365, 1, 1], 0.196995, 1, 2],
          {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281, 0.0476815,
            0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776, -0.0145575, -0.0471635,
            -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704} → SpikePositive_5, 0.247424, 3, 1],
         {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689, -0.0432748,
           0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019, 0.0728601, -0.0844032,
           -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496} → SpikePositive_20, 0.296637, 4, 1],
        {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642, -0.0491586,
         0.0387547, -0.0805303, -0.0750145, 0.0435078, 0.096307, -0.0207842, -0.074725,
         -0.0219338, -0.0702263, -0.0708028, 0.0629065, 0.0539273, -0.0472406} →
         SpikePositive_4, 0.341309, 5, 1], 0.383948, 3, 6],
       Cluster[Cluster[{-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092,
           -0.0125386, 0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416, 0.0121501,
           -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867} → SpikePositive_19,
         {-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972, -0.0821497, -0.0789604,
           -0.0537447, 0.089175, 0.0760246, 0.0874422, 0.0627384, -0.0346583, -0.0692825, 0.0851396,
           -0.0759865, -0.0253768, -0.0417439, -0.0104898} → SpikePositive_11, 0.272553, 1, 1],
        {-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127, -0.084559,
          -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588, 0.076484, 0.0945541,
          0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871} →
         SpikePositive_12, 0.334818, 2, 1], 0.459707, 9, 3],
      Cluster[Cluster[{0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891,
          -0.0575291, 0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992, -0.0922154, 0.10018,
          -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815} → SpikePositive_17,
        Cluster[{-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683, -0.0113637,
           -0.0208056, -0.0484049, 0.0489594, 0.0405395, 0.0157363, 0.0839891, 0.030142,
           -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291} → SpikePositive_14,
         {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485, -0.0941461,
           -0.0893966, -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524, 0.00305398,
           -0.0753412, 0.0791486, 0.0322394, 0.080124, -0.000969041, 0.0870857} →
         SpikePositive_13, 0.23158, 1, 1], 0.346333, 1, 2],
       Cluster[{0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254, 0.0377891,
          0.0330553, -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855, 0.0528972,
          0.0722006, -0.0375273, -0.00701134, -0.0825865, -0.0268527, -0.0449685} → SpikePositive_9,
        {0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585, -0.0327609,
          0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291, 0.0449639,
          0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327} →
         SpikePositive_8, 0.308944, 1, 1], 0.437803, 3, 2], 0.485945, 12, 5],
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 Cluster[Cluster[{0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409,
     -0.00693186, -0.0482937, 0.0280248, -0.0959175, -0.0672972,
     0.00106747, -0.0451342, -0.0567082, -0.0918568, 0.0302632,
     -0.0902741, 0.0774122, 0.0136075, 0.0648783} → SpikePositive_16,
   {0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248, -0.0347325,
     0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375, -0.041878, -0.00608792,
     0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065} → SpikePositive_6, 0.39718, 1, 1],
  {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824, -0.0808607,
    -0.0618148, -0.00363485, -0.0607952, -0.0266488, -0.0885909,
    -0.0604068, 0.0564238, 0.027816, -0.0300755, -0.00964389,
    0.0219551, 0.0830947, 0.100236} → SpikePositive_7,
  0.465014, 2, 1], 0.502616, 17, 3], InitialSplitCluster →
{Cluster[Cluster[Cluster[Cluster[Cluster[{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564,
        -0.0362021, -0.0625238, 0.0341425, -0.0893761, -0.0883628, -0.017962, -0.0386128, -0.0180346,
        0.00287015, -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174} →
       SpikePositive_1, {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915, -0.0700719,
        0.0187234, 0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485, 0.0886753, -0.0765068,
        -0.0746426, 0.0807971, -0.0126166, -0.0042573, 0.0843061} → SpikePositive_10, 0.253714, 1, 1],
      {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789, 0.0161993, 0.0873614,
       0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181, -0.0275224, 0.0821854, -0.0656115,
       0.0495169, -0.0958318, -0.0295775, 0.0577959} → SpikePositive_3, 0.30679, 2, 1], Cluster[
      Cluster[Cluster[Cluster[{0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267,
           0.0130259, 0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081, 0.0633006,
           -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478} → SpikePositive_2,
         Cluster[{0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518, -0.00286655,
            0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133, -0.00792171,
            0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659} → SpikePositive_15,
          {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917, -0.041052, 0.00572256,
           -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528, 0.00777195, -0.0217935,
           -0.0107251, 0.0930318, -0.0216511, -0.00863921, 0.0518108} → SpikePositive_18, 0.143365, 1,
          1], 0.196995, 1, 2], {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281,
          0.0476815, 0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776, -0.0145575,
          -0.0471635, -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704} → SpikePositive_5,
       0.247424, 3, 1], {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689, -0.0432748,
        0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019, 0.0728601, -0.0844032,
        -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496} → SpikePositive_20, 0.296637, 4, 1],
      {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642, -0.0491586,
       0.0387547, -0.0805303, -0.0750145, 0.0435078, 0.096307, -0.0207842, -0.074725,
       -0.0219338, -0.0702263, -0.0708028, 0.0629065, 0.0539273, -0.0472406} →
      SpikePositive_4, 0.341309, 5, 1], 0.383948, 3, 6],
    Cluster[Cluster[{-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092,
       -0.0125386, 0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416, 0.0121501,
       -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867} → SpikePositive_19,
      {-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972, -0.0821497, -0.0789604,
       -0.0537447, 0.089175, 0.0760246, 0.0874422, 0.0627384, -0.0346583, -0.0692825, 0.0851396,
       -0.0759865, -0.0253768, -0.0417439, -0.0104898} → SpikePositive_11, 0.272553, 1, 1],
     {-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127, -0.084559,
      -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588, 0.076484, 0.0945541,
      0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871} →
     SpikePositive_12, 0.334818, 2, 1], 0.459707, 9, 3],
   Cluster[Cluster[{0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891,
      -0.0575291, 0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992, -0.0922154, 0.10018,
      -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815} → SpikePositive_17,
     Cluster[{-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683, -0.0113637,
       -0.0208056, -0.0484049, 0.0489594, 0.0405395, 0.0157363, 0.0839891, 0.030142,
       -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291} → SpikePositive_14,
      {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485, -0.0941461,
       -0.0893966, -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524, 0.00305398,
       -0.0753412, 0.0791486, 0.0322394, 0.080124, -0.000969041, 0.0870857} →
      SpikePositive_13, 0.23158, 1, 1], 0.346333, 1, 2],
    Cluster[{0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254, 0.0377891,
      0.0330553, -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855, 0.0528972,
      0.0722006, -0.0375273, -0.00701134, -0.0825865, -0.0268527, -0.0449685} → SpikePositive_9,
     {0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585, -0.0327609,
      0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291, 0.0449639,
      0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327} →
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      SpikePositive_8, 0.308944, 1, 1], 0.437803, 3, 2], 0.485945, 12, 5],
  Cluster[Cluster[{0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409,
      -0.00693186, -0.0482937, 0.0280248, -0.0959175, -0.0672972,
      0.00106747, -0.0451342, -0.0567082, -0.0918568, 0.0302632,
      -0.0902741, 0.0774122, 0.0136075, 0.0648783} → SpikePositive_16,
    {0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248, -0.0347325,
      0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375, -0.041878, -0.00608792,
      0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065} → SpikePositive_6, 0.39718, 1, 1],
   {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824, -0.0808607,
     -0.0618148, -0.00363485, -0.0607952, -0.0266488,
     -0.0885909, -0.0604068, 0.0564238, 0.027816, -0.0300755,
     -0.00964389, 0.0219551, 0.0830947, 0.100236} →
    SpikePositive_7, 0.465014, 2, 1]}, IntermediateClusters →
 {Cluster[Cluster[Cluster[Cluster[Cluster[{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564,
         -0.0362021, -0.0625238, 0.0341425, -0.0893761, -0.0883628, -0.017962, -0.0386128, -0.0180346,
         0.00287015, -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174} →
        SpikePositive_1, {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915, -0.0700719,
         0.0187234, 0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485, 0.0886753, -0.0765068,
         -0.0746426, 0.0807971, -0.0126166, -0.0042573, 0.0843061} → SpikePositive_10, 0.279559, 1, 1],
      {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789, 0.0161993, 0.0873614,
        0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181, -0.0275224, 0.0821854, -0.0656115,
        0.0495169, -0.0958318, -0.0295775, 0.0577959} → SpikePositive_3, 0.311336, 2, 1],
     Cluster[Cluster[{0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585,
         -0.0327609, 0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291, 0.0449639,
         0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327} → SpikePositive_8,
       {0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254, 0.0377891, 0.0330553,
         -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855, 0.0528972, 0.0722006, -0.0375273,
         -0.00701134, -0.0825865, -0.0268527, -0.0449685} → SpikePositive_9, 0.257205, 1, 1],
      Cluster[{0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267, 0.0130259,
         0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081, 0.0633006,
         -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478} → SpikePositive_2,
       {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281, 0.0476815,
         0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776, -0.0145575,
         -0.0471635, -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704} →
        SpikePositive_5, 0.266939, 1, 1], 0.336576, 2, 2], 0.367384, 3, 4],
    {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642, -0.0491586,
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      -0.074725, -0.0219338, -0.0702263, -0.0708028, 0.0629065,
      0.0539273, -0.0472406} → SpikePositive_4, 0.397145, 7, 1],
   Cluster[Cluster[Cluster[{-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127,
        -0.084559, -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588, 0.076484, 0.0945541,
        0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871} → SpikePositive_12,
      {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485, -0.0941461, -0.0893966,
        -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524, 0.00305398, -0.0753412, 0.0791486,
        0.0322394, 0.080124, -0.000969041, 0.0870857} → SpikePositive_13, 0.317245, 1, 1],
     Cluster[{-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972, -0.0821497,
        -0.0789604, -0.0537447, 0.089175, 0.0760246, 0.0874422, 0.0627384, -0.0346583,
        -0.0692825, 0.0851396, -0.0759865, -0.0253768, -0.0417439, -0.0104898} → SpikePositive_11,
      {-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092, -0.0125386,
        0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416, 0.0121501,
        -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867} →
       SpikePositive_19, 0.266892, 1, 1], 0.343391, 2, 2],
    Cluster[Cluster[Cluster[{-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683,
         -0.0113637, -0.0208056, -0.0484049, 0.0489594, 0.0405395, 0.0157363, 0.0839891, 0.030142,
         -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291} → SpikePositive_14,
       Cluster[{0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518, -0.00286655,
          0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133, -0.00792171,
          0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659} → SpikePositive_15,
        {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917, -0.041052,
          0.00572256, -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528, 0.00777195,
          -0.0217935, -0.0107251, 0.0930318, -0.0216511, -0.00863921, 0.0518108} →
         SpikePositive_18, 0.180887, 1, 1], 0.263835, 1, 2],
      {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689, -0.0432748,
        0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019, 0.0728601, -0.0844032,
        -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496} → SpikePositive_20, 0.294117, 3, 1],
     {0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891, -0.0575291,
```

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```
      0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992, -0.0922154, 0.10018,
      -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815} →
     SpikePositive_17, 0.301453, 4, 1], 0.375883, 4, 5], 1.47437, 8, 9],
 Cluster[{0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409,
    -0.00693186, -0.0482937, 0.0280248, -0.0959175, -0.0672972,
    0.00106747, -0.0451342, -0.0567082, -0.0918568, 0.0302632,
    -0.0902741, 0.0774122, 0.0136075, 0.0648783} → SpikePositive_16,
  Cluster[{0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248,
      -0.0347325, 0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375, -0.041878,
      -0.00608792, 0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065} → SpikePositive_6,
    {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824, -0.0808607,
      -0.0618148, -0.00363485, -0.0607952, -0.0266488, -0.0885909, -0.0604068,
      0.0564238, 0.027816, -0.0300755, -0.00964389, 0.0219551, 0.0830947, 0.100236} →
     SpikePositive_7, 0.345377, 1, 1], 1.36759, 1, 2]}, SubsplitClusters →
{{Cluster[Cluster[Cluster[Cluster[{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564, -0.0362021,
         -0.0625238, 0.0341425, -0.0893761, -0.0883628, -0.017962, -0.0386128, -0.0180346, 0.00287015,
         -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174} → SpikePositive_1,
       {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915, -0.0700719, 0.0187234,
         0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485, 0.0886753, -0.0765068, -0.0746426,
         0.0807971, -0.0126166, -0.0042573, 0.0843061} → SpikePositive_10, 0.279559, 1, 1],
      {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789, 0.0161993, 0.0873614,
        0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181, -0.0275224, 0.0821854, -0.0656115,
        0.0495169, -0.0958318, -0.0295775, 0.0577959} → SpikePositive_3, 0.311336, 2, 1],
     Cluster[Cluster[{0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585,
         -0.0327609, 0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291, 0.0449639,
         0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327} → SpikePositive_8,
       {0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254, 0.0377891, 0.0330553,
         -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855, 0.0528972, 0.0722006, -0.0375273,
         -0.00701134, -0.0825865, -0.0268527, -0.0449685} → SpikePositive_9, 0.257205, 1, 1],
      Cluster[{0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267, 0.0130259,
         0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081, 0.0633006,
         -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478} → SpikePositive_2,
       {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281, 0.0476815,
         0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776, -0.0145575,
         -0.0471635, -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704} →
        SpikePositive_5, 0.266939, 1, 1], 0.336576, 2, 2], 0.367384, 3, 4],
    {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642, -0.0491586,
      0.0387547, -0.0805303, -0.0750145, 0.0435078, 0.096307, -0.0207842,
      -0.074725, -0.0219338, -0.0702263, -0.0708028, 0.0629065,
      0.0539273, -0.0472406} → SpikePositive_4, 0.397145, 7, 1],
   Cluster[Cluster[Cluster[{-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127,
        -0.084559, -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588, 0.076484, 0.0945541,
        0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871} → SpikePositive_12,
      {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485, -0.0941461, -0.0893966,
        -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524, 0.00305398, -0.0753412, 0.0791486,
        0.0322394, 0.080124, -0.000969041, 0.0870857} → SpikePositive_13, 0.317245, 1, 1],
     Cluster[{-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972, -0.0821497,
        -0.0789604, -0.0537447, 0.089175, 0.0760246, 0.0874422, 0.0627384, -0.0346583,
        -0.0692825, 0.0851396, -0.0759865, -0.0253768, -0.0417439, -0.0104898} → SpikePositive_11,
      {-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092, -0.0125386,
        0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416, 0.0121501,
        -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867} →
       SpikePositive_19, 0.266892, 1, 1], 0.343391, 2, 2],
    Cluster[Cluster[Cluster[{-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683,
         -0.0113637, -0.0208056, -0.0484049, 0.0489594, 0.0405395, 0.0157363, 0.0839891, 0.030142,
         -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291} → SpikePositive_14,
       Cluster[{0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518, -0.00286655,
          0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133, -0.00792171,
          0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659} → SpikePositive_15,
        {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917, -0.041052,
          0.00572256, -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528, 0.00777195,
          -0.0217935, -0.0107251, 0.0930318, -0.0216511, -0.00863921, 0.0518108} →
        SpikePositive_18, 0.180887, 1, 1], 0.263835, 1, 2],
      {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689, -0.0432748,
        0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019, 0.0728601, -0.0844032,
        -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496} → SpikePositive_20, 0.294117, 3, 1],
```

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      {0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891, -0.0575291,
        0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992, -0.0922154, 0.10018,
        -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815} →
       SpikePositive_17, 0.301453, 4, 1], 0.375883, 4, 5]},
  {{0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409, -0.00693186,
      -0.0482937, 0.0280248, -0.0959175, -0.0672972, 0.00106747,
      -0.0451342, -0.0567082, -0.0918568, 0.0302632, -0.0902741,
      0.0774122, 0.0136075, 0.0648783} → SpikePositive_16,
    Cluster[{0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248,
        -0.0347325, 0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375, -0.041878,
        -0.00608792, 0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065} → SpikePositive_6,
      {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824, -0.0808607,
        -0.0618148, -0.00363485, -0.0607952, -0.0266488, -0.0885909,
        -0.0604068, 0.0564238, 0.027816, -0.0300755, -0.00964389, 0.0219551,
        0.0830947, 0.100236} → SpikePositive_7, 0.345377, 1, 1]}},
Data → {{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564, -0.0362021,
    -0.0625238, 0.0341425, -0.0893761,
    -0.0883628, -0.017962, -0.0386128,
    -0.0180346, 0.00287015, -0.0573882,
    -0.0958009, 0.0379076, -0.0595687,
    -0.0529437, -0.0344174} → SpikePositive_1,
  {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915,
    -0.0700719, 0.0187234, 0.0104362,
    0.0333953, -0.0952174, -0.0348545,
    -0.0558485, 0.0886753, -0.0765068,
    -0.0746426, 0.0807971, -0.0126166,
    -0.0042573, 0.0843061} → SpikePositive_10,
  {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789,
    0.0161993, 0.0873614, 0.0491571,
    0.029947, -0.0693437, -0.0142705,
    0.0625181, -0.0275224, 0.0821854,
    -0.0656115, 0.0495169, -0.0958318,
    -0.0295775, 0.0577959} → SpikePositive_3,
  {0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585,
    -0.0327609, 0.0166862, -0.0849577,
    0.0591606, 0.0703419, -0.0412067,
    -0.0310291, 0.0449639, 0.0836001,
    -0.00965143, 0.0289184, -0.0297474,
    -0.0171145, -0.0848327} → SpikePositive_8,
  {0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254,
    0.0377891, 0.0330553, -0.0532373,
    0.0399677, 0.0862428, -0.0244445,
    -0.0794855, 0.0528972, 0.0722006,
    -0.0375273, -0.00701134, -0.0825865,
    -0.0268527, -0.0449685} → SpikePositive_9,
  {0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267,
    0.0130259, 0.0440809, 0.0904629,
    0.0612212, -0.0519196, -0.0143748,
    -0.0280081, 0.0633006, -0.0866884,
    0.00515577, -0.0372569, 0.0123246,
    0.0728383, -0.0509478} → SpikePositive_2,
  {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281,
    0.0476815, 0.0628967, -0.0423604, -0.0773945,
    0.0228186, -0.089195, 0.00937776, -0.0145575,
    -0.0471635, -0.0115995, -0.0685444, -0.065197,
    0.0709702, -0.0372704} → SpikePositive_5,
  {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642,
    -0.0491586, 0.0387547, -0.0805303, -0.0750145,
    0.0435078, 0.096307, -0.0207842, -0.074725,
    -0.0219338, -0.0702263, -0.0708028, 0.0629065,
    0.0539273, -0.0472406} → SpikePositive_4,
  {-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127,
    -0.084559, -0.0594589, 0.0148199, -0.0154587,
    -0.0374222, 0.0499588, 0.076484, 0.0945541,
    0.0610314, -0.034534, -0.0950852, 0.0403957,
    -0.0707856, 0.0799871} → SpikePositive_12,
```

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```
    {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485,
      -0.0941461, -0.0893966, -0.0641157, 0.0498908,
      -0.0603746, 0.0473787, 0.0491524, 0.00305398,
      -0.0753412, 0.0791486, 0.0322394, 0.080124,
      -0.000969041, 0.0870857} → SpikePositive_13,
    {-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972,
      -0.0821497, -0.0789604, -0.0537447, 0.089175,
      0.0760246, 0.0874422, 0.0627384, -0.0346583,
      -0.0692825, 0.0851396, -0.0759865, -0.0253768,
      -0.0417439, -0.0104898} → SpikePositive_11,
    {-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092,
      -0.0125386, 0.0806961, 0.0851796, 0.0301143,
      0.0890635, 0.0316055, 0.0537416, 0.0121501,
      -0.0133593, 0.0282534, -0.0513092, 0.0000356639,
      -0.0380747, -0.0718867} → SpikePositive_19,
    {-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683,
      -0.0113637, -0.0208056, -0.0484049, 0.0489594,
      0.0405395, 0.0157363, 0.0839891, 0.030142,
      -0.00990756, -0.014496, 0.0276552, 0.0544291,
      0.000460091, -0.0478291} → SpikePositive_14,
    {0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518,
      -0.00286655, 0.0877564, -0.011351, -0.0285781,
      -0.0462785, 0.00976108, -0.0719133, -0.00792171,
      0.0160836, -0.00852838, 0.0513166, 0.017598,
      -0.0319166, -0.0108659} → SpikePositive_15,
    {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917,
      -0.041052, 0.00572256, -0.0446275, -0.0153523,
      -0.0359252, -0.0182243, -0.0433528, 0.00777195,
      -0.0217935, -0.0107251, 0.0930318, -0.0216511,
      -0.00863921, 0.0518108} → SpikePositive_18,
    {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689,
      -0.0432748, 0.0435724, -0.00529511, 0.0323596,
      -0.0106461, -0.0842782, -0.0779019, 0.0728601,
      -0.0844032, -0.0178169, -0.0794273, -0.0571066,
      -0.0427862, 0.0441496} → SpikePositive_20,
    {0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891,
      -0.0575291, 0.0909876, -0.0209567, -0.0783119,
      0.0662179, -0.0139992, -0.0922154, 0.10018,
      -0.0673391, -0.0182609, -0.015489, -0.0206308,
      0.0352321, -0.104815} → SpikePositive_17,
    {0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409,
      -0.00693186, -0.0482937, 0.0280248, -0.0959175,
      -0.0672972, 0.00106747, -0.0451342, -0.0567082,
      -0.0918568, 0.0302632, -0.0902741, 0.0774122,
      0.0136075, 0.0648783} → SpikePositive_16,
    {0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248,
      -0.0347325, 0.0577136, 0.0329049, 0.0911482, -0.025702,
      -0.0498375, -0.041878, -0.00608792, 0.00651104, 0.0144384,
      0.0395091, -0.074232, -0.0166065} → SpikePositive_6,
    {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824,
      -0.0808607, -0.0618148, -0.00363485, -0.0607952,
      -0.0266488, -0.0885909, -0.0604068, 0.0564238,
      0.027816, -0.0300755, -0.00964389, 0.0219551,
      0.0830947, 0.100236} → SpikePositive_7},
  GroupAssociations → <|G1S1 → {SpikePositive_1, SpikePositive_10, SpikePositive_3,
      SpikePositive_8, SpikePositive_9, SpikePositive_2,
      SpikePositive_5, SpikePositive_4},
    G1S2 → {SpikePositive_12, SpikePositive_13, SpikePositive_11, SpikePositive_19,
      SpikePositive_14, SpikePositive_15, SpikePositive_18,
      SpikePositive_20, SpikePositive_17},
    G2S1 → {SpikePositive_16}, G2S2 → {SpikePositive_6, SpikePositive_7}|>|>|>
```

Let' s now label the class manually "First Class":

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In[4]:=
```
clusters1ClassLabel =
 TimeSeriesClusters[classification1["SpikeMax"], SingleAssociationLabel → "First Class"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Out[4]=
```
<|First Class → <|Cluster →
    Cluster[Cluster[Cluster[Cluster[Cluster[Cluster[{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564,
            -0.0362021, -0.0625238, 0.0341425, -0.0893761, -0.0883628, -0.017962, -0.0386128, -0.0180346,
            0.00287015, -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174} →
           SpikePositive_1, {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915, -0.0700719,
            0.0187234, 0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485, 0.0886753, -0.0765068,
            -0.0746426, 0.0807971, -0.0126166, -0.0042573, 0.0843061} → SpikePositive_10, 0.253714, 1, 1],
          {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789, 0.0161993, 0.0873614,
           0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181, -0.0275224, 0.0821854, -0.0656115,
           0.0495169, -0.0958318, -0.0295775, 0.0577959} → SpikePositive_3, 0.30679, 2, 1], Cluster[
          Cluster[Cluster[Cluster[{0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267,
               0.0130259, 0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081, 0.0633006,
               -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478} → SpikePositive_2,
             Cluster[{0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518, -0.00286655,
                0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133, -0.00792171,
                0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659} → SpikePositive_15,
              {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917, -0.041052,
                0.00572256, -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528,
                0.00777195, -0.0217935, -0.0107251, 0.0930318, -0.0216511, -0.00863921,
                0.0518108} → SpikePositive_18, 0.143365, 1, 1], 0.196995, 1, 2],
           {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281, 0.0476815,
             0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776, -0.0145575, -0.0471635,
             -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704} → SpikePositive_5, 0.247424, 3, 1],
          {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689, -0.0432748,
            0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019, 0.0728601, -0.0844032,
            -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496} → SpikePositive_20, 0.296637, 4, 1],
          {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642, -0.0491586,
           0.0387547, -0.0805303, -0.0750145, 0.0435078, 0.096307, -0.0207842, -0.074725,
           -0.0219338, -0.0702263, -0.0708028, 0.0629065, 0.0539273, -0.0472406} →
           SpikePositive_4, 0.341309, 5, 1], 0.383948, 3, 6],
         Cluster[Cluster[{-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092,
             -0.0125386, 0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416, 0.0121501,
             -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867} → SpikePositive_19,
           {-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972, -0.0821497, -0.0789604,
             -0.0537447, 0.089175, 0.0760246, 0.0874422, 0.0627384, -0.0346583, -0.0692825, 0.0851396,
             -0.0759865, -0.0253768, -0.0417439, -0.0104898} → SpikePositive_11, 0.272553, 1, 1],
          {-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127, -0.084559,
            -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588, 0.076484, 0.0945541,
            0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871} →
           SpikePositive_12, 0.334818, 2, 1], 0.459707, 9, 3],
        Cluster[Cluster[{0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891,
            -0.0575291, 0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992, -0.0922154, 0.10018,
            -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815} → SpikePositive_17,
          Cluster[{-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683, -0.0113637,
             -0.0208056, -0.0484049, 0.0489594, 0.0405395, 0.0157363, 0.0839891, 0.030142,
             -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291} → SpikePositive_14,
           {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485, -0.0941461,
             -0.0893966, -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524, 0.00305398,
             -0.0753412, 0.0791486, 0.0322394, 0.080124, -0.000969041, 0.0870857} →
           SpikePositive_13, 0.23158, 1, 1], 0.346333, 1, 2],
         Cluster[{0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254, 0.0377891,
            0.0330553, -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855, 0.0528972,
            0.0722006, -0.0375273, -0.00701134, -0.0825865, -0.0268527, -0.0449685} → SpikePositive_9,
          {0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585, -0.0327609,
            0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291, 0.0449639,
            0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327} →
           SpikePositive_8, 0.308944, 1, 1], 0.437803, 3, 2], 0.485945, 12, 5],
       Cluster[Cluster[{0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409,
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      0.00106747, -0.0451342, -0.0567082, -0.0918568, 0.0302632,
      -0.0902741, 0.0774122, 0.0136075, 0.0648783} → SpikePositive_16,
    {0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248, -0.0347325,
      0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375, -0.041878, -0.00608792,
      0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065} → SpikePositive_6, 0.39718, 1, 1],
   {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824, -0.0808607,
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     -0.0604068, 0.0564238, 0.027816, -0.0300755, -0.00964389,
     0.0219551, 0.0830947, 0.100236} → SpikePositive_7,
   0.465014, 2, 1], 0.502616, 17, 3], InitialSplitCluster →
 {Cluster[Cluster[Cluster[Cluster[Cluster[{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564,
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         0.00287015, -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174} →
        SpikePositive_1, {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915, -0.0700719,
         0.0187234, 0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485, 0.0886753, -0.0765068,
         -0.0746426, 0.0807971, -0.0126166, -0.0042573, 0.0843061} → SpikePositive_10, 0.253714, 1, 1],
      {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789, 0.0161993, 0.0873614,
        0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181, -0.0275224, 0.0821854, -0.0656115,
        0.0495169, -0.0958318, -0.0295775, 0.0577959} → SpikePositive_3, 0.30679, 2, 1], Cluster[
      Cluster[Cluster[Cluster[{0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267,
           0.0130259, 0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081, 0.0633006,
           -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478} → SpikePositive_2,
          Cluster[{0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518, -0.00286655,
             0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133, -0.00792171,
             0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659} → SpikePositive_15,
           {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917, -0.041052, 0.00572256,
             -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528, 0.00777195, -0.0217935,
             -0.0107251, 0.0930318, -0.0216511, -0.00863921, 0.0518108} → SpikePositive_18, 0.143365, 1,
          1], 0.196995, 1, 2], {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281,
          0.0476815, 0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776, -0.0145575,
          -0.0471635, -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704} → SpikePositive_5,
        0.247424, 3, 1], {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689, -0.0432748,
         0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019, 0.0728601, -0.0844032,
         -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496} → SpikePositive_20, 0.296637, 4, 1],
      {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642, -0.0491586,
        0.0387547, -0.0805303, -0.0750145, 0.0435078, 0.096307, -0.0207842, -0.074725,
        -0.0219338, -0.0702263, -0.0708028, 0.0629065, 0.0539273, -0.0472406} →
       SpikePositive_4, 0.341309, 5, 1], 0.383948, 3, 6],
    Cluster[Cluster[{-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092,
        -0.0125386, 0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416, 0.0121501,
        -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867} → SpikePositive_19,
      {-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972, -0.0821497, -0.0789604,
        -0.0537447, 0.089175, 0.0760246, 0.0874422, 0.0627384, -0.0346583, -0.0692825, 0.0851396,
        -0.0759865, -0.0253768, -0.0417439, -0.0104898} → SpikePositive_11, 0.272553, 1, 1],
     {-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127, -0.084559,
       -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588, 0.076484, 0.0945541,
       0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871} →
      SpikePositive_12, 0.334818, 2, 1], 0.459707, 9, 3],
   Cluster[Cluster[{0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891,
       -0.0575291, 0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992, -0.0922154, 0.10018,
       -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815} → SpikePositive_17,
     Cluster[{-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683, -0.0113637,
        -0.0208056, -0.0484049, 0.0489594, 0.0405395, 0.0157363, 0.0839891, 0.030142,
        -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291} → SpikePositive_14,
      {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485, -0.0941461,
        -0.0893966, -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524, 0.00305398,
        -0.0753412, 0.0791486, 0.0322394, 0.080124, -0.000969041, 0.0870857} →
       SpikePositive_13, 0.23158, 1, 1], 0.346333, 1, 2],
    Cluster[{0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254, 0.0377891,
       0.0330553, -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855, 0.0528972,
       0.0722006, -0.0375273, -0.00701134, -0.0825865, -0.0268527, -0.0449685} → SpikePositive_9,
     {0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585, -0.0327609,
       0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291, 0.0449639,
       0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327} →
      SpikePositive_8, 0.308944, 1, 1], 0.437803, 3, 2], 0.485945, 12, 5],
  Cluster[Cluster[{0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409,
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      -0.00693186, -0.0482937, 0.0280248, -0.0959175, -0.0672972,
      0.00106747, -0.0451342, -0.0567082, -0.0918568, 0.0302632,
      -0.0902741, 0.0774122, 0.0136075, 0.0648783} → SpikePositive_16,
    {0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248, -0.0347325,
      0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375, -0.041878, -0.00608792,
      0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065} → SpikePositive_6, 0.39718, 1, 1],
   {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824, -0.0808607,
     -0.0618148, -0.00363485, -0.0607952, -0.0266488,
     -0.0885909, -0.0604068, 0.0564238, 0.027816, -0.0300755,
     -0.00964389, 0.0219551, 0.0830947, 0.100236} →
    SpikePositive_7, 0.465014, 2, 1]}, IntermediateClusters →
 {Cluster[Cluster[Cluster[Cluster[Cluster[{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564,
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         0.00287015, -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174} →
        SpikePositive_1, {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915, -0.0700719,
         0.0187234, 0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485, 0.0886753, -0.0765068,
         -0.0746426, 0.0807971, -0.0126166, -0.0042573, 0.0843061} → SpikePositive_10, 0.279559, 1, 1],
      {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789, 0.0161993, 0.0873614,
        0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181, -0.0275224, 0.0821854, -0.0656115,
        0.0495169, -0.0958318, -0.0295775, 0.0577959} → SpikePositive_3, 0.311336, 2, 1],
     Cluster[Cluster[{0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585,
         -0.0327609, 0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291, 0.0449639,
         0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327} → SpikePositive_8,
       {0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254, 0.0377891, 0.0330553,
         -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855, 0.0528972, 0.0722006, -0.0375273,
         -0.00701134, -0.0825865, -0.0268527, -0.0449685} → SpikePositive_9, 0.257205, 1, 1],
      Cluster[{0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267, 0.0130259,
         0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081, 0.0633006,
         -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478} → SpikePositive_2,
       {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281, 0.0476815,
         0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776, -0.0145575,
         -0.0471635, -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704} →
        SpikePositive_5, 0.266939, 1, 1], 0.336576, 2, 2], 0.367384, 3, 4],
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      -0.074725, -0.0219338, -0.0702263, -0.0708028, 0.0629065,
      0.0539273, -0.0472406} → SpikePositive_4, 0.397145, 7, 1],
   Cluster[Cluster[Cluster[{-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127,
         -0.084559, -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588, 0.076484, 0.0945541,
         0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871} → SpikePositive_12,
       {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485, -0.0941461, -0.0893966,
         -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524, 0.00305398, -0.0753412, 0.0791486,
         0.0322394, 0.080124, -0.000969041, 0.0870857} → SpikePositive_13, 0.317245, 1, 1],
      Cluster[{-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972, -0.0821497,
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         -0.0692825, 0.0851396, -0.0759865, -0.0253768, -0.0417439, -0.0104898} → SpikePositive_11,
       {-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092, -0.0125386,
         0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416, 0.0121501,
         -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867} →
        SpikePositive_19, 0.266892, 1, 1], 0.343391, 2, 2],
     Cluster[Cluster[Cluster[{-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683,
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         -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291} → SpikePositive_14,
       Cluster[{0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518, -0.00286655,
         0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133, -0.00792171,
         0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659} → SpikePositive_15,
       {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917, -0.041052,
         0.00572256, -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528, 0.00777195,
         -0.0217935, -0.0107251, 0.0930318, -0.0216511, -0.00863921, 0.0518108} →
        SpikePositive_18, 0.180887, 1, 1], 0.263835, 1, 2],
      {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689, -0.0432748,
        0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019, 0.0728601, -0.0844032,
        -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496} → SpikePositive_20, 0.294117, 3, 1],
     {0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891, -0.0575291,
       0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992, -0.0922154, 0.10018,
       -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815} →
```

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```
      SpikePositive_17, 0.301453, 4, 1], 0.375883, 4, 5], 1.47437, 8, 9],
  Cluster[{0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409,
     -0.00693186, -0.0482937, 0.0280248, -0.0959175, -0.0672972,
     0.00106747, -0.0451342, -0.0567082, -0.0918568, 0.0302632,
     -0.0902741, 0.0774122, 0.0136075, 0.0648783} → SpikePositive_16,
   Cluster[{0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248,
      -0.0347325, 0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375, -0.041878,
      -0.00608792, 0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065} → SpikePositive_6,
    {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824, -0.0808607,
      -0.0618148, -0.00363485, -0.0607952, -0.0266488, -0.0885909, -0.0604068,
      0.0564238, 0.027816, -0.0300755, -0.00964389, 0.0219551, 0.0830947, 0.100236} →
     SpikePositive_7, 0.345377, 1, 1], 1.36759, 1, 2]}, SubsplitClusters →
 {{Cluster[Cluster[Cluster[Cluster[{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564, -0.0362021,
          -0.0625238, 0.0341425, -0.0893761, -0.0883628, -0.017962, -0.0386128, -0.0180346, 0.00287015,
          -0.0573882, -0.0958009, 0.0379076, -0.0595687, -0.0529437, -0.0344174} → SpikePositive_1,
        {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915, -0.0700719, 0.0187234,
          0.0104362, 0.0333953, -0.0952174, -0.0348545, -0.0558485, 0.0886753, -0.0765068, -0.0746426,
          0.0807971, -0.0126166, -0.0042573, 0.0843061} → SpikePositive_10, 0.279559, 1, 1],
       {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789, 0.0161993, 0.0873614,
         0.0491571, 0.029947, -0.0693437, -0.0142705, 0.0625181, -0.0275224, 0.0821854, -0.0656115,
         0.0495169, -0.0958318, -0.0295775, 0.0577959} → SpikePositive_3, 0.311336, 2, 1],
      Cluster[Cluster[{0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585,
          -0.0327609, 0.0166862, -0.0849577, 0.0591606, 0.0703419, -0.0412067, -0.0310291, 0.0449639,
          0.0836001, -0.00965143, 0.0289184, -0.0297474, -0.0171145, -0.0848327} → SpikePositive_8,
        {0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254, 0.0377891, 0.0330553,
          -0.0532373, 0.0399677, 0.0862428, -0.0244445, -0.0794855, 0.0528972, 0.0722006, -0.0375273,
          -0.00701134, -0.0825865, -0.0268527, -0.0449685} → SpikePositive_9, 0.257205, 1, 1],
       Cluster[{0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267, 0.0130259,
          0.0440809, 0.0904629, 0.0612212, -0.0519196, -0.0143748, -0.0280081, 0.0633006,
          -0.0866884, 0.00515577, -0.0372569, 0.0123246, 0.0728383, -0.0509478} → SpikePositive_2,
        {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281, 0.0476815,
          0.0628967, -0.0423604, -0.0773945, 0.0228186, -0.089195, 0.00937776, -0.0145575,
          -0.0471635, -0.0115995, -0.0685444, -0.065197, 0.0709702, -0.0372704} →
         SpikePositive_5, 0.266939, 1, 1], 0.336576, 2, 2], 0.367384, 3, 4],
     {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642, -0.0491586,
       0.0387547, -0.0805303, -0.0750145, 0.0435078, 0.096307, -0.0207842,
       -0.074725, -0.0219338, -0.0702263, -0.0708028, 0.0629065,
       0.0539273, -0.0472406} → SpikePositive_4, 0.397145, 7, 1],
    Cluster[Cluster[Cluster[{-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127,
          -0.084559, -0.0594589, 0.0148199, -0.0154587, -0.0374222, 0.0499588, 0.076484, 0.0945541,
          0.0610314, -0.034534, -0.0950852, 0.0403957, -0.0707856, 0.0799871} → SpikePositive_12,
       {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485, -0.0941461, -0.0893966,
          -0.0641157, 0.0498908, -0.0603746, 0.0473787, 0.0491524, 0.00305398, -0.0753412, 0.0791486,
          0.0322394, 0.080124, -0.000969041, 0.0870857} → SpikePositive_13, 0.317245, 1, 1],
      Cluster[{-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972, -0.0821497,
          -0.0789604, -0.0537447, 0.089175, 0.0760246, 0.0874422, 0.0627384, -0.0346583,
          -0.0692825, 0.0851396, -0.0759865, -0.0253768, -0.0417439, -0.0104898} → SpikePositive_11,
       {-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092, -0.0125386,
          0.0806961, 0.0851796, 0.0301143, 0.0890635, 0.0316055, 0.0537416, 0.0121501,
          -0.0133593, 0.0282534, -0.0513092, 0.0000356639, -0.0380747, -0.0718867} →
         SpikePositive_19, 0.266892, 1, 1], 0.343391, 2, 2],
     Cluster[Cluster[Cluster[{-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683,
          -0.0113637, -0.0208056, -0.0484049, 0.0489594, 0.0405395, 0.0157363, 0.0839891, 0.030142,
          -0.00990756, -0.014496, 0.0276552, 0.0544291, 0.000460091, -0.0478291} → SpikePositive_14,
        Cluster[{0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518, -0.00286655,
           0.0877564, -0.011351, -0.0285781, -0.0462785, 0.00976108, -0.0719133, -0.00792171,
           0.0160836, -0.00852838, 0.0513166, 0.017598, -0.0319166, -0.0108659} → SpikePositive_15,
         {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917, -0.041052,
           0.00572256, -0.0446275, -0.0153523, -0.0359252, -0.0182243, -0.0433528, 0.00777195,
           -0.0217935, -0.0107251, 0.0930318, -0.0216511, -0.00863921, 0.0518108} →
          SpikePositive_18, 0.180887, 1, 1], 0.263835, 1, 2],
       {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689, -0.0432748,
         0.0435724, -0.00529511, 0.0323596, -0.0106461, -0.0842782, -0.0779019, 0.0728601, -0.0844032,
         -0.0178169, -0.0794273, -0.0571066, -0.0427862, 0.0441496} → SpikePositive_20, 0.294117, 3, 1],
      {0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891, -0.0575291,
        0.0909876, -0.0209567, -0.0783119, 0.0662179, -0.0139992, -0.0922154, 0.10018,
```

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```
        -0.0673391, -0.0182609, -0.015489, -0.0206308, 0.0352321, -0.104815} →
       SpikePositive_17, 0.301453, 4, 1], 0.375883, 4, 5]},
    {{0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409, -0.00693186,
       -0.0482937, 0.0280248, -0.0959175, -0.0672972, 0.00106747,
       -0.0451342, -0.0567082, -0.0918568, 0.0302632, -0.0902741,
       0.0774122, 0.0136075, 0.0648783} → SpikePositive_16,
     Cluster[{0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248,
        -0.0347325, 0.0577136, 0.0329049, 0.0911482, -0.025702, -0.0498375, -0.041878,
        -0.00608792, 0.00651104, 0.0144384, 0.0395091, -0.074232, -0.0166065} → SpikePositive_6,
      {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824, -0.0808607,
        -0.0618148, -0.00363485, -0.0607952, -0.0266488, -0.0885909,
        -0.0604068, 0.0564238, 0.027816, -0.0300755, -0.00964389, 0.0219551,
        0.0830947, 0.100236} → SpikePositive_7, 0.345377, 1, 1]}},
  Data → {{0.968723, 0.0906222, 0.0464438, 0.0701767, 0.0225564, -0.0362021,
      -0.0625238, 0.0341425, -0.0893761,
      -0.0883628, -0.017962, -0.0386128,
      -0.0180346, 0.00287015, -0.0573882,
      -0.0958009, 0.0379076, -0.0595687,
      -0.0529437, -0.0344174} → SpikePositive_1,
    {0.969094, 0.058612, 0.0186321, -0.0304909, -0.048085, -0.0290915,
      -0.0700719, 0.0187234, 0.0104362,
      0.0333953, -0.0952174, -0.0348545,
      -0.0558485, 0.0886753, -0.0765068,
      -0.0746426, 0.0807971, -0.0126166,
      -0.0042573, 0.0843061} → SpikePositive_10,
    {0.960717, 0.0870398, 0.067759, -0.0201718, -0.0936406, -0.088789,
      0.0161993, 0.0873614, 0.0491571,
      0.029947, -0.0693437, -0.0142705,
      0.0625181, -0.0275224, 0.0821854,
      -0.0656115, 0.0495169, -0.0958318,
      -0.0295775, 0.0577959} → SpikePositive_3,
    {0.970133, -0.0846736, -0.0852507, -0.0488249, 0.0534284, -0.0342585,
      -0.0327609, 0.0166862, -0.0849577,
      0.0591606, 0.0703419, -0.0412067,
      -0.0310291, 0.0449639, 0.0836001,
      -0.00965143, 0.0289184, -0.0297474,
      -0.0171145, -0.0848327} → SpikePositive_8,
    {0.965591, 0.0581314, -0.0754176, -0.0800919, -0.0594074, 0.0910254,
      0.0377891, 0.0330553, -0.0532373,
      0.0399677, 0.0862428, -0.0244445,
      -0.0794855, 0.0528972, 0.0722006,
      -0.0375273, -0.00701134, -0.0825865,
      -0.0268527, -0.0449685} → SpikePositive_9,
    {0.974172, 0.0631225, -0.0430008, 0.000656502, 0.0789821, 0.0140267,
      0.0130259, 0.0440809, 0.0904629,
      0.0612212, -0.0519196, -0.0143748,
      -0.0280081, 0.0633006, -0.0866884,
      0.00515577, -0.0372569, 0.0123246,
      0.0728383, -0.0509478} → SpikePositive_2,
    {0.971235, 0.0628484, -0.00243237, -0.0443457, 0.0869513, 0.0519281,
      0.0476815, 0.0628967, -0.0423604, -0.0773945,
      0.0228186, -0.089195, 0.00937776, -0.0145575,
      -0.0471635, -0.0115995, -0.0685444, -0.065197,
      0.0709702, -0.0372704} → SpikePositive_5,
    {0.95634, -0.0656924, -0.0922242, -0.0770307, -0.0581915, -0.102642,
      -0.0491586, 0.0387547, -0.0805303, -0.0750145,
      0.0435078, 0.096307, -0.0207842, -0.074725,
      -0.0219338, -0.0702263, -0.0708028, 0.0629065,
      0.0539273, -0.0472406} → SpikePositive_4,
    {-0.0746051, 0.0230233, 0.965559, 0.0474979, 0.0463951, -0.0190127,
      -0.084559, -0.0594589, 0.0148199, -0.0154587,
      -0.0374222, 0.0499588, 0.076484, 0.0945541,
      0.0610314, -0.034534, -0.0950852, 0.0403957,
      -0.0707856, 0.0799871} → SpikePositive_12,
    {-0.090295, 0.0595713, 0.958802, -0.0637345, 0.00443784, 0.078485,
      -0.0941461, -0.0893966, -0.0641157, 0.0498908,
```

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```
    -0.0603746, 0.0473787, 0.0491524, 0.00305398,
    -0.0753412, 0.0791486, 0.0322394, 0.080124,
    -0.000969041, 0.0870857} → SpikePositive_13,
  {-0.0324948, -0.0468436, 0.957897, 0.0793537, 0.0613591, 0.0800972,
    -0.0821497, -0.0789604, -0.0537447, 0.089175,
    0.0760246, 0.0874422, 0.0627384, -0.0346583,
    -0.0692825, 0.0851396, -0.0759865, -0.0253768,
    -0.0417439, -0.0104898} → SpikePositive_11,
  {-0.0449079, -0.0330641, 0.97144, 0.0893512, 0.0689202, 0.0586092,
    -0.0125386, 0.0806961, 0.0851796, 0.0301143,
    0.0890635, 0.0316055, 0.0537416, 0.0121501,
    -0.0133593, 0.0282534, -0.0513092, 0.0000356639,
    -0.0380747, -0.0718867} → SpikePositive_19,
  {-0.0743135, -0.0295621, 0.979722, -0.0858647, -0.0685473, 0.0140683,
    -0.0113637, -0.0208056, -0.0484049, 0.0489594,
    0.0405395, 0.0157363, 0.0839891, 0.030142,
    -0.00990756, -0.014496, 0.0276552, 0.0544291,
    0.000460091, -0.0478291} → SpikePositive_14,
  {0.0115855, -0.0155871, 0.988274, 0.0137939, -0.0409004, -0.0231518,
    -0.00286655, 0.0877564, -0.011351, -0.0285781,
    -0.0462785, 0.00976108, -0.0719133, -0.00792171,
    0.0160836, -0.00852838, 0.0513166, 0.017598,
    -0.0319166, -0.0108659} → SpikePositive_15,
  {-0.0628209, -0.0167343, 0.986741, -0.0346973, 0.0238976, -0.0189917,
    -0.041052, 0.00572256, -0.0446275, -0.0153523,
    -0.0359252, -0.0182243, -0.0433528, 0.00777195,
    -0.0217935, -0.0107251, 0.0930318, -0.0216511,
    -0.00863921, 0.0518108} → SpikePositive_18,
  {-0.0790547, 0.0264771, 0.970316, -0.0620374, 0.0228402, 0.0541689,
    -0.0432748, 0.0435724, -0.00529511, 0.0323596,
    -0.0106461, -0.0842782, -0.0779019, 0.0728601,
    -0.0844032, -0.0178169, -0.0794273, -0.0571066,
    -0.0427862, 0.0441496} → SpikePositive_20,
  {0.00309429, -0.0570545, 0.959414, -0.0664378, -0.104173, 0.0441891,
    -0.0575291, 0.0909876, -0.0209567, -0.0783119,
    0.0662179, -0.0139992, -0.0922154, 0.10018,
    -0.0673391, -0.0182609, -0.015489, -0.0206308,
    0.0352321, -0.104815} → SpikePositive_17,
  {0.0629221, -0.00448095, 0.969598, -0.0506604, -0.0181881, 0.0544409,
    -0.00693186, -0.0482937, 0.0280248, -0.0959175,
    -0.0672972, 0.00106747, -0.0451342, -0.0567082,
    -0.0918568, 0.0302632, -0.0902741, 0.0774122,
    0.0136075, 0.0648783} → SpikePositive_16,
  {0.9816, 0.0108234, 0.0767583, 0.0349453, 0.0407398, 0.0300977, -0.0143248,
    -0.0347325, 0.0577136, 0.0329049, 0.0911482, -0.025702,
    -0.0498375, -0.041878, -0.00608792, 0.00651104, 0.0144384,
    0.0395091, -0.074232, -0.0166065} → SpikePositive_6,
  {0.969692, 0.00172754, -0.0899323, 0.0238704, -0.0215331, 0.0436824,
    -0.0808607, -0.0618148, -0.00363485, -0.0607952,
    -0.0266488, -0.0885909, -0.0604068, 0.0564238,
    0.027816, -0.0300755, -0.00964389, 0.0219551,
    0.0830947, 0.100236} → SpikePositive_7},
 GroupAssociations → <|G1S1 → {SpikePositive_1, SpikePositive_10, SpikePositive_3,
    SpikePositive_8, SpikePositive_9, SpikePositive_2,
    SpikePositive_5, SpikePositive_4},
  G1S2 → {SpikePositive_12, SpikePositive_13, SpikePositive_11, SpikePositive_19,
    SpikePositive_14, SpikePositive_15, SpikePositive_18,
    SpikePositive_20, SpikePositive_17},
  G2S1 → {SpikePositive_16}, G2S2 → {SpikePositive_6, SpikePositive_7}|>|>|>
```

SubclusteringDistanceFunction (1)

```
In[1]:= Needs["MathIOmica`"]
```

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SubclusteringDistanceFunction provides options for which DistanceFunction to use in the second tier clustering.

We generate some data for classification:

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
  Method → "LombScargle"
```

```
Out[2]= <|SpikeMax →
  <|SpikePositive_1 → {{0.144615, 0.148834, 0.436331, 0.348072, 0.159558, 0.256034, 0.199615, 0.199822,
      0.655562, 0.211774}, {0.970422, -0.0735747, -0.0655453, -0.0664433, 0.0417747, 0.0851783,
      0.0637713, 0.0342963, -0.00204655, -0.0098324, -0.0637451, -0.0711425, 0.0555982,
      0.0270098, -0.0390253, -0.0363671, -0.0389975, 0.0753687, -0.0825126, -0.00347466}},
   SpikePositive_2 → {{0.243515, 0.366919, 0.12755, 0.354599, 0.413141, 0.372216, 0.295704,
      0.1986, 0.422163, 0.222996}, {0.970429, 0.0804276, -0.0585675, 0.0712531, 0.0344595,
      -0.0746337, -0.0663089, 0.0715285, -0.0196533, 0.0475299, 0.0775715, -0.0596753, -0.0757236,
      0.0405674, -0.04979, 0.0407037, -0.0302229, 0.0153008, -0.0413441, -0.0206038}},
   SpikePositive_3 → {{0.288754, 0.221848, 0.144511, 0.283358, 0.431436, 0.291015, 0.271727,
      0.365578, 0.405201, 0.351755}, {0.977081, -0.0557218, -0.0456077, 0.0362593, -0.0128064,
      -0.0786343, -0.060874, 0.0301628, -0.0809874, -0.0199416, 0.0267823, -0.0514164, -0.0775337,
      -0.0182328, 0.0708994, -0.00871815, 0.0249214, -0.0596215, 0.0405216, 0.0163927}},
   SpikePositive_4 → {{0.132799, 0.154804, 0.40161, 0.223966, 0.149963, 0.296162, 0.271265,
      0.289659, 0.61931, 0.309379}, {0.968045, -0.0683278, -0.0278518, -0.0817662, -0.00420195,
      0.0822923, 0.0812262, -0.0104645, -0.0731708, 0.0355394, 0.0687445, 0.0856664, 0.0587956,
      0.0485415, -0.0304311, 0.0637853, 0.0532035, -0.00200665, -0.0366742, 0.0599366}},
   SpikePositive_5 → {{0.191562, 0.145145, 0.278537, 0.13902, 0.284285, 0.0864179, 0.192501,
      0.221403, 0.78249, 0.242227}, {0.964864, -0.0472372, 0.0320092, -0.00999021, 0.0970848,
      0.0370803, 0.0754565, 0.0746595, 0.0794876, -0.068603, -0.0387872, 0.0771029, -0.0177038,
      0.0223098, 0.0299276, -0.00653083, 0.0604525, 0.0715457, -0.0903473, 0.0803376}},
   SpikePositive_6 → {{0.276247, 0.235249, 0.300659, 0.276788, 0.299097, 0.293635, 0.451219,
      0.220267, 0.459443, 0.249907}, {0.977623, 0.0315075, 0.036761, 0.0743254, -0.000971811,
      -0.00148807, 0.0672843, -0.0129459, 0.0148489, -0.0435127, 0.0555567, -0.00898134, -0.0356825,
      0.085246, -0.0335788, -0.0171979, -0.00202351, 0.0624792, 0.0956234, -0.0582267}},
   SpikePositive_7 → {{0.158397, 0.333537, 0.301958, 0.174964, 0.196956, 0.274775, 0.356601,
      0.206379, 0.646629, 0.199232}, {0.968053, -0.0464892, 0.0081868, -0.0616556, -0.0837488,
      -0.068481, 0.0796194, -0.0754104, 0.0621339, -0.05669, 0.0491884, -0.00376478, 0.00930636,
      -0.0510119, -0.0280344, -0.0780825, 0.0414142, -0.088472, 0.0569887, 0.0352757}},
   SpikePositive_8 → {{0.286983, 0.204534, 0.317945, 0.261705, 0.276163, 0.25639, 0.240122,
      0.23961, 0.625644, 0.240258}, {0.975466, -0.0797, -0.0440971, -0.0494505, 0.0403948,
      -0.0614588, -0.00931286, -0.0604638, -0.0098713, -0.0534427, 0.0348614, 0.0109275,
      0.0818322, 0.00836638, 0.0240255, -0.00906418, 0.081572, 0.0686542, 0.0721837, -0.0167442}},
   SpikePositive_9 → {{0.329382, 0.224933, 0.19614, 0.215528, 0.343373, 0.26128, 0.308419,
      0.240606, 0.586157, 0.2706}, {0.976164, 0.0138193, 0.0837247, 0.0833099, 0.054338,
      0.0834998, 0.0435701, 0.0315396, 0.00773621, -0.00271817, 0.0276694, 0.0358482, -0.0704544,
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    -0.0447664, -0.0120772, 0.0543538, -0.0272016, 0.0845577, -0.00803157, -0.00179005}},
  SpikePositive_10 → {{0.245254, 0.147056, 0.358989, 0.237083, 0.223615, 0.339636, 0.208496,
    0.405592, 0.426472, 0.421822}, {0.979597, 0.0480624, 0.00874524, 0.00304262, 0.0276474,
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    0.0767803, -0.0144918, -0.0545586, 0.0118524, -0.0456597, 0.00331983, -0.0645432}},
  SpikePositive_11 → {{0.344964, 0.266929, 0.265361, 0.393098, 0.311618, 0.268292, 0.377265,
    0.272651, 0.362971, 0.259431}, {0.0190911, -0.0492274, 0.969874, 0.0499799, -0.0514991,
    -0.0557935, -0.0709171, -0.0366858, -0.0483137, -0.0581772, -0.082646, -0.0719475, 0.0909412,
    -0.0471911, -0.0286782, 0.00399716, 0.0873375, 0.00124518, 0.056074, -0.0456454}},
  SpikePositive_12 → {{0.14049, 0.20762, 0.218399, 0.354469, 0.468962, 0.369759, 0.359462,
    0.197341, 0.453313, 0.18307}, {-0.0423063, -0.055184, 0.968399, -0.0703284, -0.0396992,
    -0.0367487, 0.0648889, 0.0335625, -0.00673091, 0.0643687, 0.0415374, -0.0142531,
    0.0857889, -0.0815228, 0.0658988, -0.082463, 0.053615, 0.0809943, 0.0230695, 0.0541002}},
  SpikePositive_13 → {{0.11558, 0.34008, 0.36951, 0.179716, 0.44151, 0.36676, 0.285216,
    0.259656, 0.393113, 0.263439}, {0.0529517, 0.0592728, 0.968625, -0.0745921, -0.0643405,
    -0.0406406, 0.0540073, -0.0367613, -0.0130245, 0.0673241, -0.0253135, -0.0151215, 0.0812497,
    0.0477941, 0.0827504, -0.0858638, -0.0905214, 0.00861794, -0.0313945, -0.0435028}},
  SpikePositive_14 → {{0.395155, 0.316181, 0.150433, 0.265443, 0.394431, 0.417718, 0.227009,
    0.307043, 0.270159, 0.319271}, {0.0327977, 0.0321278, 0.976814, 0.0518584, -0.0138044,
    0.0934145, 0.0641857, -0.0234311, 0.01214, 0.030805, -0.0739341, 0.0516805, 0.0173853,
    0.00157357, -0.0859065, -0.0564082, -0.0184955, 0.063588, 0.054153, 0.00578928}},
  SpikePositive_15 → {{0.236913, 0.476594, 0.438642, 0.359806, 0.135863, 0.474067, 0.131147,
    0.178825, 0.272453, 0.168098}, {0.0586526, 0.0180947, 0.960686, 0.0895074, -0.0935715,
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    -0.0512704, 0.0696458, -0.0744498, -0.0484442, -0.058975, 0.0113389, 0.0779824}},
  SpikePositive_16 → {{0.270423, 0.31263, 0.265838, 0.385703, 0.486703, 0.301657, 0.243715,
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  SpikePositive_17 → {{0.182518, 0.167081, 0.33953, 0.215565, 0.544351, 0.318734, 0.262037,
    0.330208, 0.310856, 0.323698}, {-0.0544642, 0.0555371, 0.973814, -0.0762904, 0.0537609,
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    0.0661842, 0.0579094, 0.0244838, 0.0779764, -0.00996633, 0.00338773, -0.0285433}},
  SpikePositive_18 → {{0.563714, 0.310338, 0.293323, 0.411955, 0.282199, 0.283785, 0.255449,
    0.188983, 0.188713, 0.182809}, {0.0196694, 0.0432719, 0.967071, 0.0628073, -0.0688286,
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    -0.0743345, -0.070277, -0.0624285, 0.0102277, -0.0485732, -0.0238681, 0.0603957}},
  SpikePositive_19 → {{0.250165, 0.121607, 0.200181, 0.296961, 0.621995, 0.310221, 0.334185,
    0.237882, 0.289476, 0.243296}, {0.0356642, -0.0508775, 0.966793, 0.0415759, -0.0563523,
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  SpikePositive_20 → {{0.147424, 0.303107, 0.262149, 0.306429, 0.277719, 0.364156, 0.360758,
    0.285139, 0.459772, 0.301981}, {-0.0241633, -0.0487696, 0.978096, -0.0757666, 0.0449929,
    0.0391757, 0.0607199, 0.0572794, 0.00911997, -0.00526352, 0.0362069, 0.0569137, 0.0520019,
    0.0458011, 0.0409836, -0.0134161, -0.0673685, -0.0178755, -0.00157783, 0.0889721}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.281728, 0.11093, 0.11207, 0.181589, 0.242421, 0.287738,
    0.305076, 0.431108, 0.510517, 0.426234}, {-0.971933, 0.0556697, -0.0987922, -0.0698563,
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    -0.0457935, -0.0585354, -0.0680316, -0.0659124, -0.0322468, -0.00540586, 0.0555782, 0.0111247}},
  SpikeNegative_2 → {{0.132557, 0.122194, 0.248292, 0.457361, 0.234395, 0.184905, 0.111106,
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    0.0148175, -0.0338354, -0.0478327, 0.105454, -0.0494708, -0.0128437, 0.101493, 0.02757,
    -0.0783237, -0.0817058, 0.0621952, 0.0233706, -0.0628643, 0.0946252, 0.0671792}},
  SpikeNegative_3 → {{0.255134, 0.321634, 0.255469, 0.2119, 0.186103, 0.134587, 0.486557,
    0.210655, 0.575097, 0.238105}, {-0.965621, 0.0624236, -0.0914061, 0.0756922, 0.0895914,
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    -0.0741741, 0.0767565, -0.0154179, 0.0337195, -0.0298146, -0.0530662, -0.0468969}},
  SpikeNegative_4 → {{0.34448, 0.138184, 0.319868, 0.183661, 0.155841, 0.341322, 0.314833,
    0.281497, 0.576489, 0.273322}, {-0.966106, 0.0793487, -0.070697, -0.0168473, 0.0897415,
    0.0624663, -0.0475517, 0.0616311, 0.0317616, 0.0688425, 0.0505448, 0.0589167, -0.0808691,
    -0.0755496, -0.0554441, 0.0409952, -0.0573281, 0.00792862, -0.0685177, -0.0150205}},
  SpikeNegative_5 → {{0.0698036, 0.170841, 0.216406, 0.319182, 0.276109, 0.443572, 0.285108,
    0.271549, 0.555992, 0.282997}, {-0.96861, 0.0946093, 0.0250897, -0.0910517, 0.0192341,
    0.0134933, -0.0983797, 0.0623501, -0.00180692, -0.0796644, -0.0179412, -0.0526825,
    0.00135385, -0.0280059, -0.0285819, 0.080317, 0.0852038, 0.058804, 0.0392828, -0.00668206}},
  SpikeNegative_6 → {{0.482583, 0.236735, 0.317288, 0.299518, 0.397471, 0.307846, 0.164412,
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    0.285846, 0.32184, 0.235829}, {-0.955497, -0.0642821, 0.0419833, -0.0584553, 0.0772166,
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  SpikeNegative_7 → {{0.17195, 0.241966, 0.267022, 0.242393, 0.249859, 0.384702, 0.247921,
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  SpikeNegative_8 → {{0.139943, 0.212404, 0.57577, 0.305013, 0.219034, 0.218799, 0.298742,
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    -0.0882777, -0.0182276, 0.0578314, 0.047185, -0.000356488, 0.0973321, 0.0385073}},
  SpikeNegative_9 → {{0.135024, 0.341348, 0.16624, 0.404718, 0.389386, 0.201285, 0.147713,
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    0.0472334, 0.0329771, -0.060648, 0.0549063, 0.0822287, 0.0616188, 0.0401763, 0.0160265}},
  SpikeNegative_10 → {{0.18377, 0.282261, 0.260593, 0.433634, 0.149627, 0.300979, 0.189815,
    0.153822, 0.658191, 0.157249}, {-0.968045, 0.0575452, 0.0571158, 0.00369621, -0.0670718,
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    -0.00373157, 0.0660977, 0.0736771, 0.0542484, 0.0219993, -0.0554113, 0.0561661, -0.0644754}},
  SpikeNegative_11 → {{0.136972, 0.135662, 0.363925, 0.417201, 0.238029, 0.517645, 0.313807,
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    0.0466529, -0.0677002, -0.0710557, 0.0805384, -0.0832956, 0.0120152, 0.0674414}},
  SpikeNegative_12 → {{0.350379, 0.167816, 0.167026, 0.359159, 0.257184, 0.23662, 0.315274,
    0.36579, 0.448311, 0.368598}, {-0.0942925, 0.0308821, -0.967703, 0.0107139, -0.0314423,
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    0.0378048, 0.0362361, 0.0784679, -0.0198859, -0.0374415, 0.0283586, 0.0688181}},
  SpikeNegative_13 → {{0.158959, 0.206899, 0.358362, 0.485749, 0.227676, 0.507837, 0.310852,
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    0.028517, -0.0844557, -0.0816957, -0.0782261, 0.0131776, 0.0443777, 0.087283}},
  SpikeNegative_14 → {{0.205617, 0.298503, 0.239495, 0.46377, 0.316413, 0.244322, 0.26793,
    0.383284, 0.272338, 0.37882}, {-0.0164899, -0.0413022, -0.966003, 0.0599564, 0.0606842,
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    -0.0674976, 0.0575464, -0.0181283, -0.0350598, 0.0885906, -0.080689, -0.0313636}},
  SpikeNegative_15 → {{0.297805, 0.382889, 0.353067, 0.21813, 0.194903, 0.257886, 0.353772,
    0.250879, 0.468633, 0.283314}, {-0.0715669, 0.0817891, -0.969109, -0.0769127, -0.00497048,
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    0.0166835, 0.0536462, -0.074798, 0.0665309, -0.000882054, 0.00761529, -0.0839123}},
  SpikeNegative_16 → {{0.375441, 0.18512, 0.492767, 0.268183, 0.453262, 0.19978, 0.207638,
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  SpikeNegative_17 → {{0.177623, 0.171823, 0.391628, 0.29978, 0.482937, 0.427297, 0.275226,
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    -0.0539161, -0.0425768, 0.0686588, -0.013985, 0.0323945, 0.0871975, -0.0634635}},
  SpikeNegative_18 → {{0.378613, 0.245761, 0.414781, 0.229205, 0.236583, 0.180674, 0.304886,
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    -0.052798, 0.0390944, -0.0525143, 0.043583, 0.059716, -0.0740684, -0.0782111}},
  SpikeNegative_19 → {{0.348995, 0.506975, 0.375197, 0.141836, 0.212114, 0.136901, 0.385909,
    0.263301, 0.330923, 0.26228}, {-0.0618385, -0.0861214, -0.965656, -0.0201566, -0.056958,
    0.0245305, 0.060251, -0.0139389, 0.000665833, 0.0455093, 0.0203133, 0.0770208, -0.0789714,
    -0.0779588, 0.0600751, 0.0699615, 0.071614, 0.0822079, -0.0840414, -0.00260905}},
  SpikeNegative_20 → {{0.16614, 0.411343, 0.341039, 0.201789, 0.282643, 0.480774, 0.241974,
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  LinearPositive_3 → {{0.98426, 0.166348, 0.032667, 0.00238041, 0.0010704, 0.0105049, 0.0205305,
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  LinearPositive_7 → {{0.983687, 0.168795, 0.0333231, 0.00215856, 0.00153955, 0.0107881,
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  LinearPositive_8 → {{0.984328, 0.164565, 0.0333315, 0.00229822, 0.00199714, 0.0094641,
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  LinearPositive_11 → {{0.977376, 0.19853, 0.0491875, 0.0045826, 0.00133036,
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  LinearPositive_16 → {{0.981646, 0.176421, 0.0347439, 0.000201696, 0.000336153, 0.0157058,
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    0.227472, 0.233052, 0.255867, 0.286242, 0.3064, 0.315156, 0.340124, 0.345428, 0.37895}},
  LinearPositive_17 → {{0.982656, 0.174127, 0.037975, 0.00498397, 0.00373056, 0.012435,
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 LinearNegative_9 → {{0.983478, 0.163617, 0.0403193, 0.00722952, 0.00483876, 0.0170887,
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 LinearNegative_14 → {{0.987709, 0.148103, 0.0250703, 0.00267189, 0.00131148, 0.00741494,
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 LinearNegative_15 → {{0.987255, 0.147688, 0.0225272, 0.000780124, 0.00375578, 0.0164712,
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    -0.0906349, -0.11834, -0.128098, -0.156187, -0.170651, -0.196999, -0.201734, -0.232675,
    -0.250359, -0.260866, -0.273763, -0.300276, -0.310908, -0.330615, -0.349074, -0.376313}}|>,
f3 → <|Sinusoidal3_21 → {{0.00348406, 0.0739755, 0.992098, 0.088399, 0.0405084, 0.0180789,
    0.00963459, 0.0020861, 0.0194379, 0.000646693}, {0.182428, -0.0953068, -0.30408, -0.257315,
    0.00531758, 0.257802, 0.304013, 0.0964508, -0.179533, -0.317935, -0.188441, 0.101817,
    0.296928, 0.254262, 0.00182159, -0.250322, -0.302061, -0.10164, 0.19094, 0.313118}},
  Sinusoidal3_22 → {{0.00349479, 0.0698161, 0.992537, 0.0876334, 0.037979, 0.0177557, 0.00867661,
    0.00303093, 0.0214689, 0.0011105}, {0.191489, -0.0930294, -0.303799, -0.252356,
    -0.00154217, 0.258419, 0.301296, 0.102401, -0.182849, -0.318799, -0.181257, 0.0980577,
    0.296358, 0.252496, 0.00161792, -0.255131, -0.30594, -0.0921644, 0.180624, 0.318938}},
  Sinusoidal3_23 → {{0.00226736, 0.0726824, 0.992774, 0.0836203, 0.0356374, 0.0198709, 0.00914492,
    0.00266023, 0.0190551, 0.000960664}, {0.183016, -0.0961067, -0.306698, -0.255507,
    -0.00476977, 0.249925, 0.304695, 0.103791, -0.188618, -0.317013, -0.190944, 0.0967325,
    0.298611, 0.261801, 0.00536533, -0.251035, -0.295848, -0.0947483, 0.18651, 0.312869}},
  Sinusoidal3_24 → {{0.00361686, 0.0720539, 0.992571, 0.0857151, 0.0372306, 0.0186589,
    0.00954335, 0.00264029, 0.0204294, 0.000915097}, {0.183726, -0.100996, -0.302789, -0.25919,
    0.000554727, 0.25659, 0.299711, 0.0977511, -0.180615, -0.310886, -0.186154, 0.103101,
    0.302304, 0.257964, -0.00307713, -0.256818, -0.296998, -0.102041, 0.185231, 0.317143}},
  Sinusoidal3_25 → {{0.00298628, 0.0708276, 0.992888, 0.0831155, 0.0374705, 0.0181941,
    0.00909891, 0.00300946, 0.0203066, 0.00111814}, {0.18747, -0.101465, -0.301168, -0.255802,
    -0.00353661, 0.255216, 0.294332, 0.101603, -0.185359, -0.319954, -0.184438, 0.101384,
    0.299822, 0.256922, -0.00465897, -0.257922, -0.299813, -0.0982537, 0.186242, 0.31404}},
  Sinusoidal3_26 → {{0.00308809, 0.0695263, 0.992778, 0.0848772, 0.0389223, 0.0175434,
    0.00923063, 0.00231768, 0.0207694, 0.000726796}, {0.185488, -0.100532, -0.305361, -0.259078,
    0.00437922, 0.253784, 0.303334, 0.0928507, -0.179332, -0.316426, -0.189574, 0.102403,
    0.302654, 0.248447, -0.00139301, -0.257252, -0.297544, -0.0930181, 0.18886, 0.314633}},
  Sinusoidal3_27 → {{0.00273096, 0.0716837, 0.992775, 0.0835285, 0.0379642, 0.0188358,
    0.00868128, 0.00295073, 0.019829, 0.0010897}, {0.189102, -0.0986975, -0.305727, -0.253118,
    0.00224235, 0.256425, 0.296809, 0.0954209, -0.19175, -0.322019, -0.180474, 0.103902,
    0.302533, 0.250677, -0.006291, -0.257818, -0.298649, -0.092583, 0.186462, 0.311072}},
  Sinusoidal3_28 → {{0.00369267, 0.0713636, 0.992217, 0.0895349, 0.0390959, 0.0181127,
    0.00729897, 0.00228793, 0.0216133, 0.000685047}, {0.184576, -0.101445, -0.303779, -0.25849,
    0.00608058, 0.259818, 0.301773, 0.0992137, -0.186656, -0.311512, -0.183013, 0.102479,
    0.298639, 0.249618, -0.0012091, -0.250206, -0.306676, -0.0926645, 0.189812, 0.315356}},
  Sinusoidal3_29 → {{0.00276284, 0.0737334, 0.992719, 0.0830381, 0.0367343, 0.018274,
    0.00938196, 0.00372311, 0.0195249, 0.0015442}, {0.184391, -0.103184, -0.297881, -0.253258,
    -0.00586943, 0.257348, 0.297896, 0.0953433, -0.189349, -0.320026, -0.1817, 0.103002,
    0.304495, 0.250745, 0.0000769192, -0.256957, -0.296289, -0.102227, 0.186825, 0.318956}},
  Sinusoidal3_30 → {{0.00245944, 0.0714393, 0.992811, 0.0845074, 0.0356447, 0.0181358,
    0.00911504, 0.00273193, 0.019626, 0.00097972}, {0.187437, -0.0919245, -0.297757, -0.256309,
    -0.000546424, 0.250386, 0.301477, 0.103971, -0.185115, -0.321835, -0.189726, 0.0944747,
    0.296156, 0.261855, 0.00621942, -0.259615, -0.297085, -0.0951749, 0.18734, 0.314286}}|>,
f5 → <|Sinusoidal2_11 → {{0.00295348, 0.0106836, 0.0304352, 0.0896413, 0.93168, 0.347726,
    0.0328737, 0.00393939, 0.029607, 0.00120706}, {-0.093156, -0.256342, 0.253634, 0.0983485,
    -0.310897, 0.0989366, 0.256168, -0.256319, -0.0928652, 0.309958, -0.0966248, -0.260665,
    0.252914, 0.103061, -0.321014, 0.0987735, 0.257299, -0.260254, -0.0940987, 0.318869}},
  Sinusoidal2_12 → {{0.00311964, 0.0114261, 0.0353552, 0.0923083, 0.931816, 0.346733,
```

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```
    0.0283847, 0.0041574, 0.0275527, 0.00136647}, {-0.102372, -0.252162, 0.257254, 0.103164,
    -0.311622, 0.0922612, 0.249513, -0.260045, -0.0945687, 0.318561, -0.0996568, -0.259711,
    0.250887, 0.0921879, -0.319594, 0.0997953, 0.254563, -0.259465, -0.0966806, 0.317479}},
  Sinusoidal2_13 → {{0.00273963, 0.0100987, 0.0312344, 0.0952018, 0.927552, 0.357377, 0.0300185,
    0.00585348, 0.028992, 0.00227692}, {-0.0931681, -0.260687, 0.252832, 0.100203,
    -0.317439, 0.0993915, 0.251292, -0.249147, -0.0972325, 0.317508, -0.0973263, -0.254203,
    0.255422, 0.0930929, -0.318177, 0.102845, 0.254292, -0.25972, -0.0941036, 0.320121}},
  Sinusoidal2_14 → {{0.00153127, 0.0098711, 0.0279727, 0.0939576, 0.930801, 0.349448, 0.0311316,
    0.00460991, 0.0281666, 0.00164853}, {-0.092037, -0.254346, 0.254603, 0.0972334,
    -0.321367, 0.094193, 0.256326, -0.258775, -0.10147, 0.313847, -0.102704, -0.25242,
    0.254852, 0.100358, -0.318735, 0.0993499, 0.261609, -0.252226, -0.0944845, 0.311795}},
  Sinusoidal2_15 → {{0.0031345, 0.0112649, 0.0298407, 0.0946793, 0.931819, 0.346626, 0.0273949,
    0.00450013, 0.0282833, 0.00153366}, {-0.0976855, -0.254065, 0.259942, 0.101379,
    -0.317442, 0.0989585, 0.260175, -0.253012, -0.0996297, 0.317348, -0.100828, -0.254395,
    0.256954, 0.0970711, -0.317904, 0.096766, 0.251431, -0.252577, -0.0967353, 0.313096}},
  Sinusoidal2_16 → {{0.00177805, 0.0113423, 0.0314475, 0.0915031, 0.93336, 0.343141, 0.0270628,
    0.00441597, 0.0290643, 0.00146657}, {-0.0959849, -0.254434, 0.256507, 0.0944677,
    -0.312722, 0.0949905, 0.255479, -0.259663, -0.101181, 0.31879, -0.099935, -0.256236,
    0.256045, 0.100163, -0.311677, 0.100336, 0.2582, -0.256999, -0.100215, 0.314244}},
  Sinusoidal2_17 → {{0.00198445, 0.0097092, 0.0324717, 0.094077, 0.935117, 0.337453, 0.0268074,
    0.0042905, 0.030651, 0.00134322}, {-0.0995762, -0.258904, 0.2571, 0.0944413,
    -0.320832, 0.0938204, 0.253708, -0.254625, -0.0959734, 0.321369, -0.0973478, -0.253274,
    0.253155, 0.097772, -0.314037, 0.0991062, 0.254495, -0.250719, -0.10139, 0.317785}},
  Sinusoidal2_18 → {{0.00266135, 0.0118581, 0.0297554, 0.0972027, 0.936494, 0.332938, 0.0239299,
    0.00387009, 0.0325894, 0.00107875}, {-0.102165, -0.260609, 0.261343, 0.0926763,
    -0.312244, 0.103006, 0.259248, -0.249364, -0.101384, 0.316013, -0.0991545, -0.251248,
    0.258408, 0.10087, -0.313479, 0.102676, 0.250848, -0.250463, -0.102907, 0.31961}},
  Sinusoidal2_19 → {{0.00243599, 0.0101856, 0.0320001, 0.0964692, 0.930778, 0.348702, 0.0287593,
    0.00603769, 0.0273916, 0.00240947}, {-0.0941848, -0.255844, 0.257759, 0.0981586,
    -0.319736, 0.102154, 0.253858, -0.250919, -0.0966488, 0.312591, -0.0962006, -0.260107,
    0.258988, 0.0929409, -0.312086, 0.103517, 0.255879, -0.258606, -0.0961804, 0.316441}},
  Sinusoidal2_20 → {{0.00257834, 0.00973755, 0.0313965, 0.0905324, 0.935905, 0.336437,
    0.028896, 0.00501518, 0.0272843, 0.0019018}, {-0.101662, -0.259934, 0.259325, 0.0915127,
    -0.3146, 0.102672, 0.254599, -0.251761, -0.0957137, 0.319426, -0.0981541, -0.25696,
    0.251931, 0.101933, -0.314154, 0.0988812, 0.257968, -0.25793, -0.0914758, 0.313252}}|>,
f6 → <|Sinusoidal1_1 → {{0.00410568, 0.00519822, 0.0285603, 0.0508892, 0.100084, 0.987692,
    0.102691, 0.00506774, 0.0205787, 0.00177519}, {-0.20377, -0.0872915, 0.315764, -0.235926,
    -0.0299905, 0.23785, -0.281906, 0.103166, 0.177004, -0.315754, 0.162016, 0.0838873,
    -0.319288, 0.25284, -0.00156617, -0.251345, 0.310806, -0.0940053, -0.168252, 0.347552}},
  Sinusoidal1_2 → {{0.00765796, 0.00656516, 0.0207524, 0.0553043, 0.103448, 0.986151, 0.112838,
    0.00421806, 0.0214945, 0.00150817}, {-0.188108, -0.0854455, 0.304827, -0.229101,
    -0.008386, 0.265672, -0.277549, 0.0985542, 0.188514, -0.324991, 0.185759, 0.0866634,
    -0.31462, 0.234146, -0.0259564, -0.244651, 0.309743, -0.111822, -0.202892, 0.327702}},
  Sinusoidal1_3 → {{0.00194906, 0.00491313, 0.0228535, 0.0520338, 0.110713, 0.986302, 0.104616,
    0.00209359, 0.0272718, 0.000555402}, {-0.188278, -0.0901735, 0.303272, -0.272736,
    -0.0243175, 0.220608, -0.278394, 0.0960687, 0.201764, -0.327951, 0.199299, 0.0712094,
    -0.286325, 0.245985, -0.030486, -0.254011, 0.309125, -0.111049, -0.200308, 0.324136}},
  Sinusoidal1_4 → {{0.000611418, 0.00433836, 0.0206396, 0.0327711, 0.0960803, 0.986193,
    0.127604, 0.00851233, 0.0173631, 0.00398439}, {-0.185546, -0.120936, 0.298391, -0.234563,
    -0.0216129, 0.250303, -0.327492, 0.11169, 0.205286, -0.297167, 0.214579, 0.0852634,
    -0.281149, 0.263063, -0.016661, -0.24044, 0.325425, -0.0792809, -0.164797, 0.30757}},
  Sinusoidal1_5 → {{0.000166641, 0.0100721, 0.0172524, 0.0324588, 0.0901028, 0.989246, 0.106012,
    0.00318135, 0.0238543, 0.00170105}, {-0.199088, -0.0878624, 0.277172, -0.272011,
    0.0142385, 0.249821, -0.324417, 0.0753708, 0.17448, -0.316202, 0.165444, 0.120862,
    -0.324018, 0.28188, -0.0131001, -0.226907, 0.289207, -0.108403, -0.183438, 0.301229}},
  Sinusoidal1_6 → {{0.00257988, 0.00904077, 0.02972, 0.0166512, 0.0782101, 0.990389, 0.105964,
    0.0033182, 0.022899, 0.000922864}, {-0.197506, -0.126464, 0.313698, -0.222309,
    0.0165292, 0.235368, -0.321751, 0.0872528, 0.208952, -0.292407, 0.205276, 0.0794803,
    -0.322309, 0.279979, 0.0124577, -0.273342, 0.28043, -0.0692638, -0.179314, 0.282859}},
  Sinusoidal1_7 → {{0.00277503, 0.00678333, 0.015013, 0.0436675, 0.100418, 0.986827, 0.113806,
    0.0202524, 0.0200481, 0.0117964}, {-0.159496, -0.119441, 0.275685, -0.242375,
    -0.0101225, 0.28267, -0.322883, 0.122154, 0.162031, -0.29086, 0.195097, 0.0969025,
    -0.285171, 0.232217, -0.014512, -0.245441, 0.31975, -0.126497, -0.195808, 0.340264}},
  Sinusoidal1_8 → {{0.00171874, 0.00625339, 0.0151649, 0.0464966, 0.09517, 0.989039, 0.100498,
    0.00798358, 0.0109051, 0.00529571}, {-0.212378, -0.0775316, 0.269658, -0.265977,
    -0.0139263, 0.278237, -0.285019, 0.0931975, 0.206755, -0.327217, 0.201416, 0.106784,
```

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```
    -0.276104, 0.234182, 0.0218489, -0.247089, 0.296089, -0.109136, -0.15454, 0.346463}},
  Sinusoidal1_9 → {{0.00311392, 0.0011299, 0.0153662, 0.0208596, 0.0944756, 0.989536, 0.101946,
    0.00250707, 0.0284768, 0.000619056}, {-0.172333, -0.095782, 0.2834, -0.284522,
    0.027183, 0.270964, -0.302605, 0.116248, 0.213547, -0.314368, 0.166886, 0.0686509,
    -0.308751, 0.268058, -0.0174327, -0.234623, 0.298104, -0.0710555, -0.166792, 0.315203}},
  Sinusoidal1_10 → {{0.000113665, 0.00927881, 0.0104261, 0.0405947, 0.122825, 0.987035,
    0.0910759, 0.00708437, 0.0218249, 0.00336986}, {-0.196488, -0.0712922, 0.27803, -0.261255,
    -0.0189017, 0.289969, -0.338224, 0.0788056, 0.166621, -0.296911, 0.186563, 0.116821,
    -0.277541, 0.247344, -0.0250906, -0.231465, 0.310031, -0.0726631, -0.201813, 0.326799}}|>|>
```

Let's use ChessboardDistance as a distance function for the second clustering:

In[3]:=
```
clusters1SubChessboardDistance =
 TimeSeriesClusters[classification1, SubclusteringDistanceFunction → ChessboardDistance]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
<|SpikeMax → <|Cluster → Cluster[Cluster[ ··· 1 ··· ], ··· 3 ··· , 2], ··· 4 ··· , GroupAssociations →
    <|G1S1 → {SpikePositive_1, SpikePositive_9, ··· 6 ··· , SpikePositive_6, SpikePositive_10},
     G1S2 → ··· 1 ··· , G2S1 → { ··· 1 ··· }|>|>, ··· 4 ··· , f6 → ··· 1 ··· |>
```

large output | show less | show more | show all | set size limit...

In[4]:=
```
Query[All, "GroupAssociations"]@clusters1SubChessboardDistance
```

Out[4]=
```
<|SpikeMax → <|G1S1 → {SpikePositive_1, SpikePositive_9, SpikePositive_5, SpikePositive_4, SpikePositive_7,
    SpikePositive_2, SpikePositive_3, SpikePositive_8, SpikePositive_6, SpikePositive_10},
  G1S2 → {SpikePositive_20, SpikePositive_12, SpikePositive_13, SpikePositive_19, SpikePositive_17,
    SpikePositive_14, SpikePositive_16, SpikePositive_11}, G2S1 → {SpikePositive_18, SpikePositive_15}|>,
 SpikeMin → <|G1S1 → {SpikeNegative_1, SpikeNegative_4, SpikeNegative_7, SpikeNegative_5},
  G1S2 → {SpikeNegative_12}, G2S1 → {SpikeNegative_2}, G2S2 → {SpikeNegative_9, SpikeNegative_10},
  G3S1 → {SpikeNegative_3}, G3S2 → {SpikeNegative_19, SpikeNegative_15}, G4S1 → {SpikeNegative_8},
  G5S1 → {SpikeNegative_20, SpikeNegative_18, SpikeNegative_14, SpikeNegative_16},
  G5S2 → {SpikeNegative_6}, G6S1 → {SpikeNegative_17, SpikeNegative_11}, G6S2 → {SpikeNegative_13}|>,
 f1 → <|G1S1 → {LinearPositive_1, LinearPositive_3, LinearPositive_10, LinearPositive_2, LinearPositive_9,
    LinearPositive_8, LinearPositive_4, LinearPositive_5, LinearPositive_7, LinearPositive_6,
    LinearPositive_17, LinearPositive_14, LinearPositive_12, LinearPositive_13, LinearPositive_18,
    LinearPositive_16, LinearPositive_20, LinearPositive_11, LinearPositive_19, LinearPositive_15},
  G1S2 → {LinearNegative_19, LinearNegative_12, LinearNegative_11, LinearNegative_14, LinearNegative_17,
    LinearNegative_13, LinearNegative_16, LinearNegative_18, LinearNegative_15, LinearNegative_20,
    LinearNegative_10, LinearNegative_3, LinearNegative_4, LinearNegative_5, LinearNegative_6,
    LinearNegative_2, LinearNegative_1, LinearNegative_8, LinearNegative_9}, G2S1 → {LinearNegative_7}|>,
 f3 → <|G1S1 → {Sinusoidal3_21, Sinusoidal3_28}, G1S2 → {Sinusoidal3_22},
  G2S1 → {Sinusoidal3_23, Sinusoidal3_24, Sinusoidal3_30},
  G2S2 → {Sinusoidal3_26, Sinusoidal3_29, Sinusoidal3_25, Sinusoidal3_27}|>,
 f5 → <|G1S1 → {Sinusoidal2_11, Sinusoidal2_15, Sinusoidal2_16}, G1S2 → {Sinusoidal2_14},
  G1S3 → {Sinusoidal2_19, Sinusoidal2_13}, G1S4 → {Sinusoidal2_12},
  G2S1 → {Sinusoidal2_17, Sinusoidal2_18}, G2S2 → {Sinusoidal2_20}|>,
 f6 → <|G1S1 → {Sinusoidal1_1, Sinusoidal1_2, Sinusoidal1_3}, G1S2 → {Sinusoidal1_8},
  G2S1 → {Sinusoidal1_4, Sinusoidal1_7}, G3S1 → {Sinusoidal1_9},
  G3S2 → {Sinusoidal1_5, Sinusoidal1_6}, G4S1 → {Sinusoidal1_10}|>|>
```

Let's use Euclidean distance (default) for the first clustering:

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In[5]:=
```
clusters1SubEuclideanDistance =
 TimeSeriesClusters[classification1, SubclusteringDistanceFunction → EuclideanDistance]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[5]=
```
<|SpikeMax → <|Cluster → Cluster[Cluster[ ··· 1 ··· ], ··· 3 ··· , 2], ··· 4 ··· , GroupAssociations →
    <|G1S1 → {SpikePositive_1, SpikePositive_5, ··· 6 ··· , SpikePositive_2, SpikePositive_3},
     G1S2 → ··· 1 ··· , G2S1 → { ··· 1 ··· }|>|>, ··· 4 ··· , f6 → ··· 1 ··· |>
```

large output | show less | show more | show all | set size limit...

We can see that the groupings are now different:

In[6]:=
```
Query[All, "GroupAssociations"]@clusters1SubEuclideanDistance
```

Out[6]=
```
<|SpikeMax → <|G1S1 → {SpikePositive_1, SpikePositive_5, SpikePositive_4, SpikePositive_7, SpikePositive_8,
      SpikePositive_10, SpikePositive_9, SpikePositive_6, SpikePositive_2, SpikePositive_3},
    G1S2 → {SpikePositive_14, SpikePositive_16, SpikePositive_19, SpikePositive_20, SpikePositive_12,
      SpikePositive_13, SpikePositive_17, SpikePositive_11}, G2S1 → {SpikePositive_18, SpikePositive_15}|>,
  SpikeMin → <|G1S1 → {SpikeNegative_1, SpikeNegative_4, SpikeNegative_7, SpikeNegative_5},
    G1S2 → {SpikeNegative_12}, G2S1 → {SpikeNegative_2, SpikeNegative_9}, G2S2 → {SpikeNegative_10},
    G3S1 → {SpikeNegative_3}, G3S2 → {SpikeNegative_19, SpikeNegative_15}, G4S1 → {SpikeNegative_8},
    G5S1 → {SpikeNegative_20, SpikeNegative_16, SpikeNegative_18, SpikeNegative_14},
    G5S2 → {SpikeNegative_6}, G6S1 → {SpikeNegative_17}, G6S2 → {SpikeNegative_13, SpikeNegative_11}|>,
  f1 → <|G1S1 → {LinearPositive_1, LinearPositive_2, LinearPositive_9, LinearPositive_8, LinearPositive_4,
      LinearPositive_6, LinearPositive_3, LinearPositive_7, LinearPositive_5, LinearPositive_10,
      LinearPositive_17, LinearPositive_12, LinearPositive_13, LinearPositive_14, LinearPositive_20,
      LinearPositive_15, LinearPositive_11, LinearPositive_19, LinearPositive_16, LinearPositive_18},
    G1S2 → {LinearNegative_19, LinearNegative_14, LinearNegative_16, LinearNegative_11, LinearNegative_15,
      LinearNegative_18, LinearNegative_17, LinearNegative_20, LinearNegative_12, LinearNegative_13,
      LinearNegative_3, LinearNegative_10, LinearNegative_5, LinearNegative_4, LinearNegative_8,
      LinearNegative_1, LinearNegative_9, LinearNegative_6, LinearNegative_2}, G2S1 → {LinearNegative_7}|>,
  f3 → <|G1S1 → {Sinusoidal3_21, Sinusoidal3_28}, G1S2 → {Sinusoidal3_22},
    G2S1 → {Sinusoidal3_23, Sinusoidal3_30},
    G2S2 → {Sinusoidal3_26, Sinusoidal3_29, Sinusoidal3_24, Sinusoidal3_25, Sinusoidal3_27}|>,
  f5 → <|G1S1 → {Sinusoidal2_11}, G1S2 → {Sinusoidal2_19, Sinusoidal2_13},
    G1S3 → {Sinusoidal2_14, Sinusoidal2_16, Sinusoidal2_15}, G1S4 → {Sinusoidal2_12},
    G2S1 → {Sinusoidal2_17, Sinusoidal2_20}, G2S2 → {Sinusoidal2_18}|>,
  f6 → <|G1S1 → {Sinusoidal1_1, Sinusoidal1_2, Sinusoidal1_3}, G1S2 → {Sinusoidal1_8},
    G2S1 → {Sinusoidal1_4, Sinusoidal1_7}, G3S1 → {Sinusoidal1_9, Sinusoidal1_5},
    G3S2 → {Sinusoidal1_6}, G4S1 → {Sinusoidal1_10}|>|>
```

See Also

Autocorrelation ▪ **CreateTimeSeries** ▪ **GOAnalysis** ▪ **KEGGAnalysis** ▪ **KEGGPathwayVisual** ▪ **LombScargle** ▪ **MatrixClusters** ▪ **SeriesApplier** ▪ **SeriesCompare** ▪ **SeriesInternalCompare** ▪

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TimeExtractor ▪ **TimeSeriesClassification** ▪ **TimeSeriesDendrogramHeatmap** ▪ **TimeSeriesDendrogramsHeatmaps** ▪ **TimeSeriesModelFit** ▪ **TimeSeriesSingleClusters**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾ URL ▾

TimeSeriesDendrogramHeatmap

`TimeSeriesDendrogramHeatmap[data]`
generates a dendrogram and heatmap plot for time series *data* clusters.

Details

- `TimeSeriesDendrogramHeatmap[data]` generates a dendrogram and heatmap plot for one set of time series *data* clusters, typically the output of a single class of TimeSeriesClusters. The input has the form of an association:

-
```
data = <|"Cluster" → cluster object,
  "InitialSplitCluster" → {InitialSplitCluster1, InitialSplitCluster2 ...},
  "IntermediateClusters" → {IntermediateCluster11, IntermediateCluster12 ...},
  "SubsplitClusters" → {{SubsplitClusters1} {SubsplitClusters2}},
  "Data" → {{input data vector1} → Member1, ...,},
  "GroupAssociations" → <|"G1S1" → {member list G1S1},
    "G1S2" → {member list for G1S2},
    ...,
    "G2S1" → { ...}|>|>
```

- The keys of the data correspond to the following properties related to the two tier clustering results generated by TimeSeriesClusters for a single classification class:

"Cluster"	Cluster generated.
"InitialSplitCluster"	Clusters resulting from splitting the initial cluster (reported by key "Cluster") into groups using the SignificanceCriterion to determine the number of clusters.
"IntermediateClusters"	Aglomerative clustering result of hierarchical clustering of each of the initial split clusters (reported by "InitialSplitCluster")
"SubsplitClusters"	Custers generated from splitting the clusters following the second tier clustering (reported by "IntermediateClusters") into subgroups using the SignificanceCriterion to determine the number of clusters.
"Data"	Data reported in the order of clustering results as rules of `{second initial classification vector} → label` for each time series, sorted in order of the clustering results.

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"GroupAssociations"	Association denoting membership of each initial data label to groups and subgroups generated by the two tier clustering.

- The data can also be provided as a list with the corresponding values from the TimeSeriesClusters clustering for a single classification class:

- data = { cluster object$_1$, {InitialSplitCluster$_{11}$, InitialSplitCluster$_{12}$ ...},
  {IntermediateCluster$_{11}$, IntermediateCluster$_{12}$ ...}, {{SubsplitClusters$_{11}$} {SubsplitClusters$_{12}$}},
  {{input data vector$_{11}$} → Member$_{11}$, ...,},
  <|"G1S1" → {member list G1S1},
  "G1S2" → {member list for G1S2},
  ...,
  "G2S1" → { ...}|>}

- The following options can be given:

ColorBlending	{CMYKColor[1, 0, 1, 0], CMYKColor[0, 1, 1, 0]}	Color scheme for the plot. The color list is passed to an internal Blend function to create a ColorFunction for an internal ArrayPlot function.
DendrogramColor	RGBColor[1, 1, 0]	Color to highlight the dendrograms.
FrameName	"Dendrogram and Heatmap"	Label for plot frame.
GroupSubSize	{0.1, 0.1}	Relative size of group and subgroup reference column in plot.
HorizontalAxisName	"Time (arbitrary units)"	Label for the horizontal heatmap axis.
HorizontalLabels	None	Labels for horizontal axis for each column.
IndexColor	"DeepSeaColors"	Choice of color for labeling the group/subgroup index.
ImageSize	200	ImageSize is an option that specifies the overall size of an image to display for an object.
ScaleShift	None	Option to reset the blend of the colors used overall. The option is a real positive number, and is used as a multiplier for an internal Blend function's second argument.
VerticalLabels	None	Labels for vertical axis for each row.

Examples (14)

Basic Examples (2)

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First we need to load the MathIOmica package.

In[1]:=
```
Get["MathIOmica`"]
```

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

We have multiple classes:

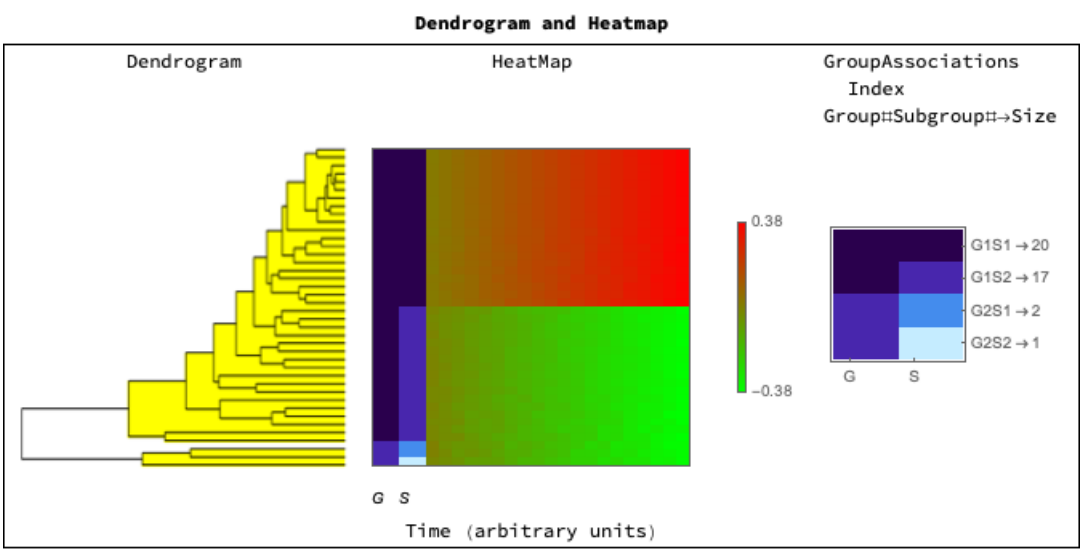
In[3]:=
```
Keys[clusters1]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"]]
```

Out[4]=



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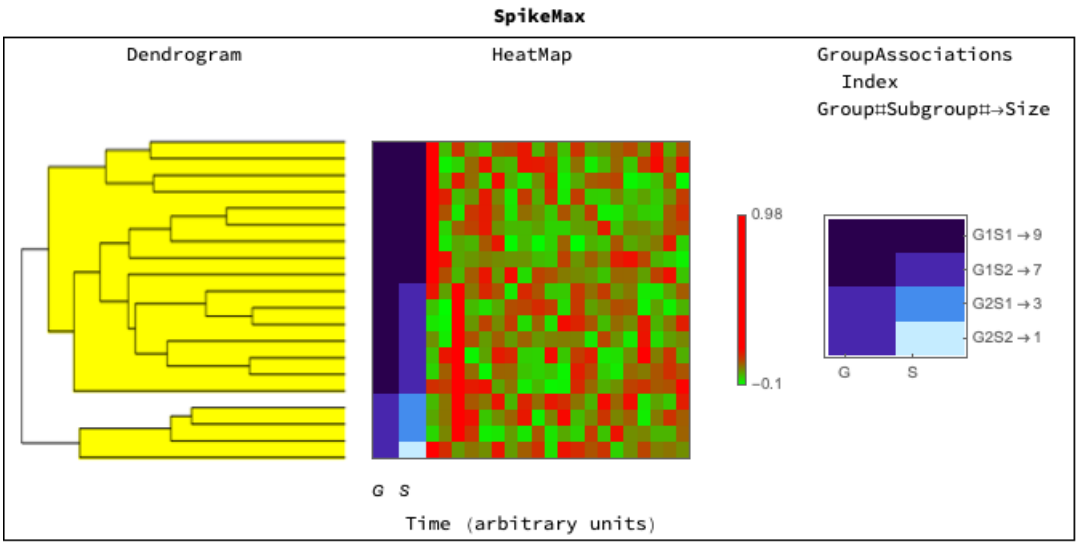
- The dendrogram is represented on the left, and is highlighted to represent the grouping level. The G, S, columns represent the groupings and subgroupings generated by the clustering. The legend shows the corresponding groupings and subgrouping, and the number of elements in each group subgroup. For example above, in Group 1, Subgroup 1 we have 19 members. We can extract the corresponding members from the input data:

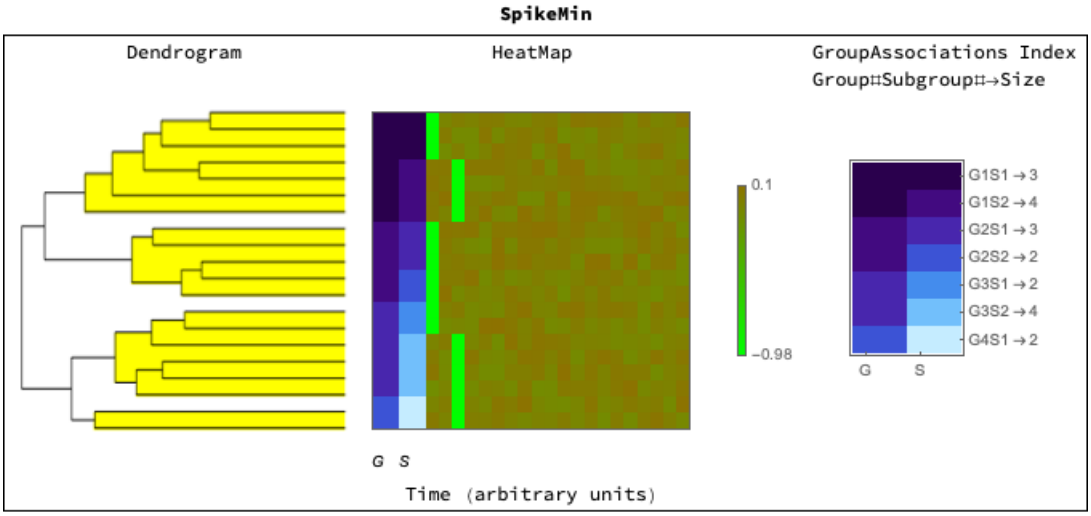
In[5]:=
```
clusters1["f1", "GroupAssociations", "G1S1"]
```

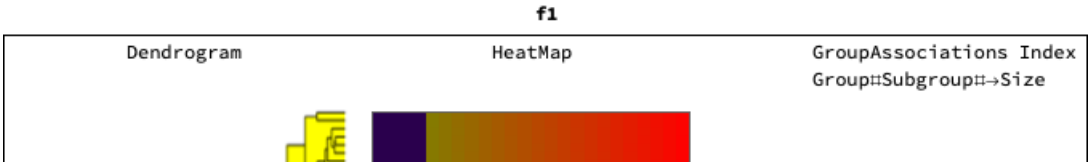
Out[5]=
```
{LinearPositive_1, LinearPositive_5, LinearPositive_2, LinearPositive_7, LinearPositive_10,
 LinearPositive_3, LinearPositive_9, LinearPositive_4, LinearPositive_6, LinearPositive_8,
 LinearPositive_12, LinearPositive_17, LinearPositive_15, LinearPositive_19, LinearPositive_14,
 LinearPositive_16, LinearPositive_11, LinearPositive_20, LinearPositive_18, LinearPositive_13}
```

- To plot all classes we use TimeSeriesDendrogramsHeatmaps .

In[6]:=
```
TimeSeriesDendrogramsHeatmaps[clusters1]
```







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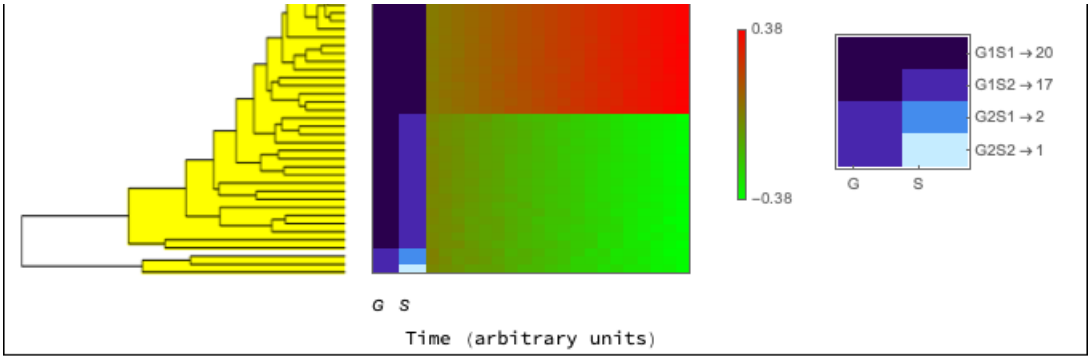
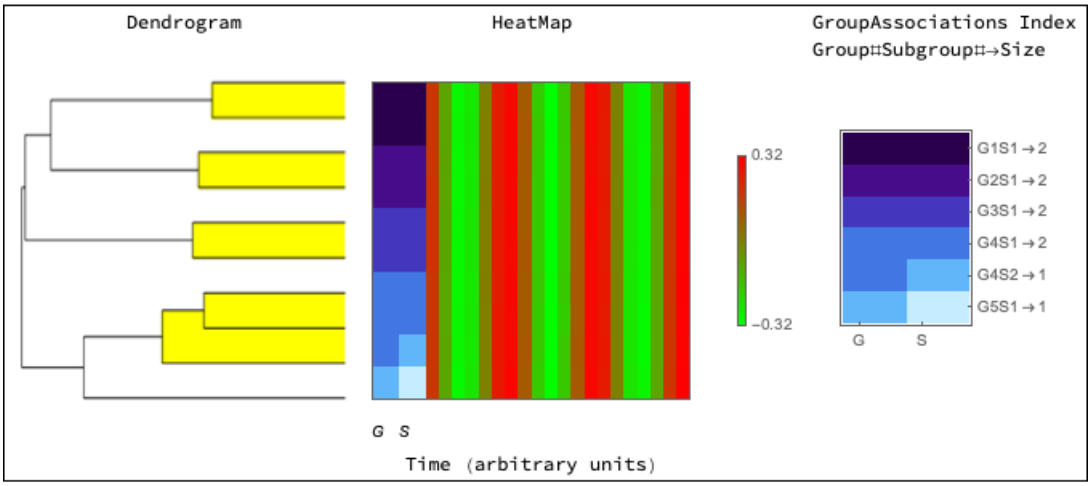
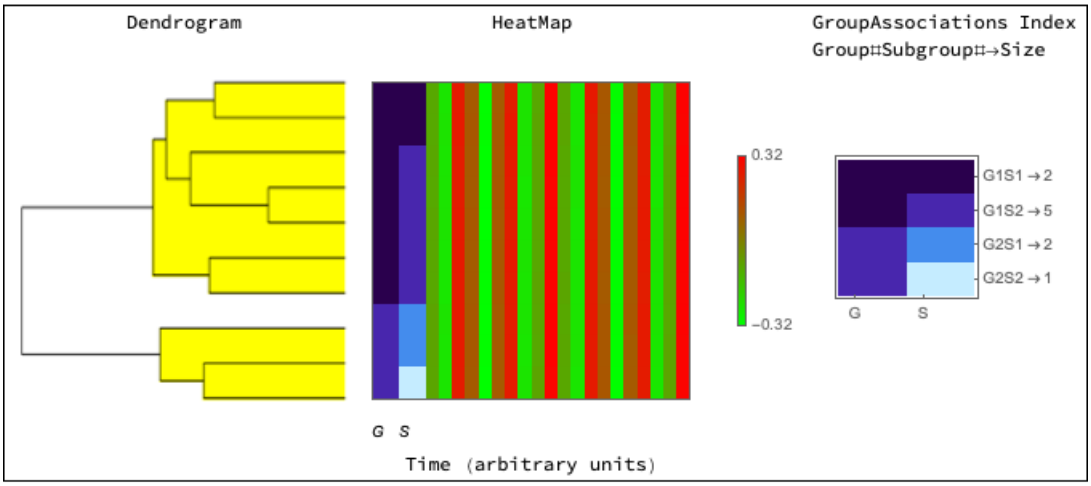


Out[6]=

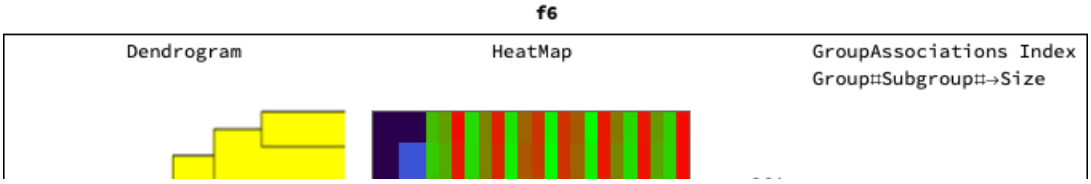
f3



f5



f6



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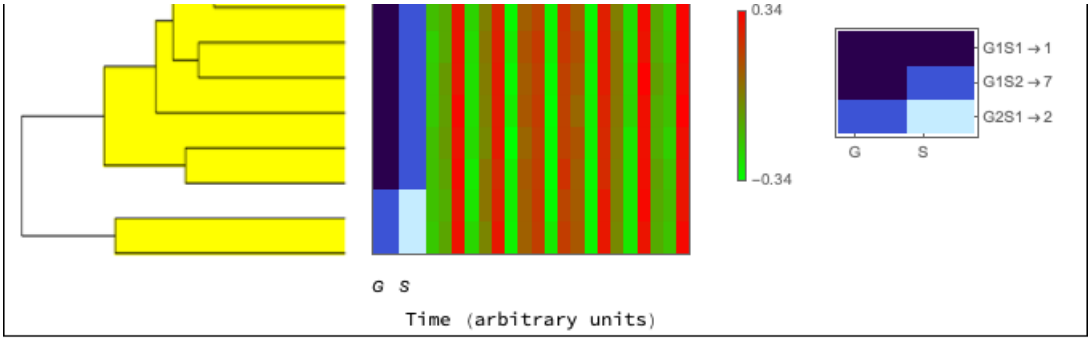


```
In[1]:= Needs["MathIOmica`"]
```

We can also consider data with missing values. We consider the previous example, with say up to 2 data points removed/set to Missing[], classify and cluster the following data for our example, for various trends and 20 time points:

```
In[2]:= classificationExample2 =
  Query[All, Nest[ReplacePart[#, RandomInteger[{1, 20}] → Missing[]] &, #, RandomInteger[{1, 2}]] &] @
   (Normalize[#] & /@ Association[Join[
       Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["Sinusoidal1_" <> ToString[i] →
         Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}], Table[
        "Sinusoidal2_" <> ToString[i] → 5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
        {i, 21, 30}]]]);
timePointsExample = Range[20];
classification2 = TimeSeriesClassification[classificationExample2, timePointsExample,
   LombScargleCutoff → 0.89, SpikeCutoffs → <|18 → {.45, -.45}, 19 → {0.43, -0.43}, 20 → {0.42, -0.42}|>];
clusters2 = TimeSeriesClusters[classification2];
```

We have again multiple classes:

```
In[3]:= Keys[clusters1]
Out[3]= {SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class, and see that Missing[] values are shown in grey:

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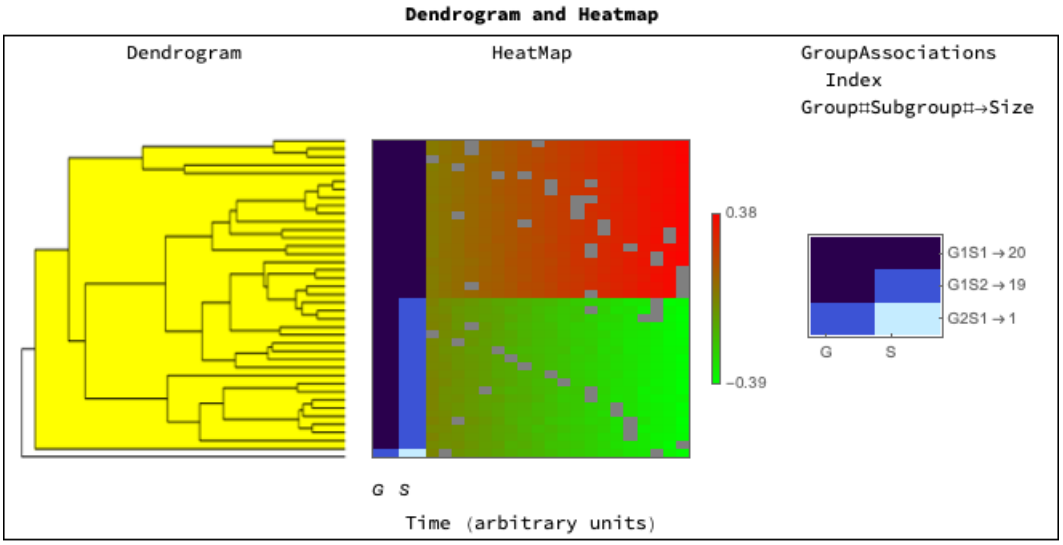
In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters2["f1"]]
```

Out[4]=



Options (11)

ColorBlending (2)

In[1]:=
```
Needs["MathIOmica`"]
```

ColorBlending provides a list of colors to be used in the plot to create gradient effects. Named colors can be used as well.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

```
Method → "LombScargle"
```

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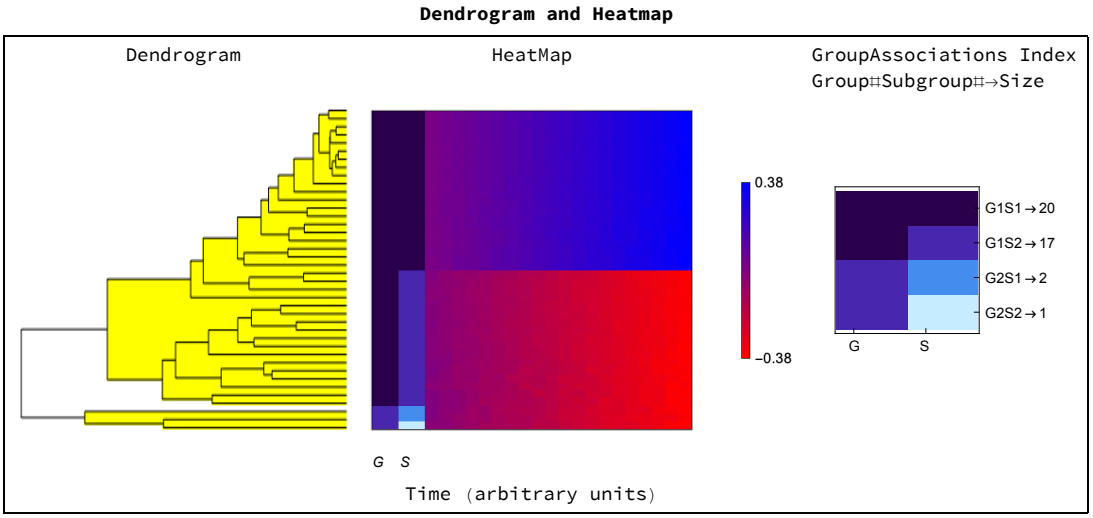
In[3]:=
```
Keys[clusters1]
```
Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

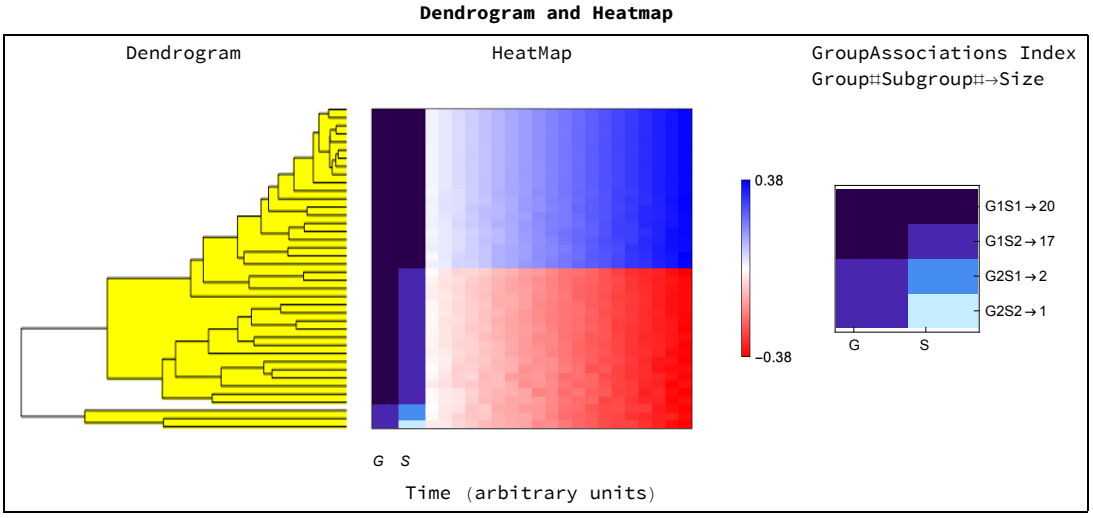
In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ColorBlending → {Red, Blue}]
```

Out[4]=



In[5]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ColorBlending → {Red, White, Blue}]
```

Out[5]=



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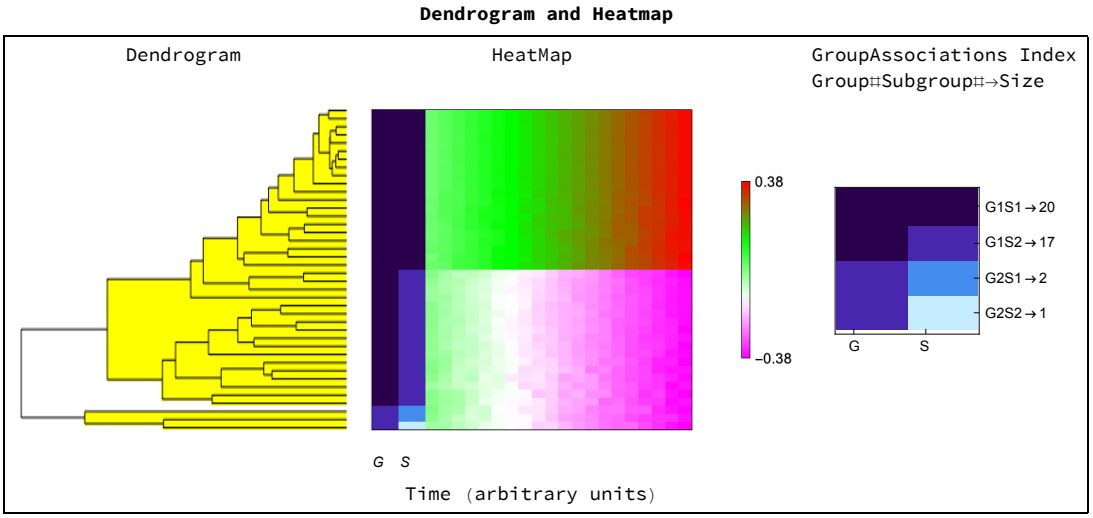
In[6]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"],
 ColorBlending → {RGBColor[1, 0, 1], White, CMYKColor[1, 0, 1, 0], CMYKColor[0, 1, 1, 0]}]
```

Out[6]=



In[1]:=
```
Needs["MathIOmica`"]
```

All of Mathematica's color gradients can be used instead of a list:

In[2]:=
```
ColorData["Gradients"]
```

Out[2]=
```
{AlpineColors, Aquamarine, ArmyColors, AtlanticColors, AuroraColors, AvocadoColors,
 BeachColors, BlueGreenYellow, BrassTones, BrightBands, BrownCyanTones, CandyColors, CherryTones,
 CMYKColors, CoffeeTones, DarkBands, DarkRainbow, DarkTerrain, DeepSeaColors, FallColors,
 FruitPunchColors, FuchsiaTones, GrayTones, GrayYellowTones, GreenBrownTerrain, GreenPinkTones,
 IslandColors, LakeColors, LightTemperatureMap, LightTerrain, MintColors, NeonColors, Pastel,
 PearlColors, PigeonTones, PlumColors, Rainbow, RedBlueTones, RedGreenSplit, RoseColors,
 RustTones, SandyTerrain, SiennaTones, SolarColors, SouthwestColors, StarryNightColors,
 SunsetColors, TemperatureMap, ThermometerColors, ValentineTones, WatermelonColors}
```

We consider the data which is classified and clustered:

In[3]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

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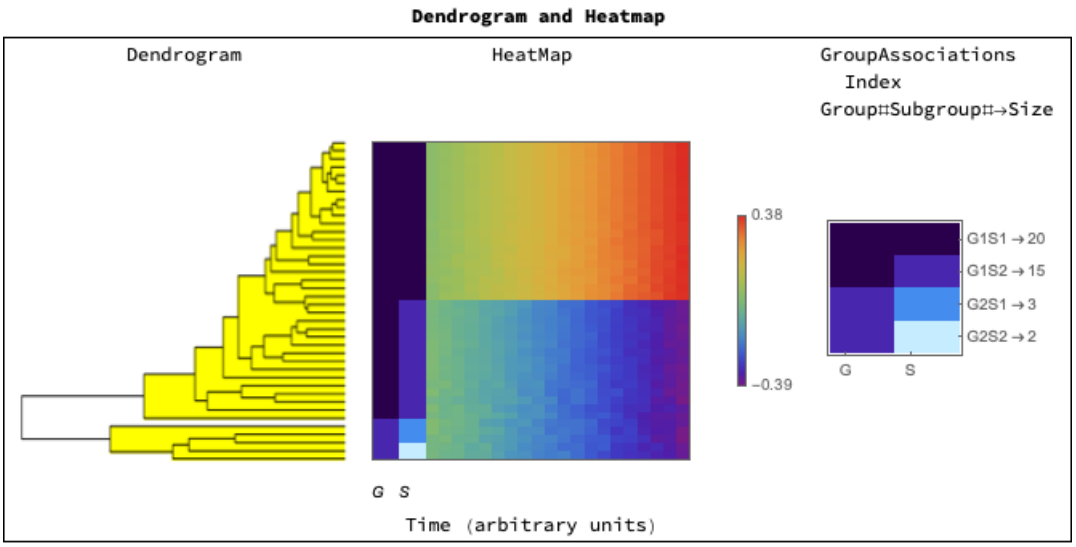
In[4]:=
```
Keys[clusters1]
```
Out[4]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

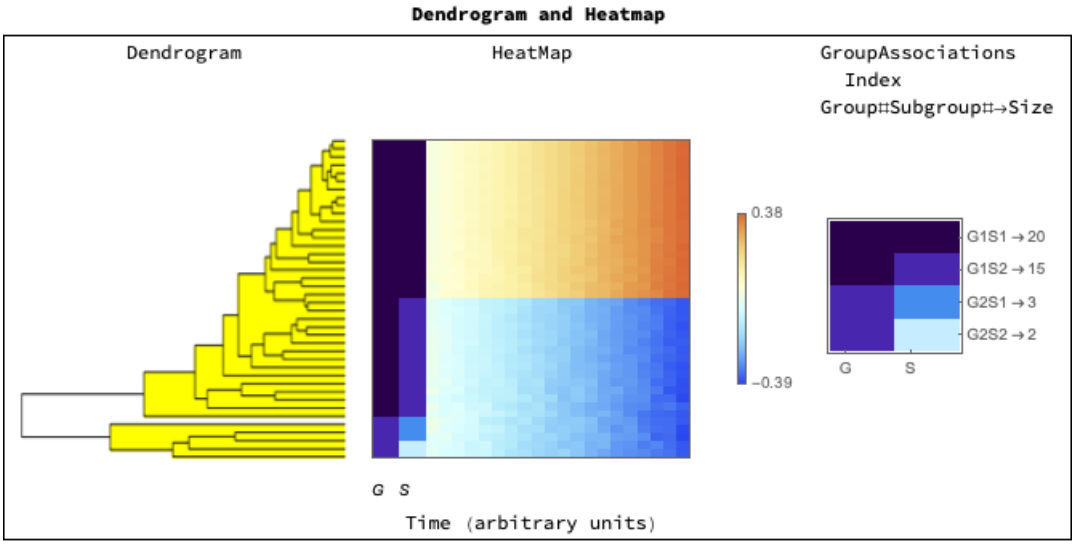
In[5]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ColorBlending → "Rainbow"]
```

Out[5]=



In[6]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ColorBlending → "LightTemperatureMap"]
```

Out[6]=



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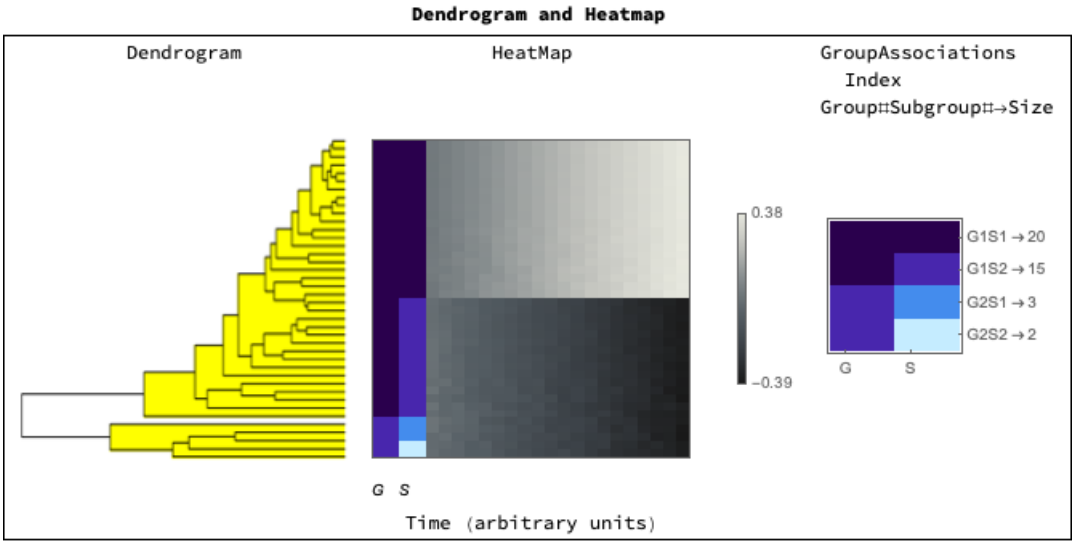
In[7]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ColorBlending → "GrayTones"]
```

Out[7]=



DendrogramColor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

DendrogramColor takes color values, for highlighting the dendrograms at the level where the groupings are called by the clustering.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

In[3]:=
```
Keys[clusters1]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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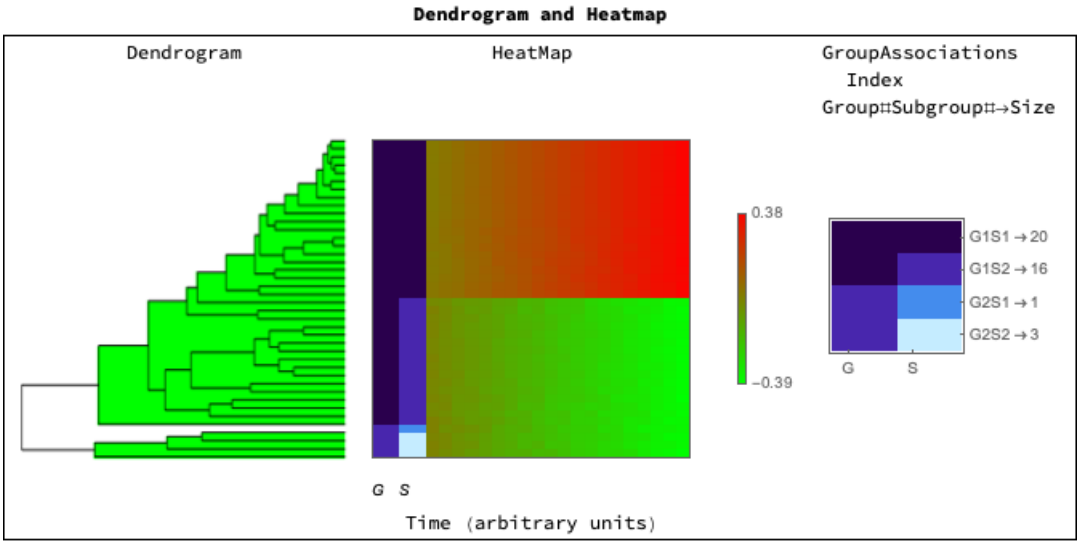
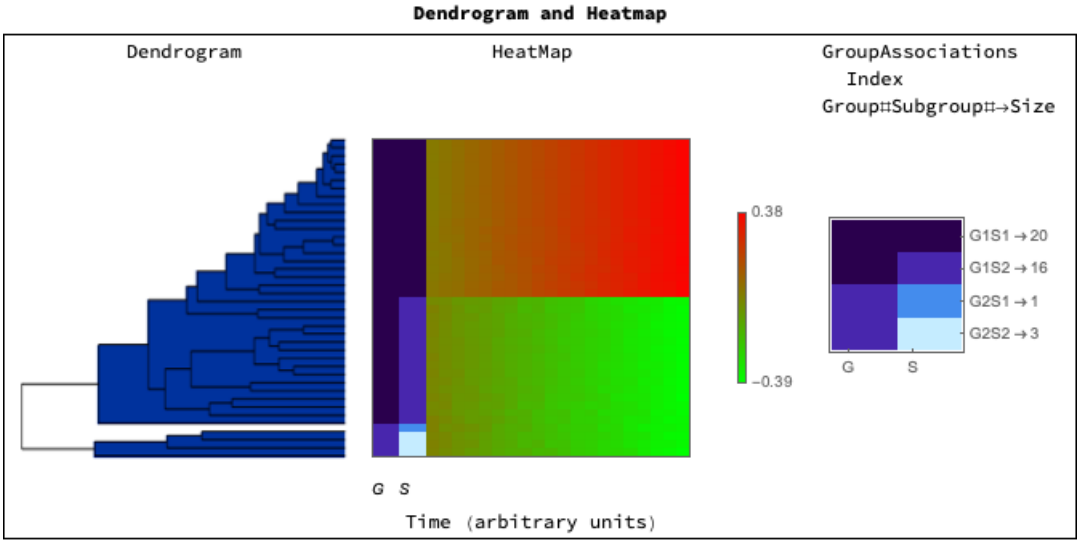
In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], DendrogramColor → RGBColor[0, 1, 0]]
```

Out[4]=



In[5]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], DendrogramColor → CMYKColor[1, .7, .05, .35]]
```

Out[5]=



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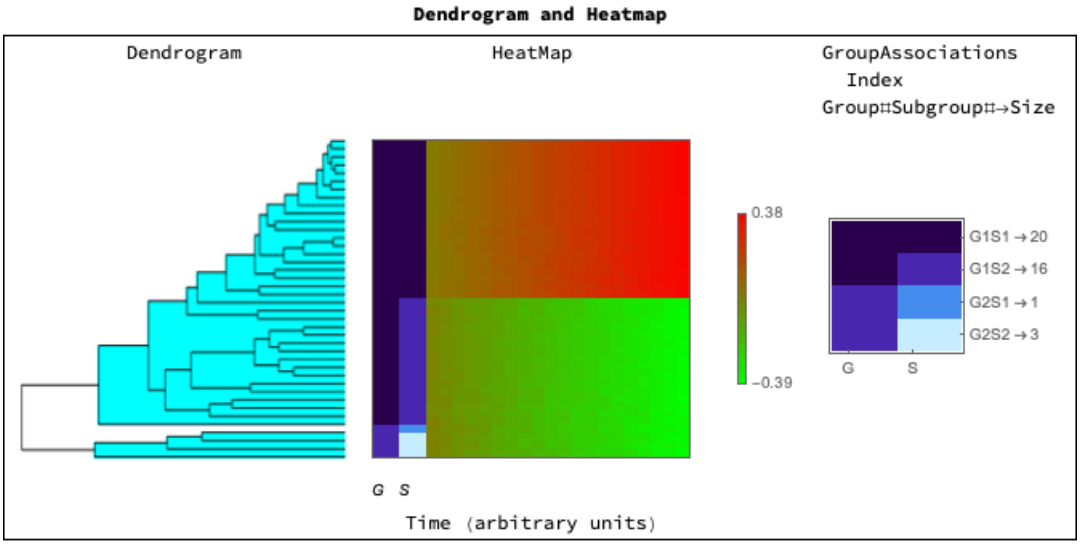
In[6]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], DendrogramColor → Cyan]
```

Out[6]=



FrameName (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The FrameName option let's us create a label for plot frame.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

In[3]:=
```
Keys[clusters1]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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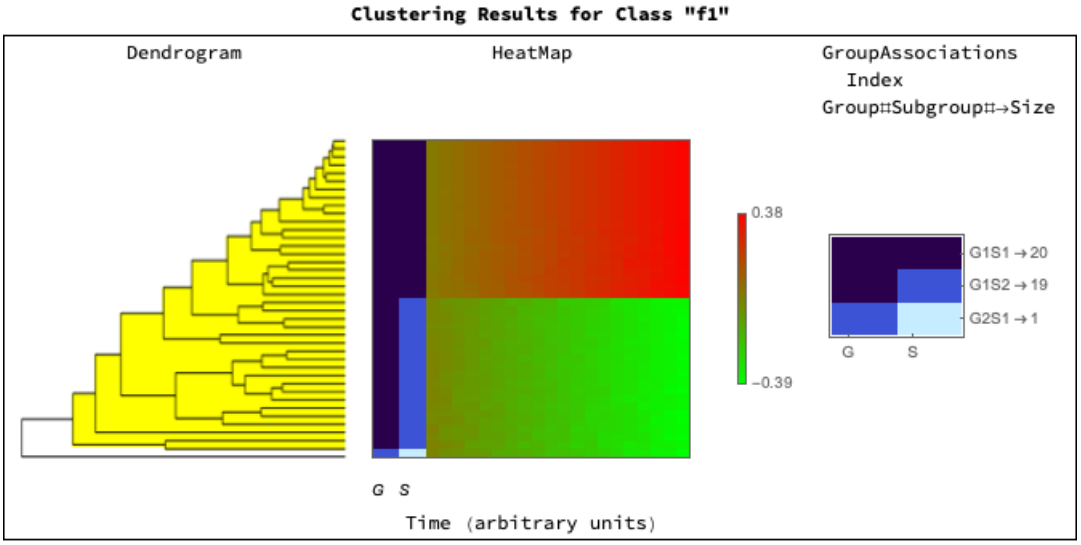
In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], FrameName → "Clustering Results for Class \"f1\""]
```

Out[4]=



GroupSubSize (1)

In[1]:=
```
Needs["MathIOmica`"]
```

GroupSubSize allows us to change the width (i.e. relative size as a fraction of the image) of group and subgroup reference columns respectively in plots.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

In[3]:=
```
Keys[clusters1]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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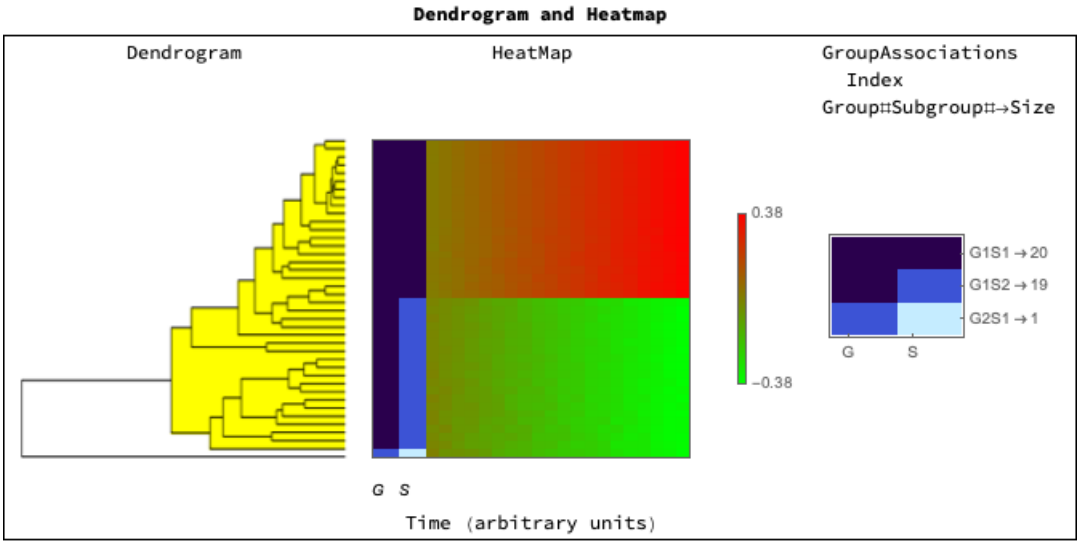
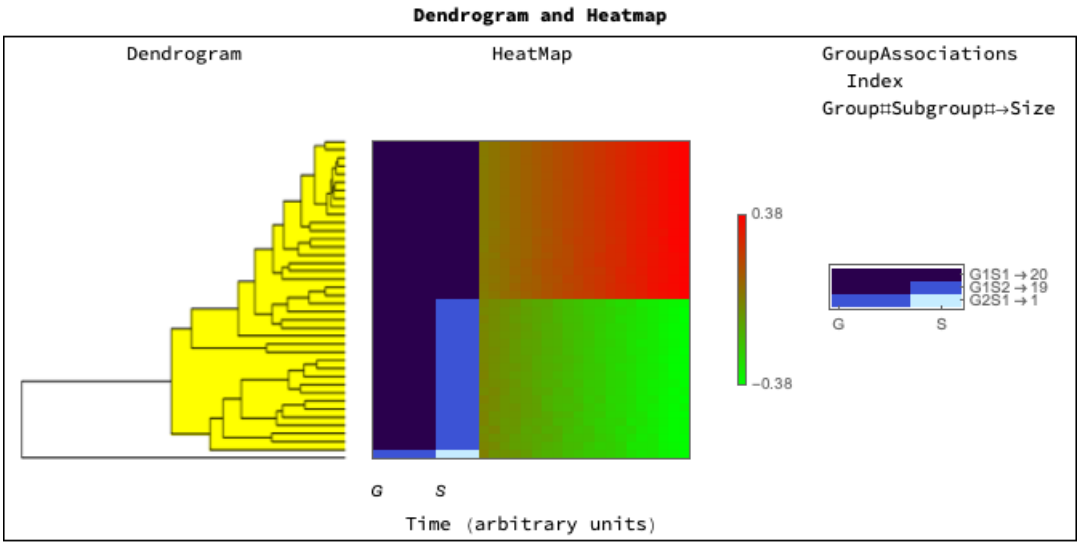
In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], GroupSubSize → {0.1, 0.1}]
```

Out[4]=



In[5]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], GroupSubSize → {0.3, 0.2}]
```

Out[5]=



HorizontalAxisName (1)

In[1]:=
```
Needs["MathIOmica`"]
```

HorizontalAxisName provides a label for the heatmap's horizontal axis.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

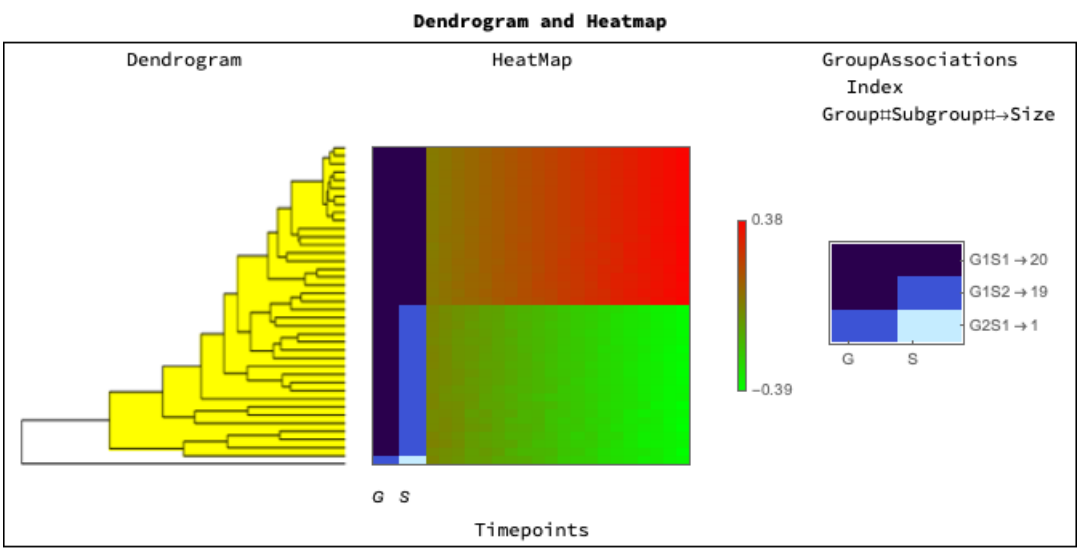
In[3]:=
```
Keys[clusters1]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], HorizontalAxisName → "Timepoints"]
```

Out[4]=



HorizontalLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

HorizontalLabels provides labels for the horizontal heatmap axis. The labels are distributed evenly in the horizontal direction.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

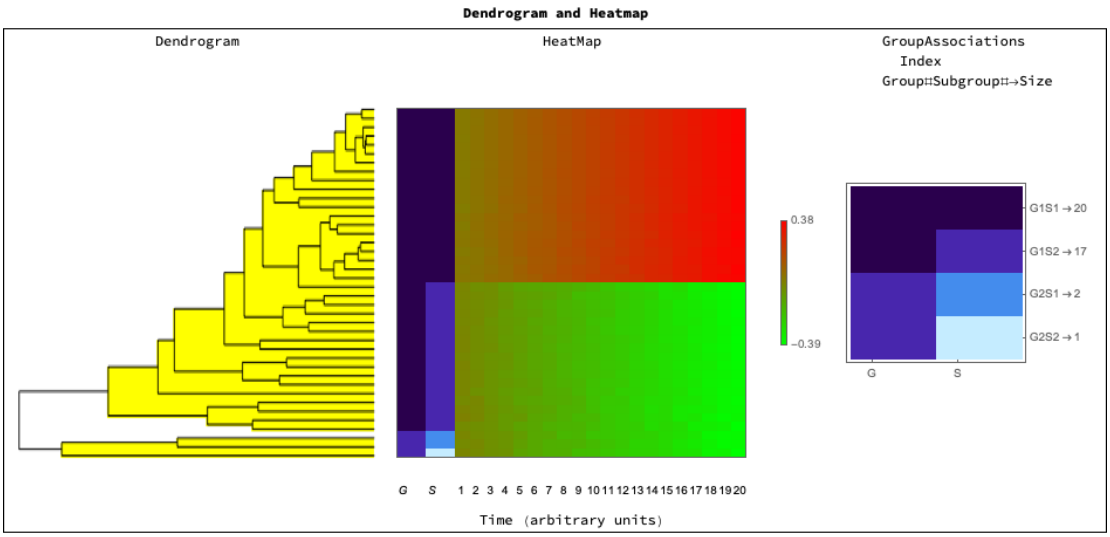
In[3]:=
```
Keys[clusters1]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class (in this example we scale up the image as well to accomodate the extra labels):

In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ImageSize → 300, HorizontalLabels → Range[20]]
```

Out[4]=



IndexColor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

IndexColor allows us to chose the color gradients for labeling the group/subgroup index. Named Mathematica gradients can be used as well:

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In[2]:=
```
ColorData["Gradients"]
```

Out[2]=
```
{AlpineColors, Aquamarine, ArmyColors, AtlanticColors, AuroraColors, AvocadoColors,
 BeachColors, BlueGreenYellow, BrassTones, BrightBands, BrownCyanTones, CandyColors, CherryTones,
 CMYKColors, CoffeeTones, DarkBands, DarkRainbow, DarkTerrain, DeepSeaColors, FallColors,
 FruitPunchColors, FuchsiaTones, GrayTones, GrayYellowTones, GreenBrownTerrain, GreenPinkTones,
 IslandColors, LakeColors, LightTemperatureMap, LightTerrain, MintColors, NeonColors, Pastel,
 PearlColors, PigeonTones, PlumColors, Rainbow, RedBlueTones, RedGreenSplit, RoseColors,
 RustTones, SandyTerrain, SiennaTones, SolarColors, SouthwestColors, StarryNightColors,
 SunsetColors, TemperatureMap, ThermometerColors, ValentineTones, WatermelonColors}
```

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[3]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

In[4]:=
```
Keys[clusters1]
```

Out[4]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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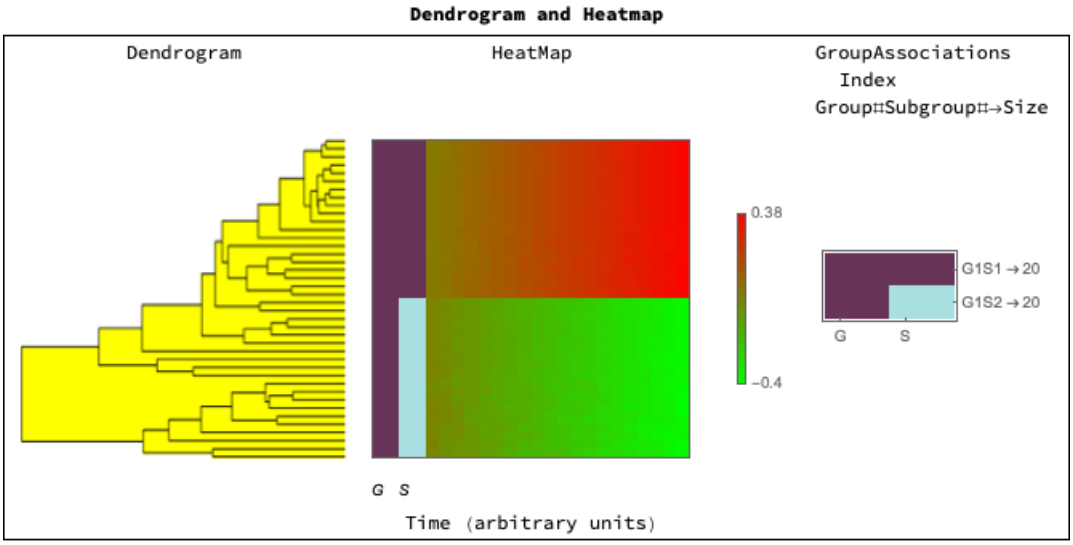
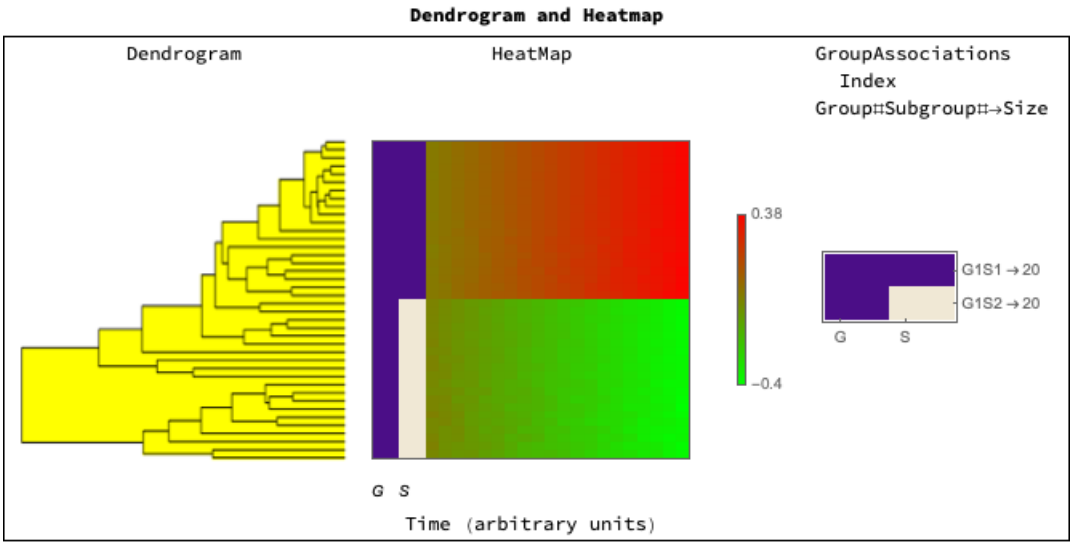
In[5]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], IndexColor → "CandyColors"]
```

Out[5]=



In[6]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], IndexColor → "LakeColors"]
```

Out[6]=



ImageSize (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ImageSize is an option that allows us to provide the overall size of the plots.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

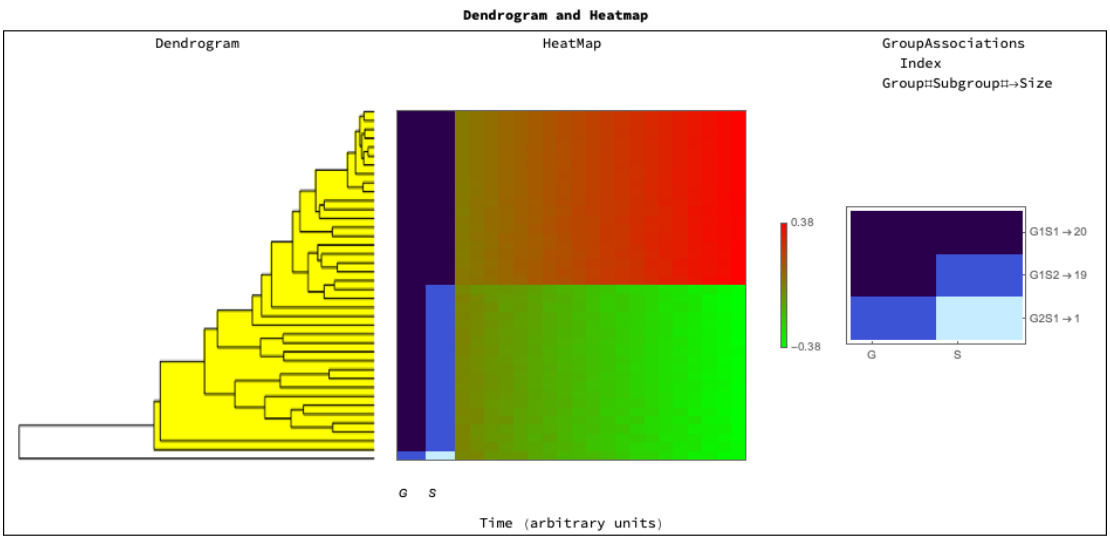
In[3]:=
```
Keys[clusters1]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ImageSize → 300]
```

Out[4]=



ScaleShift (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ScaleShift provides a shift of overall color in a heatmap, allowing for overall adjustments if necessary. We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

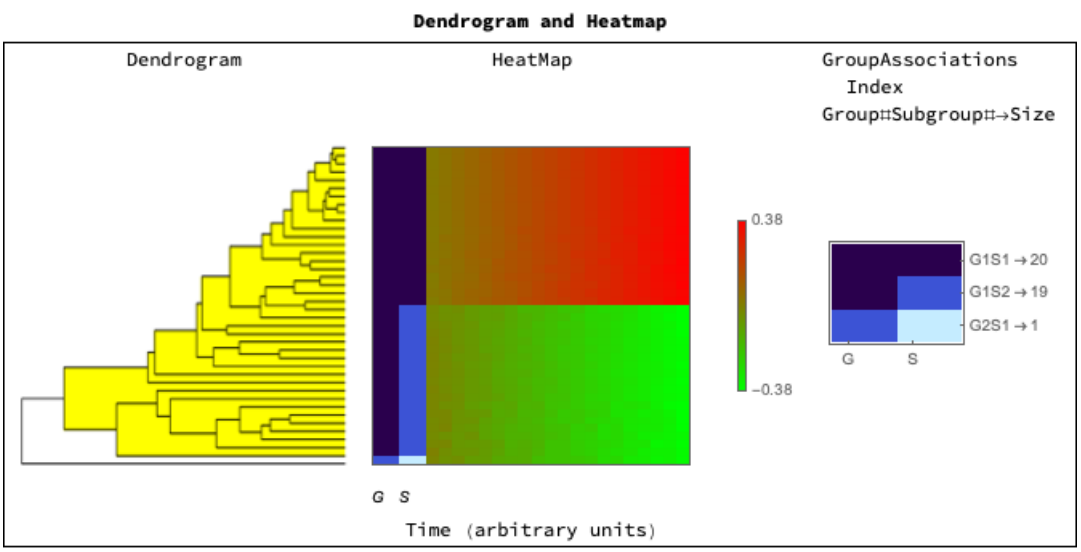
In[3]:=
```
Keys[clusters1]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

In[4]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ScaleShift → 1]
```

Out[4]=



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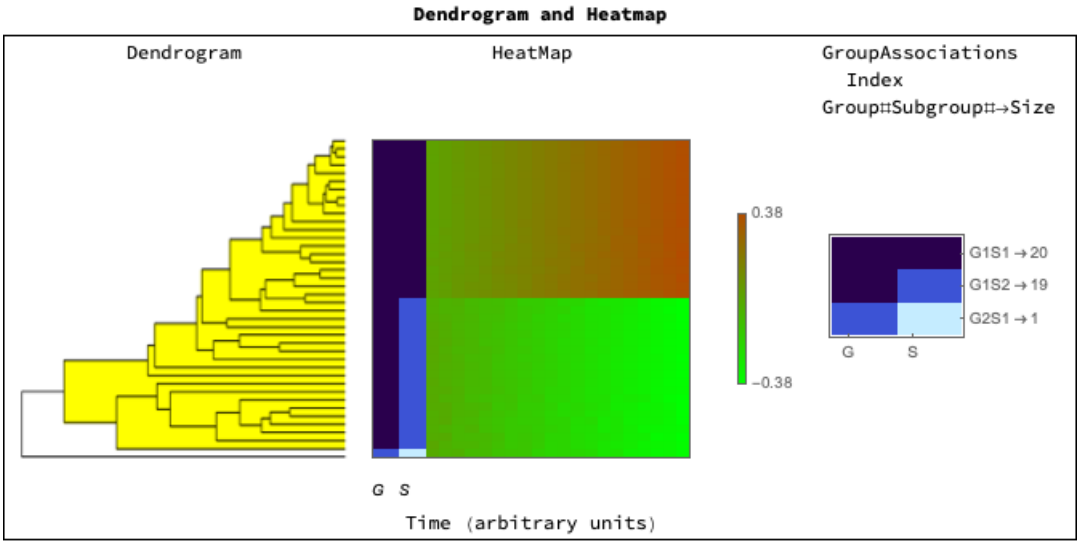
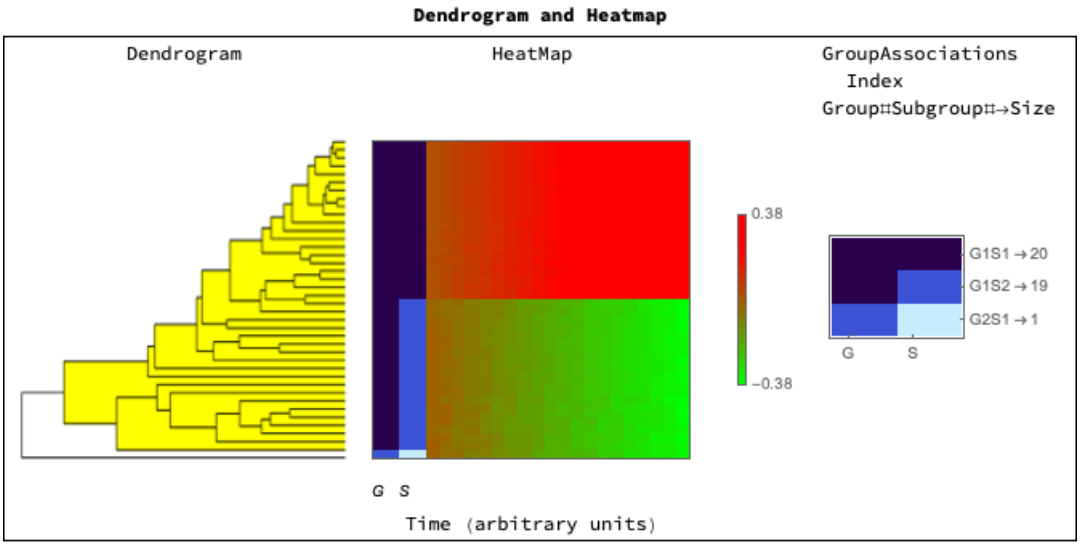
In[5]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ScaleShift → 0.7]
```

Out[5]=



In[6]:=
```
TimeSeriesDendrogramHeatmap[clusters1["f1"], ScaleShift → 1.3]
```

Out[6]=



VerticalLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

VerticalLabels provides labels for the vertical heatmap axis (the default value is None). The labels are distributed evenly in the vertical direction.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExampleSimple = Normalize[#] & /@
   Association[Join[Table["LP_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 5}],
     Table["LN_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 5}]]];
timePointsExample = Range[20];
classificationSimple = TimeSeriesClassification[classificationExampleSimple,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSimple = TimeSeriesClusters[classificationSimple];
```

In[3]:=
```
Keys[clustersSimple]
```

Out[3]= {f1}

We can extract the labels for the clustering:

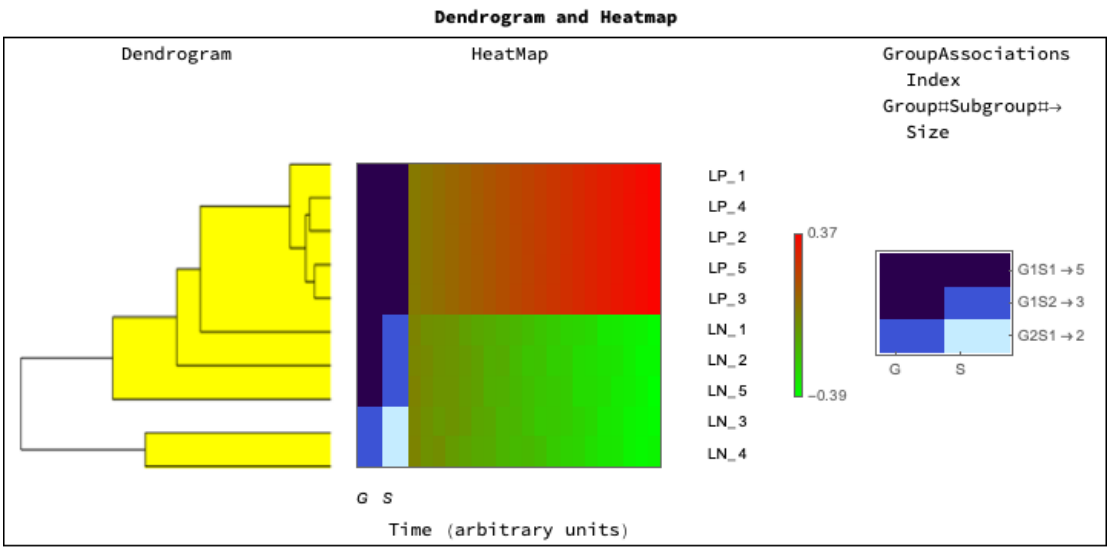
In[4]:=
```
Values@Query["f1", "Data"]@clustersSimple
```

Out[4]= {LP_1, LP_4, LP_2, LP_5, LP_3, LN_1, LN_2, LN_5, LN_3, LN_4}

We can now plot the dendrogram for any given class:

In[5]:=
```
TimeSeriesDendrogramHeatmap[clustersSimple["f1"],
 VerticalLabels → Values@Query["f1", "Data"]@clustersSimple]
```

Out[5]=



Properties & Relations (1)

TimeSeriesDendrogramsHeatmaps uses `TimeSeriesDendrogramHeatmap` repeatedly to plot multiple classes generated from clustering (e.g. by TimeSeriesClusters).

See Also

Heatmapper ▪ **MatrixClusters** ▪ **MatrixDendrogramHeatmap** ▪ **MatrixDendrogramsHeatmaps** ▪

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TimeSeriesDendrogramsHeatmaps ▪ **TimeSeriesClusters** ▪ **TimeSeriesSingleClusters** ▪ **TimeSeriesSingleDendrogramHeatmap** ▪ **TimeSeriesSingleDendrogramsHeatmaps**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾

URL ▾

TimeSeriesDendrogramsHeatmaps

`TimeSeriesDendrogramsHeatmaps[data]`
generates dendrogram and heatmap plots for all classified classes of time series data clusters.

Details

- `TimeSeriesDendrogramsHeatmaps[data]` generates dendrograms and associated heatmap plots for clustered time series data, typically the output of all classes generated by implementing TimeSeriesClusters. The input has the form of an association:

- $$\begin{aligned}&\texttt{data} = \\ &\quad \langle\!|\ \texttt{Class}_1 \to \langle\!|\texttt{Member}_{11} \to \{\{\texttt{classification vector}_{11}\}, \{\texttt{input data vector}_{11}\}\}, \\ &\qquad \texttt{Member}_{12} \to \{\{\texttt{classification vector}_{12}\}, \{\texttt{input data vector}_{12}\}\}, \ldots, \\ &\qquad \texttt{Member}_{1\,m_1} \to \{\{\texttt{classification vector}_{1\,m_1}\}, \{\texttt{input data vector}_{1\,m_1}\}\}\!|\rangle, \\ &\quad \texttt{Class}_2 \to \langle\!|\texttt{Member}_{21} \text{->} \{\{\texttt{classification vector}_{21}\}, \{\texttt{input data vector}_{21}\}\}, \\ &\qquad \texttt{Member}_{22} \text{->} \{\{\texttt{classification vector}_{22}\}, \{\texttt{input data vector}_{22}\}\}, \ldots, \\ &\qquad \texttt{Member}_{2\,m_2} \to \{\{\texttt{classification vector}_{2\,m_2}\}, \{\texttt{input data vector}_{2\,m_2}\}\}\!|\rangle, \ \ldots, \\ &\quad \texttt{Class}_M \to \langle\!|\texttt{Member}_{M1} \text{->} \{\{\texttt{classification vector}_{M1}\}, \{\texttt{input data vector}_{M1}\}\}, \\ &\qquad \texttt{Member}_{M2} \text{->} \{\{\texttt{classification vector}_{M2}\}, \{\texttt{input data vector}_{M2}\}\}, \ldots, \\ &\qquad \texttt{Member}_{Mm_M} \to \{\{\texttt{classification vector}_{Mm_M}\}, \{\texttt{input data vector}_{Mm_M}\}\}\!|\rangle\!|\rangle\end{aligned}$$

- The keys of the data correspond to the following properties related to the two tier clustering results generated by TimeSeriesClusters for each of the classification classes:

"Cluster"	Cluster generated.
"InitialSplitCluster"	Clusters resulting from splitting the initial cluster (reported by key "Cluster") into groups using the SignificanceCriterion to determine the number of clusters.
"IntermediateClusters"	Aglomerative clustering result of hierarchical clustering of each of the initial split clusters (reported by "InitialSplitCluster")
"SubsplitClusters"	Custers generated from splitting the clusters following the second tier clustering (reported by "IntermediateClusters") into subgroups using the SignificanceCriterion to determine the number of clusters.

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"Data"	Data reported in the order of clustering results as rules of {second initial classification vector} → label for each time series, sorted in order of the clustering results.
"GroupAssociations"	Association denoting membership of each initial data label to groups and subgroups generated by the two tier clustering.

- For each class a separate plot is generated: dendrograms are represented on the left, and are highlighted to represent the grouping level. The G, S, columns represent the groupings and subgroupings generated by the clustering. The legend shows the corresponding groupings and subgrouping, and the number of elements in each group subgroup.
- The following options can be given:

FunctionOptions	{ImageSize –> 200}	Options list passed to the internal TimeSeriesDendrogramHeatmap function.

Examples (3)

Basic Examples (2)

First we need to load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

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- We have multiple classes:

In[3]:=
```
Keys[clusters1]
```

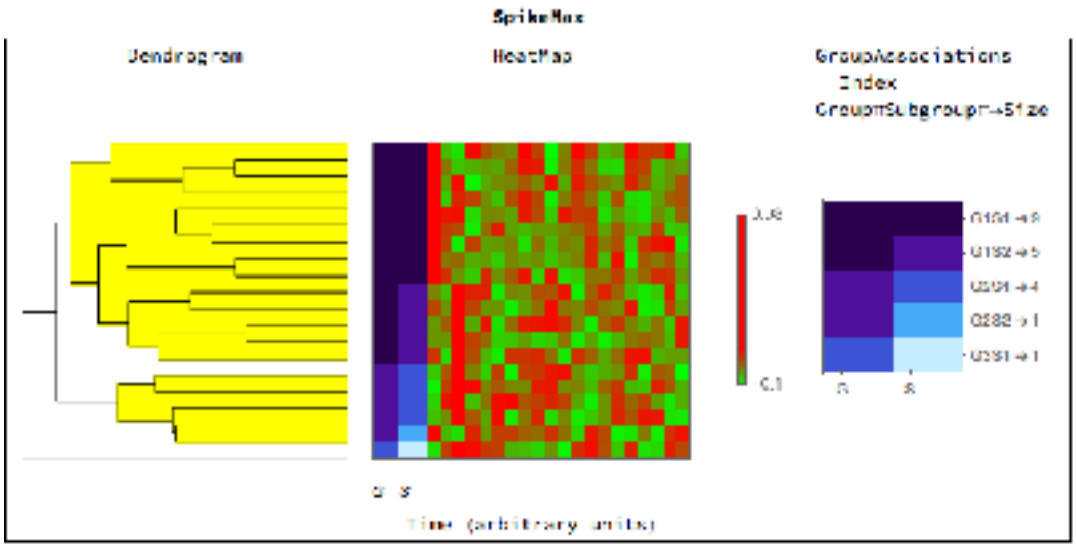
Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

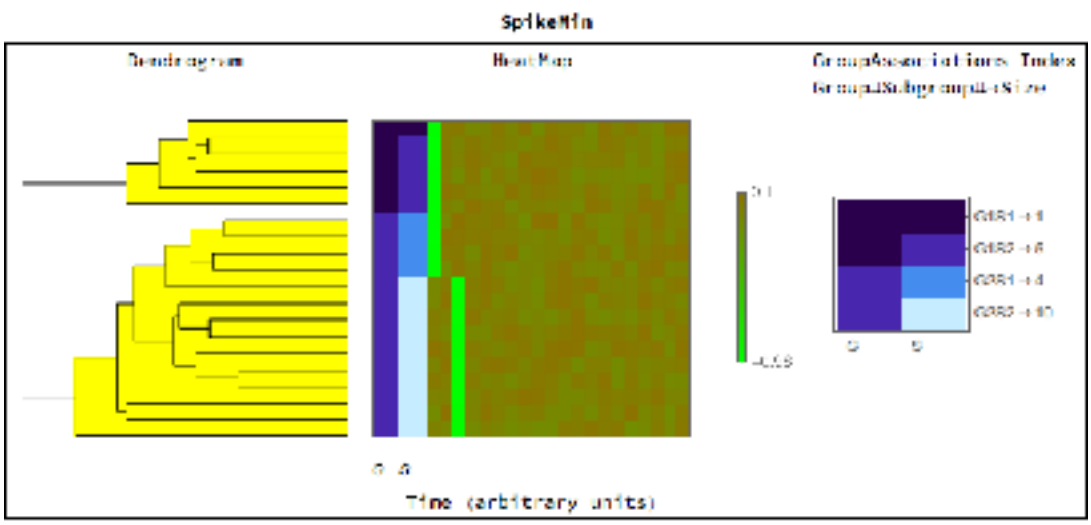
In[4]:=
```
clusters1["f1", "GroupAssociations", "G1S1"]
```

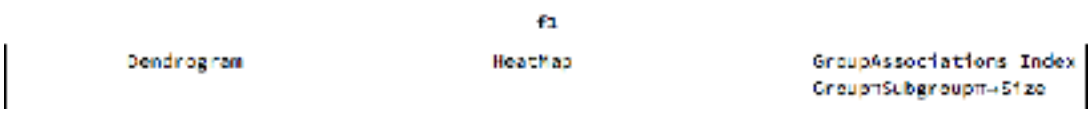
Out[4]=
```
{LinearPositive_1, LinearPositive_6, LinearPositive_7, LinearPositive_5, LinearPositive_9,
 LinearPositive_8, LinearPositive_10, LinearPositive_2, LinearPositive_3, LinearPositive_4,
 LinearPositive_12, LinearPositive_16, LinearPositive_14, LinearPositive_13, LinearPositive_20,
 LinearPositive_18, LinearPositive_19, LinearPositive_17, LinearPositive_11, LinearPositive_15}
```

- To plot all classes we use TimeSeriesDendrogramsHeatmaps .

In[5]:=
```
TimeSeriesDendrogramsHeatmaps[clusters1]
```







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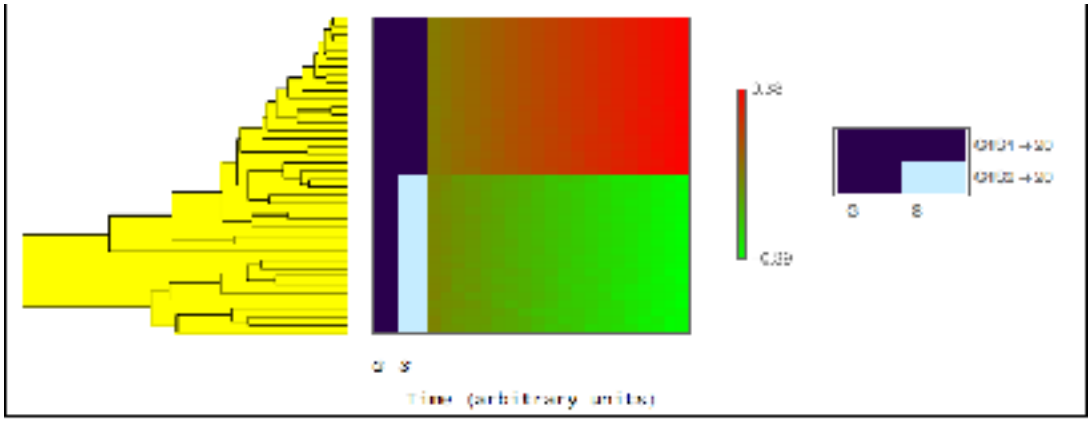
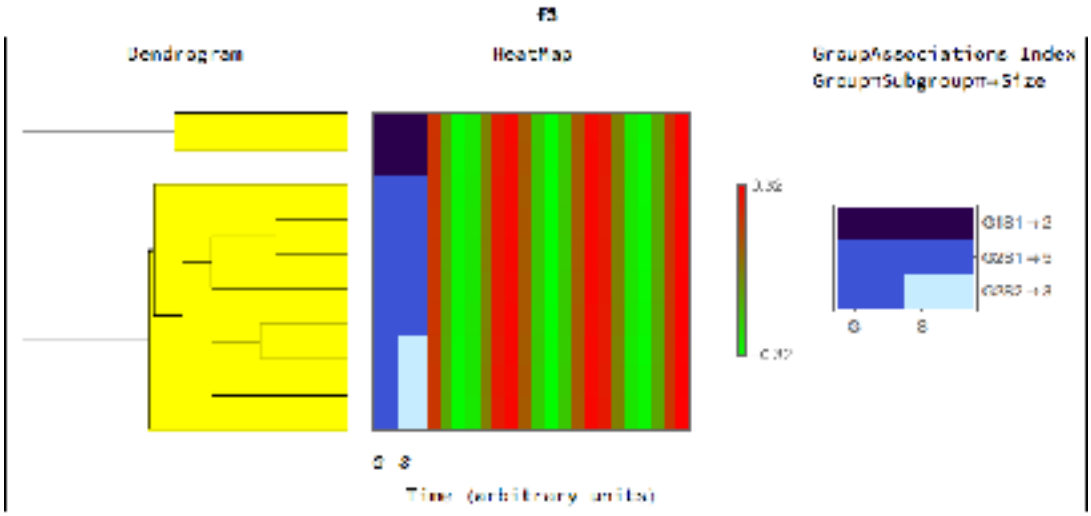
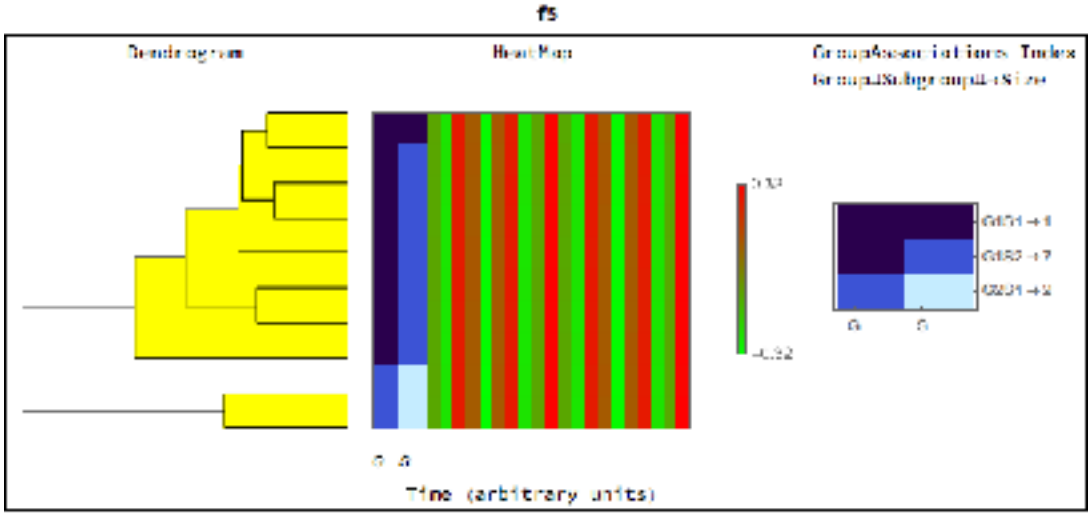


Out[5]=





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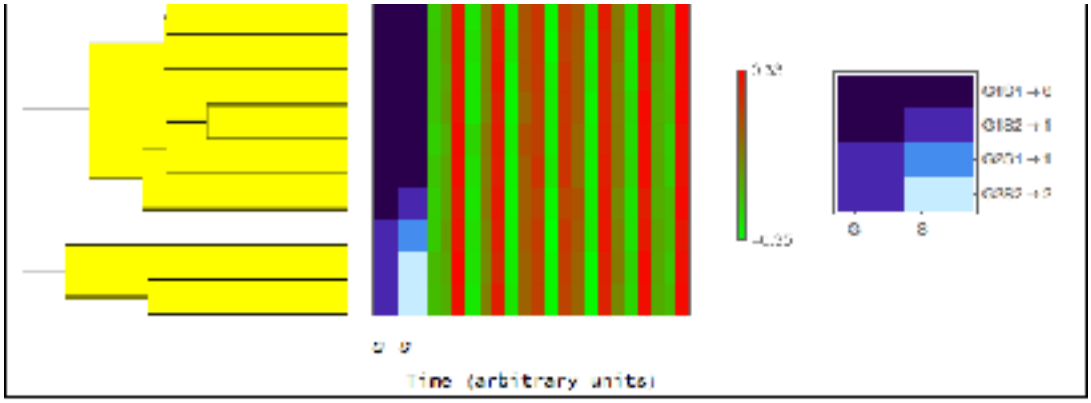



```
In[1]:= Needs["MathIOmica`"]
```

We can also consider data with missing values. We consider the previous example, with say up to 2 data points removed/set to Missing[], classify and cluster the following data for our example, for various trends and 20 time points:

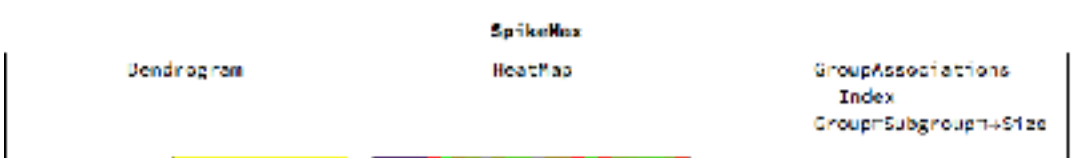
```
In[2]:= classificationExample2 =
  Query[All, Nest[ReplacePart[#, RandomInteger[{1, 20}] → Missing[]] &, #, RandomInteger[{1, 2}]] &] @
   (Normalize[#] & /@ Association[Join[
       Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
       Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["Sinusoidal1_" <> ToString[i] →
         Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}], Table[
        "Sinusoidal2_" <> ToString[i] → 5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
       Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
        {i, 21, 30}]]]);
timePointsExample = Range[20];
classification2 = TimeSeriesClassification[classificationExample2, timePointsExample,
   LombScargleCutoff → 0.89, SpikeCutoffs → <|18 → {.45, -.45}, 19 → {0.43, -0.43}, 20 → {0.42, -0.42}|>];
clusters2 = TimeSeriesClusters[classification2];
```

We have again multiple classes:

```
In[3]:= Keys[clusters1]
Out[3]= {SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class, and see Missing[] values shown in grey:

```
In[4]:= TimeSeriesDendrogramsHeatmaps[clusters2]
```



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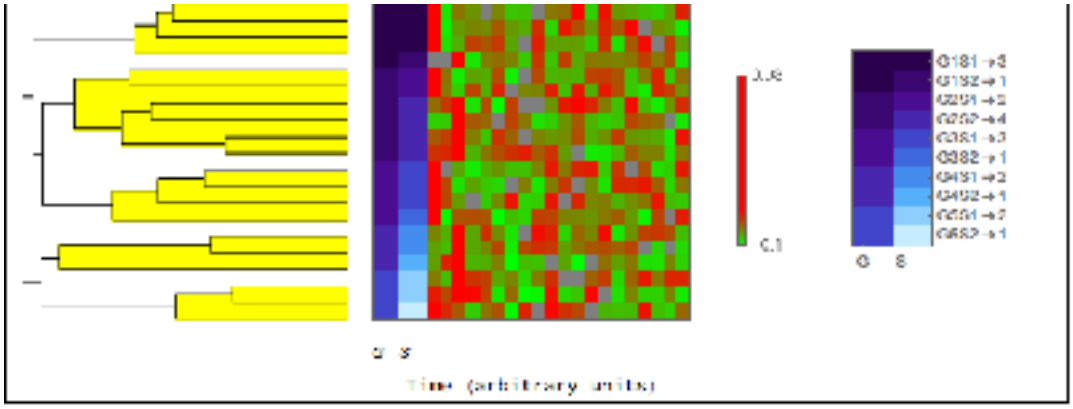

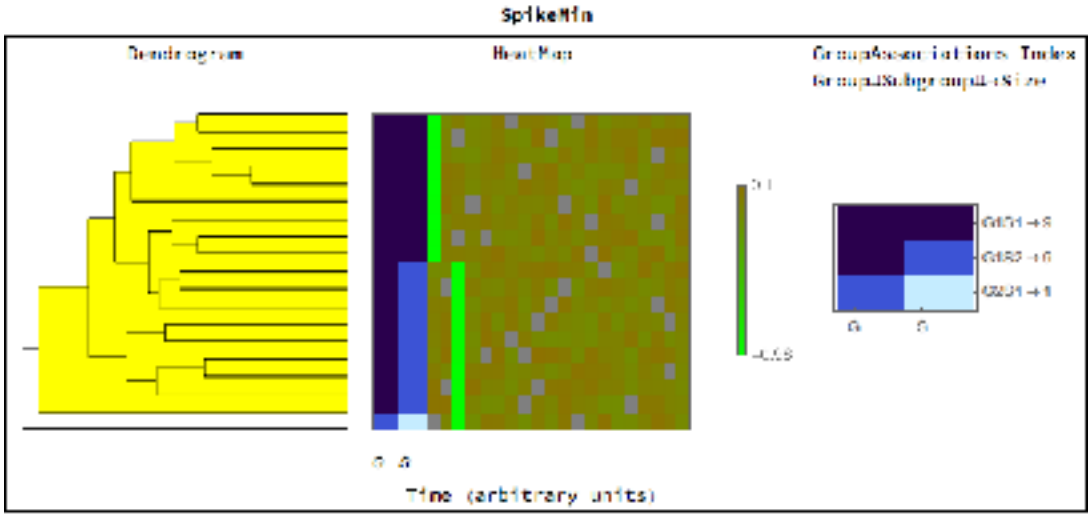

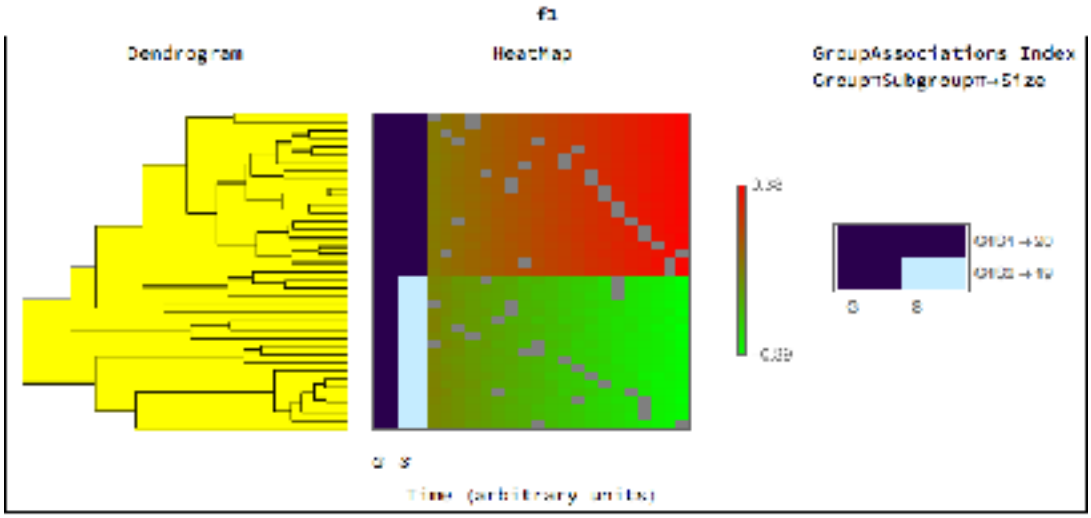

Out[4]=

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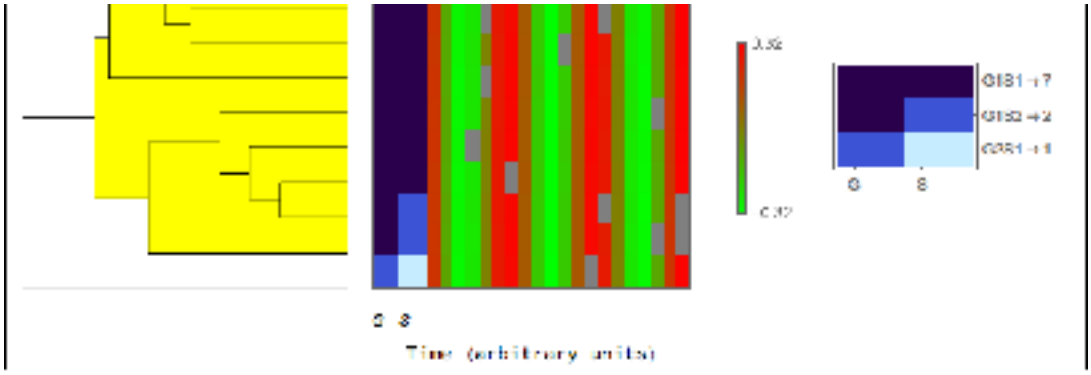
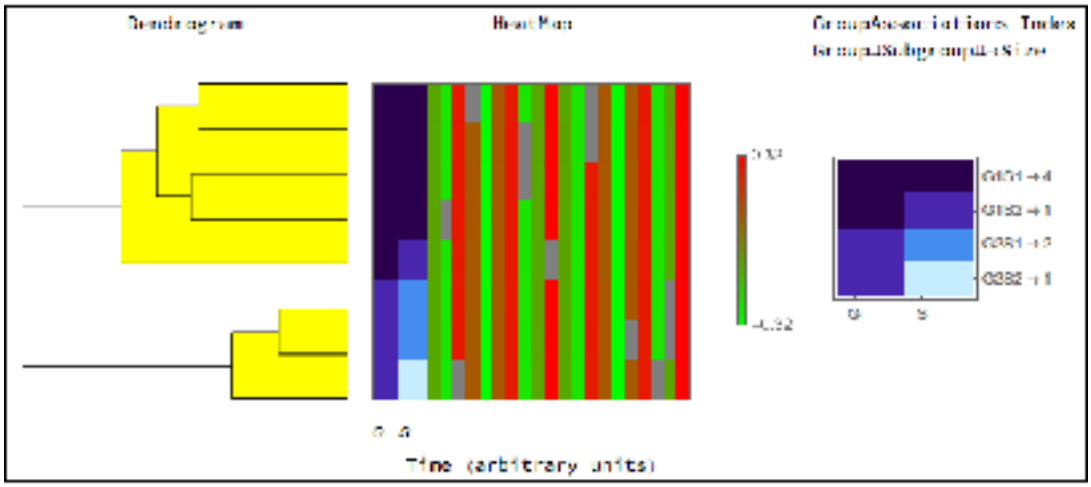
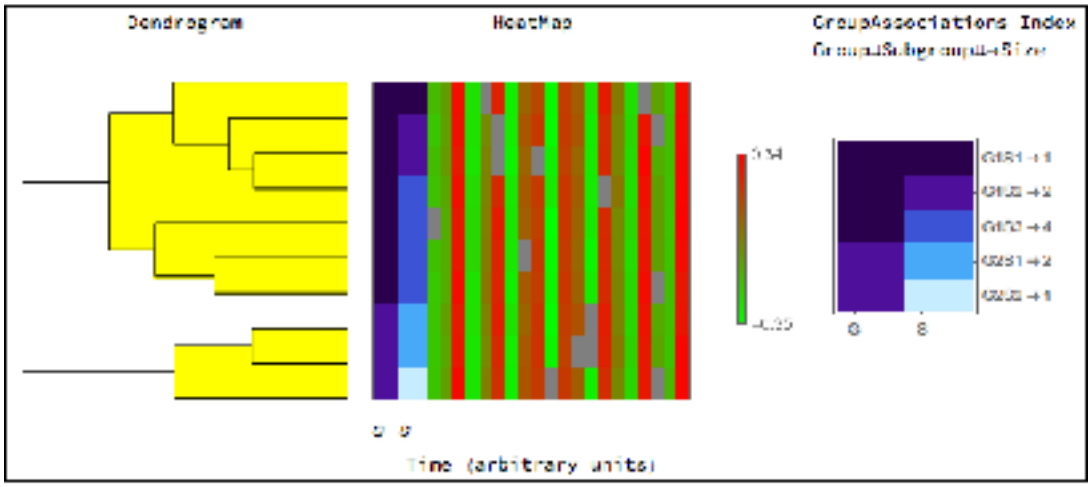


f5



f6



Options (1)

FunctionOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

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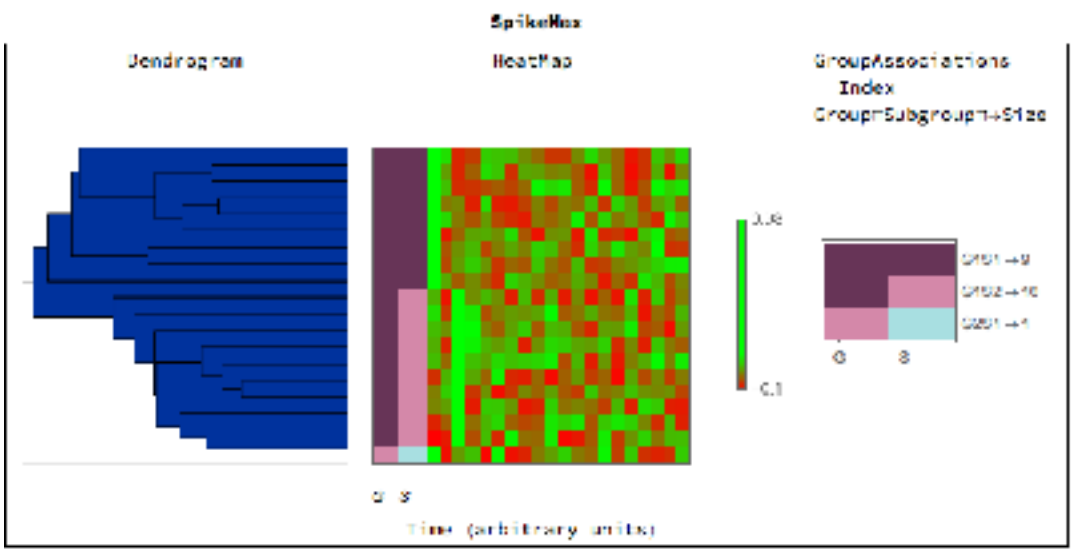
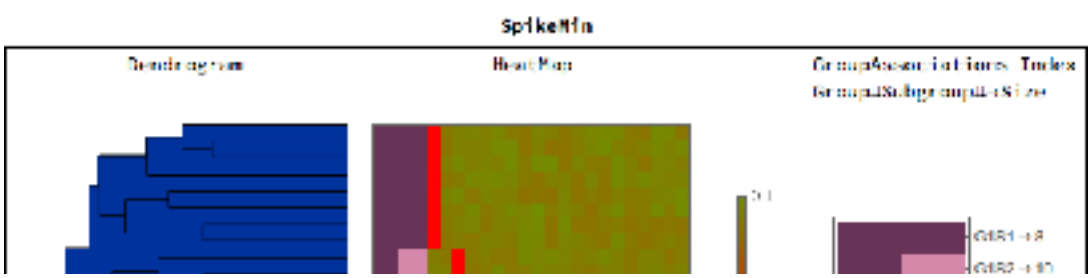
FunctionOptions provides a list of options that are used by an internal TimeSeriesDendrogramHeatmap function that is used in the plots.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clusters1 = TimeSeriesClusters[classification1];
```

In[3]:=
```
TimeSeriesDendrogramsHeatmaps[clusters1, FunctionOptions →
  {IndexColor → "CandyColors", ColorBlending → {Red, Green}, DendrogramColor → CMYKColor[1, .7, .05, .35]}]
```





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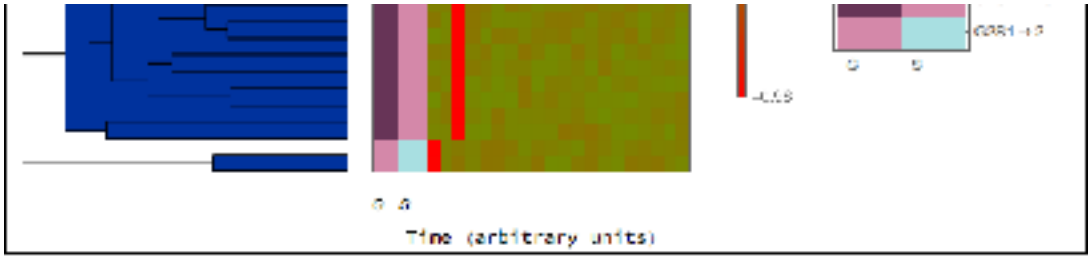
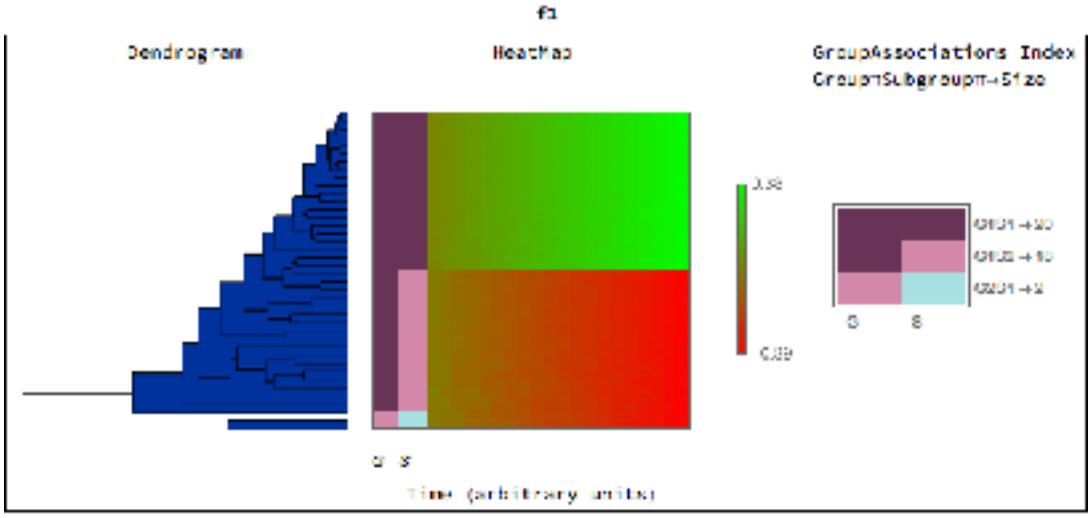
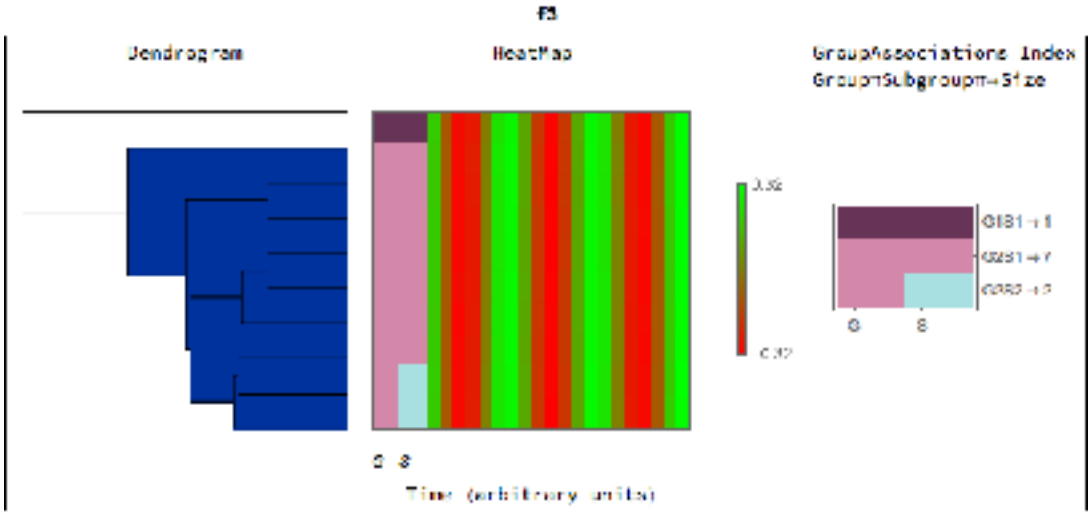
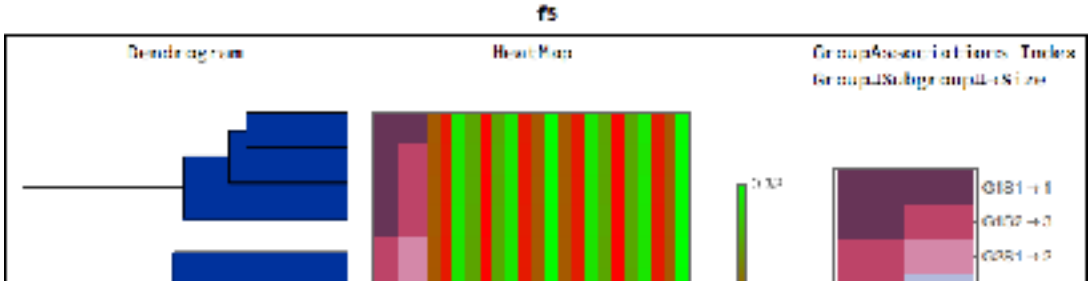




Out[3]=





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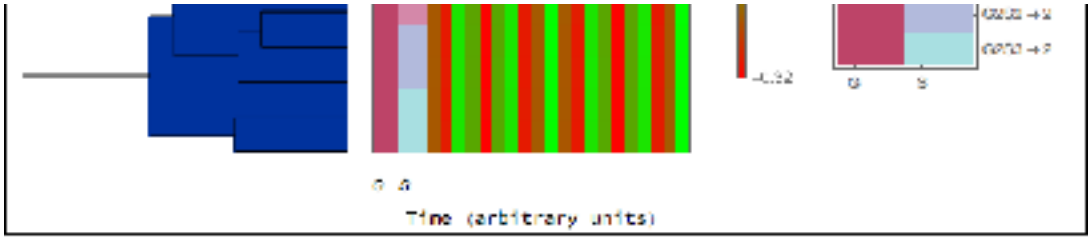

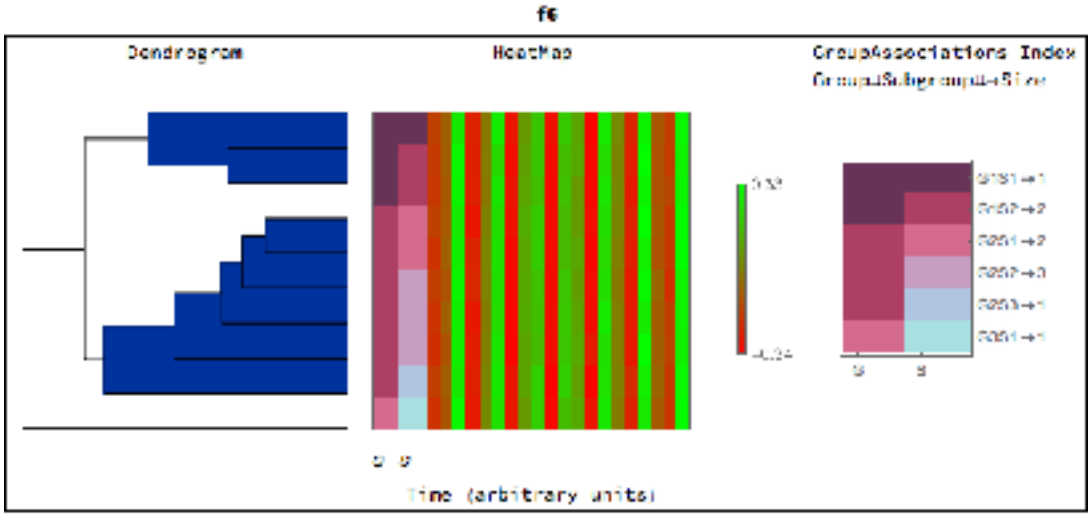

See Also

Heatmapper ▪ **MatrixClusters** ▪ **MatrixDendrogramHeatmap** ▪ **MatrixDendrogramsHeatmaps** ▪ **TimeSeriesClusters** ▪ **TimeSeriesDendrogramHeatmap** ▪ **TimeSeriesSingleClusters** ▪ **TimeSeriesSingleDendrogramHeatmap** ▪ **TimeSeriesSingleDendrogramsHeatmaps**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

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Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾

URL ▾

TimeSeriesSingleClusters

`TimeSeriesSingleClusters[data]`
performs clustering of a time series data using a single tier of hierachrical clustering to identify groups in the data.

Details

- TimeSeriesSingleClusters[data] takes as input series data, where each data is comprised of two lists and performs clustering of the data to identify groups based on similarities between the input series. The form of the input data is either an association of classes and members, where each member must have a list of two components, typically two vectors used in classification: $\{\{\text{classification vector}_1\}, \{\text{data vector}_2\}\}$.

- In the most common case of using as input data that came from performing a TimeSeriesClassification, the $\{\text{data vector}_2\}$ will correspond to input original data for the corresponding time series. In this case the input will have the form:

- $$\begin{aligned}
&\text{data} = \\
&\ <|\ \text{Class}_1 \to\ <|\text{Member}_{11} \to \{\{\text{classification vector}_{11}\}, \{\text{input data vector}_{11}\}\}, \\
&\quad \text{Member}_{12} \to\ \{\{\text{classification vector}_{12}\}, \{\text{input data vector}_{12}\}\}, \ldots, \\
&\quad \text{Member}_{1\,m_1} \to\ \{\{\text{classification vector}_{1\,m_1}\}, \{\text{input data vector}_{1\,m_1}\}\}|>, \\
&\ \text{Class}_2 \to\ <|\text{Member}_{21} \text{->} \{\{\text{classification vector}_{21}\}, \{\text{input data vector}_{21}\}\}, \\
&\quad \text{Member}_{22} \text{->} \{\{\text{classification vector}_{22}\}, \{\text{input data vector}_{22}\}\}, \ldots, \\
&\quad \text{Member}_{2\,m_2} \to\ \{\{\text{classification vector}_{2\,m_2}\}, \{\text{input data vector}_{2\,m_2}\}\}|>, \ \ldots, \\
&\ \text{Class}_M \to\ <|\text{Member}_{M1} \text{->} \{\{\text{classification vector}_{M1}\}, \{\text{input data vector}_{M1}\}\}, \\
&\quad \text{Member}_{M2} \text{->} \{\{\text{classification vector}_{M2}\}, \{\text{input data vector}_{M2}\}\}, \ldots, \\
&\quad \text{Member}_{Mm_M} \to\ \{\{\text{classification vector}_{Mm_M}\}, \{\text{input data vector}_{Mm_M}\}\}|>|>
\end{aligned}$$

- We note that in the cases where only one class of data is being considered, the input can also be provided as a list of associations, or a single association, or a list of associations, or a single list of lists.

- A single-tier hierarchical clustering of the data is performed, using $\{\text{classification vector}_1\}$ for each series to cluster the data pairwise.

- The number of groups for the clustering is automatically determinded by using internally the "Silhouette" (default) or "Gap" as "SignificanceTest" methods (see also Partitioning Data into Clusters) .

- The result is grouping of the data based on similarity, denoted as G#, where G denotes the group based on the clustering and # an index integer.

- The output is always an association of associations, providing a summary of the clustering results for each class provided in the input. The output has the form:

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```
output =
 <| Class1 → <|"Cluster" → cluster object1,
    "InitialSplitCluster" → {InitialSplitCluster11, InitialSplitCluster12 ...},
    "GroupAssociations" → <|"G1" → {member list G1},
      "G2" → {member list for G2},
      ...,
      "Gn1" → {member list for Gn1}|>|>,
  Class2 → <|"Cluster" → cluster object2,
    "InitialSplitCluster" → {InitialSplitCluster21, InitialSplitCluster22 ...},
    "GroupAssociations" → <|"G1" → {member list G1},
      "G2" → {member list for G2},
      ...,
      "Gn2" → {member list for Gn2}|>|>,
  ...,
  ClassM → <|"Cluster" → cluster objectM,
    "InitialSplitCluster" → {InitialSplitClusterM1, InitialSplitClusterM2 ...},
    "GroupAssociations" → <|"G1" → {member list G1},
      "G2" → {member list for G2},
      ...,
      "GnM" → {member list for GnM}|>|>
 |>
```

- The keys of the output correspond to the following properties related to the clustering results:

"Cluster"	Cluster generated using the input {classification vector$_1$} for similarity calculations.
"InitialSplitCluster"	Clusters resulting from splitting the initial cluster (reported by key "Cluster") into groups using the SignificanceCriterion to determine the number of clusters.
"GroupAssociations"	Association denoting membership of each initial data label to groups generated by the single tier clustering.

- The following options can be given:

ClusterLabeling	""	Additional label to append to each cluster being computed to prepend to the inbuilt G#.
DendrogramPlotOptions	{}	Options passed to the DendrogramPlot function used internally to generate the dendrograms.
DistanceFunction	EuclideanDistance	Distance function to be used in calculating the similarities between different time series in the clustering.
LinkageMeasure	"Average"	Which linkage measure to use in computing fusion coefficients.
PrintDendrograms	False	Option to print dendrograms for the clustering computed.
ReturnDendrograms	False	Option to return the dendrograms as output.

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SignificanceCriterion	"Silhouette"	Method used in determining the number of groups in the clustering.
SingleAssociationLabel	"1"	Label to use in case a list is provided to name the class of data produced.

- For a given set of series, Mathematica provides various measures of distance similarity, DistanceAndSimilarityMeasures. Three of the most common measures are the the EuclideanDistance, CorrelationDistance, and the CosineDistance.
- EuclideanDistance (default for `TimeSeriesSingleClusters`), uses the Euclidean distance between two arbitrary vectors U and V as $d_{euc}(U, V) = (\sum_i (U_i - V_i)^2)^{1/2}$, i.e. the Pythagorean distance between two vectors.
- CorrelationDistance measures the correlation distance between two arbitrary vectors U and V, as $d_{corr}(U, V) = 1 - \frac{(U - \langle U \rangle) \cdot (V - \langle V \rangle)}{\| U - \langle U \rangle \| \| V - \langle V \rangle \|}$ where * here denotes a dot product, <> denotes an average, and || || denotes a norm.
- The CosineDistance between two arbitrary vectors U and V is $d_{cos}(U, V) = 1 - \frac{U \cdot V}{\| U \| \| V \|}$. It is equal to the correlation distance in the case that the averages of U and V are zero.
- For two clusters A and B, the average linkage fusion coefficient between the two clusters is defined to be $L(A,B) = \frac{1}{|A|} \frac{1}{|B|} \sum_{a_i \in A} \sum_{b_j \in B} d(a_i, b_j)$, and thus a larger fusion coefficient means the two clusters are more well-separated. So, when deciding how to optimally cluster a given set of variables into two subsets, one chooses the partition such that the average linkage fusion coefficient is maximized, and this is the optimal partioning of this group of data into two separate clusters.

Examples (9)

Basic Examples (1)

First we need to load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

We create and classify the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

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```
Method → "LombScargle"
```

Out[2]=

```
<|SpikeMax →
  <|SpikePositive_1 → {{0.377536, 0.126534, 0.227088, 0.341425, 0.311439, 0.264319, 0.220993, 0.265013,
      0.572205, 0.244884}, {0.975645, -0.0499442, 0.0401233, 0.0389317, 0.0653422, 0.056746,
      -0.0355301, -0.0480344, 0.0165666, -0.0663353, -0.0877162, -0.0625657, 0.0239258,
      -0.0716819, 0.0704533, -0.0382771, -0.0302313, 0.0179736, 0.0331398, 0.0260595}},
   SpikePositive_2 → {{0.183878, 0.418409, 0.307359, 0.330018, 0.221003, 0.371498, 0.301183,
      0.303271, 0.356576, 0.301756}, {0.973116, -0.000804316, -0.0809772, 0.0541296, -0.083353,
      -0.0229172, -0.0345843, 0.0399539, -0.00831854, 0.0870577, -0.0351829, -0.015894, -0.0293177,
      0.0306959, -0.0828304, -0.0842261, -0.0230959, -0.0274386, -0.0147999, 0.0830133}},
   SpikePositive_3 → {{0.190822, 0.160836, 0.320254, 0.344052, 0.288156, 0.36634, 0.422387,
      0.234551, 0.45562, 0.241933}, {0.986788, -0.0375798, -0.0429245, 0.0163682, 0.0166477,
      0.0856998, -0.0353091, -0.0179756, -0.00502708, -0.0196218, 0.0256927, -0.0148214, 0.0757768,
      0.0184262, -0.0423411, 0.0390384, -0.0367786, -0.00158498, 0.0345256, -0.0173176}},
   SpikePositive_4 → {{0.185488, 0.161838, 0.385761, 0.358973, 0.224681, 0.324864, 0.34274,
      0.227775, 0.512277, 0.271903}, {0.968581, -0.0344471, -0.0765712, 0.0093056, 0.0364873,
      0.0766313, 0.0589806, -0.0766538, -0.0870111, 0.0287572, 0.0847588, 0.0477357, -0.0406988,
      0.0636941, -0.060927, 0.0462968, 0.0055593, 0.0808895, -0.0141519, -0.0441785}},
   SpikePositive_5 → {{0.0823386, 0.220825, 0.439498, 0.18011, 0.415022, 0.260699, 0.412025,
      0.21862, 0.467512, 0.206216}, {0.965984, 0.0223584, -0.0769476, 0.0111129, -0.0368375,
      0.0371604, 0.00410283, -0.0136156, 0.0677925, -0.0987696, 0.0258173, 0.0914819, 0.0767131,
      -0.0619007, -0.0333297, -0.0847753, -0.0368218, -0.0728362, -0.0648775, -0.0715446}},
   SpikePositive_6 → {{0.273001, 0.229444, 0.201224, 0.384082, 0.137518, 0.174174, 0.375493,
      0.447393, 0.27284, 0.469011}, {0.970243, 0.0445343, 0.0452492, -0.0470938, -0.0432949,
      0.0799459, -0.0600788, -0.042645, -0.066792, 0.0616696, 0.00473499, 0.0134532, -0.0993007,
      0.0899993, 0.00987543, -0.0111679, 0.0469394, -0.0309088, 0.0884848, -0.0323733}},
   SpikePositive_7 → {{0.413584, 0.231173, 0.287882, 0.278691, 0.251784, 0.138108, 0.4187,
      0.330292, 0.378179, 0.324148}, {0.968083, 0.0203132, 0.0483422, -0.029859, -0.0392207,
      0.0762786, -0.0950564, 0.0441669, 0.0603421, -0.0894993, -0.0722895, -0.0509827,
      -0.000224579, 0.0374386, 0.0557405, 0.013653, 0.0739977, 0.0616993, 0.083818, -0.0187345}},
   SpikePositive_8 → {{0.337622, 0.2448, 0.349656, 0.385675, 0.287833, 0.344473, 0.249069,
      0.288792, 0.357195, 0.283806}, {0.957044, -0.0124668, -0.0688708, 0.0756275, 0.0777307,
      0.079711, 0.0813853, 0.0815728, -0.0793447, 0.0302706, 0.0293412, -0.0698088, -0.0879294,
      -0.00882169, -0.0651249, -0.0902102, -0.00203167, 0.00182402, 0.0729092, 0.0965295}},
   SpikePositive_9 → {{0.183599, 0.19964, 0.463172, 0.312105, 0.275169, 0.258303, 0.0839067,
      0.393703, 0.425864, 0.358687}, {0.961198, -0.00660715, -0.064723, -0.099292, -0.0290666,
      0.0538273, -0.0341916, 0.0427049, -0.074944, 0.022075, -0.0913164, 0.0160681, 0.091887,
      -0.0839121, 0.080064, -0.0702979, -0.0513539, 0.0749158, -0.0608744, -0.0421906}},
   SpikePositive_10 → {{0.314067, 0.175627, 0.213734, 0.385487, 0.180438, 0.452174, 0.14742,
      0.191027, 0.571279, 0.233734}, {0.968388, 0.0590357, 0.0145383, 0.039487, -0.00355491,
      -0.0574058, 0.0193678, -0.0411893, -0.0437683, 0.0790279, -0.0878875, -0.085455,
      0.00227201, 0.078063, 0.00725375, 0.0607331, -0.10163, 0.0580699, -0.0647887, -0.0257307}},
   SpikePositive_11 → {{0.180072, 0.349916, 0.151724, 0.352401, 0.178854, 0.286106, 0.397267,
      0.349669, 0.394315, 0.385366}, {-0.0547589, -0.0436499, 0.950002, -0.0989523, -0.0126094,
      -0.0660978, -0.0418982, 0.0361536, -0.0961097, -0.0888443, 0.0883003, 0.0945619, -0.0847088,
      0.0299323, -0.0742398, 0.0273786, -0.0975514, 0.0521691, 0.0772064, 0.0938622}},
   SpikePositive_12 → {{0.18606, 0.140027, 0.352445, 0.551644, 0.29166, 0.290868, 0.296348,
      0.218987, 0.406631, 0.215521}, {0.0404589, -0.0777541, 0.966872, 0.0564372, -0.0688794,
      -0.0316483, 0.0986402, 0.0551293, -0.047029, -0.0449429, 0.0401954, -0.0157875, -0.0191132,
      -0.0890759, 0.0973962, 0.071852, 0.0249724, -0.0572762, -0.0449898, -0.0283221}},
   SpikePositive_13 → {{0.178918, 0.299452, 0.441023, 0.275168, 0.327012, 0.126542, 0.290182,
      0.252383, 0.512114, 0.273835}, {-0.0316596, -0.0435795, 0.965751, -0.0254641, 0.0771254,
      -0.0999783, 0.0229843, -0.0855508, -0.0615097, 0.0470724, 0.0193996, -0.0854435, 0.00731687,
      -0.00201888, 0.0277369, 0.0705256, -0.0108742, -0.0808313, -0.0862707, 0.0800822}},
   SpikePositive_14 → {{0.424784, 0.32815, 0.40131, 0.235815, 0.246516, 0.264477, 0.171951,
      0.250971, 0.454815, 0.255126}, {0.0701577, 0.0765725, 0.976436, -0.0157799, 0.0688371,
      0.0102558, 0.0100666, -0.079031, -0.00177166, -0.0239684, -0.0273444, -0.0491044, -0.0598414,
      -0.0107573, 0.0573085, -0.00714199, 0.00136565, -0.0809, -0.0202104, 0.0813898}},
   SpikePositive_15 → {{0.166476, 0.461996, 0.197933, 0.31338, 0.269519, 0.205326, 0.262173,
      0.380493, 0.378562, 0.387095}, {-0.0289206, -0.0292703, 0.967657, 0.0362345, 0.0609741,
      -0.0804262, 0.0622164, -0.00231658, -0.0355193, -0.055919, 0.0953032, 0.081346, -0.0168527,
      0.0591689, -0.0511003, -0.0588133, -0.0897043, -0.068773, 0.0259331, -0.0563837}},
   SpikePositive_16 → {{0.162641, 0.34839, 0.210169, 0.332637, 0.318076, 0.291214, 0.23517,
      0.444403, 0.296652, 0.413007}, {-0.0480074, 0.0228408, 0.969387, -0.0456522, 0.0305821,
```

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```
    -0.0882546, 0.010624, 0.00135594, -0.0849094, 0.0636071, -0.0558061, 0.09157, 0.0600992,
    -0.0135084, 0.0566979, -0.0820188, 0.0668288, 0.00764419, 0.0730762, -0.01359}},
  SpikePositive_17 → {{0.340371, 0.312728, 0.289065, 0.0642306, 0.331369, 0.357193, 0.251391,
    0.37921, 0.341638, 0.370888}, {-0.0229264, -0.0869165, 0.955335, 0.0226434, 0.0619697,
    0.0861752, -0.0212462, -0.101371, 0.00457296, -0.0381761, -0.0866245, -0.0825105,
    -0.0762833, 0.087413, 0.0236252, -0.0978978, -0.0454989, -0.090802, 0.0739499, -0.0396411}},
  SpikePositive_18 → {{0.082589, 0.155371, 0.283409, 0.300807, 0.413858, 0.274277, 0.433575,
    0.298348, 0.421556, 0.311477}, {0.043928, -0.0785244, 0.969703, -0.0221774, -0.0881149,
    -0.0440621, 0.0408826, 0.0428301, 0.0823653, 0.00949464, 0.0043451, -0.0529293, 0.0934254,
    0.0821909, -0.0567414, -0.00793611, -0.000406105, 0.0145316, 0.0126057, -0.0951098}},
  SpikePositive_19 → {{0.343263, 0.514203, 0.273135, 0.442318, 0.402095, 0.248105, 0.128874,
    0.183237, 0.214393, 0.16773}, {-0.000539619, 0.0645466, 0.96869, 0.0843663, -0.0265106,
    0.0754965, 0.0606102, -0.00610638, -0.0391722, 0.00540108, -0.031337, 0.0509399, 0.0795434,
    -0.0132697, -0.0135979, -0.0905822, 0.0280867, -0.0992737, -0.0158058, 0.0965149}},
  SpikePositive_20 → {{0.179041, 0.412745, 0.373056, 0.479394, 0.178821, 0.409861, 0.305272,
    0.183675, 0.265487, 0.176701}, {-0.0686623, 0.0892081, 0.969385, 0.0605215, 0.0707931,
    0.0117872, -0.0178827, -0.0145966, 0.051365, -0.0321855, 0.049711, 0.0799825, 0.0655221,
    -0.0757613, 0.0488191, 0.0606057, 0.0044402, -0.0605654, -0.0103904, -0.0764636}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.2737, 0.193299, 0.380166, 0.251616, 0.281839, 0.322197,
    0.322409, 0.279648, 0.496641, 0.26046}, {-0.981458, 0.028678, -0.0409471, -0.0271838,
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    -0.0879229, 0.017558, -0.0291186, 0.0307966, 0.0104456, -0.0361015, -0.0991689, -0.00608389}},
  SpikeNegative_2 → {{0.25017, 0.323847, 0.469791, 0.328521, 0.311454, 0.291309, 0.244944,
    0.251888, 0.393509, 0.209164}, {-0.960073, -0.0845988, 0.0131319, -0.00419922, 0.0768407,
    -0.0918345, 0.019879, 0.0612609, -0.0750127, 0.0199675, 0.0760372, -0.0453613, -0.0878043,
    0.0878892, -0.0473821, 0.0934067, 0.0623993, 0.0324588, 0.00689594, -0.0846348}},
  SpikeNegative_3 → {{0.206813, 0.263391, 0.263412, 0.235085, 0.309268, 0.238347, 0.523647,
    0.125312, 0.540186, 0.170401}, {-0.96837, -0.000161296, 0.0855302, 0.00403312, 0.0774816,
    0.0130709, 0.0195437, 0.0750072, -0.0803728, 0.0831626, -0.00662684, -0.0540657, 0.0591939,
    -0.0547884, 0.0765582, -0.0578355, 0.029509, -0.0423121, 0.0677694, 0.0586319}},
  SpikeNegative_4 → {{0.186765, 0.402397, 0.281176, 0.265048, 0.229275, 0.217172, 0.263982,
    0.275236, 0.577332, 0.274591}, {-0.977388, -0.0276319, -0.0552166, 0.0792796, 0.0806344,
    0.0741077, -0.0123994, 0.0460487, -0.0581247, -0.00216038, -0.00524078, -0.000843605,
    0.0391311, 0.0392059, -0.0239054, 0.0857963, 0.0318057, 0.0623876, -0.0320753, -0.00135886}},
  SpikeNegative_5 → {{0.250762, 0.269589, 0.376984, 0.227773, 0.292443, 0.425825, 0.342138,
    0.245778, 0.409647, 0.24149}, {-0.981048, -0.0336579, -0.0120235, -0.0762906, 0.0567084,
    0.0375414, -0.022577, -0.0471807, 0.0500128, 0.0352881, -0.0263003, 0.0689197, -0.0467611,
    -0.0203215, 0.0488475, 0.0620853, 0.0546303, 0.023892, -0.0324564, 0.0211783}},
  SpikeNegative_6 → {{0.331608, 0.301683, 0.211952, 0.263321, 0.381157, 0.198105, 0.26403,
    0.125969, 0.635323, 0.104973}, {-0.968606, -0.0604037, -0.0217052, -0.0117373, 0.0480996,
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  SpikeNegative_7 → {{0.437556, 0.287171, 0.219307, 0.193445, 0.258054, 0.289212, 0.170715,
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    0.0703398, 0.00641848, 0.0367221, -0.0903878, -0.0923014, 0.0013834, -0.0772782}},
  SpikeNegative_8 → {{0.112975, 0.151907, 0.348079, 0.237668, 0.292185, 0.432831, 0.158789,
    0.42698, 0.322292, 0.449892}, {-0.956655, -0.00869125, 0.0367912, 0.0283036, -0.0938004,
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  SpikeNegative_9 → {{0.14335, 0.314848, 0.312864, 0.311678, 0.247461, 0.350682, 0.317583,
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    0.00951344, 0.0744626, 0.0664839, -0.0481246, 0.0284149, -0.0380926, -0.0241689}},
  SpikeNegative_10 → {{0.239638, 0.277651, 0.183079, 0.312239, 0.142456, 0.258695, 0.244825,
    0.313074, 0.614074, 0.334984}, {-0.978122, -0.00624069, -0.0735614, -0.00737702, -0.0781325,
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    0.0397417, -0.0230209, 0.0553683, 0.0512275, -0.0427101, -0.0510465, -0.00792885, 0.0497494}},
  SpikeNegative_11 → {{0.289783, 0.407354, 0.279281, 0.335763, 0.175671, 0.401101, 0.241101,
    0.163804, 0.502116, 0.174729}, {-0.0668292, 0.047151, -0.966336, -0.0358278, -0.0314594,
    -0.0502751, -0.0241903, 0.0219332, -0.0162377, 0.0448167, -0.101431, -0.0495551,
    0.0441598, 0.0842858, -0.0643044, 0.0364083, 0.085304, 0.0718249, 0.0575113, -0.091458}},
  SpikeNegative_12 → {{0.201548, 0.177395, 0.311386, 0.219547, 0.333848, 0.419758, 0.414965,
    0.277174, 0.40117, 0.291781}, {0.102411, 0.0947327, -0.961059, 0.100977, 0.00293761,
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    0.0540988, 0.0641197, 0.0247426, -0.00105226, -0.0711261, -0.0593804, -0.0433988}},
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  SpikeNegative_13 → {{0.367807, 0.346244, 0.325789, 0.216576, 0.383261, 0.394869, 0.27407,
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  SpikeNegative_14 → {{0.26686, 0.259595, 0.277644, 0.20783, 0.193776, 0.27326, 0.252668,
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  SpikeNegative_15 → {{0.258699, 0.291246, 0.229373, 0.244854, 0.189405, 0.429589, 0.297236,
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  SpikeNegative_16 → {{0.328659, 0.289828, 0.43245, 0.209198, 0.364127, 0.422665, 0.290481,
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  SpikeNegative_17 → {{0.26475, 0.389365, 0.435637, 0.271051, 0.256583, 0.234757, 0.408134,
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     0.0251027, 0.0550343, 0.000847099, 0.0842775, 0.0391171, 0.0976847, -0.0265516}},
  SpikeNegative_18 → {{0.194289, 0.128338, 0.182709, 0.296765, 0.298207, 0.502697, 0.43338,
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     0.031942, 0.067682, -0.0210392, 0.00136299, 0.0994887, -0.0233012, -0.00913238, 0.0917693}},
  SpikeNegative_19 → {{0.391842, 0.199513, 0.191745, 0.406766, 0.276605, 0.313459, 0.27125,
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  SpikeNegative_20 → {{0.353308, 0.153034, 0.403829, 0.373137, 0.230081, 0.192004, 0.291367,
     0.312224, 0.411513, 0.328513}, {0.00572282, -0.00553093, -0.975483, 0.0251449, -0.0580546,
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  LinearPositive_2 → {{0.983462, 0.169976, 0.0316224, 0.00275178, 0.00158049,
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  LinearPositive_3 → {{0.984392, 0.164023, 0.0319303, 0.00243951, 0.00210556, 0.0103787,
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  LinearPositive_4 → {{0.984551, 0.163602, 0.0316921, 0.00214476, 0.00238943, 0.0112782,
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  LinearPositive_5 → {{0.983649, 0.168335, 0.0326262, 0.00288648, 0.00226863, 0.0108792,
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  LinearPositive_6 → {{0.984555, 0.163945, 0.0298417, 0.00168943, 0.00168203,
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  LinearPositive_7 → {{0.984354, 0.165065, 0.031391, 0.00242755, 0.00192761, 0.0100175,
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  LinearPositive_8 → {{0.984789, 0.161569, 0.0348001, 0.00183195, 0.00168586, 0.0112903,
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  LinearPositive_9 → {{0.983695, 0.16884, 0.0311026, 0.00210809, 0.00221345, 0.0109198,
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    0.0935818, 0.110301, 0.131118, 0.148971, 0.168532, 0.188136, 0.204207, 0.223956,
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 LinearPositive_10 → {{0.984209, 0.165025, 0.0339013, 0.00223742, 0.00180624, 0.0106092,
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 LinearPositive_11 → {{0.984658, 0.164671, 0.0339117, 0.0029376, 0.00121608, 0.00604161,
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 LinearPositive_14 → {{0.985175, 0.159792, 0.0262252, 0.00377499, 0.00135797, 0.0100061,
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 LinearPositive_16 → {{0.983788, 0.16273, 0.0436892, 0.00550545, 0.00607111, 0.0141581,
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 LinearPositive_18 → {{0.977253, 0.200866, 0.0207729, 0.00227725, 0.00301532, 0.0116246,
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    0.236523, 0.253363, 0.28506, 0.304923, 0.314404, 0.345783, 0.34911, 0.377698}},
 LinearPositive_19 → {{0.985358, 0.162891, 0.021785, 0.000999845, 0.00293066, 0.0130704,
    0.0210489, 0.0195433, 0.0230169, 0.0229397}, {0.0194704, 0.0464799, 0.0602067, 0.0698376,
    0.0837966, 0.107083, 0.122678, 0.147814, 0.16907, 0.194187, 0.203171, 0.231041,
    0.234189, 0.266125, 0.282658, 0.301069, 0.324472, 0.334657, 0.351934, 0.367803}},
 LinearPositive_20 → {{0.981457, 0.180213, 0.0356853, 0.00155774, 0.000332566, 0.0117024,
    0.015424, 0.0306402, 0.0217725, 0.03467}, {0.0199182, 0.0301676, 0.0553633, 0.0663988,
    0.0868397, 0.115421, 0.124937, 0.153948, 0.15869, 0.181977, 0.213358, 0.218207,
    0.236765, 0.256006, 0.281096, 0.305192, 0.31145, 0.343022, 0.3574, 0.37876}},
 LinearNegative_1 → {{0.990124, 0.131128, 0.0405036, 0.000648651, 0.00165951, 0.0127622,
    0.0148438, 0.00862215, 0.0147894, 0.0118069}, {-0.0316188, -0.0229558, -0.0750524, -0.0590688,
    -0.10371, -0.102502, -0.121793, -0.164356, -0.156516, -0.186793, -0.216626, -0.239216,
    -0.253787, -0.260558, -0.265944, -0.301895, -0.309615, -0.322511, -0.357934, -0.374895}},
 LinearNegative_2 → {{0.980683, 0.179465, 0.0363529, 0.00950375, 0.00120921, 0.00835715,
    0.0504078, 0.0277632, 0.0120381, 0.0333767}, {-0.0142652, -0.0310792, -0.0465593, -0.0674187,
    -0.0985199, -0.097372, -0.135642, -0.154194, -0.164679, -0.196856, -0.197957, -0.219743,
    -0.255234, -0.254995, -0.292667, -0.283701, -0.315912, -0.353666, -0.349614, -0.366051}},
 LinearNegative_3 → {{0.989959, 0.123857, 0.053797, 0.00239593, 0.00473455, 0.0307774, 0.0164006,
    0.00881652, 0.0169394, 0.0117152}, {-0.0188797, -0.0282804, -0.0637724, -0.0775291,
    -0.110195, -0.124225, -0.123724, -0.150851, -0.154901, -0.19536, -0.222346, -0.240048,
    -0.235752, -0.277911, -0.278425, -0.283234, -0.335825, -0.321195, -0.341652, -0.361499}},
 LinearNegative_4 → {{0.980341, 0.185944, 0.0488855, 0.00297492, 0.00510082, 0.0106832,
    0.0319498, 0.0149192, 0.0138634, 0.0195237}, {-0.0118744, -0.0341135, -0.0635743, -0.0719522,
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    -0.250828, -0.255598, -0.279772, -0.28835, -0.328947, -0.324574, -0.353518, -0.363274}},
 LinearNegative_5 → {{0.983375, 0.162138, 0.0464825, 0.00226587, 0.00128852, 0.0124518,
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LinearNegative_6 → {{0.983758, 0.167801, 0.0497635, 0.0013151, 0.00288713, 0.00803505,
    0.017002, 0.0101725, 0.031217, 0.0120581}, {-0.0325463, -0.02222, -0.0547532, -0.0735421,
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    -0.230127, -0.258899, -0.266972, -0.295192, -0.328064, -0.331614, -0.35358, -0.384025}},
LinearNegative_7 → {{0.983116, 0.158251, 0.064848, 0.00109101, 0.000617598, 0.0158065,
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    -0.249841, -0.250938, -0.276452, -0.289441, -0.307893, -0.345746, -0.352591, -0.376741}},
LinearNegative_8 → {{0.986129, 0.157523, 0.0368899, 0.00412251, 0.0134038, 0.0140773,
    0.0140089, 0.0149926, 0.0145574, 0.018662}, {-0.00115718, -0.0201204, -0.0730304, -0.0601412,
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    -0.229548, -0.268728, -0.268444, -0.2943, -0.324004, -0.341409, -0.366821, -0.372084}},
LinearNegative_9 → {{0.982198, 0.177007, 0.0363145, 0.00354443, 0.00146257, 0.0162265,
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    -0.231424, -0.255842, -0.270352, -0.308039, -0.320556, -0.350361, -0.347298, -0.363712}},
LinearNegative_10 → {{0.982135, 0.181361, 0.0238067, 0.00564912, 0.00354839, 0.00584574,
    0.00868449, 0.0257413, 0.0153597, 0.029982}, {-0.0114078, -0.0351473, -0.0696882, -0.0884178,
    -0.096709, -0.116625, -0.124242, -0.145992, -0.178527, -0.175988, -0.191495, -0.213466,
    -0.238418, -0.257969, -0.273814, -0.309509, -0.324481, -0.331717, -0.371364, -0.365757}},
LinearNegative_11 → {{0.979749, 0.18521, 0.0355826, 0.00433193, 0.00160226, 0.0107841,
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    -0.239382, -0.262113, -0.278355, -0.291115, -0.311438, -0.345876, -0.347504, -0.382084}},
LinearNegative_12 → {{0.980318, 0.179223, 0.0334401, 0.00130366, 0.0094814, 0.0110606,
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    -0.248508, -0.253797, -0.27434, -0.305232, -0.318243, -0.341847, -0.345518, -0.37296}},
LinearNegative_13 → {{0.983484, 0.168097, 0.0330931, 0.00123224, 0.000595679, 0.00821355,
    0.0249744, 0.0274066, 0.0316717, 0.0309866}, {-0.0233812, -0.0370288, -0.0599777, -0.0819523,
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    -0.23913, -0.255245, -0.28127, -0.305953, -0.311716, -0.343204, -0.347421, -0.372952}},
LinearNegative_14 → {{0.9813, 0.179231, 0.035265, 0.00446661, 0.00725715, 0.00971819,
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LinearNegative_15 → {{0.985723, 0.15661, 0.0232857, 0.00405901, 0.00496804, 0.0142553,
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LinearNegative_16 → {{0.980986, 0.182207, 0.0276946, 0.00387751, 0.00181689, 0.00587514,
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LinearNegative_17 → {{0.983501, 0.169085, 0.0306888, 0.00178652, 0.00159573, 0.00752165,
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LinearNegative_18 → {{0.982582, 0.172225, 0.0430764, 0.00129762, 0.000696616, 0.013354,
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    -0.242258, -0.254323, -0.278609, -0.304562, -0.31599, -0.340841, -0.358114, -0.364714}},
LinearNegative_19 → {{0.986844, 0.146106, 0.0212076, 0.00175486, 0.00155396, 0.00926879,
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LinearNegative_20 → {{0.97946, 0.18617, 0.0351038, 0.00477093, 0.000444671, 0.0107816,
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f3 → <|Sinusoidal3_21 → {{0.00282237, 0.0712402, 0.992759, 0.0845306, 0.036151, 0.0192302,
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Sinusoidal3_22 → {{0.00259744, 0.0680239, 0.992895, 0.086067, 0.0352052, 0.0184414, 0.00980373,
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  Sinusoidal3_25 → {{0.00310179, 0.0770949, 0.99206, 0.086786, 0.037962, 0.0188988, 0.00854649,
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  Sinusoidal3_26 → {{0.00259638, 0.0710446, 0.992428, 0.0878092, 0.0393509, 0.0175196,
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  Sinusoidal3_28 → {{0.00256806, 0.0687574, 0.993111, 0.0828843, 0.0352648, 0.0179976,
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  Sinusoidal3_30 → {{0.00277963, 0.0748998, 0.992009, 0.0888517, 0.0385469, 0.020321, 0.0101772,
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f5 → <|Sinusoidal2_11 → {{0.00264282, 0.0104183, 0.0330737, 0.0942986, 0.931231, 0.347584,
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  Sinusoidal2_14 → {{0.00173574, 0.0106431, 0.0314227, 0.0947047, 0.931063, 0.348445, 0.026969,
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  Sinusoidal2_15 → {{0.00273936, 0.0104807, 0.031275, 0.0912941, 0.935364, 0.338, 0.0274284,
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  Sinusoidal2_16 → {{0.00228014, 0.0121765, 0.0314211, 0.0942874, 0.92849, 0.355269, 0.0296945,
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  Sinusoidal2_17 → {{0.00216122, 0.0125529, 0.0303909, 0.0902114, 0.934765, 0.339718, 0.0284265,
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    0.257538, 0.0988031, -0.312391, 0.0972348, 0.257767, -0.25208, -0.0981886, 0.313929}},
  Sinusoidal2_18 → {{0.00185889, 0.0112968, 0.026472, 0.089911, 0.935235, 0.338958, 0.0273156,
    0.00400534, 0.0276273, 0.00129126}, {-0.0999346, -0.253023, 0.254469, 0.0926126,
    -0.313473, 0.0971886, 0.254844, -0.260652, -0.101569, 0.320119, -0.093905, -0.251597,
    0.259049, 0.101441, -0.321234, 0.0954029, 0.258691, -0.251261, -0.0941618, 0.313918}},
```

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```
    Sinusoidal2_19 → {{0.00275863, 0.0102799, 0.02839, 0.0905803, 0.934752, 0.340232, 0.0240755,
       0.00580534, 0.0271542, 0.0022776}, {-0.102304, -0.260958, 0.255763, 0.0957962,
       -0.311723, 0.0983533, 0.251216, -0.251339, -0.104118, 0.321006, -0.0979386, -0.259411,
       0.258811, 0.0932229, -0.319514, 0.0925881, 0.258918, -0.250537, -0.0979319, 0.311791}},
    Sinusoidal2_20 → {{0.00233903, 0.0115072, 0.0342345, 0.0928099, 0.93115, 0.348461, 0.0312831,
       0.00538851, 0.0244707, 0.00217405}, {-0.0985738, -0.250799, 0.254417, 0.104311,
       -0.321026, 0.0962853, 0.256321, -0.254191, -0.0959858, 0.31504, -0.101537, -0.258879,
       0.255837, 0.102562, -0.311164, 0.0972783, 0.255955, -0.261951, -0.0966271, 0.312434}}|>,
  f6 → <|Sinusoidal1_1 → {{0.00392082, 0.0110104, 0.0193521, 0.0393048, 0.0873236, 0.988454,
       0.112293, 0.00377871, 0.0255052, 0.00152342}, {-0.208741, -0.121417, 0.29004, -0.262914,
       -0.0266047, 0.224339, -0.294533, 0.0916637, 0.179675, -0.293061, 0.199487, 0.120937,
       -0.320909, 0.272986, -0.0245918, -0.273083, 0.268977, -0.11434, -0.175989, 0.31715}},
    Sinusoidal1_2 → {{0.00078854, 0.0119115, 0.00783019, 0.0370383, 0.115751, 0.986742, 0.105958,
       0.00470229, 0.0106619, 0.00194887}, {-0.215143, -0.0756135, 0.282352, -0.274215,
       -0.0111316, 0.275625, -0.274685, 0.0676022, 0.171628, -0.325726, 0.15748, 0.125108,
       -0.28209, 0.280825, -0.00601984, -0.281962, 0.313329, -0.10013, -0.1699, 0.293113}},
    Sinusoidal1_3 → {{0.00207227, 0.00778348, 0.0222643, 0.0458217, 0.115948, 0.985216, 0.111739,
       0.00635517, 0.0266977, 0.00251828}, {-0.15572, -0.0679486, 0.302484, -0.260691,
       -0.0299552, 0.265932, -0.317689, 0.0946018, 0.188425, -0.32768, 0.174666, 0.0790863,
       -0.283381, 0.24763, -0.0242454, -0.235748, 0.295892, -0.106951, -0.21055, 0.330806}},
    Sinusoidal1_4 → {{0.00269674, 0.0137778, 0.0260733, 0.0408112, 0.0840977, 0.992447, 0.0706086,
       0.00400978, 0.0207467, 0.0012365}, {-0.213107, -0.0852601, 0.32576, -0.245989,
       0.0169995, 0.240162, -0.296486, 0.0962957, 0.18491, -0.312761, 0.189241, 0.101369,
       -0.291965, 0.241837, 0.0325276, -0.263761, 0.280996, -0.0919531, -0.181654, 0.33567}},
    Sinusoidal1_5 → {{0.000218645, 0.00930363, 0.017915, 0.0334974, 0.114019, 0.984802, 0.122862,
       0.0039222, 0.0228722, 0.00137365}, {-0.172101, -0.0825161, 0.296343, -0.261072,
       -0.00445598, 0.245511, -0.30727, 0.0692245, 0.178333, -0.30576, 0.185441, 0.0955618,
       -0.295114, 0.295006, -0.0173785, -0.237536, 0.324459, -0.105937, -0.174767, 0.318424}},
    Sinusoidal1_6 → {{0.00299058, 0.00681813, 0.0115769, 0.0253521, 0.0693227, 0.990247, 0.115696,
       0.00240125, 0.0195144, 0.000610221}, {-0.192232, -0.0968191, 0.266494, -0.252668,
       0.0261661, 0.267836, -0.324947, 0.111125, 0.200409, -0.322174, 0.204294, 0.11645,
       -0.313846, 0.265905, -0.0249607, -0.238967, 0.276582, -0.0894965, -0.158167, 0.304532}},
    Sinusoidal1_7 → {{0.00216589, 0.012646, 0.0122381, 0.0458701, 0.0940669, 0.990524, 0.0816339,
       0.003606, 0.030287, 0.00125497}, {-0.167418, -0.0725458, 0.338424, -0.278488,
       0.0223571, 0.257582, -0.280715, 0.0751334, 0.176119, -0.327003, 0.178187, 0.126787,
       -0.29454, 0.244131, 0.00923144, -0.259977, 0.295629, -0.087699, -0.204926, 0.294014}},
    Sinusoidal1_8 → {{0.00117254, 0.00731166, 0.0114293, 0.0320443, 0.0961064, 0.986861,
       0.122661, 0.0126348, 0.0196368, 0.00804146}, {-0.176098, -0.107595, 0.31308, -0.274119,
       -0.0018774, 0.278776, -0.297573, 0.0685098, 0.172592, -0.309967, 0.153828, 0.119312,
       -0.320317, 0.265068, 0.00744581, -0.256587, 0.308323, -0.100255, -0.150443, 0.288131}},
    Sinusoidal1_9 → {{0.00798996, 0.0134629, 0.0165078, 0.0323132, 0.0928903, 0.987725, 0.11735,
       0.0049721, 0.0202585, 0.00170736}, {-0.183519, -0.102183, 0.309929, -0.226374,
       0.017542, 0.261708, -0.301533, 0.0738786, 0.181655, -0.33569, 0.187261, 0.0749858,
       -0.309677, 0.242912, -0.0231839, -0.280753, 0.294845, -0.110324, -0.191689, 0.294801}},
    Sinusoidal1_10 → {{0.0014161, 0.00917268, 0.0196419, 0.0456084, 0.0815281, 0.986769, 0.12856,
       0.00639631, 0.0226127, 0.00276475}, {-0.180249, -0.116682, 0.298047, -0.255977,
       -0.00803746, 0.266395, -0.286168, 0.109016, 0.190913, -0.319233, 0.190865, 0.122814,
       -0.295406, 0.275032, 0.0137159, -0.224161, 0.291322, -0.124878, -0.159457, 0.325008}}|>|>
```

We can now perform the clustering for all these classes of data:

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In[3]:=
```
clustersSingle = TimeSeriesSingleClusters[classification1]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

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General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
<|SpikeMax → <|<<1>>|>, <<4>>, f6 → <|Cluster → Cluster[<<1>>],
   InitialSplitCluster → <<1>>, GroupAssociations → <|G1 → {Sinusoidal1_1, Sinusoidal1_9,
       Sinusoidal1_8, <<2>>, Sinusoidal1_2, Sinusoidal1_3, Sinusoidal1_5}, G2 → <<1>>|>|>|>
```

large output | show less | show more | show all | set size limit...

We see that each class has different data associated with it:

In[4]:=
```
Query[All, Keys]@clustersSingle
```

Out[4]=
```
<|SpikeMax → {Cluster, InitialSplitCluster, GroupAssociations},
 SpikeMin → {Cluster, InitialSplitCluster, GroupAssociations},
 f1 → {Cluster, InitialSplitCluster, GroupAssociations},
 f3 → {Cluster, InitialSplitCluster, GroupAssociations},
 f5 → {Cluster, InitialSplitCluster, GroupAssociations},
 f6 → {Cluster, InitialSplitCluster, GroupAssociations}|>
```

For example, we look at the "f1" class clustering group associations:

In[5]:=
```
clustersSingle["f1", "GroupAssociations"]
```

Out[5]=
```
<|G1 → {LinearPositive_1, LinearPositive_2, LinearPositive_5, LinearPositive_9, LinearNegative_17,
   LinearPositive_3, LinearPositive_10, LinearPositive_4, LinearPositive_7, LinearPositive_6,
   LinearPositive_8, LinearPositive_17, LinearPositive_14, LinearPositive_11, LinearPositive_19,
   LinearNegative_8, LinearNegative_15, LinearNegative_19, LinearNegative_6, LinearNegative_4,
   LinearNegative_9, LinearNegative_11, LinearNegative_20, LinearPositive_12, LinearNegative_12,
   LinearNegative_18, LinearPositive_16, LinearNegative_5, LinearNegative_16, LinearNegative_14,
   LinearPositive_20, LinearPositive_15, LinearNegative_13, LinearNegative_10, LinearPositive_13,
   LinearPositive_18, LinearNegative_2, LinearNegative_7}, G2 → {LinearNegative_1, LinearNegative_3}|>
```

We can also obtain see the data rules in indifvidual cluster groups, by flattensing the split clusters. In the case of class "f1", looking at the second cluster:

In[6]:=
```
Query["f1", "InitialSplitCluster", 2 /* ClusterFlatten]@clustersSingle
```

Out[6]=
```
{{-0.0316188, -0.0229558, -0.0750524, -0.0590688, -0.10371, -0.102502,
   -0.121793, -0.164356, -0.156516, -0.186793, -0.216626, -0.239216, -0.253787, -0.260558,
   -0.265944, -0.301895, -0.309615, -0.322511, -0.357934, -0.374895} → LinearNegative_1,
 {-0.0188797, -0.0282804, -0.0637724, -0.0775291, -0.110195, -0.124225, -0.123724,
   -0.150851, -0.154901, -0.19536, -0.222346, -0.240048, -0.235752, -0.277911,
   -0.278425, -0.283234, -0.335825, -0.321195, -0.341652, -0.361499} → LinearNegative_3}
```

The data can be provided as a list of associations for each class (i.e. without class labels):

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In[7]:=
```
clustersSingleAssociationList = TimeSeriesSingleClusters[Values@classification1];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

The classes are automatically enumerated in order of appearance:

In[8]:=
```
Keys[clustersSingleAssociationList]
```

Out[8]=
```
{1, 2, 3, 4, 5, 6}
```

In[9]:=
```
Query[All, Keys]@clustersSingleAssociationList
```

Out[9]=
```
<|1 → {Cluster, InitialSplitCluster, GroupAssociations},
 2 → {Cluster, InitialSplitCluster, GroupAssociations},
 3 → {Cluster, InitialSplitCluster, GroupAssociations},
 4 → {Cluster, InitialSplitCluster, GroupAssociations},
 5 → {Cluster, InitialSplitCluster, GroupAssociations},
 6 → {Cluster, InitialSplitCluster, GroupAssociations}|>
```

We can also obtain the "GroupAssociations" or other information for any class as before. For example, for class 3 (which corresponds to "f1" in our fully labeled example above):

In[10]:=
```
clustersSingleAssociationList[3, "GroupAssociations"]
```

Out[10]=
```
<|G1 → {LinearPositive_1, LinearPositive_2, LinearPositive_5, LinearPositive_9, LinearNegative_17,
   LinearPositive_3, LinearPositive_10, LinearPositive_4, LinearPositive_7, LinearPositive_6,
   LinearPositive_8, LinearPositive_17, LinearPositive_14, LinearPositive_11, LinearPositive_19,
   LinearNegative_8, LinearNegative_15, LinearNegative_19, LinearNegative_6, LinearNegative_4,
   LinearNegative_9, LinearNegative_11, LinearNegative_20, LinearPositive_12, LinearNegative_12,
   LinearNegative_18, LinearPositive_16, LinearNegative_5, LinearNegative_16, LinearNegative_14,
   LinearPositive_20, LinearPositive_15, LinearNegative_13, LinearNegative_10, LinearPositive_13,
   LinearPositive_18, LinearNegative_2, LinearNegative_7}, G2 → {LinearNegative_1, LinearNegative_3}|>
```

The TimeSeriesSingleClusters can also work with data from a single class presented as an association:

In[11]:=
```
clustersSingleAssociation = TimeSeriesSingleClusters[classification1["f1"]];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

The class is by default labeled as "1":

In[12]:=
```
Keys[clustersSingleAssociation]
```

Out[12]=
```
{1}
```

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In[13]:=
```
clustersSingleAssociation["1", "GroupAssociations"]
```

Out[13]=
```
<|G1 → {LinearPositive_1, LinearPositive_2, LinearPositive_5, LinearPositive_9, LinearNegative_17,
   LinearPositive_3, LinearPositive_10, LinearPositive_4, LinearPositive_7, LinearPositive_6,
   LinearPositive_8, LinearPositive_17, LinearPositive_14, LinearPositive_11, LinearPositive_19,
   LinearNegative_8, LinearNegative_15, LinearNegative_19, LinearNegative_6, LinearNegative_4,
   LinearNegative_9, LinearNegative_11, LinearNegative_20, LinearPositive_12, LinearNegative_12,
   LinearNegative_18, LinearPositive_16, LinearNegative_5, LinearNegative_16, LinearNegative_14,
   LinearPositive_20, LinearPositive_15, LinearNegative_13, LinearNegative_10, LinearPositive_13,
   LinearPositive_18, LinearNegative_2, LinearNegative_7}, G2 → {LinearNegative_1, LinearNegative_3}|>
```

In addition, TimeSeriesSingleClusters can also work with data from a single class presented as a list:

In[14]:=
```
clustersSingleList = TimeSeriesSingleClusters[Values@classification1["f1"]];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

In[15]:=
```
Keys[clustersSingleList]
```

Out[15]=
```
{1}
```

The labeling for each time series is an index position corresponding to the position of the series in the initial input list:

In[16]:=
```
clustersSingleList["1", "GroupAssociations"]
```

Out[16]=
```
<|G1 → {1, 2, 5, 9, 37, 3, 10, 4, 7, 6, 8, 17, 14, 11, 19, 28, 35, 39, 26, 24,
   29, 31, 40, 12, 32, 38, 16, 25, 36, 34, 20, 15, 33, 30, 13, 18, 22, 27}, G2 → {21, 23}|>
```

Options (8)

ClusterLabeling (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ClusterLabeling provides a way to add a prepend text to all the cluster groups named.

We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

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```
Method → "LombScargle"
```

Out[2]=

```
<|SpikeMax →
  <|SpikePositive_1 → {{0.229557, 0.17739, 0.298737, 0.249643, 0.617624, 0.235252, 0.232899, 0.13573,
      0.478666, 0.160257}, {0.955992, 0.0164848, -0.0524196, 0.0272238, 0.0942669, -0.0684993,
      -0.0572786, 0.0574343, -0.00944892, -0.0866857, 0.0609026, 0.0899554, 0.0701144,
      0.0714032, 0.0279645, 0.0906873, -0.102718, 0.0222711, 0.0777441, 0.0815168}},
   SpikePositive_2 → {{0.0867446, 0.291302, 0.280592, 0.437638, 0.242533, 0.407746, 0.345064,
      0.19316, 0.470362, 0.18617}, {0.967378, -0.050888, -0.0668654, 0.0685551, -0.0845067,
      0.0387969, 0.0802206, 0.0176594, 0.0564915, 0.0783781, 0.047367, -0.0788505, -0.0175761,
      0.0262742, -0.00137284, -0.0910417, -0.0899303, 0.0138858, -0.0401369, -0.00701168}},
   SpikePositive_3 → {{0.113127, 0.223881, 0.170456, 0.389375, 0.115098, 0.353647, 0.295336,
      0.101658, 0.710917, 0.123039}, {0.956277, -0.0574571, -0.0219578, -0.0381778, -0.0102244,
      0.0606041, 0.0900534, -0.0923172, 0.0258003, 0.059276, 0.0858815, -0.0827851, -0.0404382,
      -0.0215864, -0.0870181, 0.0334631, -0.0852235, -0.0847604, -0.0877793, 0.0923581}},
   SpikePositive_4 → {{0.342306, 0.310357, 0.357036, 0.27328, 0.283369, 0.391899, 0.171676,
      0.188563, 0.502482, 0.181517}, {0.977687, 0.0765495, -0.0703782, 0.014362, -0.000145619,
      -0.00186992, -0.0326019, -0.0532967, -0.0751487, 0.0216965, 0.0314073, 0.0357438,
      0.0860528, -0.0386155, -0.0246417, 0.0379604, 0.019086, 0.0645538, -0.0721286, 0.0118544}},
   SpikePositive_5 → {{0.269575, 0.115997, 0.300497, 0.181041, 0.226183, 0.319019, 0.169772,
      0.288658, 0.649417, 0.32246}, {0.972255, -0.0618834, 0.00655622, -0.0612888, -0.0426931,
      -0.0364479, 0.0466336, -0.0697693, -0.0574383, -0.012952, -0.0628519, 0.0936297, 0.0450235,
      0.0423622, 0.0681387, 0.0534542, -0.0107077, 0.0662395, -0.0572637, -0.0401421}},
   SpikePositive_6 → {{0.224204, 0.446476, 0.261259, 0.11228, 0.217898, 0.247802, 0.279155,
      0.138916, 0.66582, 0.141785}, {0.963392, -0.0363784, 0.10537, -0.0000806452, -0.101898,
      -0.0836129, 0.0396876, 0.0105629, 0.0208709, -0.0511616, 0.0737177, -0.0332373, -0.0227503,
      -0.0813552, -0.0871646, -0.0469609, -0.0590188, -0.0136526, 0.00289841, 0.100895}},
   SpikePositive_7 → {{0.174704, 0.33211, 0.461258, 0.349817, 0.124863, 0.230724, 0.299366,
      0.241911, 0.498543, 0.241951}, {0.961968, -0.041276, 0.0378442, -0.0747986, -0.0475978,
      0.0561308, -0.00934272, 0.0840132, 0.0297482, 0.0371766, -0.0141519, -0.0967365, 0.0619744,
      0.0572096, -0.0783599, -0.0795267, -0.0727424, 0.0510496, 0.0779571, 0.0891484}},
   SpikePositive_8 → {{0.175172, 0.270378, 0.221847, 0.371827, 0.34245, 0.263026, 0.363325,
      0.261645, 0.494382, 0.278223}, {0.972594, -0.0714665, -0.00416933, 0.0626488, 0.0403737,
      0.0737154, -0.0127138, -0.0524928, 0.0880338, 0.0386748, 0.0178677, 0.099474, -0.039575,
      -0.00843439, 0.00484508, -0.0218234, -0.0299089, 0.03607, 0.0836651, 0.0650927}},
   SpikePositive_9 → {{0.224133, 0.473159, 0.281325, 0.203112, 0.341825, 0.307339, 0.301369,
      0.277289, 0.381598, 0.28435}, {0.972481, 0.0934263, -0.0348083, 0.0667798, -0.0868602,
      -0.0966805, 0.0147066, 0.0114999, -0.0282577, 0.0262368, 0.0312899, 0.0477617, -0.0582853,
      -0.00408684, -0.0249056, -0.091262, 0.00761949, 0.00934781, -0.0586605, -0.0440927}},
   SpikePositive_10 → {{0.16366, 0.269508, 0.194591, 0.235343, 0.361714, 0.222093, 0.298862,
      0.218053, 0.661487, 0.229642}, {0.974749, -0.0233456, 0.0660445, 0.0411115, 0.0608941,
      -0.00464854, -0.0680471, -0.0534733, 0.0803264, -0.0456851, 0.0192399, 0.0710043, 0.038336,
      -0.0588495, -0.0307418, -0.0571712, -0.0755006, -0.00466255, -0.0403163, -0.0400389}},
   SpikePositive_11 → {{0.445759, 0.327475, 0.307695, 0.319099, 0.361535, 0.216692, 0.188567,
      0.235305, 0.420413, 0.228521}, {0.0380508, 0.0135531, 0.970404, 0.0690608, -0.0320549,
      -0.0873128, 0.06045, -0.0400485, -0.0823548, -0.0729559, 0.0403636, -0.0530087, -0.0793015,
      -0.0332727, 0.0555543, -0.0613472, 0.0100647, -0.0060381, 0.0794159, 0.0277783}},
   SpikePositive_12 → {{0.300469, 0.225414, 0.331703, 0.295569, 0.284031, 0.549055, 0.384229,
      0.123645, 0.310036, 0.142624}, {-0.0424636, 0.0522229, 0.965273, -0.0190583, 0.082252,
      0.0820233, -0.0826831, 0.0450099, -0.0109654, -0.0677058, 0.0517361, -0.0220454,
      -0.0654353, 0.0111394, 0.0726991, 0.0290178, 0.024323, 0.0889113, -0.0913042, 0.0759365}},
   SpikePositive_13 → {{0.284201, 0.27443, 0.281845, 0.28611, 0.299597, 0.301064, 0.236764,
      0.319581, 0.502104, 0.303195}, {-0.00745368, -0.0865825, 0.974343, 0.0566103, 0.0317326,
      -0.0344296, 0.081772, -0.0447563, -0.00214147, -0.0550885, -0.067114, -0.0520311, 0.0486164,
      -0.0237265, 0.0350166, -0.0519948, 0.0055062, -0.0751198, 0.0602441, -0.0510646}},
   SpikePositive_14 → {{0.203389, 0.197442, 0.179862, 0.213932, 0.148601, 0.422726, 0.373189,
      0.438581, 0.303271, 0.466}, {0.0351654, 0.0637965, 0.965262, -0.0831496, 0.0371087,
      0.0719667, 0.00749899, 0.0134446, 0.0531346, 0.00575568, 0.013683, 0.0961344, -0.0902442,
      0.0186788, -0.0507972, 0.0844724, -0.101166, 0.0335328, 0.0576164, -0.0639011}},
   SpikePositive_15 → {{0.315631, 0.222029, 0.141554, 0.33669, 0.135303, 0.330452, 0.268851,
      0.378304, 0.456636, 0.407757}, {0.00627431, -0.0590489, 0.97205, -0.0427555, 0.0547316,
      0.0257813, 0.0375805, -0.0244245, 0.0154503, -0.0546737, -0.0151643, 0.0849617, -0.0771048,
      -0.071292, -0.0942647, 0.0622766, -0.0391028, 0.000588394, 0.0514175, 0.0738466}},
   SpikePositive_16 → {{0.433158, 0.182106, 0.450226, 0.312339, 0.288091, 0.0865093, 0.179037,
      0.334196, 0.363083, 0.336007}, {0.0930574, 0.0249015, 0.959142, 0.0703634, 0.026647,
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    -0.0947164, 0.0869781, 0.0612448, -0.094074, 0.0700142, -0.0739931, -0.0815047, -0.0869475,
    -0.0282018, 0.0194984, 0.0111089, 0.0305669, -0.0553038, -0.0385472, 0.0678993}},
  SpikePositive_17 → {{0.184336, 0.297965, 0.324467, 0.150497, 0.230645, 0.261094, 0.310907,
    0.430493, 0.382984, 0.446406}, {-0.0141314, -0.0850224, 0.970349, 0.0257308, 0.0678347,
    -0.00997934, 0.00711297, -0.0454983, 0.0919498, 0.0719897, -0.0232893, 0.00553686, 0.00226815,
    0.0566031, -0.0816138, 0.0287655, -0.0905716, -0.0821168, 0.0542368, -0.0267516}},
  SpikePositive_18 → {{0.159556, 0.311684, 0.352011, 0.167192, 0.26552, 0.218107, 0.485018,
    0.305789, 0.424255, 0.314191}, {0.0839969, -0.0743713, 0.972537, -0.0123447, 0.0394987,
    0.035557, -0.0762567, 0.0522619, -0.048703, 0.0314765, 0.00706774, -0.0414037, 0.0664611,
    0.093313, 0.0584456, 0.0396896, -0.0207851, -0.0388773, -0.0231012, 0.0658932}},
  SpikePositive_19 → {{0.283495, 0.452388, 0.323728, 0.439833, 0.171208, 0.271381, 0.200506,
    0.178492, 0.450144, 0.197664}, {0.0369336, 0.0769283, 0.965813, 0.0352893, 0.0573251,
    -0.0839536, -0.0349503, -0.0764346, 0.058187, -0.0836623, -0.0318186, 0.0412589, 0.0712811,
    -0.0894366, -0.0487606, 0.0287067, -0.00208687, -0.0528333, -0.0900815, 0.0314397}},
  SpikePositive_20 → {{0.246089, 0.139222, 0.2665, 0.135883, 0.314007, 0.41051, 0.296394,
    0.337346, 0.49448, 0.342476}, {-0.0240497, -0.069669, 0.966377, -0.0293453, 0.0448406,
    -0.0754659, 0.0635253, -0.0378239, 0.0630311, 0.0148336, -0.0642022, -0.0804163, -0.019965,
    -0.0311675, 0.0390918, -0.0665501, -0.0659093, 0.0860876, 0.0839589, -0.0757493}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.303269, 0.362191, 0.221329, 0.177357, 0.159601, 0.359886,
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    -0.0108568, 0.016952, 0.00771474, 0.0243929, -0.0704405, -0.0632549, 0.0629046, -0.0507205}},
  SpikeNegative_2 → {{0.335278, 0.154527, 0.429166, 0.239882, 0.274624, 0.269176, 0.278062,
    0.310382, 0.440831, 0.325764}, {-0.97599, 0.045284, 0.0542022, 0.0449958, -0.0225074,
    -0.0459232, 0.00123131, 0.0223412, 0.0667226, 0.0509244, 0.0336221, -0.0614356, -0.0545432,
    -0.0353136, -0.00168557, -0.0525425, -0.076469, -0.0763033, -0.0819001, 0.000861696}},
  SpikeNegative_3 → {{0.134212, 0.278206, 0.230157, 0.172604, 0.290839, 0.230852, 0.324911,
    0.341948, 0.56084, 0.383284}, {-0.968839, 0.0890026, -0.0429642, 0.0774255, 0.0389771,
    0.077942, 0.0319942, -0.0697241, -0.0697521, -0.0186001, -0.0144244, -0.0856914, -0.0395642,
    -0.0676809, 0.0199442, -0.0528929, 0.0144422, -0.0597485, -0.0519242, 0.0594226}},
  SpikeNegative_4 → {{0.192345, 0.232104, 0.136083, 0.342673, 0.200405, 0.274305, 0.428609,
    0.328596, 0.504925, 0.333394}, {-0.978254, 0.0156067, -0.0138612, 0.0602388, -0.0157848,
    -0.0518129, 0.0576712, 0.0637983, -0.0528065, -0.0187776, -0.017674, 0.0752962,
    0.0173854, 0.0288304, 0.0275502, -0.0283175, -0.048069, 0.082749, -0.0348031, 0.0802343}},
  SpikeNegative_5 → {{0.266796, 0.213191, 0.451853, 0.263545, 0.142882, 0.245342, 0.259993,
    0.240702, 0.572241, 0.275937}, {-0.967234, -0.0858972, -0.0316416, 0.042983, -0.0222426,
    -0.081207, -0.0667767, 0.0835317, 0.028219, -0.00734201, 0.0623961, -0.0812517, -0.0236941,
    -0.0612425, 0.0998976, 0.0121139, 0.00694716, 0.0307149, 0.0406908, -0.0852891}},
  SpikeNegative_6 → {{0.215636, 0.140087, 0.364779, 0.24054, 0.364142, 0.174333, 0.246494,
    0.267046, 0.613914, 0.266457}, {-0.97583, -0.0132062, -0.0673428, 0.0288581, -0.0331356,
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    -0.00159662, -0.0106925, -0.0473126, 0.0353561, 0.082638, 0.0320662, 0.0287677, -0.0109244}},
  SpikeNegative_7 → {{0.0423458, 0.100155, 0.284716, 0.400179, 0.328981, 0.21858, 0.351618,
    0.331264, 0.468985, 0.371006}, {-0.956208, 0.0153193, 0.0720517, 0.0963958, -0.0609996,
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    -0.0284285, -0.0635705, 0.0486603, -0.0099272, 0.087648, 0.10106, 0.0635793, 0.0818392}},
  SpikeNegative_8 → {{0.258917, 0.0994846, 0.179986, 0.283242, 0.451538, 0.279331, 0.350078,
    0.288034, 0.483837, 0.298185}, {-0.982531, 0.00977698, 0.0148612, -0.0182115, -0.0193341,
    -0.0404852, 0.00603315, -0.0154881, -0.0038047, 0.068822, 0.0412737, 0.0104208, 0.0466152,
    0.0059628, -0.0888061, -0.0918735, 0.0262471, 0.0690952, 0.0176293, 0.0286885}},
  SpikeNegative_9 → {{0.452234, 0.241653, 0.260078, 0.22109, 0.313859, 0.127376, 0.383647,
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    -0.094626, 0.067644, 0.0226909, 0.0839027, 0.089239, -0.0469565, -0.0473835, 0.0800607,
    0.0601141, -0.035456, 0.070394, -0.0932021, -0.0102194, -0.0946583, -0.00630202}},
  SpikeNegative_10 → {{0.371901, 0.279062, 0.321004, 0.261275, 0.380121, 0.31567, 0.282416,
    0.0959805, 0.515678, 0.116069}, {-0.973337, -0.0635134, 0.0397865, -0.0628728, 0.00554888,
    0.0352886, 0.0789453, 0.02634, 0.0080944, 0.0585218, 0.0176431, -0.0253325, -0.0597678,
    -0.0532766, 0.0607779, -0.0668769, 0.0767608, -0.0424396, 0.0149449, -0.0889133}},
  SpikeNegative_11 → {{0.189926, 0.258634, 0.196152, 0.269836, 0.241204, 0.319036, 0.325544,
    0.423856, 0.392491, 0.431398}, {-0.0810144, 0.0906838, -0.960296, -0.0287445, 0.0572806,
    -0.00922045, 0.0257363, 0.0376354, -0.102674, 0.0551382, -0.0133525, -0.0808784, 0.0587102,
    -0.0841456, 0.0902543, 0.0194521, -0.0871674, 0.0405671, -0.0902743, -0.00526641}},
  SpikeNegative_12 → {{0.147704, 0.32264, 0.327164, 0.352859, 0.336132, 0.302027, 0.219956,
    0.402354, 0.242596, 0.411356}, {0.1016, -0.058632, -0.968031, 0.01971, -0.0199519,
    0.0860006, -0.0408624, -0.00893327, 0.0301637, -0.00818717, -0.0186954, -0.071339,
    0.0936495, -0.0606557, 0.0342386, 0.0262391, 0.0841864, 0.0254708, 0.0547921, 0.0880851}},
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    SpikeNegative_13 → {{0.173741, 0.285518, 0.454203, 0.36118, 0.192991, 0.470721, 0.25155,
       0.296967, 0.234278, 0.29388}, {0.000549151, -0.0126935, -0.968404, -0.000808654,
       0.0834826, 0.0651037, 0.0547386, -0.0894754, -0.0379325, -0.0108714, 0.0171285, -0.0653265,
       0.0830693, 0.0721053, -0.0462074, 0.067401, 0.0821532, 0.048104, 0.034924, 0.0681466}},
    SpikeNegative_14 → {{0.175452, 0.141216, 0.335265, 0.262676, 0.433374, 0.358544, 0.30493,
       0.26446, 0.46524, 0.268583}, {-0.0875955, -0.0404707, -0.97554, 0.0576243, 0.0369264,
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       -0.0239004, -0.0432765, -0.0503029, -0.0712956, 0.0131429, 0.0404308, 0.064171}},
    SpikeNegative_15 → {{0.371829, 0.493223, 0.285799, 0.19219, 0.238252, 0.307784, 0.384489,
       0.111232, 0.412203, 0.135069}, {-0.0482849, -0.0218839, -0.96185, -0.0935463, -0.0638405,
       0.0442671, 0.0808367, 0.0775777, 0.0857884, 0.082887, -0.00622549, 0.0597791, -0.0450584,
       0.019116, -0.0599481, 0.00549017, 0.0947218, -0.083931, 0.0668242, -0.0187203}},
    SpikeNegative_16 → {{0.119152, 0.195598, 0.375235, 0.406203, 0.276788, 0.293023, 0.263282,
       0.405406, 0.266272, 0.417967}, {0.0792631, 0.0368987, -0.967917, 0.0509676, 0.0074799,
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       0.0599705, 0.0147441, 0.0931153, -0.048731, -0.0213543, 0.0590573, 0.092745, 0.0636778}},
    SpikeNegative_17 → {{0.42949, 0.173342, 0.364592, 0.315962, 0.335778, 0.192261, 0.326932,
       0.331455, 0.269725, 0.33693}, {-0.0708377, -0.050973, -0.972566, -0.0241793, -0.0149487,
       -0.0862224, -0.0212781, -0.0722039, 0.033827, 0.0339387, 0.0920776, 0.0723576, 0.0279289,
       -0.0672703, 0.0272304, -0.0502434, -0.0624423, 0.0611575, 0.0135128, -0.0136725}},
    SpikeNegative_18 → {{0.254385, 0.333763, 0.23454, 0.28226, 0.419579, 0.282818, 0.343385,
       0.279779, 0.385068, 0.297845}, {0.0490023, -0.068996, -0.975953, 0.0769728, -0.0233158,
       0.0474078, -0.0670663, 0.0517042, 0.0337078, -0.0755258, 0.0402201, 0.00737071, -0.0501713,
       0.0451592, 0.0481457, 0.0301032, 0.0573522, -0.0593154, 0.00099107, -0.0369415}},
    SpikeNegative_19 → {{0.287414, 0.210026, 0.319586, 0.434045, 0.321911, 0.193004, 0.306255,
       0.27632, 0.439714, 0.279968}, {0.0283013, 0.0606462, -0.971483, 0.0587867, 0.01733,
       0.0572995, -0.0241285, 0.00663696, 0.0706159, 0.0394575, 0.0903422, 0.0778211, -0.00801711,
       0.0783656, 0.0571845, 0.000295157, -0.00965038, 0.0918827, 0.0645407, -0.0337456}},
    SpikeNegative_20 → {{0.254416, 0.309492, 0.264784, 0.357317, 0.308149, 0.464272, 0.376454,
       0.1808, 0.348719, 0.187577}, {0.00937302, -0.0127591, -0.976716, 0.0720799, 0.0316455,
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       0.0254214, 0.0594565, 0.0508719, 0.075019, 0.0138359, -0.0132564, 0.0280138, -0.0646118}}|>,
f1 → <|LinearPositive_1 → {{0.984032, 0.166995, 0.0322908, 0.00183831, 0.00183585, 0.0109078,
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       0.242022, 0.26111, 0.278881, 0.298763, 0.318016, 0.336693, 0.355106, 0.373332}},
    LinearPositive_2 → {{0.985207, 0.158284, 0.0325639, 0.0018304, 0.00169728,
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    LinearPositive_3 → {{0.983943, 0.166446, 0.031619, 0.00233504, 0.0025841, 0.0109746,
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    LinearPositive_4 → {{0.984931, 0.162152, 0.0318881, 0.00232849, 0.00124513,
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    LinearPositive_5 → {{0.984063, 0.165524, 0.0341806, 0.00225112, 0.00204887, 0.0106605,
       0.0214928, 0.0301806, 0.0182517, 0.0349819}, {0.0171341, 0.0377385, 0.0542898, 0.0730242,
       0.0943774, 0.113691, 0.132231, 0.148636, 0.167974, 0.184803, 0.204053, 0.224004,
       0.244001, 0.261835, 0.280166, 0.298791, 0.316147, 0.335579, 0.355892, 0.373261}},
    LinearPositive_6 → {{0.984295, 0.165125, 0.0314531, 0.00166475, 0.00214803, 0.0115083,
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       0.241726, 0.260555, 0.281247, 0.299514, 0.31737, 0.334701, 0.354705, 0.375106}},
    LinearPositive_7 → {{0.984993, 0.160746, 0.0299074, 0.00211612, 0.00213385,
       0.0106483, 0.0218425, 0.0300457, 0.0185022, 0.0348048},
      {0.0172812, 0.0390811, 0.0565095, 0.075889, 0.092671, 0.112196, 0.129061, 0.147994, 0.169372, 0.188632,
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    LinearPositive_8 → {{0.983374, 0.170912, 0.0325184, 0.00278199, 0.00156893,
       0.0100068, 0.0210402, 0.0278111, 0.0183605, 0.0322961},
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       0.203637, 0.223583, 0.242056, 0.261661, 0.279511, 0.298184, 0.318875, 0.337588, 0.355254, 0.372382}},
    LinearPositive_9 → {{0.984053, 0.166776, 0.0321436, 0.00236795, 0.00223543, 0.0108628,
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    0.0931645, 0.110498, 0.132355, 0.149377, 0.167732, 0.187547, 0.203832, 0.223184,
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LinearPositive_10 → {{0.984096, 0.166359, 0.032194, 0.00198912, 0.00122933, 0.00998155,
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LinearPositive_11 → {{0.987907, 0.142141, 0.0356768, 0.0022958, 0.00533762,
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   {0.0195511, 0.0413009, 0.0533086, 0.067794, 0.0950226, 0.113856, 0.126387, 0.142338, 0.1681, 0.17943,
    0.203205, 0.227466, 0.249124, 0.269692, 0.276233, 0.299996, 0.32138, 0.33045, 0.354625, 0.373394}},
LinearPositive_12 → {{0.98304, 0.173776, 0.0337211, 0.001548, 0.0041125, 0.00779181,
    0.01368, 0.0268581, 0.0186737, 0.0309814}, {0.015734, 0.0378277, 0.0615295, 0.0738202,
    0.0864531, 0.117348, 0.136085, 0.141945, 0.161715, 0.187969, 0.207712, 0.216546,
    0.23594, 0.264576, 0.274837, 0.303347, 0.319665, 0.335056, 0.363278, 0.3715}},
LinearPositive_13 → {{0.98307, 0.173943, 0.0217689, 0.00341151, 0.00300541, 0.0161316,
    0.0198073, 0.0264742, 0.0223059, 0.0311531}, {0.0105773, 0.0318463, 0.0625117, 0.0662852,
    0.0971206, 0.110527, 0.121713, 0.152125, 0.176042, 0.192628, 0.205506, 0.222901,
    0.234456, 0.262683, 0.277756, 0.300318, 0.30978, 0.333598, 0.357806, 0.379956}},
LinearPositive_14 → {{0.982793, 0.168155, 0.0412512, 0.00363422, 0.000598744, 0.0125404,
    0.0315924, 0.0340383, 0.0156081, 0.0396063}, {0.0175016, 0.0349517, 0.0517966,
    0.0793157, 0.0981379, 0.104729, 0.131324, 0.15364, 0.159234, 0.187016, 0.209336, 0.21896,
    0.248434, 0.252868, 0.280217, 0.290359, 0.320311, 0.344354, 0.354493, 0.374989}},
LinearPositive_15 → {{0.983382, 0.165888, 0.0393631, 0.00167669, 0.000431747, 0.00674197,
    0.0257686, 0.0339059, 0.0238298, 0.0382391}, {0.0223871, 0.0429794, 0.0495936,
    0.0818754, 0.089074, 0.108593, 0.132305, 0.140953, 0.161901, 0.187417, 0.206114,
    0.228027, 0.236262, 0.254957, 0.27882, 0.301191, 0.316374, 0.344006, 0.357572, 0.37417}},
LinearPositive_16 → {{0.979627, 0.190783, 0.0345994, 0.00380234, 0.00206858, 0.00825675,
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    0.241142, 0.258798, 0.274365, 0.291929, 0.32314, 0.333663, 0.360327, 0.378745}},
LinearPositive_17 → {{0.983905, 0.163821, 0.0338227, 0.00221795, 0.00354578,
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   {0.010851, 0.0397583, 0.0596922, 0.071438, 0.0936209, 0.111291, 0.130908, 0.141833, 0.171852, 0.188216,
    0.207176, 0.229456, 0.233245, 0.265454, 0.276163, 0.292647, 0.318119, 0.342475, 0.35327, 0.375013}},
LinearPositive_18 → {{0.987507, 0.136195, 0.05002, 0.00112455, 0.00283236,
    0.0133872, 0.026465, 0.0332694, 0.0160993, 0.0390476},
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    0.210234, 0.229697, 0.249822, 0.259105, 0.27297, 0.289076, 0.317832, 0.335563, 0.355861, 0.377554}},
LinearPositive_19 → {{0.982539, 0.179961, 0.0333254, 0.00200111, 0.00115972, 0.0102927,
    0.0228046, 0.0121111, 0.00908036, 0.0161142}, {0.0178705, 0.0311769, 0.0643922, 0.069626,
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    0.23988, 0.252709, 0.287684, 0.291808, 0.325954, 0.326749, 0.363155, 0.365467}},
LinearPositive_20 → {{0.986202, 0.151601, 0.0424663, 0.00447099, 0.00109462, 0.00945047,
    0.0222463, 0.0257098, 0.0219657, 0.0295198}, {0.0209036, 0.0299207, 0.0471001,
    0.0728795, 0.0929448, 0.119098, 0.122046, 0.151927, 0.162223, 0.18536, 0.202849,
    0.232356, 0.245858, 0.25629, 0.28775, 0.29186, 0.307933, 0.336058, 0.360208, 0.378029}},
LinearNegative_1 → {{0.989193, 0.134463, 0.033273, 0.0122366, 0.00463416, 0.0136415, 0.0217159,
    0.0232319, 0.012396, 0.0280808}, {-0.00734597, -0.03506, -0.0551468, -0.0670324,
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    -0.259234, -0.268938, -0.286171, -0.283589, -0.326223, -0.343221, -0.366606, -0.368834}},
LinearNegative_2 → {{0.984347, 0.157975, 0.0263112, 0.00208168, 0.000223738, 0.00939087,
    0.0281917, 0.0414298, 0.0263626, 0.0459716}, {-0.0243221, -0.0441605, -0.049999, -0.0776565,
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    -0.251687, -0.272838, -0.293825, -0.310339, -0.30033, -0.342172, -0.3414, -0.369281}},
LinearNegative_3 → {{0.980836, 0.180195, 0.0344618, 0.00545634, 0.00277104, 0.00870568,
    0.020668, 0.0383028, 0.019548, 0.043732}, {-0.0112525, -0.0239639, -0.0431044, -0.083421,
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    -0.255364, -0.26887, -0.2802, -0.292891, -0.320417, -0.324582, -0.348452, -0.374063}},
LinearNegative_4 → {{0.984883, 0.164289, 0.0164229, 0.00377152, 0.000817277, 0.0168434,
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LinearNegative_5 → {{0.979363, 0.173022, 0.0264889, 0.00322117, 0.007271, 0.0191, 0.0251334,
    0.0628086, 0.0247816, 0.0677644}, {-0.0269755, -0.0399261, -0.0386405, -0.0826142,
    -0.0752056, -0.127049, -0.121732, -0.145044, -0.167209, -0.1901, -0.216076, -0.209046,
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    LinearNegative_6 → {{0.978834, 0.18513, 0.0526097, 0.00637124, 0.000958914, 0.01183, 0.0431018,
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    LinearNegative_7 → {{0.989622, 0.125623, 0.0203484, 0.000920876, 0.00233538, 0.0188131,
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    LinearNegative_8 → {{0.98167, 0.182555, 0.0210012, 0.00672609, 0.000402194, 0.00388633,
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    LinearNegative_9 → {{0.981286, 0.181839, 0.049084, 0.0199435, 0.00113547, 0.007865, 0.016617,
       0.0179427, 0.00808278, 0.0218862}, {-0.0331657, -0.025258, -0.0459559, -0.0773633,
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    LinearNegative_10 → {{0.989193, 0.134973, 0.0180508, 0.0045088, 0.00395087, 0.0115148,
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    LinearNegative_11 → {{0.984017, 0.168575, 0.0308096, 0.00270172, 0.00151844, 0.0073725,
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    LinearNegative_12 → {{0.985834, 0.160636, 0.021122, 0.00143503, 0.00273007, 0.00710126,
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    LinearNegative_13 → {{0.983853, 0.166447, 0.0386783, 0.00477909, 0.00188278, 0.0127449,
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    LinearNegative_15 → {{0.984911, 0.160118, 0.0276094, 0.00252165, 0.000947446, 0.0127726,
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f3 → <|Sinusoidal3_21 → {{0.00317002, 0.074109, 0.992153, 0.0886697, 0.0375327, 0.0174017,
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    0.00309489, 0.253389, 0.300953, 0.0982376, -0.189054, -0.314448, -0.191398, 0.0999263,
    0.298596, 0.259785, 0.00227449, -0.257554, -0.298002, -0.0930015, 0.186985, 0.316182}}|>,
f5 → <|Sinusoidal2_11 → {{0.0021485, 0.0122623, 0.02891, 0.090199, 0.93002, 0.352263, 0.0311963,
    0.00399926, 0.0292511, 0.00126093}, {-0.0926738, -0.253027, 0.250903, 0.103223,
    -0.313416, 0.0999185, 0.25235, -0.261082, -0.0977455, 0.317661, -0.0965129, -0.250656,
    0.257198, 0.101645, -0.32164, 0.103109, 0.254619, -0.255178, -0.0965194, 0.318261}},
  Sinusoidal2_12 → {{0.00288759, 0.0105542, 0.0303491, 0.0960558, 0.933703, 0.340797, 0.0308242,
    0.00488265, 0.0284826, 0.00175455}, {-0.0950375, -0.257589, 0.260127, 0.0966108,
    -0.318827, 0.102791, 0.259659, -0.257002, -0.0983383, 0.310707, -0.102399, -0.256376,
    0.250661, 0.0959665, -0.314225, 0.0981869, 0.256526, -0.258699, -0.099125, 0.31069}},
  Sinusoidal2_13 → {{0.00306723, 0.0105269, 0.0302048, 0.0912875, 0.93445, 0.340389, 0.0280229,
    0.00433968, 0.0276828, 0.0014454}, {-0.10377, -0.261693, 0.257432, 0.0960656,
    -0.314008, 0.096009, 0.260027, -0.256316, -0.0934067, 0.319908, -0.093365, -0.254833,
    0.256009, 0.0968868, -0.31495, 0.0918127, 0.2553, -0.254857, -0.0936769, 0.312952}},
  Sinusoidal2_14 → {{0.00274284, 0.00808739, 0.0303101, 0.0903327, 0.937647, 0.331692,
    0.0284983, 0.00491078, 0.0284156, 0.00174302}, {-0.0981357, -0.255081, 0.25029, 0.0917682,
    -0.318065, 0.100672, 0.257737, -0.252486, -0.0942907, 0.317855, -0.103104, -0.259926,
    0.249957, 0.0982428, -0.315291, 0.0936937, 0.260732, -0.252961, -0.10224, 0.319224}},
  Sinusoidal2_15 → {{0.00220203, 0.0100696, 0.0301977, 0.0929728, 0.936096, 0.335219, 0.0283751,
    0.00462066, 0.0293592, 0.00155192}, {-0.0996308, -0.259083, 0.258574, 0.0918928,
    -0.323573, 0.100662, 0.255149, -0.254062, -0.0966519, 0.311549, -0.101856, -0.258055,
    0.255751, 0.100045, -0.315038, 0.0965886, 0.251521, -0.252345, -0.0972717, 0.315269}},
  Sinusoidal2_16 → {{0.00233554, 0.0107993, 0.0315543, 0.0939632, 0.936036, 0.335148, 0.0282333,
    0.00443526, 0.0273171, 0.00151509}, {-0.102112, -0.251431, 0.259464, 0.0944396,
    -0.31558, 0.0946564, 0.250326, -0.258304, -0.100603, 0.312397, -0.0992968, -0.260179,
    0.251536, 0.097343, -0.319663, 0.096694, 0.259842, -0.256793, -0.0961074, 0.316129}},
  Sinusoidal2_17 → {{0.00166065, 0.0107851, 0.0314362, 0.0905249, 0.930692, 0.350206, 0.0305624,
    0.00436775, 0.0301819, 0.00140965}, {-0.0911387, -0.257363, 0.25119, 0.100009,
    -0.314322, 0.0933092, 0.250169, -0.258272, -0.0951845, 0.314403, -0.0990791, -0.257026,
    0.257656, 0.101298, -0.318095, 0.1024, 0.259794, -0.256055, -0.101134, 0.316503}},
  Sinusoidal2_18 → {{0.00285321, 0.0126386, 0.0290817, 0.0913069, 0.929822, 0.352632,
    0.0299377, 0.00411805, 0.0285807, 0.00132581}, {-0.0992386, -0.26257, 0.25485, 0.103071,
    -0.311735, 0.0991311, 0.256016, -0.255033, -0.0984545, 0.312418, -0.0958921, -0.256441,
    0.259614, 0.102279, -0.321201, 0.099156, 0.251793, -0.256563, -0.0949774, 0.310937}},
```

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```
    Sinusoidal2_19 → {{0.00242306, 0.00923048, 0.029239, 0.0884853, 0.934906, 0.339754, 0.0294738,
       0.00448556, 0.0291801, 0.00149388}, {-0.0936839, -0.259086, 0.257717, 0.0941326,
       -0.31336, 0.103756, 0.258283, -0.261961, -0.0936879, 0.314605, -0.10129, -0.260504,
       0.253734, 0.0955174, -0.31278, 0.0998297, 0.260465, -0.251739, -0.0958238, 0.311369}},
    Sinusoidal2_20 → {{0.00259015, 0.0104845, 0.0317279, 0.0935203, 0.933317, 0.342506, 0.0311737,
       0.00471452, 0.0272476, 0.00168515}, {-0.0982614, -0.258254, 0.252924, 0.103164,
       -0.31803, 0.094803, 0.254834, -0.25944, -0.0947796, 0.317839, -0.0974409, -0.254011,
       0.2512, 0.095761, -0.317696, 0.0947513, 0.260227, -0.256404, -0.103312, 0.310356}}|>,
  f6 → <|Sinusoidal1_1 → {{0.00265626, 0.00748442, 0.0195301, 0.0514603, 0.0886686, 0.989212,
       0.0990386, 0.00802556, 0.0249081, 0.00327817}, {-0.168698, -0.0899286, 0.307511, -0.27635,
       -0.0138816, 0.261974, -0.29244, 0.100026, 0.154827, -0.297478, 0.212215, 0.0870562,
       -0.322868, 0.243555, 0.00859735, -0.25241, 0.281436, -0.116853, -0.17869, 0.3331}},
    Sinusoidal1_2 → {{0.00455044, 0.0084327, 0.0233575, 0.0475118, 0.0999956, 0.98745, 0.106387,
       0.00301058, 0.0268424, 0.00088367}, {-0.213125, -0.125922, 0.323646, -0.241866,
       -0.0102325, 0.258289, -0.285541, 0.104174, 0.209577, -0.294379, 0.18529, 0.126338,
       -0.293835, 0.261767, -0.0093371, -0.233783, 0.291035, -0.0926483, -0.18519, 0.313391}},
    Sinusoidal1_3 → {{0.0014607, 0.00564311, 0.0165432, 0.0343438, 0.10513, 0.989353, 0.0908914,
       0.00444733, 0.0189271, 0.00151092}, {-0.198739, -0.0880265, 0.300068, -0.256305,
       0.0116843, 0.252665, -0.31665, 0.117049, 0.175831, -0.292031, 0.207327, 0.086639,
       -0.289165, 0.272243, -0.0290895, -0.245347, 0.322567, -0.0749939, -0.195786, 0.292589}},
    Sinusoidal1_4 → {{0.00361076, 0.00670356, 0.0162836, 0.038965, 0.103307, 0.986715, 0.115062,
       0.010157, 0.0226894, 0.00468882}, {-0.183691, -0.129523, 0.339368, -0.245975,
       -0.00187672, 0.293632, -0.301423, 0.0981593, 0.202886, -0.317235, 0.169799, 0.0940022,
       -0.277473, 0.23027, 0.00367662, -0.242149, 0.308816, -0.0826166, -0.167992, 0.297564}},
    Sinusoidal1_5 → {{0.00203604, 0.0110644, 0.0255919, 0.0336898, 0.0963591, 0.989763, 0.0930914,
       0.00173884, 0.0223492, 0.0002318}, {-0.187628, -0.0680063, 0.319591, -0.264895,
       0.0244925, 0.272842, -0.300061, 0.0769763, 0.187664, -0.318839, 0.203154, 0.0656472,
       -0.305857, 0.269723, 0.0253796, -0.230396, 0.279751, -0.0974417, -0.189984, 0.300875}},
    Sinusoidal1_6 → {{0.00250012, 0.0201632, 0.0211443, 0.0342903, 0.0816814, 0.987607, 0.122919,
       0.006613, 0.0275853, 0.00346878}, {-0.178331, -0.113036, 0.322943, -0.252725,
       0.0102116, 0.233272, -0.315468, 0.10279, 0.185134, -0.303644, 0.208128, 0.119876,
       -0.285354, 0.282609, -0.02276, -0.254219, 0.267924, -0.127865, -0.154326, 0.316387}},
    Sinusoidal1_7 → {{0.00265909, 0.00860401, 0.0127422, 0.0391091, 0.0940623, 0.991458, 0.0766203,
       0.00355452, 0.0225024, 0.00119721}, {-0.195606, -0.0680482, 0.315423, -0.268795,
       0.0301264, 0.254738, -0.289949, 0.0923877, 0.172469, -0.319316, 0.157685, 0.121717,
       -0.302195, 0.256053, 0.00304995, -0.252346, 0.310638, -0.0743277, -0.172949, 0.321041}},
    Sinusoidal1_8 → {{0.00170641, 0.0118431, 0.0193104, 0.0469498, 0.100069, 0.987012, 0.109804,
       0.00411663, 0.0315869, 0.0011933}, {-0.179757, -0.110362, 0.322795, -0.229783,
       -0.0224063, 0.280924, -0.277949, 0.0820535, 0.163557, -0.315118, 0.17131, 0.10962,
       -0.318535, 0.274617, 0.014939, -0.236416, 0.292915, -0.078668, -0.20981, 0.314142}},
    Sinusoidal1_9 → {{0.00094733, 0.00853224, 0.00662565, 0.0380677, 0.0873059, 0.986197,
       0.133489, 0.0069366, 0.0186757, 0.00310394}, {-0.158399, -0.0961725, 0.295506, -0.25436,
       0.00414682, 0.278906, -0.294525, 0.070388, 0.15641, -0.338296, 0.208314, 0.10672,
       -0.299369, 0.27247, 0.00519025, -0.235872, 0.333079, -0.0867432, -0.156717, 0.296464}},
    Sinusoidal1_10 → {{0.00126743, 0.00831544, 0.0215276, 0.0355426, 0.101209, 0.990378,
       0.0805881, 0.0110057, 0.0216447, 0.00510707}, {-0.170355, -0.0955602, 0.299861, -0.267626,
       0.0087676, 0.251562, -0.32368, 0.0936288, 0.183235, -0.282979, 0.207605, 0.0921288,
       -0.280951, 0.231827, 0.0180724, -0.261059, 0.315775, -0.106128, -0.212727, 0.317469}}|>|>
```

In[3]:=
```
clustersSingle = TimeSeriesSingleClusters[classification1]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

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Out[3]=
```
<|SpikeMax → <|Cluster → Cluster[ ··· 1 ··· ], InitialSplitCluster → { ··· 1 ··· },
   GroupAssociations → <|G1 → {SpikePositive_1, SpikePositive_12, SpikePositive_4, ··· 14 ···,
       SpikePositive_19, SpikePositive_3, SpikePositive_6}|>|>, ··· 4 ···, f6 → ··· 1 ···|>
```
large output | show less | show more | show all | set size limit...

We can obtain the keys for this classification, which by default follow G# for groups within each class:

In[4]:=
```
Query[All, "GroupAssociations" /* Keys]@clustersSingle
```

Out[4]=
```
<|SpikeMax → {G1}, SpikeMin → {G1, G2}, f1 → {G1, G2}, f3 → {G1, G2}, f5 → {G1, G2}, f6 → {G1, G2}|>
```

Now let's say we want to prepend a text labeling to each of these:

In[5]:=
```
clustersSingleLabels = TimeSeriesSingleClusters[classification1, ClusterLabeling → "LabelPrepend_"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[5]=
```
<| ··· 1 ··· |>
```
large output | show less | show more | show all | set size limit...

In[6]:=
```
Query[All, "GroupAssociations" /* Keys]@clustersSingleLabels
```

Out[6]=
```
<|SpikeMax → {LabelPrepend_G1}, SpikeMin → {LabelPrepend_G1, LabelPrepend_G2},
 f1 → {LabelPrepend_G1, LabelPrepend_G2}, f3 → {LabelPrepend_G1, LabelPrepend_G2},
 f5 → {LabelPrepend_G1, LabelPrepend_G2}, f6 → {LabelPrepend_G1, LabelPrepend_G2}|>
```

DendrogramPlotOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

DendrogramPlotOptions provides options for an internal DendrogramPlot in the case where either the PrintDendrograms or ReturnDendrograms option values are set to True.

We generate some data for classification:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

Method → "LombScargle"

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.317649, 0.0645686, 0.291178, 0.287706, 0.13894, 0.351824, 0.353429, 0.208994,
      0.600116, 0.235704}, {0.961907, -0.0663542, 0.0578943, 0.0350586, 0.0817456, 0.0778044,
      0.0507818, -0.0754372, -0.0621888, -0.0678777, -0.0501254, -0.0910443, 0.0357231,
      0.0772411, -0.0920714, 0.017167, -0.053944, -0.0535487, 0.0311044, 0.0520573}},
   SpikePositive_2 → {{0.421021, 0.277838, 0.254434, 0.171366, 0.40888, 0.261161, 0.201499,
      0.263757, 0.488186, 0.259926}, {0.967177, -0.0491331, -0.0612015, -0.0462464, -0.0212056,
      -0.0824781, -0.0760675, -0.0709126, -0.059994, -0.0629496, -0.0123348, 0.0788726,
      0.0195082, -0.0875618, 0.033551, 0.0595813, 0.0768343, 0.0335454, 0.0545382, 0.0392675}},
   SpikePositive_3 → {{0.186321, 0.193535, 0.327721, 0.34642, 0.191745, 0.336709, 0.10209,
      0.359195, 0.525833, 0.366522}, {0.977209, 0.0335275, 0.0228705, -0.043421, 0.0223355,
      0.0130582, 0.0373851, -0.0516496, -0.0777322, 0.0929638, -0.0170483, 0.0561751,
      0.0708102, 0.00050664, 0.066134, -0.040484, -0.0380166, 0.04893, -0.0238379, -0.0568379}},
   SpikePositive_4 → {{0.208632, 0.14333, 0.148031, 0.098426, 0.398602, 0.402727, 0.219733,
      0.274517, 0.622967, 0.267442}, {0.966562, 0.065701, 0.0582582, 0.0908827, 0.0879789,
      -0.0331988, 0.0696527, 0.0188108, 0.0214006, -0.015133, 0.0275516, 0.0572224, 0.0809586,
      -0.0633345, 0.0416776, 0.0626742, 0.0598527, -0.0929445, -0.0483169, -0.0152999}},
   SpikePositive_5 → {{0.300155, 0.184504, 0.249723, 0.327071, 0.409077, 0.289936, 0.461719,
      0.183286, 0.421238, 0.175788}, {0.969148, 0.0721269, -0.0856908, 0.0872922, 0.0358102,
      0.00887718, 0.0205674, -0.0516466, 0.0784423, -0.100548, 0.0248062, -0.0307463, 0.00454368,
      -0.00997462, 0.049402, -0.0239214, 0.0711186, -0.0284581, 0.0758886, -0.0595907}},
   SpikePositive_6 → {{0.279309, 0.379089, 0.36085, 0.308445, 0.378426, 0.128773, 0.287596,
      0.338965, 0.297239, 0.327381}, {0.964392, 0.0529843, -0.0270977, -0.0247432, -0.0474333,
      0.0838812, -0.0940839, 0.08366, -0.0724709, -0.0375525, 0.0202467, 0.00347552, -0.0969072,
      -0.0894845, -0.0434612, -0.0855264, -0.0766913, 0.0309476, 0.000776479, -0.0114616}},
   SpikePositive_7 → {{0.302217, 0.22975, 0.139672, 0.403866, 0.371446, 0.415762, 0.259177,
      0.183173, 0.474331, 0.191622}, {0.970558, 0.0327312, -0.0657766, 0.0277494, -0.0176078,
      -0.0136386, -0.0525814, -0.100913, 0.0936992, 0.0109684, -0.103676, -0.0258495,
      -0.00283064, -0.0531806, 0.06732, 0.0605964, -0.0304903, 0.0188612, -0.0405743, -0.064155}},
   SpikePositive_8 → {{0.176074, 0.175923, 0.311146, 0.359823, 0.163368, 0.262854, 0.378146,
      0.300822, 0.541817, 0.298209}, {0.96977, -0.00961901, -0.0411601, -0.0999736, 0.0221398,
      -0.00505844, -0.0423039, -0.0472912, -0.0256425, -0.0184383, 0.0896701, -0.0454494,
      0.0853281, 0.0977178, -0.0179302, -0.0459616, 0.0573109, -0.0787307, 0.0256911, -0.0520812}},
   SpikePositive_9 → {{0.163117, 0.22822, 0.353176, 0.237465, 0.448438, 0.290949, 0.408386,
      0.25003, 0.406833, 0.244193}, {0.965011, -0.0503892, -0.0807405, -0.0765858, -0.0232944,
      0.0521878, -0.0764855, 0.0132092, -0.0387573, -0.0731481, 0.0893359, 0.0474137, 0.0721364,
      -0.0706156, -0.0392538, 0.0728686, -0.0313923, -0.0637524, 0.072432, 0.011025}},
   SpikePositive_10 → {{0.290418, 0.211462, 0.247645, 0.131733, 0.192622, 0.382361, 0.234374,
      0.199883, 0.686811, 0.205821}, {0.967287, -0.0642527, 0.0943944, 0.0781782, -0.087008,
      -0.0933674, 0.0888497, -0.0689472, -0.0770399, -0.027091, -0.000730048, -0.0306504, 0.0142014,
      0.0191282, -0.00170606, -0.0499554, -0.0204459, 0.000651304, -0.0480898, 0.0535025}},
   SpikePositive_11 → {{0.077214, 0.232344, 0.321795, 0.375164, 0.337508, 0.468035, 0.366821,
      0.299942, 0.226877, 0.2946}, {-0.0862286, -0.0827602, 0.965953, -0.0453717, -0.100036,
      0.00291575, 0.0180697, 0.102925, -0.031437, -0.00588973, -0.0633668, 0.0534068, 0.0660326,
```

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```
    0.0263278, 0.0693538, -0.0550255, -0.0810156, -0.0139881, 0.00903536, -0.0451003}},
  SpikePositive_12 → {{0.32219, 0.495705, 0.192606, 0.266488, 0.28553, 0.286841, 0.302923,
    0.246012, 0.401779, 0.25464}, {-0.0531383, -0.0665485, 0.972546, 0.0513807, 0.0255179,
    -0.0377736, -0.0412504, -0.0958277, -0.0320713, -0.0585264, 0.0721541, 0.0062091, -0.02928,
    -0.0388632, -0.0784107, -0.0601481, -0.0306136, 0.00341962, 0.0839243, 0.0384119}},
  SpikePositive_13 → {{0.231059, 0.332066, 0.256035, 0.228216, 0.238581, 0.183885, 0.189078,
    0.490485, 0.349241, 0.479247}, {0.0903652, -0.0499946, 0.971523, 0.0456268, 0.012544,
    -0.0883775, -0.0583322, -0.0284296, -0.028639, 0.0761298, -0.00353677, 0.043607, -0.0627122,
    -0.0175501, -0.0481286, -0.0492613, 0.0892355, -0.0484149, 0.0527695, -0.0247184}},
  SpikePositive_14 → {{0.265578, 0.232825, 0.386112, 0.460366, 0.301056, 0.377461, 0.127925,
    0.271599, 0.33847, 0.276474}, {-0.0648816, 0.0129031, 0.969428, 0.0691067, 0.0648594,
    -0.0722478, 0.0863586, 0.0498516, 0.073479, -0.0656012, -0.0756136, 0.034176, -0.0296903,
    0.0243086, 0.024931, -0.0707182, 0.0193199, 0.00299995, -0.0831366, -0.026679}},
  SpikePositive_15 → {{0.153011, 0.303766, 0.370884, 0.285767, 0.191177, 0.202747, 0.377415,
    0.292031, 0.510919, 0.314131}, {0.0620166, -0.0218049, 0.97301, 0.0545387, 0.0756948,
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    -0.00979783, 0.0198687, 0.0787134, -0.0813662, -0.0437455, -0.023429, -0.0358258}},
  SpikePositive_16 → {{0.129184, 0.285401, 0.271764, 0.302682, 0.406306, 0.320021, 0.290752,
    0.389754, 0.265398, 0.402499}, {-0.0687796, -0.0111994, 0.97541, -0.0355948, 0.0535676,
    0.0568494, 0.0485743, 0.0130415, -0.049084, 0.0400743, -0.0637533, 0.0450199, 0.00681604,
    0.0983083, 0.0048581, 0.0302542, -0.0253094, -0.0399378, -0.0869626, -0.0571525}},
  SpikePositive_17 → {{0.25137, 0.312753, 0.230733, 0.273352, 0.548166, 0.14098, 0.332541,
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  SpikePositive_18 → {{0.307673, 0.196223, 0.319375, 0.394231, 0.254758, 0.227677, 0.346521,
    0.367121, 0.30916, 0.37715}, {-0.0611847, 0.0565762, 0.968082, -0.0485048, 0.0990627,
    -0.0573429, 0.0640607, 0.0780778, -0.0815728, 0.0468848, -0.0954449, 0.0103242, -0.0492485,
    -0.0555399, -0.0130253, 0.0132805, -0.032305, -0.00829429, -0.0715948, 0.0074015}},
  SpikePositive_19 → {{0.223692, 0.21167, 0.142079, 0.323882, 0.480465, 0.384192, 0.272493,
    0.236523, 0.454354, 0.254929}, {0.0344924, 0.0180388, 0.981226, -0.0613948, 0.0138402,
    0.059787, 0.0493929, -0.073635, -0.00220225, 0.00589341, 0.00463619, 0.0149259, 0.0437531,
    -0.0111474, -0.0220862, 0.00730416, 0.0806007, 0.0820266, -0.0625993, 0.0166048}},
  SpikePositive_20 → {{0.22507, 0.232613, 0.236338, 0.287058, 0.294685, 0.240276, 0.225186,
    0.389016, 0.500586, 0.399721}, {0.0884144, -0.0878362, 0.979373, 0.00528826, -0.0107265,
    -0.035582, 0.0188017, -0.0723907, -0.0181748, 0.0194031, 0.0431572, 0.0237123, -0.0812479,
    -0.0158746, -0.0273717, 0.0251122, 0.0748477, -0.0282688, 0.00684005, 0.0219338}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.103615, 0.299836, 0.323374, 0.149969, 0.434208, 0.411199,
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    -0.025775, 0.0220441, 0.0914044, -0.0819599, 0.0318898, 0.083921, -0.0418444, -0.0790178}},
  SpikeNegative_2 → {{0.133281, 0.234561, 0.157875, 0.209746, 0.20172, 0.538941, 0.534906,
    0.208581, 0.380028, 0.230432}, {-0.961904, 0.0532601, 0.0509629, -0.088491, 0.0749733,
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    0.048853, 0.0431339, 0.0907207, -0.0913724, -0.0354106, 0.0525202, 0.00643808, 0.0789068}},
  SpikeNegative_3 → {{0.208114, 0.291309, 0.164268, 0.206826, 0.149222, 0.286648, 0.25779,
    0.511215, 0.362536, 0.488266}, {-0.970224, 0.0680615, -0.0698319, 0.0274546, 0.0428421,
    -0.0624721, 0.0725093, -0.0326557, -0.00695631, -0.0891449, 0.0660046, 0.0352663,
    -0.0306418, 0.0874619, 0.012029, 0.0239947, -0.086955, 0.0215758, -0.0733346, 0.0055588}},
  SpikeNegative_4 → {{0.184625, 0.256643, 0.319459, 0.344082, 0.364254, 0.444654, 0.223355,
    0.27325, 0.385559, 0.27567}, {-0.977313, -0.0126757, 0.0699939, -0.0755858, -0.0234109,
    0.0545228, -0.0556218, 0.0243082, 0.0442455, -0.0345772, -0.033785, -0.0012179, -0.0310521,
    0.0151828, -0.00253263, 0.0865308, 0.022342, -0.0215575, -0.0888507, 0.0709803}},
  SpikeNegative_5 → {{0.144719, 0.327919, 0.162984, 0.244065, 0.219345, 0.291403, 0.288265,
    0.287605, 0.644196, 0.267514}, {-0.965256, 0.0705663, 0.0522363, 0.085233, 0.0243287,
    -0.00774283, -0.0390743, -0.0733518, -0.0312074, -0.0250618, -0.0455007, 0.0911324,
    0.0289105, 0.0245728, -0.0300449, -0.0681912, -0.103243, 0.0788556, 0.0666006, -0.07393}},
  SpikeNegative_6 → {{0.13351, 0.26604, 0.230652, 0.290692, 0.451726, 0.318877, 0.310559,
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  SpikeNegative_7 → {{0.249776, 0.181518, 0.202207, 0.384536, 0.270693, 0.138074, 0.26131,
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    -0.0340738, -0.0643858, 0.00659219, 0.0837693, -0.0486937, 0.0943862, 0.00787877}},
  SpikeNegative_8 → {{0.372755, 0.345717, 0.240965, 0.215638, 0.122943, 0.391599, 0.200629,
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  SpikeNegative_9 → {{0.544946, 0.148339, 0.187951, 0.279245, 0.140213, 0.204264, 0.323838,
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  SpikeNegative_10 → {{0.271695, 0.299329, 0.215908, 0.195074, 0.317957, 0.294504, 0.217287,
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  SpikeNegative_11 → {{0.283394, 0.217235, 0.308144, 0.219428, 0.339505, 0.368585, 0.437664,
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  SpikeNegative_12 → {{0.0809487, 0.129086, 0.167906, 0.452956, 0.40462, 0.448866, 0.375481,
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  SpikeNegative_13 → {{0.259201, 0.235079, 0.532866, 0.241556, 0.275625, 0.181938, 0.380469,
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    0.0874333, -0.0265103, 0.082165, 0.0178937, 0.0289866, -0.0568462, 0.0908721, -0.0653876}},
  SpikeNegative_15 → {{0.201626, 0.248375, 0.199249, 0.330689, 0.284845, 0.657957, 0.239342,
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  SpikeNegative_16 → {{0.234406, 0.129657, 0.21663, 0.320641, 0.349919, 0.409523, 0.275581,
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  SpikeNegative_17 → {{0.246566, 0.0843053, 0.220701, 0.17259, 0.549908, 0.380576, 0.273279,
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  SpikeNegative_18 → {{0.421592, 0.322415, 0.377407, 0.19652, 0.183782, 0.444633, 0.222336,
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    0.0578303, -0.0592898, 0.0987377, 0.0161916, 0.0612989, -0.0110996, 0.0370137}},
  SpikeNegative_19 → {{0.246688, 0.243671, 0.291215, 0.142395, 0.166431, 0.480573, 0.313414,
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    0.0460293, -0.0666807, -0.0779946, 0.0959169, -0.0922228, -0.0911651, -0.0736704}},
  SpikeNegative_20 → {{0.302467, 0.434687, 0.220674, 0.417926, 0.224593, 0.208491, 0.505073,
    0.218396, 0.222089, 0.223991}, {0.0777399, 0.0148584, -0.967487, -0.0259822, -0.0398998,
    -0.0858728, 0.0422119, -0.0205498, 0.086051, 0.0125045, -0.0362393, -0.0153269, -0.0495723,
    0.0608549, 0.0873292, -0.0733347, 0.0568684, 0.0875011, -0.0537834, -0.0616548}}|>,
f1 → <|LinearPositive_1 → {{0.984034, 0.165576, 0.0320348, 0.00273338, 0.00235685,
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  LinearPositive_2 → {{0.984709, 0.163338, 0.0317004, 0.0022066, 0.00144773, 0.00990713,
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  LinearPositive_3 → {{0.984492, 0.164749, 0.0311609, 0.00238192, 0.00204773, 0.0105015,
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  LinearPositive_4 → {{0.983904, 0.165647, 0.0338499, 0.00247334, 0.00228889,
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    0.205606, 0.222509, 0.24406, 0.261371, 0.278278, 0.297012, 0.3173, 0.337819, 0.353066, 0.375342}},
LinearPositive_5 → {{0.984071, 0.166104, 0.0319255, 0.00286945, 0.0016523, 0.0105909,
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LinearPositive_6 → {{0.985073, 0.160288, 0.031492, 0.00237356, 0.00201893, 0.0113909,
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LinearPositive_7 → {{0.984774, 0.16204, 0.0336916, 0.00246282, 0.00150059, 0.0120868,
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LinearPositive_8 → {{0.984564, 0.16469, 0.0339594, 0.00282071, 0.00174367, 0.0109995,
    0.0199211, 0.0253093, 0.0174895, 0.0296891}, {0.0198419, 0.0357247, 0.057249, 0.0736316,
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    0.241194, 0.262799, 0.279512, 0.297595, 0.318599, 0.336445, 0.355666, 0.372019}},
LinearPositive_9 → {{0.984144, 0.165492, 0.0320171, 0.00171, 0.00191089,
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LinearPositive_10 → {{0.984478, 0.164261, 0.0336293, 0.00325421, 0.00149638, 0.0101754,
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LinearPositive_11 → {{0.984647, 0.16723, 0.0321666, 0.00159871, 0.000219362, 0.0139602,
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LinearPositive_12 → {{0.984648, 0.164501, 0.0219171, 0.00456569, 0.00109071,
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LinearPositive_13 → {{0.98504, 0.166175, 0.0292292, 0.00321689, 0.00105008, 0.012928,
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LinearPositive_14 → {{0.988342, 0.138124, 0.0208973, 0.00291109, 0.00346294,
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    0.205831, 0.223749, 0.248052, 0.267259, 0.288336, 0.292317, 0.31509, 0.331232, 0.348171, 0.377229}},
LinearPositive_15 → {{0.986073, 0.157222, 0.0323902, 0.00126987, 0.00135606,
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LinearPositive_16 → {{0.983713, 0.168403, 0.0329718, 0.00123761, 0.00461495, 0.0167442,
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    0.216598, 0.2382, 0.268986, 0.273232, 0.303159, 0.323245, 0.333908, 0.357185, 0.365262}},
LinearPositive_17 → {{0.984306, 0.165911, 0.0255882, 0.00123055, 0.00071641, 0.0165014,
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    0.238495, 0.268201, 0.286149, 0.297984, 0.314528, 0.332123, 0.352257, 0.378987}},
LinearPositive_18 → {{0.985726, 0.159471, 0.0366058, 0.00453715, 0.000847285,
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LinearPositive_19 → {{0.981516, 0.179833, 0.0325734, 0.00186521, 0.00327453,
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LinearPositive_20 → {{0.985341, 0.155159, 0.0253817, 0.00267726, 0.00238955, 0.00998292,
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    0.244497, 0.264738, 0.281968, 0.306566, 0.311327, 0.341566, 0.348686, 0.369233}},
LinearNegative_1 → {{0.977794, 0.187787, 0.0289177, 0.000163598, 0.00405158, 0.00516271,
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LinearNegative_2 → {{0.970287, 0.234352, 0.0435813, 0.00602902, 0.00284387, 0.0015448,
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LinearNegative_3 → {{0.986477, 0.144851, 0.0160245, 0.00465276, 0.00817548, 0.00839332,
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LinearNegative_4 → {{0.98264, 0.164582, 0.0597211, 0.000539846, 0.00613353, 0.0163804,
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LinearNegative_5 → {{0.989714, 0.119206, 0.0489374, 0.000203308, 0.00819704, 0.0180694,
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LinearNegative_6 → {{0.978566, 0.201007, 0.0121723, 0.00502172, 0.00461551, 0.00808464,
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LinearNegative_7 → {{0.974363, 0.218051, 0.0253303, 0.00290097, 0.000191481, 0.00220426,
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LinearNegative_8 → {{0.985558, 0.1542, 0.0484934, 0.00704061, 0.0120374, 0.0136235, 0.0151856,
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LinearNegative_9 → {{0.985812, 0.156181, 0.0310133, 0.00172392, 0.00922624, 0.00670873,
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LinearNegative_10 → {{0.986389, 0.134062, 0.0436806, 0.00330218, 0.00828697, 0.0130188,
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LinearNegative_11 → {{0.983663, 0.162946, 0.0361403, 0.0019299, 0.00423897, 0.00583407,
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LinearNegative_12 → {{0.986585, 0.152244, 0.0334845, 0.00123524, 0.000986626, 0.0149576,
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LinearNegative_13 → {{0.983584, 0.170283, 0.028546, 0.00106715, 0.00264474, 0.0157095,
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LinearNegative_14 → {{0.980981, 0.184266, 0.0365268, 0.00174599, 0.000012139, 0.00412592,
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LinearNegative_15 → {{0.982458, 0.177874, 0.0325454, 0.00269891, 0.000846211, 0.00504817,
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LinearNegative_16 → {{0.987446, 0.140965, 0.0425444, 0.000710924, 0.00284178, 0.00919814,
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LinearNegative_17 → {{0.981818, 0.177096, 0.0336826, 0.000730455, 0.00282945, 0.0146977,
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f5 → <|Sinusoidal2_11 → {{0.00231847, 0.0106736, 0.028788, 0.0901899, 0.935443, 0.337979,
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      0.253489, 0.102048, -0.317051, 0.0908162, 0.25913, -0.254875, -0.0911868, 0.315522}},
  Sinusoidal2_12 → {{0.00214811, 0.0104961, 0.0305444, 0.0955717, 0.931817, 0.34617, 0.0288072,
      0.0046554, 0.0291285, 0.00162399}, {-0.0963757, -0.253217, 0.252535, 0.102894,
      -0.316165, 0.0970874, 0.251844, -0.252119, -0.101286, 0.319076, -0.101934, -0.250547,
      0.253164, 0.0997019, -0.320591, 0.103334, 0.260098, -0.251922, -0.100259, 0.319323}},
  Sinusoidal2_13 → {{0.00232358, 0.0102776, 0.0293118, 0.0910959, 0.93188, 0.347646, 0.0266467,
      0.00613232, 0.0267985, 0.00248607}, {-0.0919752, -0.25047, 0.253026, 0.0938724,
      -0.315834, 0.0942792, 0.25526, -0.252372, -0.101998, 0.319828, -0.0977994, -0.259302,
      0.260258, 0.095697, -0.315463, 0.0913118, 0.259662, -0.258233, -0.0977278, 0.317144}},
  Sinusoidal2_14 → {{0.00335486, 0.0107308, 0.0327631, 0.0926219, 0.93461, 0.338872, 0.0318864,
```

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```
    0.00643346, 0.0287483, 0.00262387}, {-0.0928952, -0.259338, 0.258065, 0.0990214,
    -0.320454, 0.102566, 0.249412, -0.252176, -0.0916493, 0.318399, -0.0994521, -0.252457,
    0.250798, 0.0945928, -0.315217, 0.0916625, 0.254109, -0.261547, -0.0983813, 0.320984}},
  Sinusoidal2_15 → {{0.00301847, 0.0116605, 0.0306926, 0.0891892, 0.930751, 0.350524, 0.0296544,
    0.00409467, 0.0299244, 0.00131594}, {-0.0978234, -0.262117, 0.25151, 0.102889,
    -0.310866, 0.0982631, 0.257974, -0.260732, -0.0987618, 0.322413, -0.101398, -0.251487,
    0.250012, 0.0983804, -0.316214, 0.0977151, 0.252445, -0.256166, -0.0995068, 0.314405}},
  Sinusoidal2_16 → {{0.00331774, 0.0100805, 0.0310237, 0.0951321, 0.933598, 0.341503, 0.0308789,
    0.00560897, 0.0255963, 0.00227168}, {-0.0979666, -0.252601, 0.255393, 0.0970815,
    -0.322931, 0.100529, 0.254396, -0.252073, -0.0926303, 0.318655, -0.102575, -0.251632,
    0.253993, 0.09413, -0.320204, 0.0932868, 0.254826, -0.261804, -0.0975798, 0.312616}},
  Sinusoidal2_17 → {{0.0019596, 0.0104148, 0.0308414, 0.0884832, 0.932088, 0.347438, 0.0283889,
    0.00501943, 0.0277871, 0.00189536}, {-0.0936685, -0.25537, 0.256864, 0.0929799,
    -0.314514, 0.0973972, 0.254514, -0.257286, -0.0991625, 0.321678, -0.0996272, -0.257215,
    0.255895, 0.101021, -0.313747, 0.0993177, 0.25737, -0.258617, -0.0941734, 0.31086}},
  Sinusoidal2_18 → {{0.00301437, 0.00969426, 0.031106, 0.0908948, 0.934506, 0.340414, 0.026678,
    0.00509308, 0.0272628, 0.00189793}, {-0.101562, -0.253645, 0.251498, 0.0962753,
    -0.320522, 0.0980502, 0.257139, -0.253207, -0.0947316, 0.318875, -0.101305, -0.259795,
    0.256741, 0.0946399, -0.315253, 0.0925709, 0.251198, -0.253462, -0.0990825, 0.319136}},
  Sinusoidal2_19 → {{0.00213928, 0.0110358, 0.0301506, 0.095492, 0.929698, 0.351861, 0.0290867,
    0.00465566, 0.0288221, 0.00163789}, {-0.0940571, -0.25634, 0.25704, 0.0948583,
    -0.309782, 0.0949244, 0.259003, -0.259473, -0.100661, 0.312836, -0.103737, -0.25462,
    0.255845, 0.0948323, -0.313133, 0.102298, 0.261848, -0.261533, -0.0949022, 0.313785}},
  Sinusoidal2_20 → {{0.00203527, 0.0110316, 0.0313237, 0.0972493, 0.933764, 0.340351, 0.0289975,
    0.00375764, 0.0287449, 0.00112576}, {-0.101212, -0.254026, 0.259182, 0.0998304,
    -0.315892, 0.0930679, 0.256636, -0.26141, -0.0971823, 0.312949, -0.103384, -0.251647,
    0.253581, 0.0958022, -0.315602, 0.100801, 0.260119, -0.252436, -0.0973207, 0.316131}}|>,
f6 → <|Sinusoidal1_1 → {{0.00216275, 0.0110367, 0.0113875, 0.0333156, 0.0946255, 0.990014,
    0.0961699, 0.00695854, 0.0155709, 0.00345744}, {-0.193424, -0.0820548, 0.286233, -0.227237,
    -0.000743498, 0.24921, -0.29611, 0.0803501, 0.15778, -0.31105, 0.207621, 0.0919909,
    -0.300944, 0.260836, -0.00344948, -0.286021, 0.320948, -0.0721822, -0.17328, 0.33788}},
  Sinusoidal1_2 → {{0.00363973, 0.0085336, 0.0238872, 0.0348359, 0.101943, 0.986275, 0.118027,
    0.00551957, 0.0321407, 0.00207542}, {-0.155276, -0.0867776, 0.281965, -0.243403,
    -0.01016, 0.28009, -0.306362, 0.0956848, 0.203722, -0.286084, 0.157988, 0.123837,
    -0.318048, 0.270093, -0.00653516, -0.241809, 0.280867, -0.117683, -0.21098, 0.338428}},
  Sinusoidal1_3 → {{0.00190769, 0.00968735, 0.0109604, 0.040465, 0.0891987, 0.989153, 0.107153,
    0.0090632, 0.0133971, 0.00452679}, {-0.179129, -0.0795481, 0.301052, -0.259466,
    -0.005413, 0.267223, -0.274022, 0.0776205, 0.155665, -0.346705, 0.165103, 0.101437,
    -0.303857, 0.261953, 0.0314206, -0.276479, 0.325132, -0.0975048, -0.168778, 0.294984}},
  Sinusoidal1_4 → {{0.0000692669, 0.00302635, 0.016346, 0.0280587, 0.0774052, 0.991789,
    0.093213, 0.0059664, 0.023871, 0.00211218}, {-0.179378, -0.113568, 0.291684, -0.26871,
    -0.0014155, 0.221185, -0.307742, 0.124455, 0.186459, -0.327423, 0.179657, 0.0842319,
    -0.285608, 0.274416, 0.00724696, -0.266017, 0.315138, -0.0643314, -0.166293, 0.313656}},
  Sinusoidal1_5 → {{0.000212813, 0.00323833, 0.0276226, 0.0381909, 0.0845783, 0.990432,
    0.0932576, 0.0125449, 0.027705, 0.00614219}, {-0.163481, -0.119817, 0.321515, -0.275726,
    -0.0191266, 0.219518, -0.319451, 0.124058, 0.171627, -0.283125, 0.20905, 0.0824797,
    -0.294824, 0.259021, 0.0299252, -0.236898, 0.321582, -0.0854314, -0.173467, 0.318705}},
  Sinusoidal1_6 → {{0.00239614, 0.0137099, 0.013991, 0.0263957, 0.0910341, 0.989998, 0.0989063,
    0.00482725, 0.0267352, 0.00312528}, {-0.211028, -0.115033, 0.313422, -0.240842,
    0.0306669, 0.245542, -0.309304, 0.075194, 0.168318, -0.294558, 0.180216, 0.121653,
    -0.321063, 0.280405, -0.0296038, -0.264736, 0.291277, -0.0722811, -0.164687, 0.302012}},
  Sinusoidal1_7 → {{0.0010207, 0.00345893, 0.0217, 0.0264857, 0.118749, 0.984952, 0.119755,
    0.00472272, 0.0146762, 0.0019251}, {-0.208629, -0.0977018, 0.285712, -0.271742,
    -0.0247239, 0.282807, -0.300932, 0.073303, 0.204558, -0.290292, 0.165062, 0.0791767,
    -0.319196, 0.279968, 0.00394578, -0.244695, 0.304319, -0.0955887, -0.171182, 0.289985}},
  Sinusoidal1_8 → {{0.00397638, 0.0079181, 0.0230003, 0.063951, 0.0940714, 0.988058, 0.0973252,
    0.00281035, 0.0267117, 0.000529378}, {-0.181921, -0.073252, 0.310131, -0.23201,
    0.000473446, 0.236602, -0.279002, 0.122722, 0.176044, -0.333624, 0.167761, 0.108205,
    -0.303555, 0.253185, -0.0220852, -0.229793, 0.318672, -0.107483, -0.209089, 0.337836}},
  Sinusoidal1_9 → {{0.00122631, 0.0100417, 0.0198284, 0.035212, 0.0844369, 0.991072, 0.0922432,
    0.00449693, 0.0194373, 0.00188006}, {-0.211381, -0.0847113, 0.30246, -0.254479, 0.0168569,
    0.25372, -0.325742, 0.0835532, 0.16173, -0.294729, 0.190106, 0.113056, -0.331623,
    0.259916, -0.000735403, -0.236348, 0.292264, -0.0898114, -0.158409, 0.316608}},
  Sinusoidal1_10 → {{0.00243159, 0.0108076, 0.0234248, 0.0484562, 0.0753863, 0.98763, 0.122171,
    0.0205907, 0.0196696, 0.0121423}, {-0.159361, -0.12259, 0.332356, -0.244444, -0.0273447,
    0.258635, -0.318493, 0.125622, 0.18303, -0.303641, 0.201502, 0.114583, -0.285963,
```

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Let's print the dendrograms, with a left orientation and in blue:

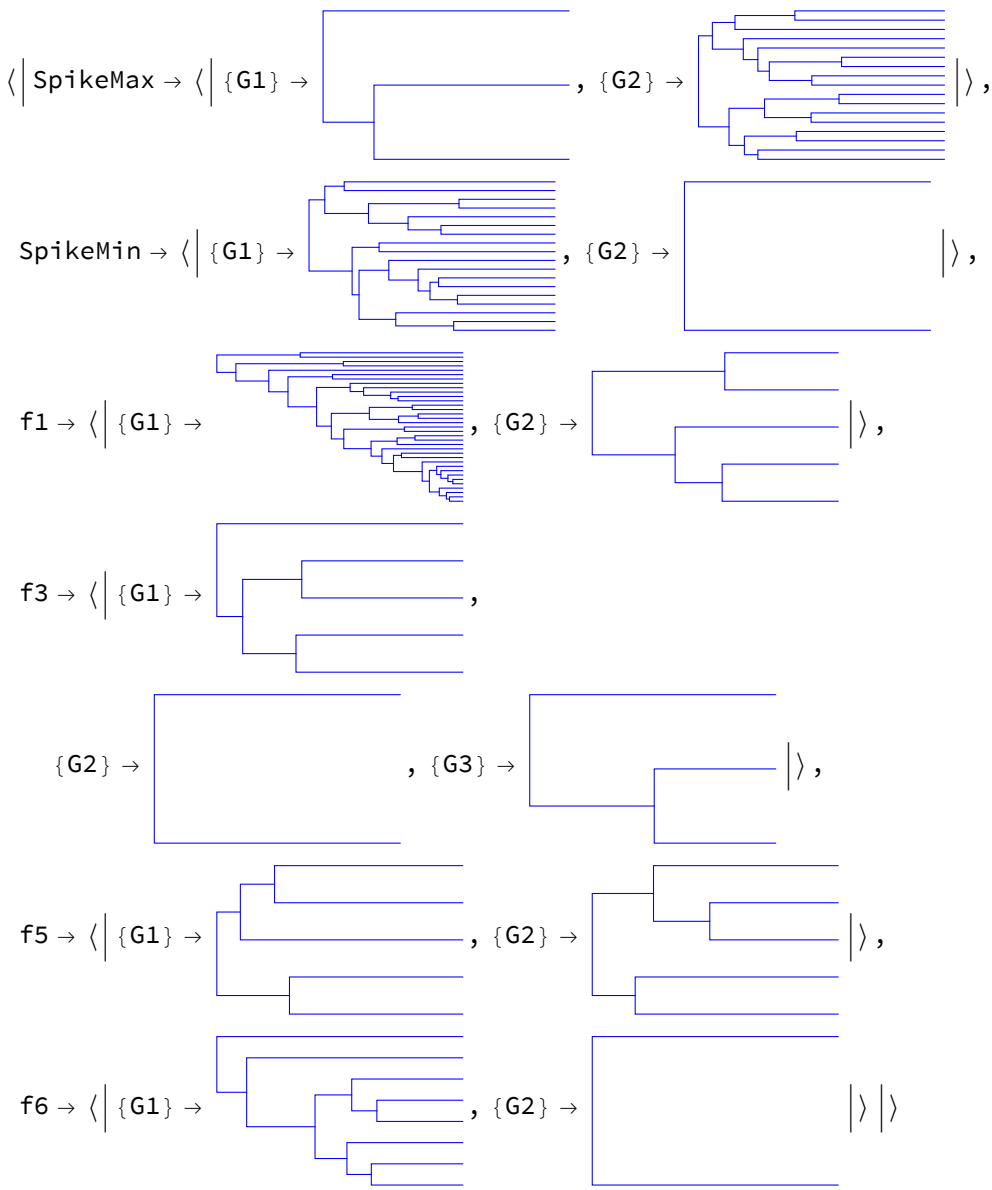
In[3]:=
```
clustersSingleDendrogramOptions = TimeSeriesSingleClusters[classification1,
  PrintDendrograms → True, DendrogramPlotOptions → {PlotStyle → Blue, Orientation → Left}];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫



DistanceFunction (1)

In[1]:=
```
Needs["MathIOmica`"]
```

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DistanceFunction provides options for which DistanceFunction to use in the clustering.

We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.213203, 0.296299, 0.285513, 0.27631, 0.281998, 0.186711, 0.371984, 0.37283,
      0.414702, 0.380987}, {0.9743, -0.0741972, -0.0644614, -0.0421534, -0.0558369, -0.0401558,
      -0.0717362, 0.0892151, 0.0232983, -0.0238502, -0.0187739, -0.0111489, -0.00485439,
      0.0819822, -0.00632645, -0.0317991, 0.082301, 0.0510931, 0.0191842, -0.0482688}},
   SpikePositive_2 → {{0.207702, 0.300878, 0.262826, 0.410641, 0.2223, 0.263391, 0.218223,
      0.19296, 0.620045, 0.201311}, {0.976754, -0.0432494, -0.0810479, -0.0423541, 0.055069,
      -0.0514568, 0.0388347, -0.0951477, 0.0606633, 0.0211584, -0.026766, -0.0406697,
      -0.0290966, -0.017112, -0.0256659, -0.0845496, 0.014448, 0.0126708, 0.0331292, 0.050648}},
   SpikePositive_3 → {{0.209632, 0.254466, 0.213618, 0.179711, 0.205569, 0.243965, 0.359047,
      0.292087, 0.650856, 0.271574}, {0.973475, -0.0828815, 0.0652842, 0.0661903, -0.0389714,
      -0.0545911, -0.0743217, 0.00587402, -0.00321313, -0.0383794, 0.0284221, -0.0211462,
      0.0650052, 0.0411155, -0.0331458, -0.0801366, 0.0169154, -0.0439268, -0.0749844, 0.0525597}},
   SpikePositive_4 → {{0.170799, 0.152459, 0.0199852, 0.561008, 0.159362, 0.336019, 0.52244,
      0.229562, 0.324309, 0.251657}, {0.945279, 0.047865, -0.0466392, 0.0988499, 0.00184076,
      0.0362555, -0.0837905, -0.0972987, 0.0757248, 0.102989, 0.0241165, -0.102294, -0.0878563,
      0.103227, 0.0195604, 0.0550401, 0.0144833, -0.0863167, -0.0837554, -0.102743}},
   SpikePositive_5 → {{0.146237, 0.219438, 0.369873, 0.227806, 0.275691, 0.177557, 0.275375,
      0.221743, 0.665605, 0.257286}, {0.955387, -0.0884152, 0.0384722, -0.0804943, -0.0959736,
      0.0120792, 0.0462763, 0.0953633, 0.0808486, -0.0251224, -0.0549271, 0.0241283, -0.0457259,
      0.0971158, 0.0815772, 0.0535714, -0.0922255, 0.0571097, -0.00651159, 0.0851089}},
   SpikePositive_6 → {{0.224573, 0.169775, 0.204155, 0.327347, 0.236944, 0.371249, 0.257693,
      0.186895, 0.65504, 0.218008}, {0.978807, -0.0265184, -0.0025605, -0.0124338, -0.000703092,
      -0.0743663, 0.046126, -0.0595596, -0.0778389, 0.0108243, 0.0811139, -0.0497488, -0.00578022,
      0.0905856, 0.0112303, 0.0511083, -0.0535075, -0.0116864, -0.0227991, 0.0118104}},
   SpikePositive_7 → {{0.344081, 0.100913, 0.182648, 0.221817, 0.273429, 0.23047, 0.2115,
      0.372961, 0.550406, 0.417377}, {0.969318, 0.0754912, 0.084589, -0.0334383, 0.0837534,
      -0.0328878, 0.0410531, -0.0155716, -0.0561623, -0.0366694, -0.0863871, 0.00726531, -0.0892358,
      0.0463142, 0.0130845, 0.0897013, -0.0130423, -0.0665359, -0.0146894, -0.0356818}},
   SpikePositive_8 → {{0.206253, 0.387965, 0.457357, 0.25461, 0.363598, 0.0745439, 0.255665,
      0.242689, 0.44046, 0.277332}, {0.957776, 0.0645473, -0.039413, -0.0784034, 0.00578501,
      -0.0566871, -0.0482532, 0.0960711, 0.080155, -0.0562845, -0.0564985, 0.0926727, -0.067996,
      0.0923466, -0.0659057, -0.0758506, -0.0287735, 0.0613157, 0.0487357, 0.0663981}},
   SpikePositive_9 → {{0.0920311, 0.176606, 0.150307, 0.213648, 0.301808, 0.412325, 0.177721,
      0.150333, 0.737023, 0.183348}, {0.971688, -0.0653497, 0.00237259, 0.00659367, 0.00927299,
      -0.0865831, 0.0829059, -0.0660903, 0.0644556, 0.0345043, 0.0449615, 0.0386944, 0.0539042,
      -0.0183447, 0.043564, 0.0613132, -0.0897402, 0.0333233, -0.0541387, -0.0531145}},
   SpikePositive_10 → {{0.300693, 0.250847, 0.166836, 0.250252, 0.210732, 0.263306, 0.258517,
```

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```
    0.32153, 0.600864, 0.333484}, {0.965868, -0.033217, 0.0903112, 0.0372052, 0.0777667,
    -0.0390693, -0.0379609, -0.0556063, -0.0502298, 0.0454747, 0.085172, 0.0613557,
    0.0522169, 0.0830927, 0.0139869, 0.0272619, 0.065538, 0.00302388, 0.0721357, 0.0930649}},
  SpikePositive_11 → {{0.228067, 0.323497, 0.220866, 0.236497, 0.398386, 0.419204, 0.331897,
    0.29277, 0.33741, 0.30735}, {-0.0166558, -0.0682954, 0.980478, -0.0369847, -0.0516715,
    0.0872132, -0.00494114, -0.0196204, -0.0435313, 0.048167, 0.0223595, 0.026473, -0.0486314,
    0.0133189, -0.0122149, -0.0421603, -0.0713999, 0.0102004, 0.0304008, 0.0752154}},
  SpikePositive_12 → {{0.370925, 0.379962, 0.281382, 0.256414, 0.261053, 0.528889, 0.211518,
    0.262458, 0.179159, 0.282003}, {-0.0407107, 0.0950274, 0.963638, 0.066862, 0.0137942,
    0.0804714, -0.0815741, 0.00100066, -0.00882515, -0.010759, -0.1033, 0.101571, -0.0502425,
    0.0677943, -0.00359804, 0.00997906, -0.0319723, 0.0987299, 0.0280591, 0.0543315}},
  SpikePositive_13 → {{0.21589, 0.239656, 0.287604, 0.288728, 0.263558, 0.258305, 0.274658,
    0.380559, 0.484453, 0.372473}, {0.053888, -0.0762893, 0.976993, -0.0514894, -0.0211056,
    -0.0554089, 0.0629739, 0.0246299, -0.0382644, 0.0836668, -0.00102749, 0.0011551,
    -0.01942, -0.084236, 0.0353149, -0.0336723, -0.0218262, -0.0478778, 0.0402433, 0.057566}},
  SpikePositive_14 → {{0.257931, 0.234062, 0.584403, 0.226925, 0.42721, 0.175861, 0.23637,
    0.312935, 0.135106, 0.316507}, {-0.00376398, 0.0463085, 0.953762, 0.0844343, -0.0914978,
    -0.0415101, -0.0631105, 0.0345409, 0.0409731, 0.083977, -0.0755788, -0.0970197, -0.0953075,
    0.0832646, -0.0915371, -0.043505, 0.00300123, -0.0871417, -0.0275863, -0.0852706}},
  SpikePositive_15 → {{0.497561, 0.169662, 0.330815, 0.436742, 0.210122, 0.287071, 0.338548,
    0.276766, 0.183852, 0.268123}, {-0.0696977, 0.0969758, 0.96724, 0.0610779, 0.0727122,
    0.0216485, 0.00893645, 0.0510784, -0.040288, -0.0690734, -0.0662068, -0.035503, -0.0530922,
    -0.0618111, 0.00620021, 0.081301, 0.0570901, 0.00870531, 0.070846, -0.0658055}},
  SpikePositive_16 → {{0.390398, 0.353815, 0.362232, 0.276107, 0.238247, 0.362869, 0.331587,
    0.300315, 0.195812, 0.296715}, {0.0360592, 0.00953796, 0.977095, 0.0859916, -0.0714312,
    -0.000267531, -0.0731075, 0.0622706, -0.0375664, 0.00956211, -0.0234636, -0.000121384,
    -0.0748238, -0.0615611, 0.00344975, -0.049348, -0.0556294, -0.00100296, 0.0715242, -0.00867468}},
  SpikePositive_17 → {{0.165792, 0.225255, 0.198764, 0.174157, 0.21718, 0.479905, 0.442145,
    0.361961, 0.330787, 0.372198}, {0.0174936, -0.00279942, 0.976116, -0.0697562, 0.0280337,
    0.0359977, -0.0189536, 0.00214493, 0.00540539, 0.0124675, -0.0907049, 0.0364283, 0.085958,
    0.0164249, 0.0389577, 0.0257443, -0.0722905, 0.0699245, 0.0723835, -0.0681192}},
  SpikePositive_18 → {{0.390387, 0.304228, 0.318403, 0.308751, 0.241641, 0.372154, 0.26828,
    0.187333, 0.457786, 0.211689}, {0.0681452, 0.0556726, 0.9771, 0.00746492, 0.0367607,
    0.0221077, 0.0326082, 0.0127644, 0.0868522, -0.0331691, -0.0568386, -0.00951086, 0.0329862,
    -0.0631096, -0.0492467, -0.0395224, -0.0688286, -0.00282587, -0.0865907, 0.0338356}},
  SpikePositive_19 → {{0.200572, 0.250288, 0.160648, 0.458437, 0.204152, 0.429539, 0.327303,
    0.294564, 0.374817, 0.317158}, {0.0948235, -0.0927256, 0.954133, 0.0818835, -0.0567917,
    -0.0654603, -0.0277149, 0.0755363, 0.0325978, -0.0993399, -0.0643148, 0.0839469, 0.0293745,
    -0.0237324, -0.0717511, -0.0601088, -0.0469831, 0.0892738, -0.0215525, -0.0916926}},
  SpikePositive_20 → {{0.272492, 0.339324, 0.176265, 0.343715, 0.206996, 0.211037, 0.393052,
    0.25985, 0.525476, 0.275456}, {-0.00418686, -0.0697099, 0.977623, -0.0296469, 0.0720201,
    0.0133134, 0.0470119, 0.00909728, -0.0172988, -0.0843302, 0.0627582, 0.00039646, 0.0427716,
    -0.0243948, -0.0638269, -0.000809094, -0.042288, -0.063654, 0.0352928, 0.0768547}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.183528, 0.151714, 0.233681, 0.437005, 0.289967, 0.24878,
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    -0.0617913, -0.0891457, 0.0832257, -0.0235717, 0.0172113, -0.0256427, -0.065283, 0.0270636,
    -0.0780908, -0.0269627, -0.0439718, 0.0278134, 0.017358, -0.0614494, -0.00510404, 0.0167709}},
  SpikeNegative_2 → {{0.191169, 0.156533, 0.319371, 0.346666, 0.121937, 0.214687, 0.253996,
    0.40164, 0.528303, 0.388439}, {-0.96852, 0.0315695, -0.0449328, 0.0840555, 0.0561742,
    -0.0853711, -0.10311, -0.026523, 0.0775456, -0.0274583, -0.00633878, 0.0573981, 0.0483904,
    -0.050677, -0.0831919, 0.0363691, -0.0366221, 0.0582851, 0.017792, -0.0424104}},
  SpikeNegative_3 → {{0.441331, 0.193081, 0.245469, 0.200602, 0.333387, 0.32619, 0.215331,
    0.251396, 0.517445, 0.26942}, {-0.967312, 0.000490023, 0.0217437, 0.024143, 0.0130749,
    0.0712279, -0.0821498, 0.0628956, 0.0803512, 0.087392, 0.054303, 0.0290355, 0.0680133,
    0.0347156, -0.0673783, -0.0687812, -0.0562157, -0.0559495, -0.050391, 0.0740635}},
  SpikeNegative_4 → {{0.246172, 0.226328, 0.439005, 0.236357, 0.289579, 0.274053, 0.207868,
    0.155862, 0.626973, 0.141515}, {-0.975013, 0.0423588, 0.0938951, -0.00282366, 0.0129695,
    0.0287542, -0.0515192, 0.037759, 0.0650345, 0.0562107, -0.081183, -0.0149278, -0.0561545,
    0.00533897, -0.0159774, 0.0514792, -0.0418059, -0.0872466, 0.0530302, -0.0345623}},
  SpikeNegative_5 → {{0.346347, 0.130164, 0.352478, 0.266545, 0.134611, 0.163162, 0.318994,
    0.30692, 0.567032, 0.324946}, {-0.965767, 0.0125736, -0.0514082, 0.015708, -0.0977946,
    -0.060737, 0.0037942, -0.0308719, 0.0350402, 0.079891, 0.0531115, 0.0798715, -0.0161959,
    -0.0589643, 0.0938065, 0.0577267, -0.0783502, -0.0814039, 0.0169785, 0.0654991}},
  SpikeNegative_6 → {{0.161701, 0.179077, 0.200031, 0.41644, 0.237913, 0.263707, 0.323087,
    0.390704, 0.436824, 0.39288}, {-0.976175, -0.0108919, 0.0247671, -0.0862598, -0.058167,
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    -0.0790978, -0.00549206, 0.0586261, -0.0522853, -0.025393, 0.0745906, 0.073347}},
  SpikeNegative_7 → {{0.268037, 0.30831, 0.246629, 0.276126, 0.39875, 0.246679, 0.421893,
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    0.0637364, 0.0175998, 0.0468708, -0.0420997, 0.055101, -0.0794416, -0.0520325, 0.0330117,
    -0.0577246, -0.0201832, -0.0270893, 0.0126916, -0.0508833, -0.0734431, -0.00788772}},
  SpikeNegative_8 → {{0.265346, 0.135091, 0.170818, 0.334036, 0.193596, 0.328322, 0.252569,
    0.186582, 0.706382, 0.166519}, {-0.975043, 0.0513999, -0.0363921, -0.0868514, -0.0214494,
    -0.0110326, 0.0129563, 0.0630441, -0.0800498, 0.00471852, 0.0463901, 0.0645997, -0.0897116,
    -0.0135215, -0.0646536, 0.0171428, -0.00574129, -0.0178563, 0.0703654, -0.0478856}},
  SpikeNegative_9 → {{0.262073, 0.478667, 0.149944, 0.420285, 0.217379, 0.309768, 0.328876,
    0.23172, 0.386014, 0.221365}, {-0.962255, -0.0294534, 0.103368, 0.0368665, 0.102579,
    0.0892724, 0.0591318, 0.072878, -0.0888403, -0.0710082, -0.0337498, 0.0767054, 0.0208215,
    -0.00184779, -0.0551778, 0.0179833, -0.0790275, 0.0100111, -0.05562, 0.025529}},
  SpikeNegative_10 → {{0.240852, 0.240776, 0.244537, 0.222346, 0.427173, 0.219767, 0.390791,
    0.392042, 0.293792, 0.388947}, {-0.962386, 0.0136552, 0.0584938, -0.0210927, 0.091926,
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    -0.0570828, -0.075766, 0.0732723, -0.0620175, 0.0399367, -0.0989478, 0.0847788}},
  SpikeNegative_11 → {{0.368162, 0.140108, 0.244676, 0.224152, 0.233209, 0.367682, 0.49291,
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    -0.0331985, 0.0629852, -0.0847891, 0.0684306, 0.00169169, 0.0281169, 0.0507051, 0.0847367,
    0.073269, -0.0203557, -0.00370386, 0.0105094, -0.0828384, 0.0175822, 0.0546643}},
  SpikeNegative_12 → {{0.347057, 0.38478, 0.324312, 0.350305, 0.235943, 0.248396, 0.292966,
    0.257141, 0.396349, 0.277833}, {0.066344, -0.0637, -0.975043, -0.0444811, -0.0879504,
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    0.0292987, 0.0181469, -0.0744141, 0.0212503, -0.0327385, -0.0546938, -0.0539847}},
  SpikeNegative_13 → {{0.228197, 0.190666, 0.275665, 0.15441, 0.285936, 0.375306, 0.347815,
    0.390047, 0.367738, 0.425184}, {0.0148061, 0.00432324, -0.968942, 0.00350249, -0.052078,
    -0.0458802, -0.00339641, 0.0839869, -0.0920891, 0.0122982, 0.0423326, 0.0259356, 0.0570133,
    -0.0762211, 0.0835084, -0.0902863, 0.0827924, -0.0415025, 0.00639228, 0.0715505}},
  SpikeNegative_14 → {{0.176639, 0.213318, 0.432605, 0.225786, 0.405744, 0.296219, 0.416187,
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    -0.078813, -0.101417, -0.00296924, -0.0211534, -0.0974859, -0.0016573, 0.0840347,
    -0.0409534, -0.0129091, -0.0801072, -0.0891318, 0.04468, 0.0706091, 0.0265406, 0.0377553}},
  SpikeNegative_15 → {{0.330686, 0.471086, 0.460538, 0.31338, 0.304381, 0.295138, 0.136817,
    0.180038, 0.299432, 0.194621}, {0.0424122, -0.080664, -0.978233, -0.0982256, -0.000465609,
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    -0.005552, -0.0266884, 0.00869151, 0.0628907, 0.0225159, 0.0237593, -0.0545753}},
  SpikeNegative_16 → {{0.262951, 0.185329, 0.133828, 0.202081, 0.182359, 0.402187, 0.458109,
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  SpikeNegative_17 → {{0.159945, 0.401107, 0.342838, 0.270457, 0.280513, 0.295305, 0.402791,
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    -0.0964345, 0.073118, -0.0514418, 0.0678314, -0.0596588, -0.0308914, 0.00912817}},
  SpikeNegative_18 → {{0.239425, 0.137969, 0.54995, 0.272471, 0.50874, 0.240757, 0.291631,
    0.183605, 0.266021, 0.201613}, {-0.0293701, -0.0478047, -0.965136, -0.0644291, 0.0665176,
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    -0.0477345, -0.0763402, -0.0755494, -0.0166772, -0.0689059, 0.0455994, -0.0246238}},
  SpikeNegative_19 → {{0.396729, 0.157811, 0.187491, 0.476307, 0.277535, 0.201631, 0.274205,
    0.409736, 0.187173, 0.399868}, {0.0616908, -0.0344618, -0.9684, -0.0245778, -0.0430929,
    0.0133005, -0.0372097, -0.0882998, 0.0912673, 0.0560062, 0.0948023, -0.00840622, 0.0475494,
    0.0127744, 0.0784664, -0.00511859, -0.0905399, -0.00909477, -0.0695718, 0.0559987}},
  SpikeNegative_20 → {{0.264693, 0.308747, 0.27698, 0.455287, 0.293323, 0.540973, 0.148594,
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    -0.0223192, 0.0138753, 0.0458871, -0.0907765, 0.0697996, -0.0423834, -0.0748526,
    0.0499077, 0.0737811, 0.00940676, 0.0663271, -0.0751591, -0.0028872, 0.0748979, 0.0522}}|>,
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  LinearPositive_2 → {{0.984087, 0.165345, 0.0332521, 0.00196025, 0.00137445, 0.0102231,
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    0.242959, 0.260344, 0.281615, 0.297694, 0.316272, 0.335894, 0.354939, 0.373962}},
  LinearPositive_3 → {{0.983904, 0.167751, 0.032146, 0.00206181, 0.00205624, 0.011974,
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  LinearPositive_4 → {{0.983857, 0.167795, 0.0325375, 0.00222092, 0.00154322, 0.0116373,
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    0.241651, 0.260862, 0.280328, 0.297871, 0.31821, 0.335773, 0.354911, 0.372764}},
  LinearPositive_5 → {{0.983427, 0.169564, 0.032244, 0.00244093, 0.00183654, 0.0109173,
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  LinearPositive_6 → {{0.983473, 0.168786, 0.0325587, 0.00223584, 0.00195293, 0.0123915,
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  LinearPositive_7 → {{0.984655, 0.1635, 0.0295333, 0.0025691, 0.00189697, 0.0123896,
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  LinearPositive_8 → {{0.983951, 0.167202, 0.0320627, 0.00229483, 0.00222546, 0.0113214,
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    0.22383, 0.241791, 0.261749, 0.27977, 0.297779, 0.317567, 0.337703, 0.353156, 0.373499}},
  LinearPositive_9 → {{0.984246, 0.165357, 0.0304527, 0.00227476, 0.00197376, 0.00993668,
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  LinearPositive_11 → {{0.986852, 0.153499, 0.0340614, 0.00439906, 0.00102227, 0.00961865,
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    0.243657, 0.257341, 0.275791, 0.303594, 0.313036, 0.344452, 0.359156, 0.37943}},
  LinearPositive_13 → {{0.978296, 0.189912, 0.0326572, 0.00391072, 0.00282273,
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  LinearPositive_14 → {{0.984124, 0.164522, 0.0255623, 0.00222797, 0.00138832, 0.00777975,
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    0.019834, 0.0212125, 0.0317727, 0.0195491, 0.0371738},
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    0.213483, 0.226152, 0.235611, 0.265073, 0.27559, 0.291338, 0.322978, 0.330504, 0.352126, 0.379277}},
  LinearPositive_17 → {{0.985842, 0.156816, 0.0379014, 0.00184753, 0.00335287,
    0.0138088, 0.0180893, 0.0236947, 0.0134104, 0.0285394},
   {0.0142489, 0.0306457, 0.0626367, 0.0738206, 0.09423, 0.11675, 0.129367, 0.142253, 0.172635, 0.191416,
    0.214754, 0.230587, 0.238399, 0.260685, 0.27776, 0.290566, 0.322449, 0.329914, 0.355805, 0.372138}},
  LinearPositive_18 → {{0.986812, 0.150439, 0.0248484, 0.0045979, 0.00278674, 0.00941991,
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    0.249142, 0.268249, 0.279977, 0.300573, 0.31298, 0.334019, 0.348818, 0.367279}},
  LinearPositive_19 → {{0.983757, 0.17118, 0.0305959, 0.00156568, 0.0039872, 0.0114017,
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    0.240635, 0.261521, 0.277342, 0.302588, 0.32031, 0.335512, 0.354785, 0.368138}},
LinearPositive_20 → {{0.984895, 0.164971, 0.0339848, 0.00113183, 0.000711663, 0.0109899,
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LinearNegative_1 → {{0.982355, 0.17568, 0.0535888, 0.00406483, 0.0036252, 0.00816896, 0.018827,
    0.0160142, 0.0115442, 0.0200738}, {-0.0359845, -0.0363874, -0.0725108, -0.0657274,
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LinearNegative_2 → {{0.983872, 0.169059, 0.0379081, 0.0000965389, 0.00100461, 0.000909553,
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    -0.238748, -0.244969, -0.278122, -0.300767, -0.317439, -0.342015, -0.356895, -0.37235}},
LinearNegative_3 → {{0.977933, 0.184049, 0.0320176, 0.00388209, 0.00631554, 0.0115626,
    0.0268196, 0.0576286, 0.0191317, 0.0644454}, {-0.0154659, -0.0508221, -0.0406288, -0.0629079,
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    -0.250673, -0.253233, -0.284722, -0.310468, -0.30833, -0.326641, -0.348788, -0.3796}},
LinearNegative_4 → {{0.980837, 0.185437, 0.0468536, 0.00309171, 0.00306363, 0.00478473,
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LinearNegative_5 → {{0.982026, 0.172949, 0.0160045, 0.00230117, 0.00143255, 0.0209135,
    0.0162202, 0.0393475, 0.0369769, 0.042827}, {-0.00696196, -0.0446751, -0.0538713, -0.0801172,
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    -0.226749, -0.26038, -0.277115, -0.311416, -0.312398, -0.344603, -0.35444, -0.374155}},
LinearNegative_6 → {{0.986028, 0.153499, 0.0396787, 0.000301954, 0.0076776, 0.00709505,
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LinearNegative_7 → {{0.982407, 0.167591, 0.0455873, 0.00405106, 0.00140387, 0.00581722,
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LinearNegative_8 → {{0.99178, 0.113178, 0.0349663, 0.00110939, 0.000251646, 0.00525677,
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    -0.253317, -0.264085, -0.282734, -0.311726, -0.297725, -0.317985, -0.365191, -0.379206}},
LinearNegative_9 → {{0.983094, 0.165424, 0.038058, 0.00190683, 0.00780248, 0.0217013,
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LinearNegative_10 → {{0.977937, 0.194756, 0.0355516, 0.0229054, 0.0104325, 0.00242642,
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LinearNegative_11 → {{0.986375, 0.150766, 0.0376432, 0.000815086, 0.00471995, 0.0188662,
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LinearNegative_12 → {{0.986904, 0.146959, 0.0379164, 0.00181161, 0.00236521, 0.0167495,
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LinearNegative_13 → {{0.98051, 0.187076, 0.0291634, 0.00377258, 0.00134168, 0.00998694,
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LinearNegative_14 → {{0.980544, 0.186566, 0.0387136, 0.00217893, 0.00645076, 0.00890981,
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LinearNegative_15 → {{0.980719, 0.182651, 0.0303746, 0.00244593, 0.00635352, 0.0101468,
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LinearNegative_16 → {{0.982975, 0.169023, 0.029083, 0.0034041, 0.00229759, 0.0127825,
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  Sinusoidal3_29 → {{0.00347466, 0.0740462, 0.992421, 0.0860222, 0.0345992, 0.0207139,
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  Sinusoidal3_30 → {{0.0031395, 0.0705166, 0.992821, 0.0860589, 0.0325904, 0.0187812, 0.00915035,
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f5 → <|Sinusoidal2_11 → {{0.00265897, 0.0115911, 0.0290342, 0.0927116, 0.934135, 0.340836,
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  Sinusoidal2_12 → {{0.0023728, 0.0117183, 0.0346677, 0.0979529, 0.933133, 0.341389, 0.0304022,
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  Sinusoidal2_15 → {{0.00124107, 0.0102532, 0.0297963, 0.0966398, 0.930185, 0.350476, 0.0277544,
    0.00444696, 0.0282309, 0.00153864}, {-0.097411, -0.253838, 0.25486, 0.0930592,
    -0.319493, 0.0911961, 0.259034, -0.258085, -0.103175, 0.319973, -0.100347, -0.248604,
    0.256282, 0.0983784, -0.311436, 0.102839, 0.259044, -0.25469, -0.0931057, 0.316065}},
  Sinusoidal2_16 → {{0.00256651, 0.0119945, 0.0304207, 0.0926425, 0.931837, 0.346704, 0.0321452,
    0.00467406, 0.0275783, 0.00165433}, {-0.0945275, -0.254365, 0.253338, 0.101229,
    -0.314806, 0.0970668, 0.2555, -0.25992, -0.0978616, 0.310204, -0.0937583, -0.258828,
    0.254556, 0.0996383, -0.317888, 0.0955747, 0.257964, -0.261456, -0.0990574, 0.315206}},
  Sinusoidal2_17 → {{0.00264169, 0.0108141, 0.0315054, 0.0944546, 0.934003, 0.340749, 0.0276689,
    0.00499592, 0.0263839, 0.00185157}, {-0.102232, -0.256394, 0.257537, 0.0990329,
    -0.317235, 0.0993583, 0.254435, -0.256592, -0.0979445, 0.312805, -0.0977739, -0.261432,
    0.256608, 0.0936714, -0.315586, 0.098595, 0.256429, -0.255891, -0.0994553, 0.310128}},
  Sinusoidal2_18 → {{0.00247226, 0.0102156, 0.0324708, 0.0928937, 0.935517, 0.336683, 0.0284643,
    0.006024, 0.0283944, 0.00235716}, {-0.0957725, -0.258292, 0.258639, 0.0951812,
    -0.3173, 0.102385, 0.251447, -0.255299, -0.0987085, 0.317543, -0.0940368, -0.259449,
    0.251116, 0.0943749, -0.310029, 0.097526, 0.258104, -0.25785, -0.0991881, 0.318312}},
  Sinusoidal2_19 → {{0.00249599, 0.0113291, 0.0304263, 0.0961514, 0.928713, 0.354467, 0.026796,
    0.00474584, 0.0282069, 0.00166031}, {-0.0958433, -0.253435, 0.257037, 0.101273,
    -0.311974, 0.0945854, 0.259947, -0.248736, -0.102193, 0.317685, -0.0953098, -0.255195,
    0.260188, 0.0996691, -0.315684, 0.101262, 0.257275, -0.255679, -0.0946062, 0.317671}},
  Sinusoidal2_20 → {{0.00199265, 0.0101552, 0.0305903, 0.0908341, 0.93534, 0.338183, 0.0259254,
    0.00547025, 0.0277536, 0.00206574}, {-0.102585, -0.259765, 0.255095, 0.0963811,
    -0.319135, 0.10329, 0.250038, -0.260097, -0.101407, 0.319188, -0.101662, -0.257898,
    0.254227, 0.0917788, -0.311087, 0.100727, 0.25468, -0.249084, -0.0976929, 0.315459}}|>,
f6 → <|Sinusoidal1_1 → {{0.00489247, 0.014921, 0.00836418, 0.0455408, 0.107635, 0.988591,
    0.0902971, 0.00596559, 0.0227455, 0.00228192}, {-0.197739, -0.0979836, 0.31329, -0.228266,
    0.00105653, 0.270186, -0.282529, 0.0942257, 0.158627, -0.317087, 0.191764, 0.109105,
    -0.27411, 0.24831, -0.0273891, -0.280756, 0.305207, -0.0731317, -0.188464, 0.338482}},
  Sinusoidal1_2 → {{0.0030646, 0.0128625, 0.0164624, 0.0473693, 0.0993663, 0.985565, 0.124954,
    0.00478314, 0.0214161, 0.00155947}, {-0.190535, -0.107546, 0.328745, -0.238209,
    -0.0212534, 0.258961, -0.282842, 0.0748681, 0.162649, -0.316028, 0.223765, 0.0885422,
    -0.310843, 0.257185, -0.0140496, -0.263777, 0.291898, -0.102796, -0.1722, 0.303298}},
  Sinusoidal1_3 → {{0.000555073, 0.0216013, 0.0175599, 0.0342086, 0.0871755, 0.986437,
    0.129697, 0.00646099, 0.0229008, 0.00321944}, {-0.170316, -0.101922, 0.31067, -0.229994,
    0.00417924, 0.283559, -0.325718, 0.0709034, 0.170496, -0.339614, 0.1543, 0.12526,
    -0.299892, 0.285513, 0.0105214, -0.225356, 0.289218, -0.106586, -0.193583, 0.284452}},
  Sinusoidal1_4 → {{0.00136807, 0.00799756, 0.0210351, 0.0444111, 0.111292, 0.985233, 0.118052,
    0.00384977, 0.0222572, 0.00144539}, {-0.171657, -0.0681876, 0.312982, -0.26897,
    -0.0233246, 0.275531, -0.299691, 0.0724831, 0.185963, -0.303913, 0.181477, 0.105324,
    -0.321215, 0.268458, -0.00878521, -0.23632, 0.292963, -0.111456, -0.208115, 0.283452}},
  Sinusoidal1_5 → {{0.00525718, 0.0121449, 0.0294669, 0.029287, 0.0892149, 0.98856, 0.110476,
    0.00517369, 0.0255888, 0.00166102}, {-0.197995, -0.125147, 0.309449, -0.226253,
    -0.00210946, 0.240951, -0.316462, 0.0840827, 0.192993, -0.298082, 0.181389, 0.0839004,
    -0.321369, 0.250954, -0.0106586, -0.272019, 0.273151, -0.109949, -0.182282, 0.326459}},
  Sinusoidal1_6 → {{0.00126575, 0.00566826, 0.0207402, 0.0623889, 0.0683859, 0.989468,
    0.107039, 0.00771162, 0.0198177, 0.00330177}, {-0.186759, -0.107764, 0.280605, -0.25893,
    -0.0183095, 0.243731, -0.277616, 0.10535, 0.167066, -0.338758, 0.172785, 0.119312,
    -0.331129, 0.229919, 0.0321919, -0.239072, 0.301712, -0.131437, -0.184473, 0.331693}},
  Sinusoidal1_7 → {{0.00203287, 0.0114798, 0.0179578, 0.0403339, 0.0889452, 0.987971, 0.115087,
    0.0102464, 0.023313, 0.00486764}, {-0.155171, -0.0971069, 0.312664, -0.26609,
    -0.0104491, 0.260212, -0.310363, 0.0821943, 0.152925, -0.312132, 0.209086, 0.080196,
    -0.315669, 0.250693, 0.00334275, -0.266999, 0.285378, -0.12436, -0.189932, 0.298821}},
  Sinusoidal1_8 → {{0.00184032, 0.00796411, 0.0346255, 0.0322142, 0.108596, 0.985222, 0.122148,
    0.00481202, 0.0171612, 0.00177146}, {-0.201562, -0.102014, 0.308942, -0.246031,
    -0.0148019, 0.229815, -0.321659, 0.0884523, 0.218596, -0.28891, 0.188903, 0.0836775,
    -0.297885, 0.270288, -0.0167725, -0.250202, 0.30669, -0.12204, -0.177013, 0.299613}},
  Sinusoidal1_9 → {{0.00128257, 0.00862532, 0.0165659, 0.0328894, 0.0825425, 0.990267,
```

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```
    0.101066, 0.00781601, 0.0288506, 0.00423076}, {-0.176521, -0.119968, 0.315676, -0.266238,
    0.0278813, 0.229126, -0.321308, 0.123922, 0.18825, -0.297393, 0.202231, 0.115685,
    -0.278471, 0.272271, -0.0198943, -0.241973, 0.306467, -0.0931539, -0.167555, 0.304275}},
 Sinusoidal1_10 → {{0.00685896, 0.0036216, 0.0166238, 0.0289726, 0.0729656, 0.989344, 0.118119,
    0.00323567, 0.0271211, 0.000789594}, {-0.175793, -0.120283, 0.304319, -0.251331, 0.0236115,
    0.278978, -0.277225, 0.129772, 0.216625, -0.326647, 0.195158, 0.0827817, -0.308764,
    0.260767, 0.000460094, -0.238956, 0.281826, -0.0831348, -0.157093, 0.311057}}|>|>
```

Let's use correlation as a distance function for the clustering:

```
In[3]:= clustersSingleCorrelationDistance =
          TimeSeriesSingleClusters[classification1, DistanceFunction → CorrelationDistance];
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

```
In[4]:= Query[All, "GroupAssociations"]@clustersSingleCorrelationDistance

Out[4]= <|SpikeMax → <|G1 → {SpikePositive_1, SpikePositive_7, SpikePositive_13, SpikePositive_2, SpikePositive_6,
          SpikePositive_9, SpikePositive_5, SpikePositive_3, SpikePositive_10, SpikePositive_20,
          SpikePositive_18, SpikePositive_19, SpikePositive_4, SpikePositive_17, SpikePositive_11},
        G2 → {SpikePositive_12, SpikePositive_16, SpikePositive_15}, G3 → {SpikePositive_14, SpikePositive_8}|>,
      SpikeMin → <|G1 → {SpikeNegative_1, SpikeNegative_6, SpikeNegative_2, SpikeNegative_5,
          SpikeNegative_3, SpikeNegative_4, SpikeNegative_8, SpikeNegative_7,
          SpikeNegative_18, SpikeNegative_14, SpikeNegative_17, SpikeNegative_16,
          SpikeNegative_11, SpikeNegative_13, SpikeNegative_10, SpikeNegative_19},
        G2 → {SpikeNegative_20, SpikeNegative_15, SpikeNegative_9, SpikeNegative_12}|>,
      f1 → <|G1 → {LinearPositive_1, LinearPositive_5, LinearPositive_6, LinearPositive_10, LinearPositive_3,
          LinearPositive_4, LinearPositive_8, LinearPositive_2, LinearPositive_9, LinearPositive_7,
          LinearNegative_16, LinearPositive_16, LinearPositive_12, LinearPositive_14, LinearNegative_18,
          LinearPositive_17, LinearPositive_20, LinearNegative_9, LinearNegative_11, LinearNegative_12,
          LinearNegative_17, LinearPositive_11, LinearPositive_18, LinearNegative_19, LinearNegative_7,
          LinearNegative_13, LinearNegative_15, LinearNegative_20, LinearPositive_19, LinearPositive_13,
          LinearNegative_5, LinearNegative_3, LinearNegative_6, LinearNegative_2, LinearNegative_1,
          LinearNegative_4, LinearNegative_14, LinearPositive_15, LinearNegative_10}, G2 → {LinearNegative_8}|>,
      f3 → <|G1 → {Sinusoidal3_21, Sinusoidal3_26, Sinusoidal3_28, Sinusoidal3_30, Sinusoidal3_22,
          Sinusoidal3_24, Sinusoidal3_27, Sinusoidal3_29, Sinusoidal3_25}, G2 → {Sinusoidal3_23}|>,
      f5 → <|G1 → {Sinusoidal2_11, Sinusoidal2_17, Sinusoidal2_20, Sinusoidal2_18, Sinusoidal2_12,
          Sinusoidal2_14, Sinusoidal2_16}, G2 → {Sinusoidal2_19, Sinusoidal2_15, Sinusoidal2_13}|>,
      f6 → <|G1 → {Sinusoidal1_1, Sinusoidal1_2, Sinusoidal1_4, Sinusoidal1_8, Sinusoidal1_3,
          Sinusoidal1_10, Sinusoidal1_5, Sinusoidal1_7, Sinusoidal1_9}, G2 → {Sinusoidal1_6}|>|>
```

Let's use Euclidean distance (default) for the clustering:

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In[5]:=
```
clustersSingleEuclideanDistance =
 TimeSeriesSingleClusters[classification1, DistanceFunction → EuclideanDistance]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[5]=
```
<|SpikeMax →
  <|Cluster → Cluster[Cluster[Cluster[Cluster[ ··· 1 ··· ], ··· 3 ···, 4], ··· 3 ···, 2], ··· 3 ···, 4], … → ··· 1 ···,
   GroupAssociations → <|G1 → {SpikePositive_1, ··· 4 ···, SpikePositive_7}, ··· 4 ···, G6 → ··· 1 ··· |> |>,
 ··· 4 ···, f6 → ··· 1 ··· |>
```

large output | show less | show more | show all | set size limit...

We can see that the groupings are now different:

In[6]:=
```
Query[All, "GroupAssociations"]@clustersSingleEuclideanDistance
```

Out[6]=
```
<|SpikeMax → <|G1 → {SpikePositive_1, SpikePositive_13, SpikePositive_3, SpikePositive_10, SpikePositive_20,
      SpikePositive_7}, G2 → {SpikePositive_17, SpikePositive_11}, G3 → {SpikePositive_4, SpikePositive_19},
    G4 → {SpikePositive_15, SpikePositive_16, SpikePositive_12, SpikePositive_18},
    G5 → {SpikePositive_8, SpikePositive_14},
    G6 → {SpikePositive_2, SpikePositive_6, SpikePositive_5, SpikePositive_9}|>,
  SpikeMin → <|G1 → {SpikeNegative_1, SpikeNegative_6, SpikeNegative_2, SpikeNegative_5, SpikeNegative_10,
      SpikeNegative_17, SpikeNegative_14, SpikeNegative_11, SpikeNegative_16, SpikeNegative_13,
      SpikeNegative_3, SpikeNegative_4, SpikeNegative_8, SpikeNegative_7, SpikeNegative_9,
      SpikeNegative_12, SpikeNegative_19}, G2 → {SpikeNegative_18, SpikeNegative_20, SpikeNegative_15}|>,
  f1 → <|G1 → {LinearPositive_1, LinearPositive_3, LinearPositive_4, LinearPositive_8, LinearPositive_5,
      LinearPositive_10, LinearPositive_6, LinearPositive_2, LinearPositive_9, LinearPositive_7,
      LinearPositive_16, LinearPositive_14, LinearNegative_16, LinearNegative_9, LinearPositive_12,
      LinearNegative_7, LinearNegative_19, LinearNegative_5, LinearPositive_13, LinearNegative_3,
      LinearNegative_10, LinearNegative_13, LinearNegative_15, LinearNegative_14, LinearPositive_15,
      LinearNegative_20, LinearPositive_19, LinearNegative_1, LinearNegative_4, LinearNegative_17,
      LinearPositive_11, LinearNegative_18, LinearPositive_17, LinearPositive_20, LinearNegative_11,
      LinearNegative_12, LinearPositive_18, LinearNegative_6, LinearNegative_2}, G2 → {LinearNegative_8}|>,
  f3 → <|G1 → {Sinusoidal3_21, Sinusoidal3_26, Sinusoidal3_28, Sinusoidal3_30, Sinusoidal3_22,
      Sinusoidal3_24, Sinusoidal3_27, Sinusoidal3_29, Sinusoidal3_25}, G2 → {Sinusoidal3_23}|>,
  f5 → <|G1 → {Sinusoidal2_11, Sinusoidal2_17, Sinusoidal2_20, Sinusoidal2_18, Sinusoidal2_12,
      Sinusoidal2_14, Sinusoidal2_16}, G2 → {Sinusoidal2_19, Sinusoidal2_15, Sinusoidal2_13}|>,
  f6 → <|G1 → {Sinusoidal1_1, Sinusoidal1_2, Sinusoidal1_4, Sinusoidal1_8, Sinusoidal1_3,
      Sinusoidal1_10, Sinusoidal1_5, Sinusoidal1_7, Sinusoidal1_9}, G2 → {Sinusoidal1_6}|>|>
```

LinkageMeasure (1)

In[1]:=
```
Needs["MathIOmica`"]
```

LinkageMeasure provides options for which Linkage to use in the hierarchical clustering.

We generate some data for classification:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

Method → "LombScargle"

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.262031, 0.515605, 0.321798, 0.200393, 0.200495, 0.198766, 0.251071, 0.265305,
      0.486816, 0.267695}, {0.977614, 0.068555, -0.00937702, -0.0428341, -0.0753933, -0.034677,
      0.0375585, 0.0942991, 0.0299715, 0.0244998, 0.00458543, -0.0290211, -0.0623508,
      0.017445, -0.0146761, -0.0253802, 0.0846189, 0.0586023, -0.0330615, 0.036849}},
   SpikePositive_2 → {{0.223113, 0.189296, 0.20006, 0.238363, 0.311528, 0.191147, 0.246047,
      0.311011, 0.679325, 0.255363}, {0.973278, -0.00495473, 0.0488842, 0.0591025, 0.0280937,
      0.0382426, 0.0104233, 0.0424415, 0.0310312, -0.0443389, 0.0604589, -0.0636102, 0.0302713,
      -0.079291, 0.0857784, -0.0920757, 0.0185353, 0.00524055, -0.0890069, -0.0264103}},
   SpikePositive_3 → {{0.348374, 0.080802, 0.306753, 0.39674, 0.320065, 0.211459, 0.242449,
      0.173281, 0.594979, 0.17505}, {0.968873, 0.0373485, -0.0405641, 0.0175992, 0.0901211,
      0.0803607, 0.0904004, 0.0130277, -0.0538515, -0.0811426, 0.00360518, -0.053144,
      -0.0747469, 0.0290527, 0.0589073, 0.008717, -0.0135857, -0.0350334, -0.067088, 0.0824756}},
   SpikePositive_4 → {{0.232622, 0.231801, 0.50543, 0.190377, 0.292934, 0.128124, 0.406184,
      0.364683, 0.276866, 0.351557}, {0.962727, 0.0931538, -0.0701008, -0.0212775, -0.0915263,
      0.0858155, -0.00587975, 0.0537035, -0.00804034, -0.0836088, 0.00832799, 0.078465,
      0.00974132, 0.0245346, 0.0471654, -0.0583499, 0.088043, 0.0405213, -0.053844, -0.0924738}},
   SpikePositive_5 → {{0.210878, 0.14213, 0.122735, 0.391745, 0.359634, 0.197983, 0.272616,
      0.374388, 0.461526, 0.41325}, {0.971049, 0.0159916, 0.00890888, 0.000647151, 0.0385269,
      0.075127, -0.0864031, 0.00463622, 0.0047049, 0.0495757, -0.0334221, 0.0686342, -0.0740603,
      0.0375439, 0.0856557, 0.0735307, -0.0426144, 0.0471819, -0.0621841, -0.0791148}},
   SpikePositive_6 → {{0.261169, 0.281963, 0.167732, 0.444412, 0.361491, 0.391995, 0.382102,
      0.163059, 0.370276, 0.180614}, {0.970697, 0.0256155, -0.0710312, 0.0718786, 0.00905697,
      0.0534335, 0.020997, -0.0927483, 0.00295895, 0.0398464, 0.0771314, 0.02028, -0.0904346,
      -0.0360662, -0.00337227, 0.0890898, -0.0276201, -0.0129936, 0.0811894, 0.044615}},
   SpikePositive_7 → {{0.263057, 0.20907, 0.155283, 0.285225, 0.364694, 0.144513, 0.248808,
      0.365101, 0.550837, 0.359323}, {0.976179, -0.0730085, 0.0408987, 0.0399843, 0.00033676,
      0.0242443, -0.0817481, 0.0891132, -0.0110932, -0.00126333, -0.031202, -0.0210058, -0.0801677,
      -0.000498351, 0.0713832, -0.0244218, -0.0235045, 0.0713244, -0.0607495, 0.0164888}},
   SpikePositive_8 → {{0.349601, 0.223949, 0.193351, 0.26264, 0.492002, 0.365388, 0.243012,
      0.279254, 0.345116, 0.299239}, {0.976042, 0.0913334, -0.0121893, 0.0844836, 0.0209955,
      -0.0846134, -0.0784591, 0.0145423, -0.0778016, -0.0151181, -0.00318551, 0.0227434, 0.00809954,
      0.0241424, 0.0264899, 0.0487303, -0.0508196, -0.00384056, 0.0110654, -0.0670301}},
   SpikePositive_9 → {{0.333246, 0.214648, 0.269155, 0.322267, 0.25816, 0.228155, 0.265315,
      0.3836, 0.422253, 0.389914}, {0.968723, 0.0424699, -0.0556903, -0.0604105, 0.0955414,
      0.0534773, -0.0654483, 0.0487035, -0.0505887, -0.0209247, -0.0682665, -0.080596, -0.0521758,
      -0.00770953, -0.0849414, -0.0171909, 0.0790178, -0.034396, -0.0413931, -0.0281419}},
   SpikePositive_10 → {{0.162955, 0.339793, 0.108439, 0.219195, 0.187832, 0.309782, 0.319639,
      0.291915, 0.604313, 0.338169}, {0.970006, 0.0304452, 0.073515, -0.0708478, -0.0273859,
      -0.0450161, -0.0571658, -0.0110263, 0.0732756, 0.0772656, -0.0224271, -0.0334241, -0.016339,
      -0.00842983, -0.0739471, 0.0981058, -0.0315599, -0.0172743, -0.0626459, -0.0892279}},
   SpikePositive_11 → {{0.441441, 0.420399, 0.288242, 0.369088, 0.111787, 0.316155, 0.201103,
      0.233346, 0.378352, 0.242058}, {0.0613771, 0.0697595, 0.963036, 0.0734871, 0.0207559,
      -0.0631523, 0.0601066, 0.0287826, 0.0421829, -0.0802404, -0.086852, 0.0636828, 0.0721699,
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    -0.0671995, -0.0342026, -0.0455056, -0.0720909, 0.0229862, 0.0889796, 0.0569413}},
  SpikePositive_12 → {{0.26786, 0.43763, 0.209573, 0.270307, 0.45836, 0.394618, 0.318091,
    0.228366, 0.228196, 0.220274}, {-0.035654, 0.0760455, 0.974934, 0.0264035, 0.0393319,
    0.036633, -0.0243453, -0.0270405, -0.0734993, 0.0809835, 0.0849702, 0.042335, -0.00548355,
    -0.0373059, 0.031824, -0.072922, 0.0300939, 0.0850747, 0.0254564, -0.00492545}},
  SpikePositive_13 → {{0.166096, 0.432773, 0.2742, 0.40712, 0.313435, 0.16659, 0.358509,
    0.306888, 0.317592, 0.307603}, {-0.0535968, 0.039994, 0.978294, -0.0152316, 0.0603358,
    -0.0687813, 0.0426913, 0.0151624, -0.0873418, 0.0681649, 0.050803, 0.0410023, 0.0544816,
    -0.0285405, -0.0285202, -0.00551805, -0.0404011, -0.0643725, -0.0282702, -0.00860574}},
  SpikePositive_14 → {{0.203211, 0.231935, 0.172064, 0.504035, 0.261979, 0.392663, 0.339808,
    0.217151, 0.422775, 0.238903}, {-0.0816366, -0.072312, 0.963185, -0.104369, 0.00749449,
    0.0206754, 0.0105317, 0.077856, 0.0353307, -0.0405319, 0.0497316, 0.0709392, -0.0060187,
    -0.0803229, -0.102249, -0.0317408, -0.00831352, -0.000251813, -0.0610604, 0.103383}},
  SpikePositive_15 → {{0.11419, 0.532144, 0.371683, 0.179141, 0.47452, 0.273849, 0.31344,
    0.165561, 0.283099, 0.166077}, {-0.0429852, 0.0123354, 0.965667, 0.0234488, -0.0271149,
    -0.0374262, -0.0831545, -0.0902304, -0.0642998, -0.00822881, 0.0900535, -0.058985, 0.0254026,
    0.0909059, 0.0477489, -0.0862319, -0.0555873, -0.0525778, -0.0599701, -0.0622793}},
  SpikePositive_16 → {{0.405565, 0.132527, 0.13173, 0.171468, 0.344677, 0.235732, 0.356294,
    0.378514, 0.42655, 0.380348}, {0.0911837, 0.0472126, 0.970606, -0.0868311, 0.077542,
    0.0634201, 0.0344849, 0.00955568, -0.0409786, -0.0198315, 0.00981953, -0.0720804,
    -0.0576423, 0.0252082, -0.033657, -0.019517, 0.0897528, 0.0557469, 0.0647229, -0.0183261}},
  SpikePositive_17 → {{0.205688, 0.25877, 0.248311, 0.167662, 0.483447, 0.231747, 0.385039,
    0.382514, 0.26989, 0.382259}, {-0.0484244, -0.0890429, 0.976557, 0.0221247, 0.0522491,
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    -0.0137081, 0.0871419, -0.046588, -0.0240991, 0.0176869, -0.0421208, 0.0336857, -0.0454476}},
  SpikePositive_18 → {{0.20969, 0.187346, 0.316932, 0.213692, 0.271216, 0.1082, 0.292696,
    0.495294, 0.326582, 0.50191}, {-0.00436761, -0.0495211, 0.96569, -0.0330497, 0.0926515,
    -0.0643679, -0.0408543, 0.0187989, -0.093213, 0.0820745, -0.0909303, -0.0237946,
    -0.0198197, 0.0839309, -0.0246714, 0.0864618, 0.076179, -0.0372221, 0.0217875, 0.0410423}},
  SpikePositive_19 → {{0.19395, 0.306681, 0.236993, 0.375537, 0.222988, 0.53949, 0.280829,
    0.251091, 0.362994, 0.23809}, {-0.0704856, -0.0431883, 0.977146, -0.0578315, -0.0444042,
    -0.0119264, -0.0215106, -0.0022079, 0.0122028, -0.0598814, -0.00743534, 0.0701433,
    0.0242108, -0.0737909, 0.060398, -0.0575935, -0.00406931, 0.0126371, 0.0934667, 0.0425159}},
  SpikePositive_20 → {{0.333698, 0.227391, 0.324465, 0.306406, 0.270805, 0.316759, 0.21301,
    0.389654, 0.325137, 0.401483}, {0.0146387, 0.0412398, 0.982731, 0.00631281, 0.0165334,
    -0.0496782, 0.0227806, 0.0500047, -0.00637053, -0.072444, -0.0754631, 0.020857, -0.0765686,
    0.0787391, -0.0109761, -0.0327196, 0.00274826, 0.0338962, 0.026175, -0.00332769}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.14448, 0.231529, 0.244834, 0.278859, 0.317198, 0.217693,
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    -0.0238484, -0.00161618, 0.0207186, 0.0245654, 0.0010237, 0.0332166, -0.0766538, -0.0364736,
    0.0913219, -0.0470595, 0.0964234, 0.0134796, 0.0166907, -0.00797038, -0.0675632, 0.0641646}},
  SpikeNegative_2 → {{0.410879, 0.23655, 0.236579, 0.333488, 0.177442, 0.307193, 0.243991,
    0.247978, 0.538588, 0.266616}, {-0.97929, -0.0425672, -0.0514822, 0.0371535, -0.0452637,
    0.0591038, 0.0433909, 0.0698452, 0.0576398, 0.0025083, 0.00745813, 0.0793889, -0.0324462,
    -0.06291, 0.028277, -0.0268306, -0.011616, -0.0155507, -0.0778632, -0.0137802}},
  SpikeNegative_3 → {{0.251506, 0.351045, 0.316724, 0.23357, 0.363713, 0.38757, 0.189124,
    0.148939, 0.54809, 0.133385}, {-0.979134, -0.0404954, -0.0113362, -0.0262341, 0.0382806,
    0.0344135, -0.0237341, -0.0733671, -0.0151662, -0.00148649, -0.0256591, 0.0637016, -0.0665723,
    0.0741999, -0.0229063, -0.0337213, 0.0883079, -0.0541626, -0.00548015, -0.0541725}},
  SpikeNegative_4 → {{0.232467, 0.341986, 0.288526, 0.227301, 0.174256, 0.231784, 0.121286,
    0.372713, 0.555746, 0.384088}, {-0.969089, 0.0300832, -0.0816174, 0.0612464, -0.00830125,
    0.0442418, 0.0521361, 0.0669856, 0.0711967, -0.0655221, 0.0659639, -0.0878101, -0.0355383,
    0.0243711, 0.0478229, 0.0818551, 0.0414154, 0.000720326, -0.024698, -0.075656}},
  SpikeNegative_5 → {{0.0924103, 0.232648, 0.233097, 0.297807, 0.229843, 0.266875, 0.272633,
    0.384843, 0.521184, 0.419758}, {-0.963324, -0.015538, -0.0384457, 0.0804909, -0.0378452,
    -0.0489894, -0.0759777, -0.0855141, 0.0257059, -0.0819458, -0.0559554, 0.00939066,
    0.0724935, 0.0191391, 0.0681024, 0.0155375, 0.0978365, 0.0814474, 0.0428796, 0.0880357}},
  SpikeNegative_6 → {{0.299254, 0.324496, 0.306306, 0.217004, 0.381494, 0.336979, 0.254358,
    0.285756, 0.425222, 0.279239}, {-0.969941, 0.0427514, 0.0826553, 0.0483104, 0.0165467,
    0.0749257, 0.0901693, -0.0397763, 0.00542138, 0.0490284, 0.045922, 0.0307883, -0.0872313,
    0.0698438, 0.0434871, -0.0289218, -0.0562658, -0.0425691, -0.0762813, 0.0334477}},
  SpikeNegative_7 → {{0.120505, 0.413766, 0.3369, 0.109014, 0.43721, 0.31961, 0.382197, 0.174029,
    0.425838, 0.194648}, {-0.970199, 0.0114464, 0.0417027, -0.0149906, 0.0873958, 0.0484727,
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    0.0614111, 0.0867789, -0.0218527, 0.0383305, -0.00578031, -0.0686246, 0.000148414}},
  SpikeNegative_8 → {{0.195875, 0.162993, 0.29885, 0.455329, 0.38518, 0.145375, 0.457798,
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  SpikeNegative_9 → {{0.200589, 0.245441, 0.347981, 0.193973, 0.240193, 0.515093, 0.250014,
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  SpikeNegative_10 → {{0.210181, 0.104157, 0.243236, 0.183016, 0.130198, 0.182289, 0.492591,
    0.358158, 0.560816, 0.34161}, {-0.964048, 0.0633365, -0.086628, 0.0147183, -0.0379561,
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  SpikeNegative_11 → {{0.165444, 0.285842, 0.134408, 0.45683, 0.299729, 0.328568, 0.397681,
    0.301146, 0.356698, 0.300493}, {-0.0306193, -0.0798668, -0.969765, 0.0674872, -0.04666,
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  SpikeNegative_12 → {{0.378931, 0.332727, 0.218716, 0.226054, 0.311391, 0.412386, 0.453359,
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    0.0788519, 0.0229568, 0.0333457, 0.0596085, -0.0935029, 0.0300871, -0.00587166}},
  SpikeNegative_13 → {{0.2923, 0.20685, 0.283588, 0.183172, 0.264258, 0.388959, 0.403478,
    0.231592, 0.515583, 0.233287}, {-0.0317843, 0.0178379, -0.972351, 0.0594339, -0.0766583,
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    0.0547267, -0.0294065, -0.034114, -0.0814727, -0.0613613, -0.0431609, -0.039945}},
  SpikeNegative_14 → {{0.178394, 0.367961, 0.434378, 0.205777, 0.430868, 0.208669, 0.260243,
    0.242726, 0.450097, 0.208164}, {0.00407205, -0.0357534, -0.968336, 0.0594338, 0.00754892,
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    -0.00249614, -0.0872426, 0.0912199, -0.0674393, 0.0940851, -0.0511439, -0.0507389}},
  SpikeNegative_15 → {{0.610804, 0.270016, 0.319252, 0.238434, 0.187819, 0.349332, 0.260176,
    0.233816, 0.253022, 0.227041}, {-0.081212, -0.0736515, -0.961897, -0.0613459, -0.0700406,
    -0.0929217, 0.0859295, -0.0337754, 0.0707243, 0.06628, 0.0534633, 0.032946, 0.0824939,
    0.014115, -0.0764981, -0.00444257, -0.0570482, -0.013483, -0.0000825451, -0.0851782}},
  SpikeNegative_16 → {{0.281867, 0.207522, 0.251876, 0.1899, 0.330024, 0.285137, 0.305206,
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  SpikeNegative_17 → {{0.479726, 0.323746, 0.170172, 0.283626, 0.42952, 0.312109, 0.160125,
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  SpikeNegative_18 → {{0.428004, 0.337232, 0.212988, 0.285548, 0.467478, 0.289138, 0.283367,
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  SpikeNegative_19 → {{0.185983, 0.426776, 0.374283, 0.266399, 0.214137, 0.516204, 0.396669,
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    0.0758994, -0.0807669, 0.0230174, 0.0647043, -0.0351233, -0.0143842, -0.0838608}},
  SpikeNegative_20 → {{0.204551, 0.174167, 0.117191, 0.336813, 0.278105, 0.368572, 0.552159,
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    -0.0762432, -0.00460178, 0.00499591, 0.0421234, 0.0911473, -0.0872384, -0.0098161,
    0.0764732, 0.0225569, 0.0971337, -0.0784129, 0.0767, -0.0511308, 0.0197344, 0.0866722}}|>,
f1 → <|LinearPositive_1 → {{0.984656, 0.162665, 0.0323294, 0.0021843, 0.00180311, 0.0124557,
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    0.241723, 0.262309, 0.280673, 0.298222, 0.316251, 0.337203, 0.353811, 0.372982}},
  LinearPositive_2 → {{0.983395, 0.169664, 0.0335789, 0.00182561, 0.00178377, 0.0118292,
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    0.222988, 0.242318, 0.261428, 0.280669, 0.29788, 0.318599, 0.337668, 0.353641, 0.37207}},
  LinearPositive_3 → {{0.983584, 0.168932, 0.0313189, 0.00193112, 0.00192672, 0.0108988,
    0.0203869, 0.0304257, 0.0185733, 0.0350912}, {0.0172428, 0.0376899, 0.0554268,
    0.0731683, 0.091643, 0.110646, 0.129275, 0.149388, 0.168074, 0.185824, 0.205825, 0.22263,
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  LinearPositive_4 → {{0.984445, 0.163629, 0.0328788, 0.00270852, 0.00232648, 0.0111756,
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    0.24414, 0.262182, 0.279125, 0.297315, 0.317487, 0.337187, 0.355189, 0.372104}},
  LinearPositive_5 → {{0.983848, 0.167653, 0.0345087, 0.00214479, 0.001928,
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  LinearPositive_6 → {{0.984054, 0.16538, 0.0350818, 0.00225871, 0.001926, 0.00949094,
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  LinearPositive_7 → {{0.98454, 0.163174, 0.0317367, 0.00273447, 0.00162815, 0.00952801,
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    0.0755092, 0.0927287, 0.111619, 0.130273, 0.147429, 0.16908, 0.187282, 0.206715,
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  LinearPositive_8 → {{0.984167, 0.165887, 0.0324721, 0.00258897, 0.00117163, 0.0109254,
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    0.242528, 0.261628, 0.281092, 0.297327, 0.31705, 0.337352, 0.353354, 0.371726}},
  LinearPositive_9 → {{0.984886, 0.16139, 0.0335065, 0.0028415, 0.00217951, 0.0114332,
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  LinearPositive_10 → {{0.9834, 0.169097, 0.0346166, 0.00224747, 0.00176146, 0.0100444,
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  LinearPositive_11 → {{0.981679, 0.179453, 0.031392, 0.00248201, 0.00024844, 0.0125935,
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  LinearPositive_12 → {{0.982551, 0.174929, 0.0348422, 0.0014502, 0.00582139,
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  LinearPositive_15 → {{0.985691, 0.158265, 0.0415331, 0.00296037, 0.00126419,
    0.00782683, 0.0184072, 0.0205343, 0.0142703, 0.0245718},
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  LinearPositive_17 → {{0.980206, 0.186224, 0.0288967, 0.00899973, 0.00172553,
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  LinearPositive_18 → {{0.985223, 0.160275, 0.0230011, 0.00252775, 0.00256867,
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  LinearPositive_19 → {{0.985086, 0.160103, 0.0300177, 0.00328998, 0.00447583, 0.00982905,
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LinearNegative_2 → {{0.974433, 0.212348, 0.0428995, 0.0131639, 0.00182814, 0.00884177,
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LinearNegative_3 → {{0.973802, 0.217617, 0.0371043, 0.00224269, 0.00393322, 0.00172276,
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LinearNegative_4 → {{0.981164, 0.175112, 0.0236026, 0.00672231, 0.0121203, 0.00134741,
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LinearNegative_5 → {{0.970266, 0.211, 0.0500085, 0.00135999, 0.00428366, 0.023469, 0.0431424,
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LinearNegative_6 → {{0.98933, 0.124858, 0.0515592, 0.00677245, 0.00191663, 0.0253303,
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LinearNegative_7 → {{0.976482, 0.199358, 0.0593132, 0.0074094, 0.00594962, 0.00404078,
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LinearNegative_8 → {{0.982033, 0.180839, 0.0356261, 0.00371577, 0.00415698, 0.0185648,
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LinearNegative_9 → {{0.974642, 0.206065, 0.0513776, 0.00593531, 0.0107462, 0.00188039,
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LinearNegative_10 → {{0.985697, 0.151226, 0.034804, 0.0162095, 0.00455025, 0.00555441,
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LinearNegative_11 → {{0.985377, 0.15543, 0.0238179, 0.0054476, 0.00172225, 0.00975408,
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LinearNegative_13 → {{0.98607, 0.154747, 0.0257421, 0.00207592, 0.000851266, 0.00692024,
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LinearNegative_14 → {{0.982745, 0.169773, 0.0467526, 0.00290513, 0.00150815, 0.00939623,
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LinearNegative_15 → {{0.983065, 0.173594, 0.0213556, 0.00174493, 0.000687068, 0.0043088,
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LinearNegative_16 → {{0.983135, 0.171519, 0.0295416, 0.00326469, 0.00122599, 0.0213993,
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    -0.00378778, 0.253931, 0.304419, 0.0976195, -0.189552, -0.31926, -0.184276, 0.101814,
    0.306855, 0.25196, -0.00448372, -0.253401, -0.303912, -0.0979719, 0.182097, 0.312096}},
  Sinusoidal3_30 → {{0.0032844, 0.0707546, 0.992947, 0.0828416, 0.0377753, 0.0169015, 0.00824842,
    0.00315568, 0.0195917, 0.00120988}, {0.183436, -0.0982542, -0.29935, -0.260086,
    0.00198862, 0.260076, 0.295736, 0.102049, -0.182656, -0.320206, -0.189321, 0.0982507,
    0.3014, 0.25198, -0.00361349, -0.259464, -0.295933, -0.0957878, 0.187044, 0.314843}}|>,
f5 → <|Sinusoidal2_11 → {{0.00278396, 0.00980635, 0.0332122, 0.0936801, 0.934687, 0.3386,
    0.0284047, 0.00464955, 0.0299324, 0.00160565}, {-0.0962384, -0.257827, 0.260505, 0.0918557,
    -0.316687, 0.101685, 0.258089, -0.250785, -0.0966075, 0.317318, -0.101046, -0.258399,
    0.249813, 0.100794, -0.31193, 0.101611, 0.254088, -0.259434, -0.0992464, 0.314511}},
  Sinusoidal2_12 → {{0.00309191, 0.0114524, 0.0325938, 0.0970742, 0.936192, 0.33369, 0.0272474,
    0.00581262, 0.0280632, 0.00227487}, {-0.103805, -0.260387, 0.261388, 0.0932128,
    -0.316092, 0.100226, 0.250123, -0.250053, -0.102179, 0.318672, -0.0928022, -0.254279,
    0.249667, 0.095202, -0.315189, 0.0948244, 0.254505, -0.262088, -0.0977322, 0.318362}},
  Sinusoidal2_13 → {{0.00326127, 0.00987637, 0.0319603, 0.0954726, 0.931551, 0.347095,
    0.0281142, 0.00473546, 0.026011, 0.00172236}, {-0.101387, -0.252164, 0.25363, 0.0963944,
    -0.311729, 0.0978179, 0.257902, -0.254491, -0.0986101, 0.318334, -0.0954345, -0.25964,
    0.250983, 0.0919275, -0.317554, 0.100485, 0.259018, -0.262655, -0.0962481, 0.314943}},
  Sinusoidal2_14 → {{0.00283585, 0.0117289, 0.030673, 0.0949722, 0.925035, 0.363945, 0.0293476,
```

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```
    0.0048848, 0.0293311, 0.00169825}, {-0.0954193, -0.261849, 0.250459, 0.102575,
    -0.312566, 0.0953334, 0.260167, -0.256272, -0.0979746, 0.317937, -0.0946487, -0.251913,
    0.257838, 0.0921307, -0.312627, 0.100805, 0.251512, -0.261026, -0.0941116, 0.320489}},
  Sinusoidal2_15 → {{0.00262196, 0.0103469, 0.0317936, 0.0990032, 0.933976, 0.339489,
    0.0278381, 0.00447707, 0.026699, 0.00154794}, {-0.102559, -0.251408, 0.2604, 0.0925851,
    -0.317397, 0.0975437, 0.258368, -0.254682, -0.0926816, 0.31337, -0.0977197, -0.254774,
    0.258394, 0.0923161, -0.314531, 0.10047, 0.256799, -0.26013, -0.0940216, 0.316238}},
  Sinusoidal2_16 → {{0.00206764, 0.0107335, 0.0311459, 0.0934424, 0.929988, 0.351447, 0.0304756,
    0.00481277, 0.0288301, 0.00173008}, {-0.0920729, -0.25203, 0.251227, 0.0998683,
    -0.314127, 0.0927703, 0.252575, -0.250812, -0.0992494, 0.317208, -0.101982, -0.252929,
    0.255115, 0.103624, -0.320278, 0.100113, 0.261122, -0.259292, -0.0979151, 0.320406}},
  Sinusoidal2_17 → {{0.0027976, 0.00980949, 0.0317477, 0.0944654, 0.934261, 0.339877, 0.0294744,
    0.00543363, 0.0264954, 0.00212237}, {-0.100017, -0.255997, 0.261186, 0.0960125,
    -0.319967, 0.0939745, 0.249736, -0.253916, -0.096083, 0.314687, -0.100922, -0.258625,
    0.252191, 0.0928662, -0.321542, 0.0925187, 0.258972, -0.257767, -0.0935494, 0.311781}},
  Sinusoidal2_18 → {{0.00210524, 0.0124539, 0.0284017, 0.0973056, 0.934171, 0.339608, 0.028245,
    0.00523618, 0.0269675, 0.00197436}, {-0.102239, -0.259032, 0.258535, 0.093086,
    -0.318424, 0.0943334, 0.254806, -0.257375, -0.102837, 0.316043, -0.0912257, -0.248486,
    0.258454, 0.0964511, -0.315988, 0.0912264, 0.257035, -0.259428, -0.0951829, 0.313458}},
  Sinusoidal2_19 → {{0.00228044, 0.0117335, 0.0284726, 0.0943892, 0.930387, 0.350605, 0.0256501,
    0.00370827, 0.0303354, 0.00106528}, {-0.100134, -0.259468, 0.250969, 0.0918539,
    -0.313158, 0.0958691, 0.255158, -0.260927, -0.103581, 0.319722, -0.0958573, -0.251544,
    0.258055, 0.0933034, -0.320686, 0.103164, 0.249864, -0.257746, -0.102044, 0.311941}},
  Sinusoidal2_20 → {{0.00202398, 0.0104558, 0.0310868, 0.0959762, 0.931167, 0.347799, 0.0282167,
    0.00519005, 0.0290932, 0.00188985}, {-0.0955139, -0.258676, 0.256542, 0.10117,
    -0.321732, 0.0992282, 0.255243, -0.256237, -0.104397, 0.315102, -0.101898, -0.256471,
    0.252145, 0.0953161, -0.312349, 0.103088, 0.255207, -0.251711, -0.100956, 0.312842}}|>,
f6 → <|Sinusoidal1_1 → {{0.00180426, 0.00722039, 0.0173069, 0.0404013, 0.103617, 0.988079,
    0.102542, 0.00434129, 0.0209801, 0.00157832}, {-0.196738, -0.095746, 0.284972, -0.252927,
    -0.0223783, 0.229066, -0.305151, 0.0677152, 0.167948, -0.319847, 0.192793, 0.0733285,
    -0.317952, 0.239646, -0.0256613, -0.275008, 0.311485, -0.0960515, -0.201788, 0.318492}},
  Sinusoidal1_2 → {{0.000908585, 0.0133628, 0.0201405, 0.0432163, 0.0718202, 0.992592,
    0.0818257, 0.00894984, 0.0189214, 0.00405682}, {-0.205461, -0.104126, 0.324626, -0.242711,
    -0.00517235, 0.258439, -0.334443, 0.106564, 0.15871, -0.327563, 0.191095, 0.108496,
    -0.292671, 0.230713, 0.0288677, -0.245762, 0.275697, -0.0783146, -0.179834, 0.311853}},
  Sinusoidal1_3 → {{0.000803748, 0.0023944, 0.0307844, 0.0353459, 0.087524, 0.990572, 0.0914791,
    0.00777354, 0.0214219, 0.00399567}, {-0.189047, -0.0883025, 0.328109, -0.273479,
    -0.00291637, 0.232537, -0.316505, 0.119597, 0.189911, -0.293863, 0.169855, 0.0856639,
    -0.323006, 0.260312, 0.0132984, -0.232948, 0.309535, -0.0851566, -0.163919, 0.300625}},
  Sinusoidal1_4 → {{0.0031152, 0.0144705, 0.0244922, 0.0396681, 0.0962524, 0.987111, 0.116305,
    0.00269431, 0.0204828, 0.000618064}, {-0.174811, -0.0677771, 0.31613, -0.251141,
    -0.00759742, 0.238276, -0.272396, 0.0882635, 0.212258, -0.324069, 0.20333, 0.101819,
    -0.279297, 0.275875, -0.00015304, -0.278785, 0.287865, -0.12374, -0.176474, 0.316345}},
  Sinusoidal1_5 → {{0.00511538, 0.0139913, 0.0223733, 0.0294797, 0.100346, 0.986137, 0.121888,
    0.00399322, 0.0316051, 0.000971159}, {-0.171048, -0.120713, 0.292484, -0.239581,
    0.0312333, 0.265678, -0.306473, 0.0967801, 0.195206, -0.320612, 0.175424, 0.0779049,
    -0.286276, 0.271248, -0.0232282, -0.238192, 0.283464, -0.133749, -0.189582, 0.337116}},
  Sinusoidal1_6 → {{0.00342531, 0.0154005, 0.0254294, 0.0486856, 0.0733891, 0.989898, 0.104924,
    0.00557383, 0.0201357, 0.0022786}, {-0.196675, -0.0933062, 0.317219, -0.244676,
    -0.0129846, 0.226877, -0.323959, 0.106637, 0.17707, -0.325249, 0.186147, 0.119586,
    -0.31671, 0.240639, -0.017396, -0.261678, 0.265998, -0.126988, -0.191504, 0.295835}},
  Sinusoidal1_7 → {{0.00321799, 0.0119492, 0.0139239, 0.0376277, 0.0857979, 0.99181, 0.083678,
    0.003996, 0.0129501, 0.00166159}, {-0.217038, -0.0818892, 0.297892, -0.239846,
    0.0313663, 0.274519, -0.285012, 0.11816, 0.191279, -0.311466, 0.217487, 0.11619,
    -0.269933, 0.269086, 0.0178921, -0.246704, 0.304601, -0.0814787, -0.170779, 0.314555}},
  Sinusoidal1_8 → {{0.00117977, 0.00896874, 0.0266083, 0.0290931, 0.118087, 0.988078, 0.0862118,
    0.00127229, 0.0262131, 0.000376701}, {-0.213234, -0.0841553, 0.307188, -0.270073,
    -0.0107618, 0.264508, -0.286065, 0.0749114, 0.204132, -0.310136, 0.158493, 0.0776777,
    -0.285161, 0.284335, 0.0146852, -0.252882, 0.271119, -0.0769714, -0.181126, 0.339186}},
  Sinusoidal1_9 → {{0.00340454, 0.011917, 0.0201244, 0.0642893, 0.12726, 0.982663, 0.11386,
    0.0101136, 0.0198906, 0.00505458}, {-0.178167, -0.0801708, 0.31542, -0.241079,
    -0.0295255, 0.272898, -0.295834, 0.0849626, 0.161891, -0.33583, 0.167221, 0.0837731,
    -0.272033, 0.237477, -0.0151109, -0.232963, 0.32163, -0.12473, -0.197099, 0.342664}},
  Sinusoidal1_10 → {{0.00165418, 0.00486053, 0.0134427, 0.0420518, 0.100973, 0.988631, 0.10073,
    0.00937566, 0.0133975, 0.00479156}, {-0.178801, -0.0696355, 0.276001, -0.279183,
    -0.00670003, 0.246072, -0.312785, 0.113792, 0.206342, -0.30543, 0.165177, 0.131571,
```

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The default linkage is "Average" as a distance function for the first clustering:

In[3]:=
```
clustersSingle = TimeSeriesSingleClusters[classification1, LinkageMeasure → "Average"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
<|SpikeMax →
  <|Cluster → Cluster[Cluster[Cluster[Cluster[ ··· 1 ··· ], ··· 3 ··· , 5], ··· 3 ··· , 8], {-0.0429852, 0.0123354,
      ··· 17 ··· , -0.0622793} → SpikePositive_15, ··· 19 ··· , 19, 1], ··· 1 ··· , ··· 1 ··· |>, ··· 5 ··· |>
```

large output | show less | show more | show all | set size limit...

In[4]:=
```
Query[All, "GroupAssociations"]@clustersSingle
```

Out[4]=
```
<|SpikeMax → <|G1 → {SpikePositive_1, SpikePositive_11, SpikePositive_13, SpikePositive_6, SpikePositive_14,
     SpikePositive_19, SpikePositive_2, SpikePositive_5, SpikePositive_7, SpikePositive_10,
     SpikePositive_3, SpikePositive_4, SpikePositive_16, SpikePositive_9, SpikePositive_20,
     SpikePositive_18, SpikePositive_17, SpikePositive_8, SpikePositive_12}, G2 → {SpikePositive_15}|>,
 SpikeMin → <|G1 → {SpikeNegative_1, SpikeNegative_8, SpikeNegative_11, SpikeNegative_20, SpikeNegative_2,
     SpikeNegative_6, SpikeNegative_16, SpikeNegative_13, SpikeNegative_4, SpikeNegative_5,
     SpikeNegative_10, SpikeNegative_9, SpikeNegative_18, SpikeNegative_17, SpikeNegative_15,
     SpikeNegative_3, SpikeNegative_14, SpikeNegative_7, SpikeNegative_19, SpikeNegative_12}|>,
 f1 → <|G1 → {LinearPositive_1, LinearPositive_9, LinearPositive_4, LinearPositive_7, LinearPositive_6,
     LinearPositive_8, LinearPositive_2, LinearPositive_10, LinearPositive_3, LinearPositive_5,
     LinearPositive_19, LinearNegative_20, LinearNegative_17, LinearPositive_18, LinearNegative_15,
     LinearNegative_16, LinearPositive_11, LinearPositive_12, LinearNegative_14, LinearPositive_13,
     LinearPositive_17, LinearPositive_14, LinearNegative_8, LinearNegative_12, LinearNegative_13,
     LinearNegative_11, LinearNegative_19, LinearNegative_10, LinearNegative_18, LinearPositive_20,
     LinearPositive_16, LinearPositive_15, LinearNegative_4, LinearNegative_3, LinearNegative_2,
     LinearNegative_9, LinearNegative_7, LinearNegative_5}, G2 → {LinearNegative_6, LinearNegative_1}|>,
 f3 → <|G1 → {Sinusoidal3_21, Sinusoidal3_23, Sinusoidal3_28, Sinusoidal3_29},
   G2 → {Sinusoidal3_22, Sinusoidal3_27, Sinusoidal3_30, Sinusoidal3_26},
   G3 → {Sinusoidal3_25, Sinusoidal3_24}|>,
 f5 → <|G1 → {Sinusoidal2_11, Sinusoidal2_17, Sinusoidal2_15, Sinusoidal2_18, Sinusoidal2_12,
     Sinusoidal2_20, Sinusoidal2_13, Sinusoidal2_16, Sinusoidal2_19}, G2 → {Sinusoidal2_14}|>,
 f6 → <|G1 → {Sinusoidal1_1, Sinusoidal1_10, Sinusoidal1_4, Sinusoidal1_5, Sinusoidal1_2,
     Sinusoidal1_7, Sinusoidal1_3, Sinusoidal1_6, Sinusoidal1_8}, G2 → {Sinusoidal1_9}|>|>
```

In[5]:=
```
clustersSingleLinkageSingle = TimeSeriesSingleClusters[classification1, LinkageMeasure → "Single"]
```

Out[5]=
```
<|SpikeMax → <|Cluster → Cluster[ ··· 1 ··· ], ··· 1 ··· ,
   GroupAssociations → <|G1 → {SpikePositive_1, SpikePositive_11, SpikePositive_13, ··· 14 ··· ,
       SpikePositive_14, SpikePositive_19, SpikePositive_3}|>|>, ··· 4 ··· , f6 → <| ··· 1 ··· |>|>
```

large output | show less | show more | show all | set size limit...

We can see that the groupings are now different:

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In[6]:=
```
Query[All, "GroupAssociations"]@clustersSingleLinkageSingle
```

Out[6]=
```
<|SpikeMax → <|G1 → {SpikePositive_1, SpikePositive_11, SpikePositive_13, SpikePositive_9, SpikePositive_20,
      SpikePositive_7, SpikePositive_5, SpikePositive_2, SpikePositive_16, SpikePositive_18,
      SpikePositive_10, SpikePositive_4, SpikePositive_8, SpikePositive_12, SpikePositive_15,
      SpikePositive_17, SpikePositive_6, SpikePositive_14, SpikePositive_19, SpikePositive_3}|>,
 SpikeMin → <|G1 → {SpikeNegative_1, SpikeNegative_5, SpikeNegative_16, SpikeNegative_6, SpikeNegative_14,
      SpikeNegative_7, SpikeNegative_3, SpikeNegative_13, SpikeNegative_18, SpikeNegative_17,
      SpikeNegative_4, SpikeNegative_20, SpikeNegative_11, SpikeNegative_8, SpikeNegative_10,
      SpikeNegative_12, SpikeNegative_2, SpikeNegative_19, SpikeNegative_9}, G2 → {SpikeNegative_15}|>,
 f1 → <|G1 → {LinearPositive_1, LinearPositive_9, LinearPositive_4, LinearPositive_7, LinearPositive_6,
      LinearPositive_8, LinearPositive_10, LinearPositive_2, LinearPositive_3, LinearPositive_5,
      LinearPositive_19, LinearNegative_20, LinearNegative_17, LinearPositive_12, LinearPositive_18,
      LinearNegative_12, LinearNegative_13, LinearNegative_11, LinearPositive_11, LinearNegative_16,
      LinearNegative_15, LinearPositive_17, LinearPositive_13, LinearPositive_14, LinearNegative_14,
      LinearPositive_15, LinearNegative_18, LinearPositive_20, LinearPositive_16, LinearNegative_19,
      LinearNegative_10, LinearNegative_8, LinearNegative_7, LinearNegative_2, LinearNegative_3,
      LinearNegative_9, LinearNegative_4, LinearNegative_1, LinearNegative_6}, G2 → {LinearNegative_5}|>,
 f3 → <|G1 → {Sinusoidal3_21, Sinusoidal3_28, Sinusoidal3_23, Sinusoidal3_29},
   G2 → {Sinusoidal3_27, Sinusoidal3_22, Sinusoidal3_30, Sinusoidal3_26, Sinusoidal3_24},
   G3 → {Sinusoidal3_25}|>,
 f5 → <|G1 → {Sinusoidal2_11, Sinusoidal2_17, Sinusoidal2_15, Sinusoidal2_18, Sinusoidal2_12,
      Sinusoidal2_13, Sinusoidal2_20, Sinusoidal2_16, Sinusoidal2_19}, G2 → {Sinusoidal2_14}|>,
 f6 → <|G1 → {Sinusoidal1_1, Sinusoidal1_10, Sinusoidal1_4, Sinusoidal1_5, Sinusoidal1_3,
      Sinusoidal1_7, Sinusoidal1_2, Sinusoidal1_6, Sinusoidal1_8}, G2 → {Sinusoidal1_9}|>|>
```

PrintDendrograms (1)

In[1]:=
```
Needs["MathIOmica`"]
```

PrintDendrograms provides the option to print the associated dendrograms for the groupings (if the cluster contains more than 2 members).

We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.139603, 0.173158, 0.306117, 0.103904, 0.283261, 0.380772, 0.354363, 0.264505,
      0.586766, 0.284551}, {0.964431, -0.0763187, 0.0618974, -0.0373706, -0.0717686,
      0.0293627, 0.0228842, 0.0213041, -0.0973033, -0.0565211, 0.0332251, 0.0423411, 0.0430305,
      -0.0923421, -0.0716407, 0.0660293, -0.097426, -0.0225919, -0.0515643, -0.0611379}},
   SpikePositive_2 → {{0.186332, 0.273561, 0.187083, 0.448727, 0.297439, 0.296725, 0.242463,
```

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```
    0.223897, 0.572852, 0.201233}, {0.979116, 0.0150889, -0.0460036, 0.00691092, 0.0628092,
    -0.00688088, 0.0274263, -0.0223928, 0.0716318, 0.0334815, 0.061184, -0.0859721, 0.00247714,
    -0.0407816, 0.063177, -0.0548415, 0.0151693, -0.0617815, 0.0435518, 0.0411769}},
  SpikePositive_3 → {{0.20861, 0.22357, 0.301871, 0.231928, 0.321042, 0.273735, 0.236957,
    0.276503, 0.616124, 0.267155}, {0.98038, -0.0730539, 0.0213493, -0.0464398, -0.0254496,
    0.0144711, -0.0494357, 0.0588998, -0.0413789, -0.0250951, -0.0301895, -0.0347643, 0.0431284,
    -0.073272, 0.00761343, -0.0000242675, -0.0939655, 0.0425406, -0.0405846, 0.00998093}},
  SpikePositive_4 → {{0.236173, 0.235418, 0.167233, 0.229635, 0.462521, 0.357198, 0.465586,
    0.175908, 0.429444, 0.185602}, {0.973135, 0.0207371, -0.0797469, 0.0840174, -0.0500596,
    -0.0981119, -0.0484946, 0.0160433, 0.0589451, -0.0382736, 0.0509197, 0.0152259, 0.0044412,
    0.0777621, 0.0307863, 0.069977, 0.0164469, -0.059591, -0.0303562, 0.000433519}},
  SpikePositive_5 → {{0.249291, 0.208524, 0.579464, 0.208146, 0.208393, 0.366647, 0.315873,
    0.232482, 0.34646, 0.252097}, {0.971134, 0.0299732, -0.0674381, -0.0332008, -0.0683827,
    -0.0101144, 0.0780638, 0.0195841, -0.0886576, -0.0676456, -0.0215324, -0.01236, 0.0502086,
    0.0790484, -0.0847988, -0.0310409, 0.00475339, 0.034161, 0.0786992, -0.0416482}},
  SpikePositive_6 → {{0.195541, 0.179674, 0.369562, 0.264478, 0.335808, 0.19982, 0.249534,
    0.235242, 0.629361, 0.237824}, {0.976162, 0.0109322, 0.0164602, -0.0615586, 0.0447799,
    0.0657531, -0.0159831, 0.0819455, 0.0106872, -0.0535965, -0.0304359, -0.0295563, 0.0521748,
    -0.0500269, 0.00752722, -0.00377874, -0.0810205, 0.0677547, -0.071203, -0.0576301}},
  SpikePositive_7 → {{0.229806, 0.241025, 0.422821, 0.245905, 0.38646, 0.410194, 0.254765,
    0.12702, 0.485495, 0.124477}, {0.954149, 0.0341866, -0.0807026, 0.0926856, 0.0938635,
    -0.0585943, 0.0656275, -0.00376349, -0.0128924, -0.0904209, 0.083156, -0.0381472, 0.0904582,
    -0.0540832, -0.0916075, -0.0882032, 0.00502663, 0.0438799, 0.0792304, -0.0674001}},
  SpikePositive_8 → {{0.147935, 0.150014, 0.210323, 0.166605, 0.369665, 0.13222, 0.295068,
    0.340667, 0.633329, 0.353921}, {0.967284, -0.0636712, 0.0241452, 0.0194986, 0.0588822,
    -0.0730189, 0.0883649, 0.0382393, 0.0415047, -0.0502167, 0.0368422, 0.0876878, -0.0595052,
    0.0777435, 0.0823588, -0.0604527, 0.0874274, 0.00801529, 0.00694649, -0.0143568}},
  SpikePositive_9 → {{0.152684, 0.228352, 0.383065, 0.299961, 0.538426, 0.299586, 0.201517,
    0.145035, 0.476092, 0.140946}, {0.968934, 0.0801344, -0.090907, -0.00227879, 0.020907,
    -0.0544364, 0.0141734, 0.0479159, 0.0942644, -0.0750392, -0.0273817, -0.0147725, 0.0780924,
    -0.0482779, 0.0490779, -0.0277807, -0.0842605, 0.00264186, -0.00431546, -0.0797434}},
  SpikePositive_10 → {{0.172397, 0.0593778, 0.270612, 0.266261, 0.241976, 0.426235, 0.185468,
    0.475146, 0.305868, 0.478207}, {0.956568, -0.0589781, -0.0466581, 0.0814565, 0.0513147,
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    0.0403119, 0.0843222, -0.0499161, 0.0627514, -0.0165298, 0.0769656, -0.0792587}},
  SpikePositive_11 → {{0.214058, 0.417205, 0.235873, 0.169721, 0.134702, 0.334627, 0.212617,
    0.229803, 0.63407, 0.255926}, {0.05433, -0.064429, 0.939097, -0.0871296, 0.0985329,
    -0.0641875, -0.0932996, -0.0997323, 0.0942622, -0.093888, -0.0833658, 0.0230485, 0.0657012,
    -0.0607797, -0.0549921, -0.0824991, -0.0924953, -0.0721891, -0.0772698, 0.0903478}},
  SpikePositive_12 → {{0.253455, 0.165492, 0.235245, 0.191778, 0.406637, 0.470589, 0.491888,
    0.172503, 0.360111, 0.167494}, {-0.0751916, 0.0102051, 0.967387, -0.0466811, 0.0761783,
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    -0.056698, 0.00749422, -0.0434542, 0.0397629, 0.0976378, 0.042359, -0.0705581}},
  SpikePositive_13 → {{0.220721, 0.284913, 0.161607, 0.323736, 0.353094, 0.39228, 0.276642,
    0.301871, 0.442646, 0.311502}, {0.0149324, -0.0463859, 0.971483, -0.0303441, 0.0667607,
    0.0107339, 0.052351, 0.0689298, -0.0870556, -0.0163982, 0.0371825, 0.0764935, -0.0320093,
    0.0193253, 0.0586868, -0.0915726, 0.000297253, 0.0648495, -0.0547181, 0.0731653}},
  SpikePositive_14 → {{0.101373, 0.220362, 0.260553, 0.419846, 0.443856, 0.545183, 0.197891,
    0.226439, 0.252041, 0.220935}, {-0.0485689, -0.0510203, 0.972107, 0.0136159, -0.0585878,
    0.0492256, 0.0149436, -0.00454662, 0.042685, 0.0689748, -0.0808354, 0.0853935, 0.0863835,
    -0.0280406, 0.046121, -0.035152, 0.0615839, 0.0337688, -0.0821512, -0.00791745}},
  SpikePositive_15 → {{0.203094, 0.302906, 0.338817, 0.341445, 0.236868, 0.331214, 0.327834,
    0.305364, 0.40413, 0.325217}, {-0.0307232, -0.0263193, 0.976811, -0.0831622, -0.0425598,
    -0.0827629, -0.0769521, -0.0621172, -0.0459749, -0.000900566, 0.0220369, 0.0106499, -0.0871833,
    -0.0613261, -0.012829, 0.0484066, -0.0340709, -0.00747633, -0.0105028, 0.0306053}},
  SpikePositive_16 → {{0.182133, 0.193135, 0.202607, 0.463961, 0.402555, 0.434022, 0.174415,
    0.274947, 0.354908, 0.301356}, {-0.0437639, 0.0464104, 0.966801, -0.0344085, 0.0361691,
    0.0828144, 0.0940843, -0.0601786, 0.0213259, -0.0348835, 0.0420217, 0.089459, -0.0546068,
    0.0348891, -0.00149698, 0.0832397, 0.0712742, 0.0455017, -0.0932172, 0.0315103}},
  SpikePositive_17 → {{0.174415, 0.439747, 0.298656, 0.461241, 0.207827, 0.328376, 0.282877,
    0.20506, 0.386705, 0.227227}, {-0.0930768, -0.00887103, 0.975806, 0.010716, 0.0544974,
    -0.0582415, -0.0269492, -0.0418753, 0.028923, -0.0285629, 0.0297661, 0.0844567, 0.0596374,
    -0.0608177, -0.0329793, 0.0474126, -0.025668, -0.0077553, -0.0263815, 0.0917962}},
  SpikePositive_18 → {{0.267984, 0.275839, 0.232718, 0.482813, 0.442374, 0.399864, 0.163616,
    0.287638, 0.164783, 0.269418}, {-0.0550497, 0.0296405, 0.961186, 0.0795716, -0.0195804,
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    0.0272537, 0.0238438, -0.0612766, 0.0823901, 0.0273862, 0.0688015, 0.0394461}},
  SpikePositive_19 → {{0.232151, 0.275987, 0.254255, 0.215574, 0.379443, 0.349311, 0.444859,
    0.295077, 0.347455, 0.295177}, {0.0221344, -0.0277336, 0.988949, -0.0437262, -0.00124103,
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    0.00698123, -0.0237059, -0.050558, -0.0265937, -0.0090807, -0.00149299, -0.0105948}},
  SpikePositive_20 → {{0.324777, 0.261411, 0.401887, 0.288548, 0.425095, 0.363361, 0.368143,
    0.160034, 0.288849, 0.155242}, {-0.0237394, 0.0737083, 0.964705, -0.086938, -0.0826668,
    0.0736465, -0.0559265, 0.00223441, 0.0714315, -0.0919996, -0.049177, -0.0940865, 0.039591,
    0.0161322, -0.0602852, -0.0577299, 0.0194352, -0.0631869, 0.0365186, 0.0326185}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.273353, 0.311518, 0.221207, 0.499805, 0.274153, 0.202898,
    0.299951, 0.289538, 0.400596, 0.280873}, {-0.978029, -0.00383559, 0.0275075, -0.0427462,
    -0.0452455, -0.0791621, 0.0660528, -0.00786309, -0.0256058, -0.0657684, -0.0377776, 0.00870464,
    0.0301873, -0.0345455, -0.0228268, 0.029219, -0.018194, -0.0436978, -0.0708332, -0.104406}},
  SpikeNegative_2 → {{0.212469, 0.174606, 0.31858, 0.249458, 0.251319, 0.330012, 0.243886,
    0.370958, 0.500375, 0.375651}, {-0.978888, 0.0196595, 0.02025, 0.0932749, 0.0625934,
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    -0.0404582, -0.0584408, -0.0579249, 0.0161112, 0.0117478, 0.0411087, 0.0498611}},
  SpikeNegative_3 → {{0.171952, 0.197564, 0.128713, 0.246769, 0.177336, 0.286938, 0.159169,
    0.408392, 0.628555, 0.391097}, {-0.971083, 0.0913797, -0.0424025, 0.0449219, -0.0234004,
    0.0456246, -0.0619769, 0.069521, 0.0128269, -0.0779213, 0.0174254, 0.00571033, 0.0234734,
    0.0655938, -0.0923583, 0.0453414, -0.0807692, 0.0662328, -0.022883, -0.00906523}},
  SpikeNegative_4 → {{0.308178, 0.395739, 0.282403, 0.138127, 0.28498, 0.319156, 0.247878,
    0.398457, 0.322268, 0.377419}, {-0.96529, -0.0849312, -0.0515247, -0.0731766, 0.0192338,
    0.0377249, -0.0197211, -0.0454323, 0.0748961, -0.014502, -0.0401656, -0.0695137, -0.00623443,
    0.0557939, 0.0231714, 0.0653931, -0.083588, 0.0808812, -0.0827656, -0.0902091}},
  SpikeNegative_5 → {{0.179668, 0.274535, 0.311791, 0.165031, 0.337383, 0.124683, 0.350747,
    0.223338, 0.646965, 0.216933}, {-0.962843, 0.00259798, -0.0258785, 0.105752, -0.0369854,
    -0.0468649, 0.0384641, -0.00927059, -0.102951, 0.0710442, -0.0950529, -0.0862348, -0.0989826,
    0.0332026, -0.00835638, -0.0423861, -0.0909184, -0.0103824, -0.0435248, -0.0281412}},
  SpikeNegative_6 → {{0.150502, 0.252027, 0.14886, 0.264872, 0.267851, 0.207418, 0.125552,
    0.334237, 0.673849, 0.353834}, {-0.971828, 0.080947, -0.080628, -0.0219086, -0.0815854,
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    0.0201114, 0.0470693, 0.0130922, 0.0894166, 0.0682914, -0.0710743, 0.0616145, 0.0254284}},
  SpikeNegative_7 → {{0.211992, 0.134043, 0.406543, 0.313642, 0.320831, 0.192811, 0.354677,
    0.237929, 0.532982, 0.258571}, {-0.976612, -0.0307568, 0.0481401, 0.0774888, -0.0190506,
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    0.0038081, -0.0775255, -0.03226, -0.0320663, 0.00133655, 0.0542884, 0.00858839, -0.011162}},
  SpikeNegative_8 → {{0.210928, 0.45998, 0.159, 0.112959, 0.334254, 0.259208, 0.321368, 0.15339,
    0.607113, 0.177708}, {-0.968543, -0.0696978, -0.00489993, -0.00289883, 0.0044149,
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    0.0738794, 0.0853344, -0.0974057, -0.0769651, 0.00991955, 0.0552079, -0.0461145}},
  SpikeNegative_9 → {{0.146624, 0.150396, 0.147436, 0.3461, 0.211329, 0.177891, 0.140813,
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    -0.0591954, -0.0218034, 0.0315876, 0.0430964, -0.0912474, -0.0345406, -0.0772367, 0.0468641,
    0.0114773, -0.0898343, -0.0488545, 0.00935063, -0.00295362, 0.0694061, 0.0297022}},
  SpikeNegative_10 → {{0.238753, 0.231903, 0.143861, 0.328481, 0.430074, 0.155352, 0.463464,
    0.279631, 0.434478, 0.264124}, {-0.964143, 0.0732921, 0.0686973, -0.0390418, -0.046176,
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    0.0194041, -0.0670764, -0.0241126, -0.101145, 0.0292221, -0.0736272, -0.0681365}},
  SpikeNegative_11 → {{0.142591, 0.248022, 0.239727, 0.379463, 0.234435, 0.47043, 0.238904,
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    0.0445593, 0.0336278, 0.00897117, -0.012475, 0.0887516, 0.0752123, -0.0734175, -0.0414447,
    -0.00956767, -0.0435995, 0.0235962, -0.0203181, -0.0311413, 0.0781577, -0.0154093}},
  SpikeNegative_12 → {{0.303459, 0.328877, 0.234438, 0.366009, 0.248532, 0.320684, 0.315988,
    0.179969, 0.517968, 0.213762}, {-0.0868488, -0.00124643, -0.973067, -0.0345716, -0.00500647,
    -0.0539257, -0.0723407, 0.0731668, -0.0180531, 0.00310669, -0.0425214, -0.0101748,
    -0.0447723, 0.0734618, 0.0268663, -0.0951252, 0.0560425, 0.00959325, 0.0324254, -0.0847286}},
  SpikeNegative_13 → {{0.209854, 0.348132, 0.311011, 0.553404, 0.367735, 0.1859, 0.379571,
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    0.0855484, -0.0369704, -0.0671949, 0.0881656, 0.0891899, -0.0852712, 0.0428454, -0.0648444,
    0.010485, 0.0111101, 0.0290237, 0.0045872, 0.00349227, 0.00917078, -0.0555009}},
  SpikeNegative_14 → {{0.376023, 0.227099, 0.156392, 0.296898, 0.266717, 0.286313, 0.372564,
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    -0.00271052, -0.0540645, -0.0349982, -0.0791213, 0.0745438, -0.0791581, 0.0605174, -0.0179372,
    0.0794887, 0.0913266, 0.0666125, -0.00732944, -0.0652516, 0.0220882, -0.0219685}},
  SpikeNegative_15 → {{0.149832, 0.221482, 0.309144, 0.444624, 0.355096, 0.287328, 0.377267,
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  SpikeNegative_16 → {{0.168999, 0.208703, 0.330732, 0.287591, 0.410699, 0.242195, 0.443132,
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  SpikeNegative_17 → {{0.124512, 0.132295, 0.338021, 0.338617, 0.183472, 0.275913, 0.216396,
    0.373236, 0.549312, 0.374713}, {-0.081603, 0.0731496, -0.971635, 0.0378921, -0.0473306,
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  SpikeNegative_18 → {{0.286595, 0.258158, 0.185231, 0.289575, 0.376898, 0.541439, 0.271325,
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    0.0552216, -0.0070587, 0.0586783, 0.0273356, -0.084843, 0.0721957, -0.0382943}},
  SpikeNegative_19 → {{0.236995, 0.229766, 0.438685, 0.324255, 0.33772, 0.340796, 0.293415,
    0.247777, 0.393426, 0.246957}, {0.0544889, -0.0108166, -0.981347, 0.0645786, -0.0624785,
    -0.00540784, 0.0130994, -0.023456, -0.0719932, 0.00109494, 0.0714159, 0.0405416, -0.0378696,
    0.0188841, -0.00691337, 0.0135403, -0.0233054, 0.0742091, 0.0588444, -0.039813}},
  SpikeNegative_20 → {{0.174413, 0.572335, 0.241379, 0.367185, 0.259813, 0.365273, 0.188512,
    0.21463, 0.357036, 0.197278}, {0.0627042, -0.0764204, -0.969974, 0.00826208, -0.0162539,
    0.0510032, 0.0141814, 0.0815016, -0.0156703, 0.0180097, -0.0882601, -0.0847999, -0.0349803,
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f1 → <|LinearPositive_1 → {{0.983508, 0.168516, 0.0334786, 0.00206362, 0.00239714,
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  LinearPositive_2 → {{0.983528, 0.1694, 0.0313443, 0.00172823, 0.00193798, 0.0115158,
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  LinearPositive_3 → {{0.984257, 0.164621, 0.0318287, 0.00233499, 0.00150264, 0.0108312,
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  LinearPositive_4 → {{0.984186, 0.166218, 0.0322579, 0.00251302, 0.00165442, 0.0103529,
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  LinearPositive_7 → {{0.983261, 0.170652, 0.0320475, 0.00265523, 0.0017659, 0.0107545,
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  LinearPositive_8 → {{0.984226, 0.165633, 0.0309667, 0.00218201, 0.00216477, 0.0104582,
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LinearPositive_14 → {{0.984568, 0.165578, 0.0330146, 0.00285364, 0.00249474,
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LinearPositive_16 → {{0.984636, 0.156381, 0.0402167, 0.000970259, 0.00368043, 0.0135432,
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LinearPositive_17 → {{0.981994, 0.177561, 0.0361845, 0.00229526, 0.00168945, 0.00608066,
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LinearPositive_18 → {{0.982605, 0.173693, 0.0356202, 0.00145254, 0.00166369,
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LinearPositive_19 → {{0.985898, 0.149917, 0.0274397, 0.00266935, 0.000129462, 0.0133988,
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LinearPositive_20 → {{0.977878, 0.195306, 0.0357161, 0.00212212, 0.00208537, 0.0174858,
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LinearNegative_1 → {{0.99072, 0.120059, 0.0201698, 0.00539866, 0.00124491, 0.0308753,
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LinearNegative_2 → {{0.974624, 0.21017, 0.0183388, 0.00211449, 0.00510898, 0.0102544,
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LinearNegative_3 → {{0.98462, 0.150008, 0.0283362, 0.000912683, 0.0125714, 0.0204543,
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LinearNegative_4 → {{0.972837, 0.210432, 0.0445605, 0.0013097, 0.00597106, 0.0113243,
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LinearNegative_5 → {{0.964738, 0.246367, 0.0620877, 0.00485903, 0.0151181, 0.0278604,
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LinearNegative_6 → {{0.986354, 0.144017, 0.0373073, 0.00168246, 0.00200573, 0.0157975,
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LinearNegative_7 → {{0.985949, 0.159059, 0.0354131, 0.00621036, 0.00276281, 0.00949204,
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LinearNegative_8 → {{0.986781, 0.142867, 0.0602096, 0.00605667, 0.00297972, 0.0151172,
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  Sinusoidal3_24 → {{0.00336575, 0.0725162, 0.992616, 0.0854972, 0.0354166, 0.0187903,
    0.00981913, 0.0025733, 0.0205522, 0.000873626}, {0.185601, -0.101923, -0.305421, -0.256308,
    0.0000113177, 0.251227, 0.303237, 0.0922656, -0.179814, -0.315517, -0.185253, 0.0970033,
```

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```
    0.304217, 0.256679, -0.000422492, -0.262023, -0.298668, -0.0983544, 0.182513, 0.3126}},
  Sinusoidal3_25 → {{0.00331797, 0.0718565, 0.992577, 0.0855245, 0.0380086, 0.0194563,
    0.00774127, 0.00321931, 0.0201989, 0.00122209}, {0.183751, -0.100411, -0.300994, -0.255716,
    -0.00026775, 0.253919, 0.297493, 0.10003, -0.185757, -0.313727, -0.189585, 0.0945243,
    0.304789, 0.250702, -0.00143616, -0.256287, -0.303438, -0.0999373, 0.186978, 0.317675}},
  Sinusoidal3_26 → {{0.0025504, 0.0696483, 0.992891, 0.0849576, 0.034613, 0.0198931, 0.00859834,
    0.0034502, 0.0202696, 0.00136819}, {0.189058, -0.10267, -0.304464, -0.252797,
    -0.00387765, 0.25256, 0.304056, 0.0982572, -0.186084, -0.317255, -0.181467, 0.0915441,
    0.304896, 0.253329, 0.00284001, -0.257354, -0.295781, -0.0910805, 0.187279, 0.316837}},
  Sinusoidal3_27 → {{0.00319205, 0.0708506, 0.992075, 0.0922752, 0.036929, 0.0182165, 0.00791052,
    0.00196288, 0.0219243, 0.000553052}, {0.18691, -0.102053, -0.301659, -0.262426,
    0.0039017, 0.260648, 0.297469, 0.0974666, -0.180757, -0.310844, -0.190027, 0.0923358,
    0.296552, 0.261521, -0.00378511, -0.250681, -0.305287, -0.0939923, 0.191806, 0.311279}},
  Sinusoidal3_28 → {{0.00383707, 0.0727799, 0.99289, 0.0819417, 0.0357702, 0.0196913, 0.007968,
    0.00238697, 0.0201355, 0.000787348}, {0.179454, -0.0915893, -0.294676, -0.253987,
    0.00442181, 0.249938, 0.303639, 0.102001, -0.18276, -0.318147, -0.190031, 0.0916913,
    0.304159, 0.256234, -0.00457587, -0.260824, -0.302442, -0.0989292, 0.186304, 0.318826}},
  Sinusoidal3_29 → {{0.00265557, 0.0752882, 0.992259, 0.0876039, 0.0350697, 0.0183511,
    0.0083376, 0.00343494, 0.0205583, 0.00133398}, {0.18741, -0.103213, -0.303158, -0.260295,
    -0.00512705, 0.260185, 0.292975, 0.0940242, -0.189882, -0.317117, -0.184281, 0.0944924,
    0.303885, 0.25824, -0.000615996, -0.255749, -0.299352, -0.100341, 0.178573, 0.310889}},
  Sinusoidal3_30 → {{0.00274097, 0.0724118, 0.992366, 0.087837, 0.0363148, 0.0173692, 0.00777818,
    0.00195308, 0.0236384, 0.000483094}, {0.185816, -0.104262, -0.299055, -0.262614,
    0.00386926, 0.250705, 0.296854, 0.0982316, -0.184236, -0.318858, -0.186871, 0.0948812,
    0.295995, 0.260854, 0.00124566, -0.256897, -0.304108, -0.0931579, 0.18407, 0.315164}}|>,
f5 → <|Sinusoidal2_11 → {{0.0021863, 0.00959448, 0.0285668, 0.0949592, 0.933843, 0.341087,
    0.0297988, 0.00399401, 0.027603, 0.00128804}, {-0.0978063, -0.250788, 0.255721, 0.0943006,
    -0.321353, 0.101567, 0.255239, -0.261793, -0.0915417, 0.316466, -0.0967716, -0.251099,
    0.25697, 0.0919787, -0.320731, 0.103066, 0.256093, -0.252231, -0.0944481, 0.314535}},
  Sinusoidal2_12 → {{0.00224336, 0.0105988, 0.027602, 0.0941147, 0.928606, 0.355225, 0.0291108,
    0.00513538, 0.0298848, 0.00181515}, {-0.0929565, -0.25935, 0.250422, 0.0921213,
    -0.315584, 0.100816, 0.254726, -0.256311, -0.0997627, 0.311634, -0.0973668, -0.255242,
    0.259731, 0.0924005, -0.317254, 0.102227, 0.253156, -0.259697, -0.0927791, 0.321911}},
  Sinusoidal2_13 → {{0.00262329, 0.00968297, 0.0268626, 0.0895483, 0.932759, 0.345949,
    0.025171, 0.00453595, 0.027958, 0.00154404}, {-0.0984483, -0.252959, 0.25124, 0.0936347,
    -0.310245, 0.103566, 0.260877, -0.253729, -0.100155, 0.318332, -0.0995411, -0.259222,
    0.261107, 0.0967166, -0.315963, 0.100587, 0.2567, -0.249627, -0.0927355, 0.319775}},
  Sinusoidal2_14 → {{0.00261937, 0.0104693, 0.0302275, 0.0958453, 0.93156, 0.346655, 0.0284019,
    0.00426434, 0.0313651, 0.00135846}, {-0.0925158, -0.258123, 0.258935, 0.0924964,
    -0.312698, 0.09608, 0.259177, -0.251668, -0.100968, 0.315198, -0.0936748, -0.256425,
    0.253025, 0.0998625, -0.317926, 0.100446, 0.256569, -0.259375, -0.0989909, 0.315521}},
  Sinusoidal2_15 → {{0.0018857, 0.00986411, 0.0328309, 0.0919788, 0.935002, 0.338101, 0.0301171,
    0.00445953, 0.0298383, 0.00148656}, {-0.0952776, -0.259945, 0.258045, 0.0947106,
    -0.320541, 0.098042, 0.24941, -0.254939, -0.0925626, 0.314999, -0.100664, -0.257508,
    0.254321, 0.101816, -0.317218, 0.102325, 0.25668, -0.255624, -0.102273, 0.31011}},
  Sinusoidal2_16 → {{0.002589, 0.0122407, 0.0305735, 0.0921313, 0.935065, 0.338173, 0.0299374,
    0.00471157, 0.0281505, 0.00164196}, {-0.10206, -0.258796, 0.259787, 0.0943925,
    -0.317351, 0.102273, 0.252725, -0.261095, -0.102348, 0.313124, -0.0920329, -0.257921,
    0.249427, 0.0985654, -0.314536, 0.0958209, 0.25048, -0.259489, -0.091701, 0.317734}},
  Sinusoidal2_17 → {{0.00197809, 0.0119424, 0.0308672, 0.091655, 0.93478, 0.339018, 0.029709,
    0.00421171, 0.0291809, 0.00135381}, {-0.0978688, -0.259009, 0.260498, 0.0927053,
    -0.318885, 0.0979968, 0.255295, -0.258247, -0.091778, 0.31672, -0.0944336, -0.250607,
    0.260721, 0.103538, -0.312537, 0.0973553, 0.251944, -0.257564, -0.0943136, 0.314176}},
  Sinusoidal2_18 → {{0.00171249, 0.0103916, 0.0319618, 0.0895411, 0.931894, 0.347436, 0.0286685,
    0.00520224, 0.0293334, 0.00186741}, {-0.0930394, -0.260225, 0.255618, 0.101291,
    -0.318619, 0.0977972, 0.25166, -0.259943, -0.0937511, 0.319758, -0.0969108, -0.256278,
    0.258732, 0.0957414, -0.309916, 0.101147, 0.256247, -0.250323, -0.0982336, 0.315555}},
  Sinusoidal2_19 → {{0.0024306, 0.0102924, 0.0316874, 0.0925639, 0.929954, 0.35181, 0.0306688,
    0.00392925, 0.0278163, 0.00125596}, {-0.0992077, -0.252782, 0.251156, 0.099905,
    -0.320071, 0.0928177, 0.255564, -0.262417, -0.0950867, 0.3201, -0.0963666, -0.254065,
    0.25027, 0.0938593, -0.319054, 0.0992109, 0.252455, -0.25652, -0.0938053, 0.318123}},
  Sinusoidal2_20 → {{0.00297307, 0.0112148, 0.0302667, 0.0916457, 0.93611, 0.335642, 0.0278324,
    0.00500241, 0.0281157, 0.00180909}, {-0.101334, -0.258604, 0.261993, 0.0986418,
    -0.313248, 0.102087, 0.25044, -0.253046, -0.0959372, 0.318938, -0.0956894, -0.253968,
    0.255929, 0.0975745, -0.319324, 0.095645, 0.256211, -0.252314, -0.0929326, 0.317057}}|>,
f6 → <|Sinusoidal1_1 → {{0.000324761, 0.00677835, 0.0308677, 0.0439898, 0.0814845, 0.987513,
```

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```
    0.11883, 0.00226312, 0.0334318, 0.000269637}, {-0.168419, -0.106072, 0.299122, -0.274366,
    -0.0200933, 0.228498, -0.282257, 0.0734256, 0.20367, -0.335725, 0.174712, 0.0962315,
    -0.314693, 0.26182, 0.0303708, -0.237699, 0.278229, -0.124311, -0.176202, 0.339211}},
Sinusoidal1_2 → {{0.00200759, 0.0158537, 0.0123066, 0.065699, 0.101547, 0.985227, 0.118255,
    0.00856298, 0.0146295, 0.00458194}, {-0.189289, -0.0764228, 0.291036, -0.228708,
    -0.0178454, 0.278773, -0.27753, 0.0924438, 0.160979, -0.324755, 0.205822, 0.128397,
    -0.278397, 0.250389, -0.00679117, -0.242213, 0.313273, -0.126628, -0.175789, 0.351426}},
Sinusoidal1_3 → {{0.000744805, 0.00396843, 0.0153685, 0.0499942, 0.086149, 0.989283, 0.102696,
    0.00243995, 0.0243401, 0.000628255}, {-0.183541, -0.0819158, 0.314088, -0.277272,
    -0.0253743, 0.228184, -0.274238, 0.0839815, 0.181841, -0.345891, 0.169951, 0.115949,
    -0.311414, 0.261157, 0.0100975, -0.247422, 0.316484, -0.072513, -0.172951, 0.303698}},
Sinusoidal1_4 → {{0.0012403, 0.00771552, 0.0224583, 0.0300259, 0.0956104, 0.989866, 0.0940288,
    0.0117756, 0.0231749, 0.00629418}, {-0.156057, -0.0908831, 0.31941, -0.276729,
    0.0125883, 0.270753, -0.317074, 0.0993571, 0.180195, -0.29003, 0.175982, 0.0934268,
    -0.303644, 0.261073, 0.0260883, -0.251924, 0.29963, -0.108038, -0.199678, 0.287746}},
Sinusoidal1_5 → {{0.00464079, 0.00598005, 0.0171991, 0.0372672, 0.0774216, 0.993218,
    0.0732305, 0.00537635, 0.019595, 0.00237943}, {-0.212747, -0.113513, 0.284236, -0.263218,
    -0.00857183, 0.236529, -0.299942, 0.105478, 0.202988, -0.304307, 0.218618, 0.112673,
    -0.289318, 0.229473, 0.024331, -0.278879, 0.286401, -0.0737334, -0.207995, 0.308093}},
Sinusoidal1_6 → {{0.00179329, 0.0066258, 0.00995313, 0.0281132, 0.081752, 0.990689, 0.101325,
    0.00416992, 0.0251169, 0.00112691}, {-0.157155, -0.0928229, 0.294699, -0.264917,
    0.0165258, 0.259834, -0.311222, 0.100239, 0.209815, -0.322368, 0.209343, 0.109624,
    -0.281119, 0.248271, -0.00745596, -0.264388, 0.300143, -0.072788, -0.189588, 0.298711}},
Sinusoidal1_7 → {{0.00132979, 0.00636795, 0.0200559, 0.0383354, 0.0886724, 0.990697,
    0.0900422, 0.00653938, 0.0241969, 0.00266961}, {-0.184061, -0.109508, 0.314913, -0.252401,
    0.000564479, 0.246188, -0.311193, 0.0807909, 0.201924, -0.331801, 0.195092, 0.0825744,
    -0.286778, 0.215996, 0.018972, -0.261467, 0.31075, -0.0797952, -0.205813, 0.297689}},
Sinusoidal1_8 → {{0.00628111, 0.00307298, 0.0177952, 0.0244957, 0.082268, 0.990604, 0.102734,
    0.00535337, 0.0194784, 0.00267303}, {-0.19365, -0.0981125, 0.281187, -0.259894,
    0.00864784, 0.242141, -0.274735, 0.125042, 0.204242, -0.289212, 0.173953, 0.10637,
    -0.331003, 0.285694, -0.0116858, -0.288402, 0.293574, -0.0914007, -0.168643, 0.303366}},
Sinusoidal1_9 → {{0.00123265, 0.0124651, 0.0270966, 0.0391426, 0.0930526, 0.988206, 0.108858,
    0.00611635, 0.0217606, 0.00245508}, {-0.187962, -0.105139, 0.289834, -0.254104,
    -0.0096671, 0.237993, -0.321966, 0.0781107, 0.193943, -0.298541, 0.22154, 0.0902549,
    -0.292739, 0.245565, 0.00529907, -0.247269, 0.28767, -0.129026, -0.182529, 0.338661}},
Sinusoidal1_10 → {{0.00386502, 0.00738369, 0.0191405, 0.0324693, 0.0956762, 0.991763,
    0.0690746, 0.00292594, 0.0313447, 0.00040121}, {-0.19376, -0.10068, 0.311172, -0.269204,
    0.0271798, 0.229924, -0.318579, 0.0978162, 0.189502, -0.299215, 0.187231, 0.0842308,
    -0.29927, 0.224835, -0.0214239, -0.268628, 0.293472, -0.0754236, -0.205815, 0.322271}}|>|>
```

We now cluster the data and also print the dendrograms in the notebook:

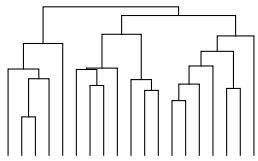
```
In[3]:= clustersSingleDendrogramPrint = TimeSeriesSingleClusters[classification1, PrintDendrograms → True]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

⟨|SpikeMax → ⟨|{G1} →  ,

```
    {G2} → {{0.956568, -0.0589781, -0.0466581, 0.0814565, 0.0513147, 0.0082198,
        0.0708303, -0.0490454, -0.0926812, 0.0692334, -0.0927865,
        0.0892166, 0.0704922, 0.0403119, 0.0843222, -0.0499161, 0.0627514,
        -0.0165298, 0.0769656, -0.0792587} → SpikePositive_10}|⟩,
```

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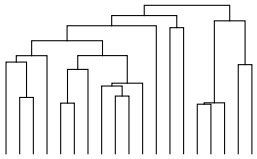
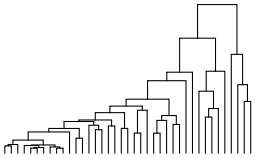
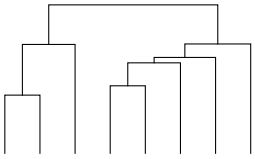
SpikeMin → ⟨| {G1} →  , {G2} →

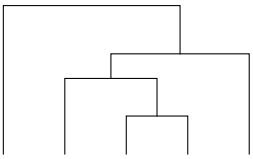
{{0.0827623, -0.0588837, -0.969842, 0.01951, 0.0468457, 0.0855484, -0.0369704, -0.0671949, 0.0881656, 0.0891899, -0.0852712, 0.0428454, -0.0648444, 0.010485, 0.0111101, 0.0290237, 0.0045872, 0.00349227, 0.00917078, -0.0555009} → SpikeNegative_13} |⟩,

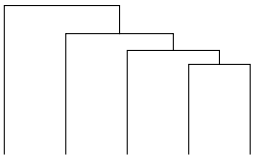
f1 → ⟨| {G1} →  , {G2} →

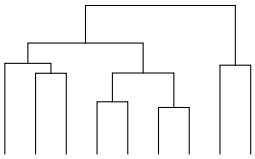
{{-0.00136933, -0.0192948, -0.0669584, -0.0635999, -0.0999356, -0.125464, -0.136925, -0.157574, -0.174999, -0.189751, -0.225655, -0.209208, -0.236751, -0.252947, -0.264884, -0.292009, -0.336532, -0.353623, -0.340838, -0.361294} → LinearNegative_5} |⟩,

f3 → ⟨| {G1} →  , {G2} → |⟩,

f5 →

⟨| {G1} →  ,

{G2} →  |⟩,

f6 → ⟨| {G1} →  ,

{G2} → {{-0.189289, -0.0764228, 0.291036, -0.228708, -0.0178454, 0.278773, -0.27753, 0.0924438, 0.160979, -0.324755, 0.205822, 0.128397, -0.278397, 0.250389, -0.00679117, -0.242213, 0.313273, -0.126628, -0.175789, 0.351426} → Sinusoidal1_2} |⟩ |⟩

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Out[3]=
```
<|SpikeMax → <|Cluster → Cluster[Cluster[Cluster[ ··· 1 ··· ], Cluster[ ··· 1 ··· ], 0.493857, 5, 14],
      {0.956568, ··· 18 ···, -0.0792587} → SpikePositive_10, 0.543473, 19, 1],
   ··· 1 ···, ··· → ··· 1 ···|>, ··· 4 ···, f6 → ··· 1 ···|>
```

large output | show less | show more | show all | set size limit...

ReturnDendrograms (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ReturnDendrograms provides the option to return the dendrograms instead of the clustering information (if the cluster contains more than 2 members).

We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.186057, 0.284953, 0.44937, 0.272487, 0.249688, 0.225565, 0.162872, 0.274526,
      0.562173, 0.277214}, {0.973406, 0.0433581, -0.059313, -0.0916115, 0.0596847, -0.0167239,
      -0.0190323, 0.0558582, -0.0544698, -0.00816693, 0.000414807, 0.0141137, 0.0217771,
      0.031485, -0.0839875, -0.0865681, 0.0085147, -0.0332072, -0.0659995, 0.08117}},
   SpikePositive_2 → {{0.144249, 0.369536, 0.32711, 0.255665, 0.276283, 0.184693, 0.339036,
      0.302645, 0.507546, 0.309329}, {0.980414, -0.016971, -0.0368637, -0.0731845, -0.0391038,
      0.0119513, -0.00358485, 0.0280359, 0.0682032, 0.000828929, -0.0276565, 0.0334874, -0.0605033,
      -0.0200575, -0.065865, -0.0678932, 0.0000974058, -0.0736708, -0.00920246, 0.0652114}},
   SpikePositive_3 → {{0.271542, 0.13846, 0.35268, 0.263374, 0.297275, 0.353907, 0.143114,
      0.265509, 0.5697, 0.290152}, {0.9765, -0.0469841, -0.0274786, -0.0436017, 0.0850257,
      -0.0463719, 0.0349388, 0.0244622, -0.0930344, -0.0256027, -0.0894578, -0.040037, 0.0364655,
      0.00999363, -0.0403726, 0.0220905, -0.0624992, 0.0129691, 0.0439993, 0.0437193}},
   SpikePositive_4 → {{0.206074, 0.351196, 0.317101, 0.124306, 0.209449, 0.122759, 0.292748,
      0.27725, 0.652409, 0.266544}, {0.964475, -0.0677296, 0.0778997, -0.0620513, -0.0955366,
      0.0190931, -0.0597538, -0.0118405, -0.052236, -0.0704986, 0.0561131, 0.0618892, -0.0253668,
      -0.0800025, -0.0501208, -0.0877321, -0.0154919, 0.0391237, -0.0887379, 0.0224404}},
   SpikePositive_5 → {{0.109771, 0.256021, 0.225271, 0.235463, 0.191098, 0.464696, 0.308721,
      0.269941, 0.574472, 0.256044}, {0.959803, -0.0272423, 0.0654207, -0.042125, -0.0834555,
      -0.00344186, 0.0996709, 0.0239578, 0.0688813, 0.0642002, 0.0675744, -0.0612362, 0.090522,
      -0.0274587, 0.0790637, 0.067888, 0.00208826, -0.0944741, 0.0916774, 0.0131056}},
   SpikePositive_6 → {{0.131228, 0.378837, 0.237421, 0.308329, 0.331075, 0.254092, 0.232548,
      0.40265, 0.35825, 0.411223}, {0.968246, -0.0447082, 0.0119759, -0.0392046, -0.0544432,
      -0.000589631, -0.0348838, 0.0336854, 0.0490456, 0.0762185, -0.0552132, 0.0554762, -0.084511,
```

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    -0.0741623, 0.00783961, -0.0854182, -0.0913937, -0.0264057, 0.100509, -0.00350417}},
  SpikePositive_7 → {{0.107458, 0.291707, 0.252243, 0.303918, 0.310839, 0.366234, 0.408686,
    0.206086, 0.498316, 0.242496}, {0.973104, -0.0776564, -0.0763351, 0.00138343, -0.00909098,
    0.0593921, 0.0605275, 0.0491998, 0.00290933, 0.0416834, 0.0892761, -0.0125215, -0.0675164,
    0.0084043, -0.0801667, 0.0816204, -0.0451946, 0.0358085, 0.0237805, -0.00581378}},
  SpikePositive_8 → {{0.167621, 0.306083, 0.183794, 0.202458, 0.115204, 0.318399, 0.441703,
    0.352438, 0.460036, 0.397303}, {0.965295, 0.0304342, 0.0316001, 0.0491686, -0.0313052,
    0.0466561, 0.0895529, 0.0543664, 0.0497039, 0.0822315, -0.0108576, -0.0229684, -0.0785151,
    0.0770893, -0.0914743, 0.0104667, 0.0827173, 0.0246495, -0.0669045, -0.0856856}},
  SpikePositive_9 → {{0.227111, 0.315736, 0.380185, 0.212101, 0.240329, 0.385624, 0.331792,
    0.218197, 0.497715, 0.217543}, {0.975437, 0.0361853, 0.0216175, 0.0106477, -0.055278,
    0.0348754, 0.0433696, -0.0892221, -0.0634533, -0.0301576, 0.0693699, 0.080302, 0.0542414,
    -0.0680912, -0.0610044, -0.00161622, -0.0183852, -0.060353, 0.00938006, 0.0308474}},
  SpikePositive_10 → {{0.0682845, 0.226724, 0.254541, 0.324355, 0.161418, 0.215455, 0.265539,
    0.350463, 0.614308, 0.361593}, {0.976876, -0.058815, -0.0161151, -0.0742256, 0.053581,
    0.0430444, 0.0111858, 0.0161628, 0.0205862, 0.0642683, 0.0324183, -0.0185917, -0.00562065,
    -0.00313993, -0.0737493, -0.0907463, -0.00958956, -0.0397722, -0.0793111, -0.0611882}},
  SpikePositive_11 → {{0.236121, 0.308709, 0.187199, 0.447701, 0.416484, 0.416285, 0.383295,
    0.100557, 0.314049, 0.105166}, {-0.0789219, -0.0558099, 0.972922, 0.0536209, -0.0531991,
    0.00482322, 0.0471701, 0.0123594, -0.0619907, -0.0674399, 0.0304956, -0.0160545, 0.0716681,
    -0.0872272, 0.0174328, -0.0648436, -0.0552441, 0.0746119, -0.0223623, -0.00469093}},
  SpikePositive_12 → {{0.294766, 0.382554, 0.215209, 0.224646, 0.226705, 0.359563, 0.397313,
    0.301513, 0.374635, 0.31652}, {0.00851864, -0.00442541, 0.978006, -0.0721774, -0.0373053,
    -0.0254686, -0.0767492, -0.0534583, -0.0519531, -0.0338598, 0.0281634, -0.00240526,
    -0.069083, -0.0482155, -0.0418077, -0.0246109, -0.0838032, 0.0231295, 0.075381, 0.00888262}},
  SpikePositive_13 → {{0.239755, 0.232606, 0.244111, 0.317766, 0.172253, 0.418295, 0.318376,
    0.321619, 0.441899, 0.350896}, {-0.0332878, 0.0121969, 0.979681, -0.0107867, 0.0855229,
    -0.0434934, 0.027402, -0.0476206, 0.0353046, -0.0712524, -0.0132807, 0.0429851, -0.0164436,
    -0.0402051, 0.00853344, 0.0819211, -0.0559528, 0.0752833, -0.00278093, -0.0283559}},
  SpikePositive_14 → {{0.240115, 0.219398, 0.33796, 0.343674, 0.340733, 0.17021, 0.521313,
    0.306707, 0.251059, 0.296552}, {-0.0686488, 0.0322823, 0.972457, -0.0888313, -0.0055965,
    0.000432748, -0.0268747, 0.050057, -0.0879038, 0.0145354, -0.0551008, -0.0803193, 0.0766122,
    -0.00464608, -0.0170553, 0.0638282, 0.0185789, -0.0576855, 0.0769681, 0.0119985}},
  SpikePositive_15 → {{0.215183, 0.349147, 0.384889, 0.42659, 0.362142, 0.371506, 0.234531,
    0.272285, 0.189436, 0.259772}, {-0.0622426, -0.0144091, 0.978598, 0.0731152, -0.0905665,
    -0.0335278, -0.0514277, -0.011573, -0.0381371, -0.0114003, -0.0857887, 0.0285693, 0.059129,
    0.0234184, 0.0446504, -0.00675618, 0.0495864, -0.0125197, 0.0479933, -0.00709912}},
  SpikePositive_16 → {{0.13061, 0.273336, 0.370356, 0.407372, 0.284451, 0.463258, 0.243897,
    0.330726, 0.200425, 0.317108}, {-0.0290631, -0.034495, 0.976801, 0.050151, -0.0612509,
    0.0102965, -0.0619418, -0.0144713, -0.019884, 0.0618643, -0.0389644, 0.0918211, 0.0265873,
    -0.0369695, 0.0875098, 0.0546521, 0.0713745, -0.0205497, 0.0140258, -0.0283216}},
  SpikePositive_17 → {{0.11717, 0.0903535, 0.354703, 0.273959, 0.439013, 0.211557, 0.360101,
    0.446129, 0.161749, 0.429981}, {-0.065007, -0.0255826, 0.9572, -0.061188, -0.0752202,
    0.0484095, 0.0127936, 0.0418707, -0.0814211, 0.0952334, 0.00929213, -0.0580687,
    -0.0791487, 0.0603657, 0.0538425, 0.0699691, 0.073026, -0.086321, 0.088508, -0.0880196}},
  SpikePositive_18 → {{0.157625, 0.263757, 0.272326, 0.240826, 0.292871, 0.162953, 0.342061,
    0.484441, 0.271223, 0.485644}, {0.00921355, -0.0119804, 0.979056, -0.0146489, -0.0223254,
    -0.0588834, -0.00097976, -0.000412144, -0.0640614, 0.0373787, 0.0195259, 0.00699577,
    -0.0502738, 0.0739539, -0.0510249, 0.034355, -0.0118272, -0.0691248, 0.0898334, -0.0796252}},
  SpikePositive_19 → {{0.428028, 0.229406, 0.226992, 0.443339, 0.314009, 0.306425, 0.179428,
    0.189116, 0.455985, 0.218428}, {0.0644446, 0.0679107, 0.968934, 0.0558452, 0.0494749,
    0.0221025, 0.0788116, -0.0616285, -0.0111148, -0.0625198, 0.0353004, 0.0135149, -0.0532479,
    -0.0456996, -0.00190593, 0.0638591, 0.0778967, 0.0722161, -0.0786244, 0.0663836}},
  SpikePositive_20 → {{0.291039, 0.285291, 0.22477, 0.460775, 0.222065, 0.427024, 0.330835,
    0.245109, 0.32355, 0.255328}, {-0.0202577, 0.096643, 0.967613, -0.0535363, 0.0418324,
    0.052326, 0.0960591, 0.0663893, 0.0273902, 0.0369966, 0.0755439, 0.0959062, -0.0193928,
    -0.0922504, 0.0179765, 0.00850002, -0.0619573, 0.0226551, 0.0218299, 0.0430291}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.17342, 0.154088, 0.217128, 0.0831435, 0.16819, 0.255416,
    0.35111, 0.201426, 0.768465, 0.210265}, {-0.965382, 0.0889278, -0.0560649, 0.075434,
    -0.00806055, -0.0118783, -0.0123091, 0.038572, -0.00978923, 0.0840861, -0.0521253, 0.0219723,
    -0.0840704, 0.0717033, 0.0579256, -0.0780611, -0.0751462, -0.00465005, 0.077664, 0.0756724}},
  SpikeNegative_2 → {{0.153414, 0.324356, 0.18775, 0.168624, 0.200722, 0.241794, 0.239741,
    0.518811, 0.327243, 0.524491}, {-0.973552, 0.0102451, -0.0104519, 0.0183611, 0.067344,
    0.0738206, 0.0832414, -0.0513097, 0.0450722, -0.0796698, 0.0252012, -0.0505906,
    0.00397519, -0.0081093, 0.0388634, 0.0721374, -0.069014, 0.0299736, 0.0220672, 0.0870693}},
  SpikeNegative_3 → {{0.268384, 0.189026, 0.311077, 0.428439, 0.138612, 0.201425, 0.281476,
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    0.151629, 0.652253, 0.156428}, {-0.965938, 0.0796745, 0.0109961, -0.0106168, -0.0126973,
    -0.0515114, 0.0736918, 0.0814467, 0.0450959, 0.0309065, 0.00742083, 0.07595, -0.025174,
    -0.0634925, 0.0688054, 0.0837421, 0.0806663, -0.0617525, 0.0661966, -0.0746727}},
SpikeNegative_4 → {{0.346218, 0.292011, 0.261489, 0.496707, 0.407135, 0.159068, 0.149975,
    0.19843, 0.440606, 0.180847}, {-0.969212, -0.0824169, 0.0348615, -0.0537201, -0.0842795,
    -0.0399014, -0.00561527, -0.0569735, -0.0243843, -0.00947515, -0.0112643, 0.0622174,
    0.0819859, 0.0453069, -0.062635, 0.0953947, 0.0718421, -0.0508388, 0.00379233, -0.0593391}},
SpikeNegative_5 → {{0.0728803, 0.263743, 0.369318, 0.274514, 0.299226, 0.381061, 0.187318,
    0.296863, 0.520868, 0.290021}, {-0.968987, 0.0182037, -0.00197997, 0.00951669, 0.0534982,
    0.0866407, -0.0655922, -0.0787107, -0.0193378, -0.0753267, -0.0300273, -0.00269029,
    -0.0705823, -0.0514412, -0.0676465, 0.0545087, 0.0850109, 0.0849199, -0.0214012, -0.0523795}},
SpikeNegative_6 → {{0.12397, 0.281259, 0.218551, 0.33489, 0.289616, 0.236451, 0.181252,
    0.30184, 0.621414, 0.309366}, {-0.978886, 0.0721348, 0.0127744, 0.0465883, -0.00661601,
    0.0796811, -0.0437941, -0.0446638, -0.0637284, -0.0406465, 0.0301998, 0.0594883, 0.0430653,
    -0.00544088, -0.0574549, 0.0757701, 0.0257071, -0.0243195, 0.00159893, 0.0399345}},
SpikeNegative_7 → {{0.208512, 0.509435, 0.230333, 0.216693, 0.247901, 0.181345, 0.299842,
    0.220246, 0.560142, 0.224669}, {-0.978112, -0.0104321, -0.0394489, 0.0732634, 0.0984939,
    0.0238204, -0.0116736, -0.0325259, -0.0699797, -0.000632841, -0.0367821, 0.0153191, 0.0969571,
    0.0726149, 0.0199523, 0.00441849, 0.000809935, 0.00477566, -0.00401969, -0.0564368}},
SpikeNegative_8 → {{0.277578, 0.198049, 0.146895, 0.238083, 0.261854, 0.193143, 0.38689,
    0.34388, 0.55605, 0.34995}, {-0.975408, 0.0674887, -0.0481068, 0.0169408, -0.0272948,
    -0.0226999, 0.0761121, -0.0785916, -0.0455542, 0.0168341, 0.031644, 0.0658954, 0.0262556,
    -0.0528805, -0.0122532, -0.0801485, -0.0716298, 0.0312954, -0.0132706, -0.0643814}},
SpikeNegative_9 → {{0.237391, 0.223306, 0.339995, 0.276494, 0.314913, 0.284268, 0.243947,
    0.372708, 0.388865, 0.414872}, {-0.961404, -0.058575, -0.0392626, 0.0420178, 0.0445832,
    -0.0490034, -0.092666, -0.0132395, -0.00116857, -0.0115535, 0.0688895, -0.0936724, 0.084168,
    -0.0343476, -0.0886135, -0.0310264, 0.0355253, -0.0958633, -0.0680449, 0.0999805}},
SpikeNegative_10 → {{0.257437, 0.339787, 0.350088, 0.171562, 0.252315, 0.18698, 0.157719,
    0.43732, 0.413002, 0.42539}, {-0.967054, -0.0406288, 0.0209802, 0.0822812, 0.0662753,
    0.021601, 0.088852, -0.0937102, 0.0232389, -0.0602233, 0.0518085, -0.0903627, -0.0789964,
    -0.0333453, -0.0208295, -0.00571432, -0.0741004, -0.0200417, 0.0522385, -0.0543523}},
SpikeNegative_11 → {{0.113916, 0.334182, 0.467694, 0.483976, 0.362365, 0.361491, 0.232121,
    0.217361, 0.120539, 0.211507}, {0.0887104, -0.0348674, -0.952527, -0.0328708, 0.0617161,
    -0.0769026, 0.0567175, 0.0778484, 0.0678741, -0.0949992, -0.0996427, -0.0710342, 0.0813831,
    0.0459356, -0.0667231, -0.0964028, -0.0386698, 0.0962838, 0.0362633, 0.0189939}},
SpikeNegative_12 → {{0.508764, 0.227165, 0.300878, 0.150168, 0.377462, 0.163016, 0.341204,
    0.317555, 0.272555, 0.340409}, {-0.0466733, -0.0317445, -0.96295, -0.058428, -0.0544759,
    -0.0920069, 0.051441, 0.0193413, 0.0434336, -0.0529278, 0.0751078, 0.0893565, 0.0573978,
    -0.0767066, 0.0924429, -0.0779277, -0.0410687, -0.0207671, -0.0435635, -0.0744828}},
SpikeNegative_13 → {{0.275215, 0.326212, 0.460967, 0.273006, 0.521838, 0.198137, 0.193742,
    0.201335, 0.305248, 0.219085}, {0.0290113, -0.0410936, -0.971861, -0.0789099, 0.0120188,
    0.0938584, -0.0392047, -0.0155785, 0.0247058, -0.0988287, -0.0227592, 0.0494964, 0.0640304,
    -0.0424762, 0.00549242, 0.0614506, 0.0108776, -0.0554831, 0.0617388, -0.07701}},
SpikeNegative_14 → {{0.307789, 0.337992, 0.260578, 0.159327, 0.272456, 0.327739, 0.354549,
    0.33695, 0.401394, 0.340204}, {-0.0554839, -0.0915638, -0.960776, 0.0431363, -0.104742,
    0.0416074, 0.0355399, 0.00703476, 0.0862097, 0.104251, 0.000379487, 0.0319954, 0.0172933,
    -0.102113, -0.0949109, 0.0429361, 0.0140405, -0.042826, -0.00373929, 0.0813975}},
SpikeNegative_15 → {{0.282862, 0.315814, 0.126143, 0.294467, 0.25315, 0.349134, 0.516802,
    0.211643, 0.419836, 0.208587}, {0.0154146, -0.00538657, -0.97133, 0.0526383, -0.0697879,
    -0.0371785, -0.0221002, -0.081792, 0.0198333, 0.0709144, -0.0735156, -0.00353376, -0.0853131,
    0.0444826, 0.0128331, 0.0883123, 0.0330355, -0.0599481, -0.0849809, -0.00908492}},
SpikeNegative_16 → {{0.277991, 0.195359, 0.419772, 0.221438, 0.167162, 0.383402, 0.252125,
    0.361348, 0.395848, 0.365427}, {-0.0143895, -0.0568899, -0.974285, 0.00436456, -0.033776,
    0.063454, -0.0121051, 0.0672053, -0.0850502, 0.0103415, 0.0245305, 0.019177, 0.0881644,
    0.0513637, -0.0335946, -0.0664228, 0.0407874, 0.0176396, -0.05335, 0.0916098}},
SpikeNegative_17 → {{0.284895, 0.37671, 0.398086, 0.152346, 0.375655, 0.12394, 0.411786,
    0.278564, 0.330831, 0.286617}, {-0.10236, 0.0461428, -0.967784, -0.101984, 0.0256545,
    0.033326, 0.0962205, -0.0045107, 0.0482414, -0.0822168, -0.0359052, 0.10425, 0.000217704,
    -0.0630273, 0.0469423, 0.00529443, -0.00666536, 0.0168614, -0.0191977, -0.0345373}},
SpikeNegative_18 → {{0.129983, 0.236193, 0.179675, 0.584754, 0.396566, 0.238712, 0.331692,
    0.20003, 0.376723, 0.216555}, {0.0671732, -0.00272445, -0.957977, 0.0230087, -0.0305195,
    0.0390183, -0.0913498, -0.0651508, -0.036516, -0.0723957, -0.0983365, -0.0771741, -0.0961899,
    0.0618581, 0.0752779, -0.0263087, -0.0875141, -0.0807013, 0.0364927, -0.0710437}},
SpikeNegative_19 → {{0.189969, 0.350793, 0.533739, 0.264815, 0.371425, 0.27261, 0.171073,
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    0.298527, 0.392802, 0.295471}, {0.0490005, 0.0826038, -0.963012, -0.0342477, -0.0368504,
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    -0.0209771, 0.0498523, 0.0436247, 0.0320582, -0.0912719, 0.04218, 0.039325, -0.0666511}}|>,
f1 → <|LinearPositive_1 → {{0.98475, 0.162296, 0.0318315, 0.00301455, 0.00182373,
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    0.241935, 0.261941, 0.281138, 0.300331, 0.319074, 0.334249, 0.354074, 0.371761}},
  LinearPositive_3 → {{0.984111, 0.166573, 0.0317621, 0.00135537, 0.00181677, 0.0117803,
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    0.241327, 0.262036, 0.281007, 0.298483, 0.319231, 0.335095, 0.353911, 0.373479}},
  LinearPositive_4 → {{0.984473, 0.163801, 0.0309613, 0.00195318, 0.00188463,
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  LinearPositive_7 → {{0.984046, 0.166637, 0.0341384, 0.00243163, 0.00209441,
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  LinearPositive_12 → {{0.980545, 0.188041, 0.0324654, 0.00301278, 0.0031811,
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  LinearPositive_14 → {{0.98339, 0.171523, 0.0269283, 0.00358849, 0.0028756,
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 LinearNegative_2 → {{0.976589, 0.202842, 0.0332704, 0.00531539, 0.00679751, 0.0271891,
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 LinearNegative_3 → {{0.972997, 0.208861, 0.0275352, 0.00280136, 0.00954368, 0.0304265,
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 LinearNegative_4 → {{0.986731, 0.143106, 0.0231978, 0.00839047, 0.0075225, 0.00508414,
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 LinearNegative_6 → {{0.980539, 0.186072, 0.0434641, 0.00488078, 0.00396361, 0.0117633,
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 LinearNegative_7 → {{0.989152, 0.134581, 0.0232009, 0.00118239, 0.00258281, 0.00750078,
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 LinearNegative_8 → {{0.987402, 0.146533, 0.0165892, 0.00656197, 0.000301414, 0.0130954,
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 LinearNegative_9 → {{0.975359, 0.177161, 0.0315429, 0.00287551, 0.00485556, 0.0152767,
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 LinearNegative_11 → {{0.988356, 0.136873, 0.0397626, 0.0032238, 0.00323321, 0.0125752,
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 LinearNegative_12 → {{0.978853, 0.190286, 0.0204606, 0.00235819, 0.00380515, 0.00805408,
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    0.0262983, 0.0314445, 0.0178179, 0.0365332}, {-0.0164204, -0.0337779, -0.0547249, -0.0766537,
    -0.0921471, -0.116547, -0.138752, -0.156148, -0.162677, -0.186623, -0.210874, -0.227364,
    -0.245417, -0.255416, -0.286793, -0.290101, -0.309665, -0.337488, -0.356178, -0.371519}},
  LinearNegative_20 → {{0.983692, 0.169185, 0.0414812, 0.00393031, 0.000580035, 0.0068466,
    0.015117, 0.024406, 0.0178976, 0.0282541}, {-0.0280679, -0.0306632, -0.0512357, -0.072462,
    -0.0927335, -0.116204, -0.138128, -0.144678, -0.169712, -0.186035, -0.207093, -0.22972,
    -0.237083, -0.267079, -0.27696, -0.298832, -0.310582, -0.33177, -0.359767, -0.373765}}|>,
f3 → <|Sinusoidal3_21 → {{0.00355531, 0.0742648, 0.992187, 0.0881519, 0.0375958, 0.0191982,
    0.00787121, 0.00276551, 0.0203614, 0.000973375}, {0.182344, -0.0929162, -0.304235, -0.257915,
    0.00211209, 0.255655, 0.304653, 0.102344, -0.188113, -0.310059, -0.183752, 0.101517,
    0.30165, 0.254203, 0.00583859, -0.251189, -0.303417, -0.0988828, 0.180963, 0.318535}},
  Sinusoidal3_22 → {{0.0031089, 0.0701813, 0.992518, 0.0875818, 0.0381054, 0.0190182, 0.00847639,
    0.00295976, 0.0201716, 0.00108652}, {0.188452, -0.0926518, -0.299679, -0.253896,
    0.00353829, 0.251551, 0.299408, 0.0999664, -0.183961, -0.314942, -0.181602, 0.0991463,
    0.302488, 0.254208, 0.00295958, -0.260002, -0.302718, -0.0964704, 0.189075, 0.32006}},
  Sinusoidal3_23 → {{0.00329529, 0.0700991, 0.99232, 0.089902, 0.037368, 0.0198159, 0.0076683,
    0.00234303, 0.0209867, 0.000764148}, {0.182763, -0.0931976, -0.306592, -0.258547,
    0.00462913, 0.251396, 0.297078, 0.0955226, -0.182727, -0.312158, -0.183866, 0.09298,
    0.303363, 0.256366, -0.0042742, -0.258119, -0.307382, -0.0938042, 0.18545, 0.317979}},
  Sinusoidal3_24 → {{0.00270536, 0.0723514, 0.992356, 0.087696, 0.0377297, 0.019052, 0.00761229,
    0.00286835, 0.0210405, 0.00100623}, {0.187071, -0.0991947, -0.305541, -0.261947,
    -0.000733293, 0.249892, 0.299387, 0.101571, -0.190897, -0.316068, -0.189886, 0.0946894,
    0.29774, 0.253304, 0.00561168, -0.254426, -0.303403, -0.098298, 0.180914, 0.31211}},
  Sinusoidal3_25 → {{0.00271299, 0.0718094, 0.992417, 0.0878902, 0.0361741, 0.0206941,
    0.00928781, 0.00320346, 0.019608, 0.00126011}, {0.184688, -0.102062, -0.302369, -0.252662,
    4.29826×10^-6, 0.254612, 0.29939, 0.0933696, -0.193139, -0.313328, -0.190369, 0.0949648,
    0.298563, 0.252679, -0.00301176, -0.258027, -0.297315, -0.0993173, 0.192343, 0.318535}},
  Sinusoidal3_26 → {{0.00341143, 0.0736422, 0.992328, 0.0871718, 0.0366661, 0.0212402,
    0.00839779, 0.00283855, 0.0193906, 0.00104447}, {0.181692, -0.0943077, -0.306123, -0.256572,
    0.00185915, 0.250617, 0.296842, 0.0997239, -0.188239, -0.310585, -0.186483, 0.0957397,
    0.303453, 0.259763, -0.00313757, -0.259133, -0.302552, -0.103036, 0.182653, 0.315604}},
  Sinusoidal3_27 → {{0.00377459, 0.0719121, 0.992619, 0.0850128, 0.0381506, 0.0186494, 0.00710648,
    0.00281646, 0.0207722, 0.000979886}, {0.190594, -0.0917081, -0.295466, -0.250952,
    0.00475161, 0.260813, 0.303513, 0.102598, -0.181804, -0.313203, -0.189485, 0.0958399,
    0.307837, 0.250839, -0.00130701, -0.251543, -0.305479, -0.0926764, 0.187742, 0.316137}},
  Sinusoidal3_28 → {{0.00261923, 0.0754694, 0.992038, 0.0891226, 0.0362814, 0.0195988,
    0.00785671, 0.00278538, 0.0210917, 0.000960827}, {0.188278, -0.100685, -0.304993, -0.252415,
    0.00220452, 0.25253, 0.298371, 0.0995009, -0.191167, -0.31309, -0.18677, 0.0956776,
    0.300627, 0.26086, 0.00581569, -0.254108, -0.305037, -0.0933558, 0.184107, 0.312543}},
```

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    Sinusoidal3_29 → {{0.00275379, 0.0738614, 0.992167, 0.0896737, 0.0361232, 0.0188224,
        0.0103429, 0.00292536, 0.0180103, 0.00114815}, {0.179493, -0.0928928, -0.301251, -0.25724,
        -0.00344132, 0.261608, 0.299771, 0.0938614, -0.185094, -0.317074, -0.187245, 0.0953869,
        0.29664, 0.260269, 0.000688658, -0.253688, -0.295966, -0.103995, 0.190678, 0.318258}},
    Sinusoidal3_30 → {{0.00355136, 0.0695558, 0.992554, 0.0864546, 0.0408223, 0.0188979, 0.00860697,
        0.00220346, 0.0202138, 0.000682475}, {0.185824, -0.0958723, -0.304663, -0.259212,
        0.00539201, 0.253249, 0.301672, 0.101362, -0.181298, -0.320804, -0.18753, 0.0970998,
        0.29583, 0.250332, -0.00310213, -0.253962, -0.303056, -0.0987462, 0.190341, 0.31294}}|〉,
f5 → ‹| Sinusoidal2_11 → {{0.00253552, 0.0107028, 0.0283465, 0.0901249, 0.931334, 0.34896,
        0.0309276, 0.0060493, 0.0282565, 0.00239969}, {-0.0926105, -0.259032, 0.251576, 0.104116,
        -0.312685, 0.0985291, 0.253439, -0.255022, -0.102439, 0.312657, -0.0991142, -0.257896,
        0.253857, 0.0984422, -0.315388, 0.093153, 0.263427, -0.252387, -0.0927589, 0.323864}},
    Sinusoidal2_12 → {{0.00224528, 0.00968796, 0.0341054, 0.0915867, 0.934298, 0.340149, 0.0292908,
        0.00463257, 0.0292316, 0.00157428}, {-0.0969792, -0.258894, 0.258469, 0.0984789,
        -0.317991, 0.0937412, 0.248889, -0.257533, -0.0920553, 0.319277, -0.0987638, -0.257835,
        0.25145, 0.0955839, -0.317026, 0.0987866, 0.258291, -0.254554, -0.100341, 0.313109}},
    Sinusoidal2_13 → {{0.00258083, 0.011127, 0.0320827, 0.092831, 0.931151, 0.348849, 0.0259521,
        0.00499198, 0.02797, 0.00182128}, {-0.0994749, -0.257752, 0.259634, 0.096924,
        -0.316578, 0.0926748, 0.254147, -0.250113, -0.101298, 0.320363, -0.0972071, -0.258586,
        0.257974, 0.0987496, -0.317203, 0.0963386, 0.251926, -0.256975, -0.0961103, 0.311056}},
    Sinusoidal2_14 → {{0.00203932, 0.0105526, 0.0339722, 0.0959858, 0.933918, 0.340254, 0.0287681,
        0.00402245, 0.0263768, 0.00132502}, {-0.103205, -0.25118, 0.259563, 0.0941588,
        -0.323031, 0.0925099, 0.257281, -0.258453, -0.0917462, 0.317055, -0.100592, -0.254121,
        0.256345, 0.0974935, -0.31271, 0.0993375, 0.253624, -0.259294, -0.0961551, 0.311135}},
    Sinusoidal2_15 → {{0.00297203, 0.0113028, 0.0326736, 0.0866152, 0.936747, 0.335, 0.0287496,
        0.00505221, 0.0267992, 0.00188129}, {-0.0978636, -0.251079, 0.256984, 0.102987,
        -0.312528, 0.100128, 0.253906, -0.260913, -0.0917341, 0.319042, -0.102466, -0.25988,
        0.255536, 0.0975341, -0.311743, 0.0918227, 0.257989, -0.253667, -0.0991913, 0.317932}},
    Sinusoidal2_16 → {{0.00309188, 0.0124392, 0.028516, 0.0877439, 0.935292, 0.339365, 0.0255196,
        0.00560993, 0.0263759, 0.00218768}, {-0.0985335, -0.250238, 0.260486, 0.0969513,
        -0.310301, 0.103436, 0.253858, -0.26186, -0.103365, 0.318149, -0.103107, -0.259061,
        0.259059, 0.0927989, -0.313414, 0.0913793, 0.254517, -0.253909, -0.0918574, 0.317467}},
    Sinusoidal2_17 → {{0.00345217, 0.0118403, 0.0320879, 0.094159, 0.935336, 0.3368, 0.0308654,
        0.00532049, 0.0260654, 0.00206644}, {-0.10255, -0.256586, 0.251881, 0.103595,
        -0.310678, 0.0989632, 0.255218, -0.254416, -0.0944942, 0.314887, -0.0928084, -0.25568,
        0.252729, 0.0975301, -0.315726, 0.0916148, 0.261833, -0.262207, -0.101841, 0.319504}},
    Sinusoidal2_18 → {{0.00218129, 0.00938919, 0.0346551, 0.0933245, 0.928873, 0.354419,
        0.0294813, 0.00485937, 0.0261259, 0.00180657}, {-0.0993102, -0.25452, 0.252862, 0.101956,
        -0.321493, 0.0929633, 0.253774, -0.254638, -0.0951006, 0.320106, -0.100371, -0.259326,
        0.252814, 0.0956327, -0.314791, 0.103548, 0.255486, -0.257578, -0.0955245, 0.311968}},
    Sinusoidal2_19 → {{0.00231439, 0.0136683, 0.0314768, 0.0918852, 0.933529, 0.342542, 0.0274833,
        0.00484336, 0.0279488, 0.00171361}, {-0.0977172, -0.253818, 0.261492, 0.103663,
        -0.315714, 0.0972864, 0.25347, -0.25752, -0.0977711, 0.316933, -0.0957286, -0.254152,
        0.262747, 0.100665, -0.313247, 0.0952965, 0.251906, -0.253814, -0.0976278, 0.315682}},
    Sinusoidal2_20 → {{0.00199557, 0.0126584, 0.0296439, 0.0907448, 0.929896, 0.352363, 0.0318499,
        0.00487554, 0.0285484, 0.00176259}, {-0.0922665, -0.257493, 0.254988, 0.0968375,
        -0.318005, 0.0950675, 0.253958, -0.258563, -0.0947943, 0.312454, -0.103985, -0.250903,
        0.262439, 0.102151, -0.316717, 0.0945428, 0.252343, -0.262284, -0.0932684, 0.314911}}|›,
f6 → ‹| Sinusoidal1_1 → {{0.00578966, 0.00472902, 0.0263054, 0.0465122, 0.0983159, 0.989438,
        0.0853475, 0.00106889, 0.0339062, 0.0000616584}, {-0.200043, -0.10423, 0.323203, -0.243478,
        0.00875965, 0.23356, -0.276095, 0.109638, 0.205835, -0.330546, 0.159345, 0.0764526,
        -0.301442, 0.242619, -0.0137553, -0.244226, 0.300605, -0.077243, -0.201097, 0.336601}},
    Sinusoidal1_2 → {{0.00810342, 0.00653519, 0.0209024, 0.0339932, 0.104117, 0.988302, 0.101406,
        0.0117046, 0.0161769, 0.00596028}, {-0.181832, -0.0936339, 0.308954, -0.242841,
        0.0225537, 0.287571, -0.282659, 0.0961719, 0.189373, -0.304464, 0.161659, 0.07311,
        -0.303763, 0.236916, 0.0222327, -0.261818, 0.319223, -0.114178, -0.160571, 0.336435}},
    Sinusoidal1_3 → {{0.00400841, 0.0061327, 0.0195223, 0.0239513, 0.115737, 0.985846, 0.113472,
        0.0055561, 0.0281827, 0.00176283}, {-0.166325, -0.110319, 0.272646, -0.280769,
        0.00819272, 0.279648, -0.31593, 0.111692, 0.209627, -0.308011, 0.171198, 0.0673646,
        -0.269824, 0.270984, -0.0257943, -0.24401, 0.280535, -0.122408, -0.19911, 0.322503}},
    Sinusoidal1_4 → {{0.00495053, 0.013176, 0.0151062, 0.0442701, 0.0844689, 0.989584, 0.0984023,
        0.00158896, 0.0389256, 0.00128538}, {-0.198121, -0.127173, 0.269287, -0.272971,
        0.0239745, 0.245393, -0.269858, 0.10216, 0.178628, -0.325968, 0.173545, 0.127663,
        -0.306014, 0.280097, -0.017369, -0.233946, 0.268148, -0.126541, -0.211789, 0.330173}},
    Sinusoidal1_5 → {{0.00493794, 0.00964439, 0.00693658, 0.0475007, 0.0838059, 0.991077,
```

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```
    0.0898398, 0.00546309, 0.0145672, 0.0029465}, {-0.197504, -0.0712738, 0.310925, -0.244514,
    0.0138147, 0.28745, -0.274115, 0.0924708, 0.170366, -0.350252, 0.219084, 0.0996091,
    -0.288994, 0.226212, 0.00648717, -0.264141, 0.302523, -0.067535, -0.17636, 0.302713}},
Sinusoidal1_6 → {{0.002636, 0.0137174, 0.0149399, 0.0380844, 0.0794973, 0.988181, 0.121791,
    0.00444116, 0.0213324, 0.00149695}, {-0.18894, -0.114146, 0.287703, -0.233905,
    0.00238088, 0.248959, -0.295036, 0.102869, 0.172449, -0.334122, 0.192661, 0.108203,
    -0.300289, 0.278202, -0.0175038, -0.261674, 0.289141, -0.11555, -0.181721, 0.312482}},
Sinusoidal1_7 → {{0.0000458859, 0.00813927, 0.014741, 0.0314676, 0.102649, 0.986064,
    0.123826, 0.00649842, 0.0220293, 0.00251273}, {-0.166296, -0.103919, 0.305753, -0.26747,
    -0.0176523, 0.240392, -0.314322, 0.0855238, 0.185005, -0.33738, 0.191867, 0.0769827,
    -0.263321, 0.280517, -0.00908763, -0.26048, 0.320579, -0.0931721, -0.178267, 0.286927}},
Sinusoidal1_8 → {{0.00328896, 0.0206494, 0.0180387, 0.0305919, 0.0846769, 0.991923, 0.0824971,
    0.00439326, 0.0197634, 0.00208394}, {-0.206913, -0.0723008, 0.27699, -0.226666,
    0.0211854, 0.271297, -0.31804, 0.0747828, 0.169398, -0.311484, 0.190472, 0.112492,
    -0.308027, 0.261381, 0.0133875, -0.270253, 0.264509, -0.0961712, -0.209916, 0.329725}},
Sinusoidal1_9 → {{0.000907661, 0.0078569, 0.0288663, 0.0325463, 0.094869, 0.989786, 0.0948249,
    0.00404135, 0.0189544, 0.00124734}, {-0.196197, -0.0822149, 0.309029, -0.250726,
    0.0100052, 0.231608, -0.320474, 0.0898615, 0.194581, -0.319573, 0.156997, 0.0934043,
    -0.292318, 0.278255, 0.0241797, -0.227597, 0.323457, -0.0892371, -0.169922, 0.319031}},
Sinusoidal1_10 → {{0.009691, 0.00642574, 0.0134791, 0.0283452, 0.115109, 0.988376, 0.092684,
    0.00769383, 0.00863196, 0.0042313}, {-0.218031, -0.0853087, 0.290593, -0.237114,
    0.0259807, 0.285407, -0.276146, 0.10953, 0.210241, -0.314659, 0.161904, 0.0682331,
    -0.27922, 0.248638, -0.011386, -0.293722, 0.328823, -0.088923, -0.179267, 0.29274}}|>|⟩
```

We now cluster and return the dendrograms as output

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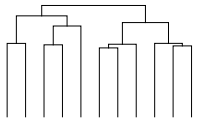
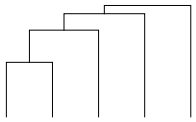
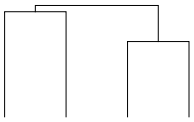
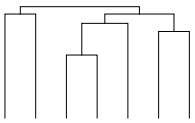
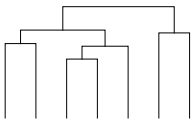
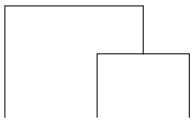
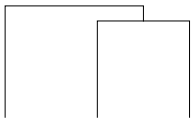
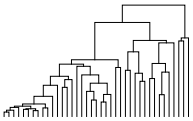
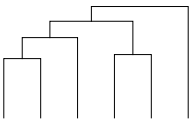
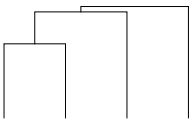
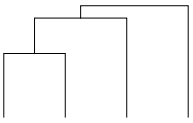
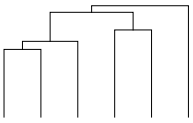
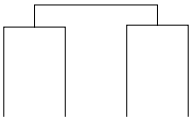
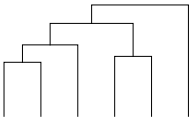
In[3]:=
```
clustersSingleDendrogramsReturn = TimeSeriesSingleClusters[classification1, ReturnDendrograms → True]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

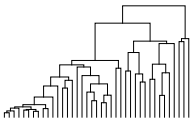
Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
⟨|SpikeMax → ⟨|{G1} →  , {G2} →  , {G3} →  |⟩,
SpikeMin → ⟨|{G1} →  , {G2} →  ,
{G3} →  , {G4} →  |⟩, f1 →
⟨|{G1} →  , {G2} → {{-0.00413326, -0.0426122, -0.0424214, -0.091468, -0.080986, -0.118982,
-0.131633, -0.139847, -0.171527, -0.198047, -0.209967, -0.221144, -0.233244, -0.25001, -0.287256,
-0.283226, -0.313567, -0.350353, -0.341338, -0.389285} → LinearNegative_9}|⟩,
f3 → ⟨|{G1} →  , {G2} →  |⟩,
f5 → ⟨|{G1} →  , {G2} →  |⟩,
f6 → ⟨|{G1} →  , {G2} →  |⟩|⟩
```

For example for class "f1" we have for each group the following dendrograms:

In[4]:=
```
clustersSingleDendrogramsReturn["f1"]
```

Out[4]=
```
⟨|{G1} →  ,
{G2} → {{-0.00413326, -0.0426122, -0.0424214, -0.091468, -0.080986, -0.118982, -0.131633,
-0.139847, -0.171527, -0.198047, -0.209967, -0.221144, -0.233244, -0.25001, -0.287256,
-0.283226, -0.313567, -0.350353, -0.341338, -0.389285} → LinearNegative_9}|⟩
```

We note that group {G2} is only one datapoint so no dendrogram plot was generated:

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In[5]:=
```
clustersSingleDendrogramsReturn["f1", {"G2"}]
```

Out[5]=
```
{{-0.00413326, -0.0426122, -0.0424214, -0.091468, -0.080986, -0.118982,
   -0.131633, -0.139847, -0.171527, -0.198047, -0.209967, -0.221144, -0.233244, -0.25001,
   -0.287256, -0.283226, -0.313567, -0.350353, -0.341338, -0.389285} → LinearNegative_9}
```

We note also that dendrogram plots are referenced by curly brackets arount text indexes.

SignificanceCriterion (1)

In[1]:=
```
Needs["MathIOmica`"]
```

SignificanceCriterion provides an option for which method to use for determining the number of clusters in the groupings.

We generate some data for classification:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
```

```
Method → "LombScargle"
```

Out[2]=
```
<|SpikeMax →
  <|SpikePositive_1 → {{0.231635, 0.127012, 0.371103, 0.3616, 0.39872, 0.137645, 0.212773, 0.252691,
      0.55995, 0.247282}, {0.970804, 0.0055172, -0.0971827, -0.0967522, 0.0837954, 0.0521942,
      -0.00301911, -0.058448, -0.0259389, -0.070911, 0.00208692, 0.0846819, 0.00299234,
      -0.0130132, 0.073597, -0.00610181, 0.0361755, -0.0415473, -0.0254373, 0.0578016}},
   SpikePositive_2 → {{0.176289, 0.343681, 0.115171, 0.312737, 0.233768, 0.314783, 0.225061,
      0.288792, 0.59804, 0.307076}, {0.980444, -0.0323017, 0.0260442, -0.0103456, -0.0133957,
      -0.0783444, -0.00372869, -0.0368195, -0.0496866, 0.0888213, 0.0742354, -0.0452147, -0.0841188,
      -0.0210654, -0.0214555, -0.0176604, -0.0325115, -0.0184703, -0.0360506, -0.0176605}},
   SpikePositive_3 → {{0.206626, 0.331126, 0.407373, 0.322197, 0.367522, 0.358736, 0.209549,
      0.165039, 0.456051, 0.187088}, {0.966022, 0.0465207, -0.0678872, 0.0227955, 0.0249703,
      -0.0381213, 0.0763162, 0.0577334, 0.0885493, -0.0205545, -0.0773964, -0.0414142, 0.00764708,
      -0.0429703, -0.0734319, -0.0627559, -0.0851024, 0.0786182, 0.0323381, -0.0812525}},
   SpikePositive_4 → {{0.208367, 0.22869, 0.35001, 0.218188, 0.170962, 0.230926, 0.318647,
      0.318595, 0.594315, 0.308816}, {0.978589, -0.0158801, 0.0237429, -0.0163171, -0.0718786,
      0.0317038, 0.0845922, 0.0298798, 0.0677049, -0.00119884, -0.0514771, 0.00655001,
      0.0105094, 0.053671, 0.084314, -0.030778, 0.0754205, 0.00973014, -0.0382212, 0.0386344}},
   SpikePositive_5 → {{0.315941, 0.277965, 0.461586, 0.179649, 0.173473, 0.285541, 0.252624,
      0.368818, 0.351872, 0.37722}, {0.964601, 0.00252704, 0.082767, 0.0116754, -0.10214,
      0.0733494, -0.00686185, -0.0318008, -0.102957, -0.0132254, -0.0809355, 0.0940556, 0.0134242,
      -0.0196314, -0.0472405, -0.0847583, -0.0453281, 0.0547669, 0.0636669, 0.0204922}},
   SpikePositive_6 → {{0.303594, 0.32678, 0.427135, 0.352759, 0.321742, 0.23242, 0.264962,
      0.204946, 0.417026, 0.224737}, {0.972137, 0.0556179, -0.0502547, -0.0774199, -0.0537787,
```

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```
    0.0640427, -0.043339, 0.00713312, 0.0535145, 0.0028891, -0.0712325, 0.0546772,
    0.0262392, 0.034552, 0.0100378, 0.06671, -0.0311377, 0.0858697, 0.0652283, 0.0666914}},
  SpikePositive_7 → {{0.451074, 0.220027, 0.181445, 0.243886, 0.116429, 0.253569, 0.236887,
    0.231252, 0.637766, 0.248047}, {0.97115, 0.00685532, 0.0859537, -0.0309878, -0.0146072,
    0.0960689, 0.0158916, -0.0697751, -0.045903, 0.00251557, -0.0547753, -0.0506728, -0.0617838,
    -0.0589158, -0.0149981, 0.0865538, 0.0413541, 0.0674612, -0.0605393, 0.0360118}},
  SpikePositive_8 → {{0.299258, 0.211383, 0.25382, 0.186362, 0.279739, 0.158062, 0.248256,
    0.198595, 0.721906, 0.202853}, {0.973994, -0.0571045, 0.0913812, 0.0319366, 0.0210366,
    0.022805, 0.0428367, 0.0953903, -0.0070739, -0.0560586, 0.0205246, -0.0646, -0.053091,
    -0.00949398, -0.00230283, -0.0324272, -0.0426894, 0.0686406, -0.0473281, 0.0792543}},
  SpikePositive_9 → {{0.231274, 0.247713, 0.302558, 0.307632, 0.18576, 0.181947, 0.260318,
    0.359891, 0.566735, 0.335983}, {0.981988, -0.0119843, 0.0242128, -0.0593673, -0.0513045,
    -0.00288677, -0.0447631, 0.0167196, 0.0619154, -0.00409621, -0.0511381, -0.0404097,
    0.0512361, 0.0308402, 0.0785498, -0.0713587, 0.0485374, 0.0115252, -0.0290708, -0.0158424}},
  SpikePositive_10 → {{0.258018, 0.224019, 0.182473, 0.268694, 0.266091, 0.115523, 0.260904,
    0.478683, 0.366807, 0.511707}, {0.966259, 0.0618121, 0.0515567, -0.0171071, 0.0626677,
    0.0284539, -0.0606364, 0.0793513, -0.00140559, 0.0596505, -0.00228256, 0.0888921,
    -0.0465762, 0.103608, 0.0462677, 0.0374834, 0.0910273, 0.0718944, 0.0384022, -0.0449021}},
  SpikePositive_11 → {{0.453975, 0.246393, 0.313281, 0.320948, 0.327868, 0.316362, 0.364356,
    0.262359, 0.242908, 0.252724}, {-0.0761151, -0.0781174, 0.963818, 0.0315869, -0.0664098,
    0.0128587, -0.0727258, 0.020553, -0.0345735, -0.0301584, -0.0221052, -0.084294, -0.102952,
    -0.0949217, -0.0753284, -0.0634776, 0.0131458, -0.0211067, 0.086401, 0.0279011}},
  SpikePositive_12 → {{0.344695, 0.293857, 0.357158, 0.351475, 0.362928, 0.293624, 0.316884,
    0.294833, 0.202022, 0.312491}, {-0.0770546, 0.0595143, 0.967192, 0.0927699, 0.0734907,
    0.0420414, 0.0195969, 0.0569099, -0.0708712, -0.0107643, 0.0320865, 0.0195686, -0.0952872,
    0.0946077, 0.0188549, 0.0779035, -0.00156154, 0.0556194, 0.0238589, 0.0314875}},
  SpikePositive_13 → {{0.210915, 0.115636, 0.509029, 0.388436, 0.414054, 0.405385, 0.211315,
    0.163372, 0.302395, 0.183261}, {-0.0960531, 0.0137381, 0.95477, -0.0409739, -0.0578675,
    -0.0837937, -0.0481146, 0.07087, 0.0896267, -0.0704387, -0.0734234, -0.0844348, -0.0581679,
    0.0754952, -0.0175571, -0.0374868, 0.0683292, 0.0754585, -0.0953164, 0.0620686}},
  SpikePositive_14 → {{0.202895, 0.196595, 0.269012, 0.580828, 0.470761, 0.267612, 0.335416,
    0.155713, 0.233105, 0.161663}, {-0.0140682, 0.0306125, 0.969459, 0.0627603, -0.0874352,
    0.0976857, 0.0957556, 0.00567254, 0.00745021, -0.0508928, 0.047163, -0.0157311, 0.0388849,
    0.0183307, -0.0394411, 0.0911511, 0.0748513, -0.050999, -0.0419827, -0.0434777}},
  SpikePositive_15 → {{0.240719, 0.271994, 0.274231, 0.182626, 0.453368, 0.462996, 0.188303,
    0.252183, 0.433109, 0.230161}, {0.0437529, -0.0198375, 0.961971, -0.0383272, -0.0164214,
    0.0573805, -0.0442233, -0.0964422, 0.103104, 0.0697833, -0.0955153, -0.0253095, 0.0967699,
    -0.0595282, 0.0176845, -0.0835667, 0.090835, -0.0153295, 0.0142298, 0.0431323}},
  SpikePositive_16 → {{0.0792822, 0.197749, 0.310438, 0.349581, 0.319285, 0.465525, 0.192929,
    0.3665, 0.353948, 0.347205}, {-0.048953, -0.0633941, 0.972613, -0.0864037, -0.0867341,
    -0.0376291, 0.0472286, 0.00183335, 0.0379066, 0.0459666, -0.0182835, 0.07046, -0.010278,
    -0.0445743, 0.0713467, -0.0690639, 0.0000707509, -0.0715315, 0.012247, -0.0538743}},
  SpikePositive_17 → {{0.2684, 0.155787, 0.263448, 0.318696, 0.384926, 0.2544, 0.321351,
    0.382546, 0.339009, 0.394078}, {0.0328151, -0.0393512, 0.978823, 0.0574934, -0.00531358,
    -0.0745638, 0.0510764, 0.0553694, -0.0122667, 0.0532257, -0.0568207, -0.0375045, -0.0186179,
    -0.00473004, -0.0537367, -0.0108755, 0.0142541, 0.0785825, 0.0246968, -0.0820348}},
  SpikePositive_18 → {{0.309113, 0.488772, 0.309683, 0.240091, 0.328227, 0.284261, 0.225828,
    0.285017, 0.319991, 0.298058}, {-0.0397884, 0.0349372, 0.97753, 0.0689563, 0.0837776,
    -0.00199056, -0.0175822, -0.0888026, -0.0191219, 0.0148956, -0.0375517, 0.035255,
    0.0472028, 0.070622, 0.00879753, 0.0369919, 0.00732228, 0.0256336, 0.0473194, 0.0825078}},
  SpikePositive_19 → {{0.181854, 0.111471, 0.246175, 0.0509372, 0.271526, 0.235879, 0.31936,
    0.494427, 0.409311, 0.497953}, {0.0886066, -0.0891141, 0.955765, -0.0955824, 0.0555432,
    -0.0254482, -0.0453141, 0.0365502, 0.043223, 0.0979586, -0.0799527, -0.0839224, -0.0441189,
    0.0990981, 0.00497859, -0.0659274, 0.0117601, 0.0519556, 0.0990019, -0.028022}},
  SpikePositive_20 → {{0.249001, 0.350206, 0.206078, 0.267233, 0.37948, 0.326706, 0.478972,
    0.261302, 0.268783, 0.284243}, {-0.00921595, -0.075659, 0.963561, 0.0581728, -0.0549483,
    0.0557199, -0.0860652, -0.0351729, -0.0945953, 0.00327257, -0.0444181, 0.0111816, 0.0839352,
    0.088854, -0.0269132, 0.0921451, -0.00133634, 0.0817685, 0.0598814, 0.0458451}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.27641, 0.265784, 0.336803, 0.434557, 0.304165, 0.297379,
    0.117923, 0.226748, 0.516693, 0.193489}, {-0.968766, 0.00503028, 0.0632635, -0.0306565,
    -0.0119271, 0.0502831, 0.0267222, -0.0118103, 0.0862596, -0.0381405, -0.070072, 0.0413867,
    -0.0826555, -0.0485017, -0.0820665, 0.0762073, 0.0255585, -0.0862917, 0.00861934, -0.0870756}},
  SpikeNegative_2 → {{0.165716, 0.187494, 0.212016, 0.185989, 0.452357, 0.264026, 0.484212,
    0.274831, 0.421859, 0.309106}, {-0.968043, 0.0329819, 0.0778328, -0.037568, 0.0733535,
    0.05902, 0.0818742, -0.0303037, 0.0254041, 0.0688082, -0.00843283, -0.0586369, 0.0574702,
    -0.0655312, 0.0450836, -0.0273778, 0.047317, 0.0630449, 0.0859084, 0.0706224}},
```

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```
SpikeNegative_3 → {{0.0867231, 0.223293, 0.138282, 0.237292, 0.345876, 0.254484, 0.342315,
   0.399258, 0.501242, 0.393659}, {-0.970227, 0.0681026, -0.0132683, -0.0426283, 0.0400495,
   0.0764913, 0.0750908, -0.0845037, 0.0111491, -0.0424036, -0.0775258, 0.00506349, 0.00502102,
   -0.0672474, -0.0358614, 0.0479507, 0.0255814, 0.0856381, 0.0813343, 0.0331612}},
SpikeNegative_4 → {{0.220706, 0.189027, 0.219765, 0.17183, 0.372092, 0.455154, 0.221214,
   0.342594, 0.4632, 0.333552}, {-0.973004, 0.00160696, 0.0445183, -0.0214869, 0.0127617,
   0.0683137, -0.03778, -0.0581259, -0.0318291, 0.00998972, 0.0681251, 0.0209424, -0.0913193,
   0.0312682, -0.0853618, -0.0602592, -0.0757207, 0.0269143, -0.0169352, 0.0894932}},
SpikeNegative_5 → {{0.375082, 0.138097, 0.310382, 0.107296, 0.26979, 0.135846, 0.297932,
   0.350809, 0.525967, 0.390745}, {-0.966082, -0.0913418, -0.098272, 0.00112055, -0.0546253,
   -0.0735305, -0.0192325, -0.0380109, 0.0201766, 0.0887577, 0.0939298, -0.0811833, 0.0578012,
   -0.00192415, 0.0666636, -0.0229404, -0.0241527, 0.0102525, 0.0701629, 0.0292208}},
SpikeNegative_6 → {{0.112942, 0.104542, 0.113356, 0.235771, 0.416916, 0.301821, 0.197358,
   0.245157, 0.68636, 0.269852}, {-0.969824, 0.0955812, -0.0150389, -0.00607449, -0.0329995,
   0.0842598, -0.0602328, -0.0326223, 0.0443762, -0.00658482, -0.0623925, 0.0151555,
   0.0483257, -0.0177022, -0.0961048, -0.0698866, 0.087463, 0.0492988, 0.0629934, 0.0144423}},
SpikeNegative_7 → {{0.215632, 0.14079, 0.272384, 0.24513, 0.248631, 0.222984, 0.238852,
   0.435917, 0.515163, 0.4188}, {-0.975412, 0.0760954, -0.0738481, -0.0063881, -0.000970129,
   -0.0641479, -0.0757353, -0.0510591, 0.0722788, -0.0019098, -0.011396, 0.0349746, 0.0233094,
   -0.00248382, -0.0883477, 0.0779107, -0.0352241, -0.0284149, -0.0336371, 0.0253519}},
SpikeNegative_8 → {{0.226309, 0.083853, 0.116152, 0.324388, 0.238886, 0.241791, 0.326551,
   0.405638, 0.510302, 0.419426}, {-0.976303, 0.0294086, -0.0905423, 0.0126873, -0.0766744,
   -0.0717946, 0.0900117, 0.0129382, 0.0271543, -0.0264695, 0.0256822, 0.0198201, -0.0230559,
   -0.0383159, -0.0530544, -0.0734999, 0.0207356, 0.05819, 0.00518505, 0.0418962}},
SpikeNegative_9 → {{0.296257, 0.100687, 0.121596, 0.261682, 0.237137, 0.230485, 0.154644,
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   -0.064208, -0.0705883, -0.0688746, -0.0256698, 0.0314167, 0.0413442, -0.0420767}},
SpikeNegative_10 → {{0.200649, 0.340604, 0.216585, 0.189576, 0.177364, 0.306337, 0.288681,
   0.44044, 0.412865, 0.433357}, {-0.966496, -0.0791238, -0.0933902, -0.0200744, 0.0401185,
   0.0368338, 0.073441, -0.105224, -0.0484407, -0.0964378, 0.0323598, 0.0446077, -0.0456092,
   -0.0460905, 0.0164798, -0.00900904, -0.052784, 0.0845029, 0.0421583, -0.0110827}},
SpikeNegative_11 → {{0.308665, 0.304411, 0.343321, 0.182374, 0.418419, 0.376387, 0.286245,
   0.296485, 0.28461, 0.305527}, {0.0765649, 0.0526624, -0.964994, -0.0681373, -0.091813,
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   -0.0284843, 0.0963662, 0.0207142, -0.0446878, -0.0217161, -0.0260451, -0.000906771}},
SpikeNegative_12 → {{0.259531, 0.401245, 0.318829, 0.263249, 0.131649, 0.34113, 0.43843,
   0.238508, 0.382147, 0.268048}, {-0.013268, -0.0194088, -0.973121, -0.0212022, -0.0943601,
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   -0.0741038, 0.013993, -0.0316564, 0.0806968, -0.0234642, -0.00482436, -0.0589265}},
SpikeNegative_13 → {{0.204474, 0.401143, 0.251676, 0.317423, 0.386495, 0.337897, 0.315231,
   0.295218, 0.308894, 0.296115}, {-0.0167688, 0.0029019, -0.988145, 0.0202247, 0.024768,
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   -0.055727, 0.00616158, 0.0387314, -0.0299293, 0.0140238, 0.0342016, -0.0274436}},
SpikeNegative_14 → {{0.231099, 0.3124, 0.202821, 0.296848, 0.348054, 0.205361, 0.314164,
   0.25676, 0.556635, 0.286289}, {-0.0590047, -0.0401618, -0.971711, 0.0696084, -0.0375952,
   0.0689487, 0.0185439, 0.0627442, -0.0000215089, 0.0715985, -0.0932229, 0.0327478, -0.0160633,
   -0.0575975, 0.0778759, -0.0130651, -0.0751085, -0.0353268, 0.0459743, -0.0410668}},
SpikeNegative_15 → {{0.34604, 0.316156, 0.269344, 0.27722, 0.294052, 0.427924, 0.266233,
   0.266372, 0.386667, 0.264524}, {-0.017594, 0.0878457, -0.978045, -0.0384094, -0.0202168,
   -0.0690458, 0.0665935, 0.0196486, -0.000568922, 0.0846965, 0.0824445, 0.00860091, -0.000795724,
   -0.0179418, -0.00927521, 0.0564372, -0.0414626, 0.0208256, 0.0211178, -0.060755}},
SpikeNegative_16 → {{0.0911008, 0.449867, 0.134176, 0.368068, 0.171205, 0.291728, 0.435205,
   0.306625, 0.37483, 0.312262}, {-0.0514598, 0.0158602, -0.963925, 0.0703626, 0.0496291,
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   0.0378208, 0.0353802, -0.0494164, 0.0538654, 0.0892101, -0.0227273, 0.0716227}},
SpikeNegative_17 → {{0.162382, 0.264485, 0.4069, 0.364363, 0.360254, 0.316526, 0.285059,
   0.262843, 0.406722, 0.244155}, {-0.0847169, 0.0412444, -0.975128, -0.0560307, 0.0816705,
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   0.052153, -0.0533618, 0.0216582, -0.0620018, 0.0569594, 0.056589, 0.0552481}},
SpikeNegative_18 → {{0.315463, 0.212757, 0.209287, 0.39018, 0.318533, 0.414943, 0.324741,
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   -0.00380975, 0.0280319, 0.0041074, 0.0059955, -0.0678945, 0.0815715, 0.0398886}},
SpikeNegative_19 → {{0.460392, 0.270747, 0.348778, 0.278732, 0.32876, 0.23303, 0.237211,
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    SpikeNegative_20 → {{0.314522, 0.307708, 0.182626, 0.355532, 0.170148, 0.107149, 0.208503,
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  f1 → <|LinearPositive_1 → {{0.983395, 0.171368, 0.0317627, 0.00262773, 0.00152459, 0.0106471,
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    LinearPositive_2 → {{0.983763, 0.167707, 0.03293, 0.00218543, 0.00157278, 0.0106994,
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      0.243059, 0.260512, 0.280832, 0.297588, 0.316591, 0.336284, 0.353489, 0.373157}},
    LinearPositive_3 → {{0.9851, 0.159938, 0.0331717, 0.00180471, 0.00171922, 0.00924119,
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      0.244401, 0.259932, 0.27977, 0.298984, 0.315575, 0.337001, 0.356379, 0.372256}},
    LinearPositive_4 → {{0.98444, 0.16465, 0.0301371, 0.00201931, 0.00189418,
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    LinearPositive_5 → {{0.984093, 0.166093, 0.0351717, 0.00266431, 0.0020133, 0.0110125,
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    LinearPositive_6 → {{0.984121, 0.16606, 0.0311294, 0.00236946, 0.00163533, 0.0116212,
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    LinearPositive_7 → {{0.985086, 0.159969, 0.0322341, 0.00278862, 0.00189372, 0.011764,
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    LinearPositive_8 → {{0.984739, 0.16237, 0.0322579, 0.0016883, 0.00174199, 0.0096794,
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    LinearPositive_9 → {{0.984274, 0.165567, 0.0332257, 0.00186419, 0.00154652, 0.0106616,
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    LinearPositive_11 → {{0.983789, 0.163784, 0.04855, 0.00483351, 0.00249784,
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      0.200193, 0.225749, 0.25297, 0.256093, 0.28086, 0.293337, 0.324011, 0.343363, 0.354379, 0.370262}},
    LinearPositive_12 → {{0.983342, 0.169374, 0.0386388, 0.00592099, 0.000506119, 0.00695176,
      0.0194786, 0.0288271, 0.0218478, 0.0329801}, {0.0230674, 0.0309986, 0.0567725, 0.0826395,
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      0.237742, 0.261863, 0.276127, 0.298845, 0.311341, 0.342747, 0.355564, 0.370487}},
    LinearPositive_13 → {{0.985387, 0.156092, 0.0455891, 0.00294201, 0.00104763, 0.0101187,
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      0.0672196, 0.0934525, 0.110196, 0.137305, 0.151159, 0.16303, 0.188981, 0.212172,
      0.22911, 0.251088, 0.264298, 0.280635, 0.289515, 0.312502, 0.336603, 0.359231, 0.366}},
    LinearPositive_14 → {{0.985666, 0.158341, 0.0325252, 0.0049885, 0.00568011, 0.00710732,
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    LinearPositive_15 → {{0.984009, 0.163165, 0.051888, 0.00132387, 0.00169336,
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LinearPositive_16 → {{0.983459, 0.169823, 0.0280156, 0.00372544, 0.000587821, 0.0155963,
   0.0219102, 0.0296009, 0.0201204, 0.0341303}, {0.0176596, 0.0425456, 0.0558716, 0.0783394,
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   0.235032, 0.265369, 0.283165, 0.298268, 0.318254, 0.339499, 0.355184, 0.369008}},
LinearPositive_17 → {{0.984712, 0.163104, 0.0266023, 0.000480986, 0.00023573, 0.0118453,
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   0.23664, 0.256378, 0.282624, 0.304448, 0.318006, 0.329102, 0.354719, 0.373994}},
LinearPositive_18 → {{0.982903, 0.173119, 0.0215078, 0.000944607, 0.0010796, 0.00844423,
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LinearPositive_19 → {{0.98417, 0.160566, 0.0470687, 0.00555796, 0.000768027, 0.0159719,
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LinearPositive_20 → {{0.982094, 0.173623, 0.0382673, 0.00275342, 0.00706849,
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LinearNegative_1 → {{0.979052, 0.195975, 0.031001, 0.00577881, 0.00365944, 0.00918715,
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   -0.229274, -0.263476, -0.274706, -0.310673, -0.319475, -0.328303, -0.361832, -0.360014}},
LinearNegative_2 → {{0.985694, 0.157175, 0.0224155, 0.00242781, 0.00562126, 0.0222114,
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LinearNegative_3 → {{0.986881, 0.147218, 0.0271477, 0.00239579, 0.000474715, 0.00677325,
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LinearNegative_4 → {{0.981082, 0.178395, 0.0531702, 0.00424393, 0.00354503, 0.00528428,
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LinearNegative_5 → {{0.974941, 0.211714, 0.0418163, 0.0000829623, 0.0105382, 0.0097203,
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   -0.232279, -0.245878, -0.272715, -0.310174, -0.33096, -0.322036, -0.370479, -0.364229}},
LinearNegative_6 → {{0.97939, 0.191159, 0.0255597, 0.0171374, 0.00516641, 0.00365737,
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LinearNegative_7 → {{0.985959, 0.146543, 0.0200263, 0.00161163, 0.00821057, 0.00641485,
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LinearNegative_8 → {{0.984301, 0.158014, 0.0199399, 0.0100077, 0.00739794, 0.01659, 0.0328648,
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   -0.254093, -0.272685, -0.297273, -0.282784, -0.326937, -0.339581, -0.338273, -0.364391}},
LinearNegative_9 → {{0.976364, 0.194496, 0.0206728, 0.00300634, 0.00273546, 0.00802011,
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   -0.235321, -0.274441, -0.291326, -0.310988, -0.298289, -0.342785, -0.336256, -0.349795}},
LinearNegative_10 → {{0.98715, 0.146513, 0.032857, 0.000144075, 0.00154595, 0.0103906,
   0.0282788, 0.0286816, 0.00794871, 0.0345387}, {-0.00743748, -0.0226851, -0.0465315, -0.0614444,
   -0.0810216, -0.102901, -0.133547, -0.143944, -0.16039, -0.175868, -0.207807, -0.231897,
   -0.253787, -0.252663, -0.296139, -0.296924, -0.328268, -0.326251, -0.349497, -0.379093}},
LinearNegative_11 → {{0.979931, 0.189367, 0.0372188, 0.00120984, 0.000905268, 0.00735488,
   0.0212743, 0.0272784, 0.0139661, 0.0322827}, {-0.0153178, -0.0290084, -0.059707, -0.0675303,
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   -0.242005, -0.251747, -0.283057, -0.296033, -0.310792, -0.336772, -0.362336, -0.37473}},
LinearNegative_12 → {{0.987323, 0.14133, 0.0379758, 0.00209893, 0.00150295, 0.0145111,
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    -0.0965112, -0.114964, -0.123905, -0.143963, -0.162924, -0.183681, -0.210142, -0.226477,
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  LinearNegative_13 → {{0.985232, 0.156402, 0.0378932, 0.0015253, 0.00311556, 0.0220663,
    0.030836, 0.0260404, 0.0182709, 0.030949}, {-0.0102606, -0.0423886, -0.0590648, -0.0674797,
    -0.0968307, -0.109291, -0.131952, -0.142641, -0.16124, -0.183254, -0.204839, -0.229696,
    -0.233433, -0.266759, -0.28289, -0.289291, -0.325332, -0.34424, -0.353007, -0.371961}},
  LinearNegative_14 → {{0.982878, 0.172687, 0.0310814, 0.0018436, 0.00104531, 0.0170575,
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    -0.235152, -0.263953, -0.277205, -0.30107, -0.317182, -0.341816, -0.353991, -0.378665}},
  LinearNegative_15 → {{0.984317, 0.167528, 0.0338548, 0.00474701, 0.000906504, 0.00857942,
    0.016972, 0.0237806, 0.0133826, 0.0279067}, {-0.0203359, -0.028689, -0.0617725, -0.0743195,
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    -0.242096, -0.263054, -0.284686, -0.302238, -0.317155, -0.341793, -0.354689, -0.363019}},
  LinearNegative_16 → {{0.984826, 0.158405, 0.0398812, 0.00171686, 0.00295837, 0.0126547,
    0.0182113, 0.0342821, 0.0144556, 0.0393346}, {-0.024565, -0.0443067, -0.0605353, -0.0660784,
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  LinearNegative_17 → {{0.987088, 0.151349, 0.0407029, 0.00511773, 0.0014826, 0.00353701,
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  LinearNegative_18 → {{0.983828, 0.168063, 0.0237763, 0.00611178, 0.00049456, 0.00946036,
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    -0.237633, -0.265284, -0.286574, -0.300185, -0.311647, -0.337487, -0.349791, -0.368213}},
  LinearNegative_19 → {{0.984309, 0.163371, 0.0378626, 0.00377453, 0.003015, 0.00685889,
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    -0.249193, -0.268078, -0.275472, -0.300157, -0.310785, -0.340962, -0.357969, -0.367547}},
  LinearNegative_20 → {{0.982749, 0.174775, 0.0394341, 0.00505765, 0.00123465, 0.0117571,
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    -0.244503, -0.25481, -0.283506, -0.290803, -0.321846, -0.339833, -0.362359, -0.375558}}|>,
f3 → <|Sinusoidal3_21 → {{0.0033914, 0.0713904, 0.992371, 0.0874491, 0.0381688, 0.0201349,
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    0.296436, 0.252683, -0.00503455, -0.252594, -0.300926, -0.0976967, 0.184563, 0.320317}},
  Sinusoidal3_22 → {{0.00296815, 0.0777505, 0.992243, 0.0864319, 0.0346243, 0.0169382,
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    0.300348, 0.259271, 0.00439223, -0.256258, -0.301514, -0.0983207, 0.180466, 0.311007}},
  Sinusoidal3_23 → {{0.00312424, 0.0713375, 0.992333, 0.0882085, 0.0388388, 0.0187502,
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    0.301917, 0.251794, -0.00051312, -0.257347, -0.299051, -0.0970992, 0.183589, 0.322599}},
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  Sinusoidal3_25 → {{0.00275734, 0.0732189, 0.992479, 0.0861988, 0.0367625, 0.0186967,
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  Sinusoidal3_26 → {{0.00350993, 0.070707, 0.992182, 0.0918069, 0.0353893, 0.0192547, 0.00996283,
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  Sinusoidal3_27 → {{0.00424635, 0.0734029, 0.992613, 0.0848938, 0.0363472, 0.0166925, 0.00915735,
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    0.300003, 0.253819, -0.00497814, -0.255747, -0.307919, -0.101095, 0.182152, 0.312448}},
  Sinusoidal3_28 → {{0.00360476, 0.0728697, 0.992385, 0.088125, 0.0365882, 0.0178232,
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    0.298817, 0.261922, -0.00110191, -0.258941, -0.299818, -0.099765, 0.192202, 0.313364}},
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    Sinusoidal3_29 → {{0.00350002, 0.0712086, 0.992745, 0.0852598, 0.0352607, 0.0203947,
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       0.301652, 0.256014, -0.00436728, -0.25838, -0.30256, -0.0995602, 0.186079, 0.310085}},
    Sinusoidal3_30 → {{0.00296397, 0.0703285, 0.992923, 0.0830484, 0.0371613, 0.0170387,
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f5 → <|Sinusoidal2_11 → {{0.00216072, 0.0106675, 0.0285168, 0.100569, 0.930626, 0.348248,
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    Sinusoidal2_12 → {{0.00229902, 0.00951773, 0.0300892, 0.0930584, 0.931662, 0.347653,
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    Sinusoidal2_13 → {{0.00212951, 0.0127109, 0.0311251, 0.0934516, 0.936571, 0.333555,
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    Sinusoidal2_14 → {{0.00227279, 0.0114952, 0.0305116, 0.0947886, 0.934038, 0.340585, 0.0284085,
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    Sinusoidal2_15 → {{0.0016141, 0.0125358, 0.0319882, 0.0939057, 0.932451, 0.344847, 0.0307151,
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       0.261056, 0.101913, -0.310916, 0.0987814, 0.261798, -0.259863, -0.0929558, 0.317805}},
    Sinusoidal2_16 → {{0.00219775, 0.00961946, 0.0299144, 0.0944737, 0.930777, 0.349245, 0.0310084,
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    Sinusoidal2_17 → {{0.00188652, 0.010426, 0.0273486, 0.0873316, 0.932507, 0.346793, 0.0286597,
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    Sinusoidal2_18 → {{0.00251718, 0.0112501, 0.0318539, 0.0946148, 0.936315, 0.333917, 0.0277148,
       0.00373048, 0.0305114, 0.00106039}, {-0.102062, -0.259074, 0.260281, 0.0993512,
       -0.317038, 0.0949568, 0.258768, -0.255415, -0.0954669, 0.31808, -0.0957705, -0.251787,
       0.253411, 0.101657, -0.313939, 0.0954859, 0.254183, -0.249981, -0.101134, 0.317345}},
    Sinusoidal2_19 → {{0.0017472, 0.0110449, 0.0298418, 0.0876281, 0.935393, 0.338708, 0.0264486,
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       0.25912, 0.103389, -0.316074, 0.103423, 0.250469, -0.251677, -0.103134, 0.315807}},
    Sinusoidal2_20 → {{0.00170956, 0.0108259, 0.026457, 0.0887948, 0.931885, 0.34821, 0.0280074,
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f6 → <|Sinusoidal1_1 → {{0.0042858, 0.00989316, 0.0136987, 0.0381234, 0.0688449, 0.98588,
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       -0.318108, 0.247014, -0.0196663, -0.26661, 0.293723, -0.122443, -0.184386, 0.317792}},
    Sinusoidal1_2 → {{0.00114266, 0.0107328, 0.0114304, 0.0407167, 0.110262, 0.989198, 0.0826316,
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    Sinusoidal1_3 → {{0.000442851, 0.010943, 0.0164297, 0.0357659, 0.104933, 0.988327, 0.100189,
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       -0.0217788, 0.259701, -0.334103, 0.0970165, 0.171653, -0.332377, 0.165053, 0.0874093,
       -0.277286, 0.268213, -0.0227175, -0.254034, 0.297574, -0.0838384, -0.215818, 0.306517}},
    Sinusoidal1_4 → {{0.00256177, 0.00989642, 0.0159148, 0.04357, 0.106322, 0.982907, 0.141327,
       0.00400222, 0.0184448, 0.00173337}, {-0.174485, -0.0866047, 0.299765, -0.222189,
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       -0.277782, 0.271995, -0.0297964, -0.248169, 0.305539, -0.0958841, -0.205876, 0.292028}},
    Sinusoidal1_5 → {{0.0016597, 0.00788244, 0.0234746, 0.0389518, 0.113411, 0.985669, 0.114833,
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    -0.275391, 0.256188, -0.0150063, -0.243249, 0.298405, -0.123482, -0.167882, 0.300152}},
Sinusoidal1_6 → {{0.0001706, 0.00267387, 0.0237978, 0.0389141, 0.0885118, 0.989287, 0.103875,
    0.00665206, 0.0234474, 0.00243147}, {-0.191632, -0.127898, 0.286087, -0.265546,
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    -0.312101, 0.229346, 0.013662, -0.230263, 0.332781, -0.106601, -0.169797, 0.327467}},
Sinusoidal1_7 → {{0.00634386, 0.0111713, 0.0195865, 0.0451848, 0.0914914, 0.988704, 0.104522,
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Sinusoidal1_8 → {{0.00120642, 0.012149, 0.0147163, 0.036543, 0.0922969, 0.98871, 0.106805,
    0.00362442, 0.0284572, 0.00135586}, {-0.166526, -0.0776441, 0.279207, -0.273491,
    0.00960522, 0.248772, -0.322097, 0.066154, 0.171174, -0.330402, 0.15361, 0.123925,
    -0.317938, 0.259866, -0.0149687, -0.245059, 0.285803, -0.117604, -0.195533, 0.321442}},
Sinusoidal1_9 → {{0.00132163, 0.00569102, 0.0272635, 0.0403651, 0.0898484, 0.990641,
    0.0878248, 0.00487265, 0.0202472, 0.00204088}, {-0.181136, -0.0704119, 0.28558, -0.24468,
    0.0191615, 0.250639, -0.315567, 0.0846315, 0.179088, -0.307336, 0.205238, 0.0786919,
    -0.318952, 0.243541, 0.0236864, -0.220152, 0.323026, -0.0950151, -0.201582, 0.334594}},
Sinusoidal1_10 → {{0.00251832, 0.0096177, 0.0160585, 0.0300419, 0.0682723, 0.986822, 0.13909,
    0.00482743, 0.0298058, 0.00200483}, {-0.153291, -0.11914, 0.290252, -0.238204, 0.0170784,
    0.244772, -0.288776, 0.0743898, 0.205828, -0.343281, 0.165507, 0.122183, -0.321543,
    0.263098, 0.00774918, -0.258717, 0.294899, -0.114232, -0.165818, 0.320227}}|>|>
```

The default SignificanceCriterion is "Silhouette":

In[3]:=
```
clustersSingle = TimeSeriesSingleClusters[classification1, SignificanceCriterion → "Silhouette"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[3]=
```
<|SpikeMax → <|Cluster → Cluster[Cluster[ ··· 1 ··· ],
    Cluster[{-0.0140682, 0.0306125, ··· 16 ···, -0.0419827, -0.0434777} → SpikePositive_14, ··· 3 ···, 1],
    ··· 18 ···, 18, 2], ··· 1 ···, ··· 1 ···|>, ··· 5 ···|>
```

large output | show less | show more | show all | set size limit...

In[4]:=
```
Query[All, "GroupAssociations" /* Keys]@clustersSingle
```

Out[4]=
```
<|SpikeMax → {G1, G2}, SpikeMin → {G1, G2}, f1 → {G1, G2}, f3 → {G1, G2}, f5 → {G1, G2}, f6 → {G1, G2}|>
```

In[5]:=
```
clustersSingleGap = TimeSeriesSingleClusters[classification1, SignificanceCriterion → "Gap"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

General::stop : Further output of Agglomerate::ties will be suppressed during this calculation. ≫

Out[5]=
```
<|SpikeMax → <|Cluster → Cluster[Cluster[ ··· 1 ··· ],
    Cluster[{-0.0140682, 0.0306125, ··· 16 ···, -0.0419827, -0.0434777} → SpikePositive_14, ··· 3 ···, 1],
    ··· 18 ···, 18, 2], ··· 1 ···, ··· 1 ···|>, ··· 5 ···|>
```

large output | show less | show more | show all | set size limit...

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We can see that the number of groups generated is different:

```
In[6]:= Query[All, "GroupAssociations" /* Keys]@clustersSingleGap
Out[6]= <|SpikeMax → {G1}, SpikeMin → {G1, G2}, f1 → {G1, G2}, f3 → {G1}, f5 → {G1}, f6 → {G1}|>
```

SingleAssociationLabel (1)

```
In[1]:= Needs["MathIOmica`"]
```

SingleAssociationLabel provides an option for what to label the class if a single class is provided as input in the form of a list. The default label is "1".

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
  timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>]
  Method → "LombScargle"
Out[2]= <|SpikeMax →
  <|SpikePositive_1 → {{0.260388, 0.245711, 0.150891, 0.297354, 0.342784, 0.178015, 0.301023, 0.194064,
      0.662492, 0.210418}, {0.984595, 0.0426538, 0.0179441, -0.0228628, 0.0250083, -0.0278621,
      -0.0652766, -0.0604749, 0.0729085, -0.0203339, 0.026914, 0.0384599, -0.00443374,
      0.0214493, 0.0470012, 0.0542644, 0.000931502, -0.0266604, -0.0612261, 0.0237265}},
   SpikePositive_2 → {{0.258197, 0.313229, 0.283166, 0.376839, 0.255183, 0.29414, 0.129824,
      0.163721, 0.629143, 0.148033}, {0.970907, -0.00593115, 0.0210836, -0.058253, 0.0015684,
      -0.0431886, -0.0209517, -0.097558, 0.0191591, -0.000431375, -0.00686202, -0.0594855,
      0.0716292, -0.0952797, 0.0536522, -0.063791, -0.0974441, 0.0173567, 0.0563725, 0.0596441}},
   SpikePositive_3 → {{0.278888, 0.229765, 0.292629, 0.525801, 0.234082, 0.285231, 0.380042,
      0.196092, 0.371749, 0.223829}, {0.966576, 0.0396294, -0.0684005, 0.0197313, 0.0649133,
      -0.00424926, -0.0689057, -0.0837356, 0.0322856, -0.020455, -0.0225326, -0.0600544, 0.0082849,
      0.0941703, -0.0974221, -0.0422418, -0.0263268, 0.0443156, 0.0974553, -0.0718231}},
   SpikePositive_4 → {{0.134377, 0.160499, 0.210143, 0.369042, 0.211988, 0.321542, 0.253611,
      0.314417, 0.591107, 0.338997}, {0.971727, -0.0596889, 0.0474448, -0.0640848, -0.000744131,
      0.0568001, 0.0606394, -0.0352061, 0.0621654, 0.0802062, -0.0349508, 0.0319642, -0.00523245,
      0.044493, 0.0821664, 0.0731019, -0.0532013, -0.0455357, 0.0520489, 0.0585355}},
   SpikePositive_5 → {{0.213386, 0.146304, 0.180393, 0.2751, 0.372654, 0.103536, 0.262599,
      0.202151, 0.7169, 0.226894}, {0.957834, -0.0838027, -0.0202768, -0.0447831, 0.0898779,
      -0.0260558, -0.0909962, 0.0393741, 0.0762775, -0.0946617, -0.0849301, -0.0512037, -0.0799125,
      0.0210224, -0.0376881, -0.0060933, -0.0535727, -0.0547708, -0.0976687, 0.07886}},
   SpikePositive_6 → {{0.292532, 0.224272, 0.28103, 0.331868, 0.280526, 0.120558, 0.124022,
      0.320145, 0.59204, 0.336747}, {0.973177, -0.0143179, 0.017454, -0.0815008, 0.0640615,
      -0.0718526, -0.020035, 0.0468446, -0.0351388, -0.026056, -0.0783309, -0.0574767, -0.0713074,
      0.0296903, 0.0391121, -0.0842894, -0.0214224, 0.0842498, -0.00426514, -0.0195874}},
   SpikePositive_7 → {{0.237606, 0.24978, 0.196464, 0.22107, 0.217644, 0.207519, 0.148806,
      0.502634, 0.415638, 0.505678}, {0.961868, -0.0121292, 0.0454807, -0.0987756, 0.00861658,
      0.0563813, 0.0195099, 0.0702466, -0.0892035, 0.0811513, -0.0577825, 0.0549826, -0.0791978,
```

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```
    -0.0619687, 0.0176499, 0.0675396, 0.083561, -0.0549534, 0.0268929, 0.0874893}},
  SpikePositive_8 → {{0.292096, 0.240631, 0.380341, 0.438396, 0.329456, 0.15914, 0.354918,
    0.264993, 0.344313, 0.267059}, {0.970565, 0.0563423, -0.0356883, -0.0918923, -0.0354868,
    0.0814418, -0.0590716, 0.0424911, -0.082389, -0.0730024, 0.0344587, -0.0578783, -0.0782079,
    0.00597631, 0.00796937, -0.00564963, -0.0759616, -0.0188232, 0.0536684, 0.00422988}},
  SpikePositive_9 → {{0.211622, 0.201214, 0.22236, 0.432351, 0.174577, 0.195114, 0.173965,
    0.354716, 0.579695, 0.343042}, {0.966423, -0.0674757, 0.0554647, -0.0432617, 0.0597318,
    0.0312359, -0.0146744, -0.101786, -0.0521611, 0.0758959, 0.0712873, 0.0182951,
    0.0242038, 0.0207882, 0.102946, -0.0851805, 0.0231602, 0.0501532, 0.0735243, 0.0133773}},
  SpikePositive_10 → {{0.130535, 0.130824, 0.195574, 0.216103, 0.241791, 0.352877, 0.684441,
    0.206417, 0.371119, 0.221617}, {0.96379, -0.0948729, -0.0252853, 0.0827415, -0.0532786,
    0.0877364, 0.0347807, 0.0299562, 0.0698768, -0.0707597, 0.0516924, -0.0689011, 0.00595017,
    0.0754929, -0.0433978, 0.0682848, 0.0278066, -0.0330652, 0.0622196, -0.0815615}},
  SpikePositive_11 → {{0.196024, 0.25445, 0.429421, 0.58272, 0.256495, 0.370549, 0.145442,
    0.181022, 0.296787, 0.166626}, {0.00840957, 0.0853478, 0.964152, -0.0619487, -0.0761645,
    -0.0371389, 0.0267932, 0.0773386, -0.000715143, -0.0403987, -0.00252004, 0.0520121,
    -0.0283832, -0.0640981, 0.0813266, -0.0655443, 0.0510528, -0.0833161, -0.0978328, 0.077786}},
  SpikePositive_12 → {{0.19224, 0.139094, 0.327675, 0.12945, 0.394882, 0.398754, 0.408241,
    0.260988, 0.432161, 0.288258}, {0.0500355, -0.0685108, 0.975847, -0.0570955, -0.0412712,
    0.0755937, 0.0204554, 0.0170235, 0.0554969, 0.0920522, -0.0136969, -0.0725248,
    -0.0180233, 0.0342937, 0.01804, 0.016408, -0.0746403, 0.054622, -0.00722388, 0.0378922}},
  SpikePositive_13 → {{0.244514, 0.139541, 0.272318, 0.301463, 0.33181, 0.525157, 0.477406,
    0.213356, 0.206334, 0.23196}, {-0.0432619, -0.0325615, 0.972197, 0.0255384, -0.0749987,
    0.101228, -0.0550282, 0.0577603, 0.0748688, -0.0624347, -0.0131491, -0.0213904, -0.0596143,
    0.0307112, -0.0564378, 0.0196663, -0.0250186, 0.0728887, 0.0200498, -0.0668496}},
  SpikePositive_14 → {{0.405008, 0.343741, 0.223641, 0.419721, 0.300941, 0.174706, 0.295623,
    0.229116, 0.426941, 0.219947}, {0.0558479, 0.0585074, 0.975087, 0.059428, 0.0865757,
    -0.0195558, 0.0437175, -0.0121055, -0.059396, 0.00279565, -0.00467662, -0.0163185, 0.0921236,
    -0.0810352, -0.00573544, 0.0107053, 0.0954525, -0.00134351, -0.000141434, 0.0325192}},
  SpikePositive_15 → {{0.324818, 0.313595, 0.424905, 0.362429, 0.289987, 0.297547, 0.304719,
    0.289096, 0.226874, 0.28935}, {-0.0348226, 0.0207203, 0.973886, 0.102139, 0.0937659,
    0.0986344, -0.0129664, 0.0218629, 0.0236153, 0.0251701, 0.018967, 0.0269387, -0.02418,
    0.024597, 0.00700588, 0.0889882, 0.0672893, -0.0561361, 0.0182105, 0.0293179}},
  SpikePositive_16 → {{0.291139, 0.229457, 0.356605, 0.309834, 0.408183, 0.37253, 0.386601,
    0.214812, 0.309388, 0.206655}, {-0.0466938, 0.00775181, 0.973392, -0.026675, -0.0137985,
    0.0653713, -0.0746897, -0.0288424, 0.0796465, -0.0156034, -0.0740683, -0.0604558,
    0.0863012, -0.0237339, -0.0304634, 0.039449, 0.0785187, -0.0295269, 0.0659963, 0.0326474}},
  SpikePositive_17 → {{0.364453, 0.389423, 0.433733, 0.330073, 0.257626, 0.329576, 0.276587,
    0.205372, 0.280764, 0.214366}, {-0.00634892, 0.0469787, 0.975649, 0.00800729, -0.0857652,
    -0.0733767, -0.0444004, 0.0414565, -0.028985, -0.0509261, -0.0875459, -0.0151254, -0.0029478,
    -0.0152558, -0.0190962, -0.0716269, -0.0762463, 0.032735, 0.0303479, 0.0670751}},
  SpikePositive_18 → {{0.116775, 0.274752, 0.0796023, 0.409028, 0.35308, 0.222014, 0.269727,
    0.454748, 0.300693, 0.439675}, {0.0261203, -0.0459348, 0.960193, -0.0535144, -0.0796904,
    -0.0385966, 0.0668307, 0.0443286, -0.0742133, 0.0352114, 0.0024666, 0.100321, 0.0775953,
    -0.0165483, -0.100866, -0.0889614, 0.063578, -0.00742959, 0.0912017, -0.0669753}},
  SpikePositive_19 → {{0.198373, 0.198798, 0.440801, 0.312832, 0.427136, 0.445232, 0.213476,
    0.203801, 0.350603, 0.195585}, {-0.00854676, 0.0858518, 0.965705, -0.0126694, -0.0605102,
    -0.0160961, 0.0455675, -0.073144, 0.0961231, 0.090109, -0.00755778, -0.0155226, 0.0525843,
    -0.0435363, 0.0950979, 0.0628887, 0.0859513, 0.0399965, 0.0644759, -0.00107979}},
  SpikePositive_20 → {{0.238367, 0.346055, 0.534441, 0.229237, 0.26479, 0.297432, 0.234236,
    0.192716, 0.438042, 0.206843}, {0.0844609, 0.0592278, 0.971989, -0.0221568, -0.0503454,
    -0.0670139, 0.0116156, 0.0450434, 0.0504005, -0.0432833, 0.0256569, -0.0409855, -0.0319116,
    0.0493455, 0.0487706, -0.0895384, -0.0911685, -0.0381602, -0.0419681, 0.0527794}}|>,
SpikeMin → <|SpikeNegative_1 → {{0.318543, 0.169641, 0.186495, 0.275646, 0.341289, 0.273471,
    0.193343, 0.269342, 0.605321, 0.302303}, {-0.970463, 0.0292309, -0.0828502, -0.0604229,
    -0.00665921, 0.0839047, -0.00148688, 0.056199, 0.0394746, 0.0277076, 0.0609057, 0.00751375,
    0.0568776, -0.0277868, -0.0499463, 0.046385, 0.0861317, -0.0899138, 0.0179878, 0.0775533}},
  SpikeNegative_2 → {{0.117729, 0.167454, 0.189108, 0.242647, 0.458894, 0.274782, 0.436336,
    0.213768, 0.520943, 0.264394}, {-0.958043, 0.0439645, 0.0148129, -0.063333, -0.0649309,
    0.0765257, 0.068547, -0.00923035, -0.0848928, 0.0616155, -0.0422219, -0.0979222,
    -0.0608249, -0.091055, 0.0775452, -0.0687884, 0.0713927, -0.022196, -0.015522, 0.100959}},
  SpikeNegative_3 → {{0.332594, 0.287772, 0.421526, 0.21009, 0.350474, 0.366138, 0.250671,
    0.205878, 0.4118, 0.230341}, {-0.979722, -0.0803607, 0.0131085, 0.0261506, 0.0640096,
    0.0146427, 0.0014714, 0.00542047, 0.0768372, 0.0462248, 0.0196202, -0.0437175, -0.0320476,
    0.0295895, 0.0365406, -0.0629048, 0.0728549, -0.0554827, -0.0348965, 0.0367728}},
  SpikeNegative_4 → {{0.103821, 0.139037, 0.42892, 0.191533, 0.216307, 0.307455, 0.292286,
```

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```
    0.425818, 0.399396, 0.4262}, {-0.970769, 0.0525318, 0.0707741, 0.0482433, 0.076337,
    -0.0316713, -0.0613821, -0.0330202, 0.0755618, 0.0228373, 0.066596, -0.0247929, -0.00318789,
    -0.00586691, 0.0223311, 0.0859136, -0.000498284, 0.0871622, 0.0650011, 0.0692533}},
SpikeNegative_5 → {{0.272295, 0.299517, 0.218009, 0.172337, 0.288952, 0.402216, 0.208151,
    0.316323, 0.510062, 0.331808}, {-0.962076, 0.0210887, -0.0516851, -0.0617211, 0.0545953,
    0.0927954, -0.0584114, -0.0385042, 0.0244566, -0.0116392, 0.0879369, 0.0798407, 0.0763973,
    0.0779802, 0.0578946, 0.0834642, 0.0655166, 0.0000367346, 0.0381559, 0.0904087}},
SpikeNegative_6 → {{0.130083, 0.359262, 0.259644, 0.265026, 0.281821, 0.216489, 0.298034,
    0.309187, 0.552699, 0.316492}, {-0.974823, 0.0876679, -0.066298, 0.0213095, 0.0165679,
    0.0147248, 0.020837, -0.0348346, -0.0293177, -0.044101, -0.0945735, -0.0425154, -0.0216562,
    -0.0061356, 0.00136604, 0.0627185, 0.0286156, -0.0799317, -0.0990344, -0.00558016}},
SpikeNegative_7 → {{0.374646, 0.412203, 0.323625, 0.299188, 0.376429, 0.349996, 0.232698,
    0.186757, 0.32323, 0.194375}, {-0.972026, -0.0960549, 0.0912705, -0.0568929, 0.0528073,
    0.00411893, 0.0659282, -0.0676534, 0.0184713, -0.018727, 0.0639034, 0.0223991, 0.0226277,
    0.0139122, 0.0640245, -0.0428062, 0.0419348, -0.0791334, -0.0110535, -0.0508509}},
SpikeNegative_8 → {{0.159862, 0.107531, 0.341298, 0.260371, 0.234713, 0.238153, 0.294837,
    0.139875, 0.723789, 0.190872}, {-0.961362, 0.0401187, 0.0209914, 0.0700343, 0.0281124,
    0.0123564, -0.101827, 0.0848511, -0.0900803, 0.0986202, 0.0451721, -0.0295946,
    0.00353828, -0.102892, -0.0316313, -0.0485393, 0.102203, -0.0508, 0.0457176, 0.0220815}},
SpikeNegative_9 → {{0.29301, 0.284872, 0.408927, 0.216902, 0.337763, 0.362393, 0.36569,
    0.258843, 0.35019, 0.223496}, {-0.968574, -0.089523, 0.101336, -0.0352164, 0.0844694,
    -0.00367364, -0.0317037, -0.0414654, 0.0621643, 0.0780272, -0.0999487, 0.0452828, -0.0364943,
    0.0171792, -0.0244018, 0.0182332, -0.0759164, -0.00247154, 0.0301257, 0.0352708}},
SpikeNegative_10 → {{0.179702, 0.48369, 0.250786, 0.293342, 0.277385, 0.258275, 0.368631,
    0.214667, 0.447534, 0.242695}, {-0.978436, -0.0637402, -0.0247001, -0.0082031, 0.0751406,
    0.0280849, 0.0235381, 0.0432936, -0.0839759, -0.0277196, -0.0202634, -0.0513935, 0.0615891,
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SpikeNegative_11 → {{0.426523, 0.101644, 0.265676, 0.39495, 0.253536, 0.321521, 0.510073,
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SpikeNegative_12 → {{0.215972, 0.145986, 0.417923, 0.285238, 0.288568, 0.305217, 0.29231,
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SpikeNegative_13 → {{0.179214, 0.273178, 0.23495, 0.386216, 0.415546, 0.374561, 0.20098,
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SpikeNegative_17 → {{0.263024, 0.395295, 0.300151, 0.238924, 0.32208, 0.648924, 0.215268,
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SpikeNegative_19 → {{0.24538, 0.371762, 0.333591, 0.347016, 0.305689, 0.403541, 0.446099,
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SpikeNegative_20 → {{0.144793, 0.243782, 0.530771, 0.253771, 0.468271, 0.273254, 0.350486,
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LinearNegative_11 → {{0.98449, 0.166737, 0.0305391, 0.00183374, 0.00392343, 0.0120626,
    0.0221104, 0.0208824, 0.0184581, 0.0248023}, {-0.0144941, -0.0305378, -0.0633965, -0.0696761,
    -0.0885522, -0.115724, -0.12314, -0.152395, -0.159387, -0.194971, -0.205338, -0.219688,
    -0.242933, -0.257821, -0.28294, -0.293097, -0.322714, -0.335954, -0.355939, -0.375987}},
LinearNegative_12 → {{0.983058, 0.168322, 0.0254275, 0.00140346, 0.0043042, 0.0177536,
    0.0154835, 0.0404788, 0.0162672, 0.0462509}, {-0.0148871, -0.0465102, -0.0623852, -0.0740241,
    -0.0941809, -0.115291, -0.134019, -0.156294, -0.175334, -0.18221, -0.21367, -0.214928,
    -0.247838, -0.267133, -0.275037, -0.298644, -0.316063, -0.32968, -0.352458, -0.370772}},
LinearNegative_13 → {{0.983108, 0.173037, 0.0282577, 0.00280281, 0.00101853, 0.0135896,
    0.0167039, 0.0295113, 0.0156016, 0.0342236}, {-0.015714, -0.0371518, -0.0522033, -0.0691653,
    -0.0951901, -0.111442, -0.137192, -0.149371, -0.165077, -0.185808, -0.212965, -0.216673,
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    -0.236296, -0.268764, -0.282848, -0.303841, -0.314287, -0.32841, -0.358954, -0.371893}},
  LinearNegative_14 → {{0.979568, 0.189596, 0.0431711, 0.00353421, 0.00118874, 0.00919193,
    0.0158507, 0.0297253, 0.0147023, 0.0344515}, {-0.0226673, -0.0285807, -0.0590313, -0.0745851,
    -0.0987489, -0.109982, -0.138172, -0.15227, -0.167396, -0.179324, -0.206394, -0.219938,
    -0.243563, -0.260188, -0.271531, -0.30537, -0.322871, -0.344529, -0.350913, -0.366415}},
  LinearNegative_15 → {{0.98375, 0.16809, 0.028338, 0.00524876, 0.00124156, 0.00837112,
    0.0159829, 0.0334162, 0.0156323, 0.0382407}, {-0.027454, -0.0357832, -0.0602119, -0.0771882,
    -0.0904181, -0.11745, -0.134185, -0.146582, -0.172653, -0.182929, -0.2046, -0.215573,
    -0.241761, -0.266455, -0.286027, -0.295126, -0.309328, -0.338338, -0.355472, -0.374755}},
  LinearNegative_16 → {{0.983302, 0.172169, 0.0274593, 0.00430988, 0.00173809, 0.0112221,
    0.0233003, 0.0260533, 0.0214123, 0.0298916}, {-0.0240558, -0.0306542, -0.0537539, -0.0669803,
    -0.0892249, -0.113844, -0.127405, -0.157576, -0.16074, -0.193442, -0.204803, -0.214517,
    -0.245748, -0.265327, -0.287433, -0.296174, -0.311519, -0.338394, -0.349333, -0.378402}},
  LinearNegative_17 → {{0.981787, 0.170425, 0.0428221, 0.00156052, 0.000347459, 0.00996377,
    0.0268935, 0.0423645, 0.0165315, 0.0481903}, {-0.0243081, -0.0428655, -0.0512256, -0.0803895,
    -0.0940658, -0.112217, -0.138408, -0.14552, -0.17245, -0.17803, -0.209708, -0.230672,
    -0.239436, -0.252252, -0.282437, -0.293638, -0.311377, -0.341314, -0.356008, -0.375425}},
  LinearNegative_18 → {{0.985015, 0.157547, 0.0253292, 0.00816751, 0.00139604, 0.0161979,
    0.0175278, 0.0370182, 0.0227603, 0.0419106}, {-0.0188888, -0.0393474, -0.0609787, -0.0837959,
    -0.0997794, -0.115402, -0.121814, -0.15327, -0.175281, -0.179323, -0.200775, -0.216975,
    -0.242109, -0.268016, -0.279604, -0.293511, -0.310324, -0.3405, -0.355825, -0.376634}},
  LinearNegative_19 → {{0.985763, 0.155843, 0.0309198, 0.00328164, 0.00518766, 0.0165203,
    0.0232856, 0.0276804, 0.0194587, 0.0321124}, {-0.0211988, -0.0426853, -0.0475655, -0.0709076,
    -0.0994447, -0.109678, -0.125476, -0.14254, -0.169408, -0.182461, -0.198712, -0.225818,
    -0.24069, -0.269692, -0.278136, -0.302102, -0.325988, -0.331627, -0.350799, -0.376019}},
  LinearNegative_20 → {{0.987248, 0.140226, 0.0352556, 0.00532824, 0.0014789, 0.0102804,
    0.0267144, 0.0374332, 0.0193086, 0.0425579}, {-0.0229396, -0.0454202, -0.0487709, -0.0851539,
    -0.0982256, -0.107814, -0.124549, -0.143277, -0.162672, -0.189933, -0.208619, -0.220399,
    -0.251254, -0.259578, -0.280319, -0.294846, -0.316754, -0.338702, -0.354156, -0.373274}}|>,
f3 → <|Sinusoidal3_21 → {{0.00393196, 0.0730876, 0.992163, 0.0883546, 0.0393739, 0.0195983,
    0.0100064, 0.0026097, 0.0201412, 0.00090379}, {0.182593, -0.0994387, -0.307591, -0.251938,
    0.00547376, 0.254617, 0.298414, 0.0919814, -0.181503, -0.311401, -0.190295, 0.100126,
    0.300618, 0.252141, -0.00525157, -0.26015, -0.303318, -0.101815, 0.186126, 0.318593}},
  Sinusoidal3_22 → {{0.00322681, 0.0734902, 0.992588, 0.0836605, 0.0374297, 0.0209669,
    0.00863508, 0.00288517, 0.0208504, 0.0010227}, {0.183093, -0.104038, -0.29628, -0.252467,
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    0.304592, 0.253188, 0.000706396, -0.253337, -0.296515, -0.103253, 0.191294, 0.323004}},
  Sinusoidal3_23 → {{0.00306571, 0.0709852, 0.992797, 0.0851472, 0.0361914, 0.0178061,
    0.00771481, 0.00343824, 0.0188339, 0.00139443}, {0.187918, -0.0922354, -0.296438, -0.255644,
    -0.0000867738, 0.257668, 0.304362, 0.101082, -0.188267, -0.315172, -0.184706, 0.0995107,
    0.305029, 0.249432, 0.00544209, -0.25796, -0.29982, -0.0943208, 0.189333, 0.313752}},
  Sinusoidal3_24 → {{0.00258184, 0.0713358, 0.992757, 0.084013, 0.0366518, 0.0176537,
    0.00776563, 0.00249983, 0.0236143, 0.000754715}, {0.18775, -0.101841, -0.294868, -0.25699,
    -0.00245683, 0.257286, 0.301315, 0.0930634, -0.184378, -0.321088, -0.1892, 0.0938712,
    0.304065, 0.249713, -0.00307558, -0.249808, -0.301591, -0.091814, 0.184068, 0.321775}},
  Sinusoidal3_25 → {{0.00294445, 0.0716883, 0.992504, 0.0877983, 0.0349317, 0.0192157,
    0.00934308, 0.00263234, 0.0198862, 0.000926399}, {0.185107, -0.0937609, -0.300807, -0.24946,
    -0.00368283, 0.261166, 0.300373, 0.0983199, -0.190176, -0.314704, -0.189094, 0.0965295,
    0.2944, 0.260606, -0.00488801, -0.253156, -0.302564, -0.0930939, 0.19043, 0.317274}},
  Sinusoidal3_26 → {{0.00259526, 0.07148, 0.992506, 0.0876439, 0.0361723, 0.0183876, 0.00775777,
    0.00272792, 0.0204657, 0.000960651}, {0.184209, -0.0919739, -0.305473, -0.261648,
    -6.02238×10^-6, 0.256309, 0.299821, 0.0930316, -0.186459, -0.311693, -0.18779, 0.0974013,
    0.307035, 0.254151, 0.000444525, -0.254307, -0.300396, -0.0919838, 0.181362, 0.315903}},
  Sinusoidal3_27 → {{0.00392268, 0.0736346, 0.992125, 0.0894711, 0.0387608, 0.018788, 0.00799147,
    0.00378135, 0.0175868, 0.00165925}, {0.183648, -0.0930997, -0.300941, -0.254876,
    0.00580887, 0.26189, 0.296631, 0.103122, -0.188264, -0.313514, -0.184094, 0.0978014,
    0.300364, 0.251314, 0.00221433, -0.259597, -0.302063, -0.102484, 0.190728, 0.314243}},
  Sinusoidal3_28 → {{0.00261313, 0.0715877, 0.992758, 0.083475, 0.0383481, 0.0196263, 0.00917329,
    0.00268812, 0.0195927, 0.000957507}, {0.18454, -0.0952822, -0.303492, -0.25661,
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    0.303551, 0.259667, 0.00338218, -0.249999, -0.29641, -0.0993918, 0.187495, 0.317659}},
  Sinusoidal3_29 → {{0.00271538, 0.0737797, 0.992421, 0.0858555, 0.0380423, 0.0191077,
    0.00868441, 0.00324763, 0.0194572, 0.00126937}, {0.187311, -0.102172, -0.306355, -0.258761,
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    0.301047, 0.253318, 0.00299172, -0.250284, -0.296154, -0.100081, 0.184983, 0.31019}},
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    Sinusoidal3_30 → {{0.00357542, 0.0712888, 0.992491, 0.0873181, 0.0379892, 0.0169087,
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        0.29935, 0.252935, 0.00554842, -0.261867, -0.305736, -0.0925331, 0.190617, 0.313882}}|〉,
f5 → ‹|Sinusoidal2_11 → {{0.00281686, 0.0084638, 0.0311803, 0.0950863, 0.936015, 0.334724,
        0.0288941, 0.00490623, 0.0296836, 0.00170252}, {-0.0925024, -0.252391, 0.261804, 0.0949073,
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        0.252703, 0.0945153, -0.321488, 0.100899, 0.259506, -0.250929, -0.100114, 0.315503}},
    Sinusoidal2_12 → {{0.00256682, 0.011503, 0.0299913, 0.0969546, 0.934301, 0.339079, 0.0301738,
        0.00482265, 0.0270394, 0.0017803}, {-0.0997103, -0.254485, 0.253556, 0.101836,
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        0.260287, 0.0957265, -0.31566, 0.0921673, 0.257442, -0.255403, -0.102763, 0.316019}},
    Sinusoidal2_13 → {{0.00261804, 0.0104493, 0.0327596, 0.0932705, 0.931214, 0.34821, 0.0278915,
        0.00527928, 0.0298809, 0.00191118}, {-0.0934352, -0.258396, 0.25944, 0.102164,
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        0.252221, 0.0941186, -0.315406, 0.103138, 0.256505, -0.253599, -0.0979757, 0.317231}},
    Sinusoidal2_14 → {{0.00227697, 0.011913, 0.0322904, 0.0884078, 0.936373, 0.335295, 0.0287715,
        0.00376869, 0.0305491, 0.00108073}, {-0.0958187, -0.256098, 0.262448, 0.0975879,
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        0.253557, 0.104227, -0.311473, 0.0956505, 0.254812, -0.253333, -0.0989094, 0.315391}},
    Sinusoidal2_15 → {{0.00264627, 0.0110901, 0.0300565, 0.091207, 0.933401, 0.343368, 0.0247317,
        0.00560338, 0.0293336, 0.00214722}, {-0.0972913, -0.261439, 0.259934, 0.0946222,
        -0.312494, 0.10338, 0.252244, -0.254174, -0.104322, 0.32185, -0.10136, -0.256575,
        0.256357, 0.0938093, -0.314063, 0.100187, 0.253159, -0.254097, -0.0989871, 0.311243}},
    Sinusoidal2_16 → {{0.00261369, 0.0107816, 0.0273437, 0.0953078, 0.935087, 0.337919,
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        0.259095, 0.100036, -0.319403, 0.0923476, 0.251595, -0.251953, -0.100224, 0.321737}},
    Sinusoidal2_17 → {{0.00306387, 0.010055, 0.0311425, 0.088682, 0.930804, 0.350615, 0.0302341,
        0.0048513, 0.0280701, 0.0017212}, {-0.0970539, -0.261196, 0.253236, 0.0944534,
        -0.315214, 0.101953, 0.258812, -0.258097, -0.0940835, 0.31379, -0.0999959, -0.26327,
        0.253577, 0.0952638, -0.312437, 0.098095, 0.251174, -0.261592, -0.0925556, 0.314052}},
    Sinusoidal2_18 → {{0.00313075, 0.00937136, 0.0301513, 0.0950644, 0.932408, 0.345162,
        0.0249045, 0.00391213, 0.0282369, 0.00129103}, {-0.10151, -0.250291, 0.250599, 0.096394,
        -0.312822, 0.09768, 0.261135, -0.25052, -0.0938805, 0.317925, -0.0918853, -0.260746,
        0.261072, 0.0940949, -0.320369, 0.103158, 0.25478, -0.252147, -0.10144, 0.318143}},
    Sinusoidal2_19 → {{0.00242551, 0.0117218, 0.0310044, 0.0870479, 0.935228, 0.338947, 0.0278964,
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        -0.310472, 0.0986034, 0.255, -0.261535, -0.101044, 0.320707, -0.0996266, -0.256683,
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    Sinusoidal2_20 → {{0.00249505, 0.0112337, 0.0314717, 0.0944674, 0.931921, 0.346162, 0.0260778,
        0.00354041, 0.0309029, 0.00101227}, {-0.0988454, -0.254859, 0.259992, 0.0946886,
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        0.251163, 0.0946484, -0.316854, 0.103092, 0.254627, -0.25594, -0.097935, 0.315059}}|›,
f6 → ‹|Sinusoidal1_1 → {{0.00242276, 0.0093411, 0.00910904, 0.0410019, 0.0937532, 0.990279,
        0.0904247, 0.00505574, 0.0222734, 0.00179277}, {-0.212188, -0.0999616, 0.27479, -0.25771,
        0.000823954, 0.264749, -0.301555, 0.111621, 0.158613, -0.318777, 0.172098, 0.118809,
        -0.290023, 0.255504, -0.0291429, -0.259228, 0.291499, -0.0889868, -0.167864, 0.347203}},
    Sinusoidal1_2 → {{0.00716923, 0.00781515, 0.0196069, 0.0422324, 0.113883, 0.985278, 0.113983,
        0.00245192, 0.0312804, 0.000322441}, {-0.193636, -0.12019, 0.322617, -0.254704,
        -0.00747086, 0.28816, -0.28223, 0.0883687, 0.204, -0.310639, 0.195326, 0.0785247,
        -0.293043, 0.244686, -0.0216511, -0.238028, 0.273796, -0.0982342, -0.195454, 0.316906}},
    Sinusoidal1_3 → {{0.00185957, 0.00728847, 0.0180757, 0.0389176, 0.0820034, 0.991024,
        0.0924908, 0.00488114, 0.0258746, 0.00142265}, {-0.163454, -0.101927, 0.305027, -0.231416,
        0.0306473, 0.260901, -0.279585, 0.0924574, 0.170975, -0.313902, 0.212337, 0.0943165,
        -0.316169, 0.252156, 0.0281256, -0.243443, 0.333682, -0.0733566, -0.212348, 0.305626}},
    Sinusoidal1_4 → {{0.00830792, 0.00574957, 0.0172162, 0.0342911, 0.0887013, 0.989385, 0.105323,
        0.00849964, 0.0223038, 0.00364294}, {-0.165376, -0.0945384, 0.294768, -0.268981,
        0.00547141, 0.278722, -0.291465, 0.118823, 0.18206, -0.294773, 0.210882, 0.0722241,
        -0.312666, 0.246451, -0.00837558, -0.271456, 0.274216, -0.115707, -0.171855, 0.328009}},
    Sinusoidal1_5 → {{0.000859877, 0.000254868, 0.0313177, 0.0426916, 0.0935456, 0.988922,
        0.0992448, 0.0060627, 0.0242192, 0.00223745}, {-0.194921, -0.113903, 0.302678, -0.27259,
        -0.0253657, 0.234915, -0.290618, 0.117753, 0.212649, -0.299943, 0.155136, 0.0857743,
        -0.321098, 0.241618, 0.0166473, -0.229632, 0.318426, -0.0909468, -0.168206, 0.33151}},
    Sinusoidal1_6 → {{0.00092075, 0.00996182, 0.00867829, 0.0346619, 0.0925016, 0.988664,
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    0.111076, 0.0115132, 0.00961286, 0.00693268}, {-0.178751, -0.0655419, 0.27386, -0.237352,
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    -0.268245, 0.262243, -0.0151267, -0.269787, 0.320947, -0.0892703, -0.169814, 0.312358}},
Sinusoidal1_7 → {{0.00202551, 0.0100417, 0.0188363, 0.0263553, 0.0796213, 0.990514,
    0.105057, 0.0036338, 0.0183605, 0.001272}, {-0.202824, -0.109332, 0.290084, -0.269003,
    -0.00331824, 0.249122, -0.309607, 0.0811477, 0.212804, -0.33586, 0.203505, 0.0898667,
    -0.281695, 0.259762, 0.0230823, -0.27048, 0.270568, -0.101282, -0.176441, 0.288424}},
Sinusoidal1_8 → {{0.00372194, 0.0119278, 0.0273178, 0.0341682, 0.11153, 0.987112, 0.103575,
    0.00445953, 0.018755, 0.00144668}, {-0.193409, -0.0909943, 0.303997, -0.234664,
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    -0.298209, 0.275829, 0.0171893, -0.270533, 0.316295, -0.118365, -0.20542, 0.31355}},
Sinusoidal1_9 → {{0.000658801, 0.00517548, 0.0189464, 0.0457291, 0.0778028, 0.988673,
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    -0.0186558, 0.23391, -0.296235, 0.0877631, 0.175016, -0.341285, 0.212271, 0.0866696,
    -0.303468, 0.256182, 0.0299947, -0.241273, 0.328692, -0.101436, -0.17687, 0.312626}},
Sinusoidal1_10 → {{0.000850813, 0.0049151, 0.024096, 0.0232946, 0.0807771, 0.991342,
    0.0922717, 0.00829457, 0.0311945, 0.00345396}, {-0.153119, -0.115014, 0.282732, -0.261708,
    0.0272211, 0.242714, -0.31643, 0.105565, 0.180159, -0.302865, 0.164673, 0.0779684,
    -0.314669, 0.269124, 0.0289465, -0.24498, 0.310534, -0.0978127, -0.195506, 0.331775}}|>|>
```

Let's cluster only the "SpikeMax" class extracted from the data

```
In[3]:= clustersSingleClass = TimeSeriesSingleClusters[classification1["SpikeMax"]]
```

```
Out[3]= <|1 →
  <|Cluster → Cluster[Cluster[Cluster[Cluster[Cluster[Cluster[Cluster[{0.984595, 0.0426538, 0.0179441, -0.0228628,
            0.0250083, -0.0278621, -0.0652766, -0.0604749, 0.0729085, -0.0203339, 0.026914, 0.0384599,
            -0.00443374, 0.0214493, 0.0470012, 0.0542644, 0.000931502, -0.0266604, -0.0612261, 0.0237265} →
           SpikePositive_1, {0.957834, -0.0838027, -0.0202768, -0.0447831, 0.0898779, -0.0260558,
            -0.0909962, 0.0393741, 0.0762775, -0.0946617, -0.0849301, -0.0512037, -0.0799125, 0.0210224,
            -0.0376881, -0.0060933, -0.0535727, -0.0547708, -0.0976687, 0.07886} → SpikePositive_5,
          0.157065, 1, 1], {0.970907, -0.00593115, 0.0210836, -0.058253, 0.0015684, -0.0431886, -0.0209517,
           -0.097558, 0.0191591, -0.000431375, -0.00686202, -0.0594855, 0.0716292, -0.0952797, 0.0536522,
           -0.063791, -0.0974441, 0.0173567, 0.0563725, 0.0596441} → SpikePositive_2, 0.328567, 2, 1],
         Cluster[Cluster[{0.971727, -0.0596889, 0.0474448, -0.0640848, -0.000744131, 0.0568001,
            0.0606394, -0.0352061, 0.0621654, 0.0802062, -0.0349508, 0.0319642, -0.00523245, 0.044493,
            0.0821664, 0.0731019, -0.0532013, -0.0455357, 0.0520489, 0.0585355} → SpikePositive_4,
          {0.966423, -0.0674757, 0.0554647, -0.0432617, 0.0597318, 0.0312359, -0.0146744,
            -0.101786, -0.0521611, 0.0758959, 0.0712873, 0.0182951, 0.0242038, 0.0207882, 0.102946,
            -0.0851805, 0.0231602, 0.0501532, 0.0735243, 0.0133773} → SpikePositive_9, 0.193079, 1, 1],
         {0.973177, -0.0143179, 0.017454, -0.0815008, 0.0640615, -0.0718526, -0.020035,
           0.0468446, -0.0351388, -0.026056, -0.0783309, -0.0574767, -0.0713074, 0.0296903,
           0.0391121, -0.0842894, -0.0214224, 0.0842498, -0.00426514, -0.0195874} →
          SpikePositive_6, 0.257644, 2, 1], 0.332385, 3, 3], Cluster[
         Cluster[Cluster[Cluster[{-0.00634892, 0.0469787, 0.975649, 0.00800729, -0.0857652, -0.0733767,
             -0.0444004, 0.0414565, -0.028985, -0.0509261, -0.0875459, -0.0151254, -0.0029478, -0.0152558,
            -0.0190962, -0.0716269, -0.0762463, 0.032735, 0.0303479, 0.0670751} → SpikePositive_17,
           {-0.0348226, 0.0207203, 0.973886, 0.102139, 0.0937659, 0.0986344, -0.0129664, 0.0218629,
            0.0236153, 0.0251701, 0.018967, 0.0269387, -0.02418, 0.024597, 0.00700588, 0.0889882,
            0.0672893, -0.0561361, 0.0182105, 0.0293179} → SpikePositive_15, 0.16385, 1, 1],
          {0.0844609, 0.0592278, 0.971989, -0.0221568, -0.0503454, -0.0670139, 0.0116156,
            0.0450434, 0.0504005, -0.0432833, 0.0256569, -0.0409855, -0.0319116, 0.0493455, 0.0487706,
            -0.0895384, -0.0911685, -0.0381602, -0.0419681, 0.0527794} → SpikePositive_20, 0.290051, 2, 1],
         Cluster[Cluster[{0.966576, 0.0396294, -0.0684005, 0.0197313, 0.0649133, -0.00424926,
            -0.0689057, -0.0837356, 0.0322856, -0.020455, -0.0225326, -0.0600544, 0.0082849, 0.0941703,
            -0.0974221, -0.0422418, -0.0263268, 0.0443156, 0.0974553, -0.0718231} → SpikePositive_3,
           {0.970565, 0.0563423, -0.0356883, -0.0918923, -0.0354868, 0.0814418, -0.0590716,
            0.0424911, -0.082389, -0.0730024, 0.0344587, -0.0578783, -0.0782079, 0.00597631, 0.00796937,
            -0.00564963, -0.0759616, -0.0188232, 0.0536684, 0.00422988} → SpikePositive_8, 0.220501, 1,
          1], {0.0558479, 0.0585074, 0.975087, 0.059428, 0.0865757, -0.0195558, 0.0437175, -0.0121055,
           -0.059396, 0.00279565, -0.00467662, -0.0163185, 0.0921236, -0.0810352, -0.00573544, 0.0107053,
           0.0954525, -0.00134351, -0.000141434, 0.0325192} → SpikePositive_14, 0.260663, 2, 1],
         0.363707, 3, 3], {0.00840957, 0.0853478, 0.964152, -0.0619487, -0.0761645, -0.0371389,
          0.0267932, 0.0773386, -0.000715143, -0.0403987, -0.00252004, 0.0520121, -0.0283832,
```

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```
        -0.0640981, 0.0813266, -0.0655443, 0.0510528, -0.0833161, -0.0978328, 0.077786} →
       SpikePositive_11, 0.398224, 6, 1], 0.486106, 6, 7],
    Cluster[{0.0261203, -0.0459348, 0.960193, -0.0535144, -0.0796904, -0.0385966, 0.0668307,
       0.0443286, -0.0742133, 0.0352114, 0.0024666, 0.100321, 0.0775953, -0.0165483,
       -0.100866, -0.0889614, 0.063578, -0.00742959, 0.0912017, -0.0669753} → SpikePositive_18,
      {0.961868, -0.0121292, 0.0454807, -0.0987756, 0.00861658, 0.0563813, 0.0195099,
       0.0702466, -0.0892035, 0.0811513, -0.0577825, 0.0549826, -0.0791978,
       -0.0619687, 0.0176499, 0.0675396, 0.083561, -0.0549534, 0.0268929, 0.0874893} →
      SpikePositive_7, 0.342411, 1, 1], 0.538803, 13, 2],
   Cluster[{0.96379, -0.0948729, -0.0252853, 0.0827415, -0.0532786, 0.0877364,
       0.0347807, 0.0299562, 0.0698768, -0.0707597, 0.0516924,
       -0.0689011, 0.00595017, 0.0754929, -0.0433978, 0.0682848,
       0.0278066, -0.0330652, 0.0622196, -0.0815615} → SpikePositive_10,
    Cluster[Cluster[Cluster[{-0.0466938, 0.00775181, 0.973392, -0.026675, -0.0137985, 0.0653713,
         -0.0746897, -0.0288424, 0.0796465, -0.0156034, -0.0740683, -0.0604558, 0.0863012, -0.0237339,
         -0.0304634, 0.039449, 0.0785187, -0.0295269, 0.0659963, 0.0326474} → SpikePositive_16,
       {-0.00854676, 0.0858518, 0.965705, -0.0126694, -0.0605102, -0.0160961, 0.0455675,
         -0.073144, 0.0961231, 0.090109, -0.00755778, -0.0155226, 0.0525843, -0.0435363, 0.0950979,
         0.0628887, 0.0859513, 0.0399965, 0.0644759, -0.00107979} → SpikePositive_19, 0.232815, 1, 1],
      {0.0500355, -0.0685108, 0.975847, -0.0570955, -0.0412712, 0.0755937, 0.0204554, 0.0170235,
        0.0554969, 0.0920522, -0.0136969, -0.0725248, -0.0180233, 0.0342937, 0.01804, 0.016408,
        -0.0746403, 0.054622, -0.00722388, 0.0378922} → SpikePositive_12, 0.303895, 2, 1],
      {-0.0432619, -0.0325615, 0.972197, 0.0255384, -0.0749987, 0.101228, -0.0550282,
        0.0577603, 0.0748688, -0.0624347, -0.0131491, -0.0213904, -0.0596143, 0.0307112,
        -0.0564378, 0.0196663, -0.0250186, 0.0728887, 0.0200498, -0.0668496} →
      SpikePositive_13, 0.329013, 3, 1], 0.405326, 1, 4], 0.605384, 15, 5],
InitialSplitCluster → {Cluster[Cluster[Cluster[Cluster[Cluster[
        Cluster[{0.984595, 0.0426538, 0.0179441, -0.0228628, 0.0250083, -0.0278621, -0.0652766,
           -0.0604749, 0.0729085, -0.0203339, 0.026914, 0.0384599, -0.00443374, 0.0214493,
           0.0470012, 0.0542644, 0.000931502, -0.0266604, -0.0612261, 0.0237265} → SpikePositive_1,
         {0.957834, -0.0838027, -0.0202768, -0.0447831, 0.0898779, -0.0260558, -0.0909962,
           0.0393741, 0.0762775, -0.0946617, -0.0849301, -0.0512037, -0.0799125, 0.0210224, -0.0376881,
           -0.0060933, -0.0535727, -0.0547708, -0.0976687, 0.07886} → SpikePositive_5, 0.157065, 1, 1],
        {0.970907, -0.00593115, 0.0210836, -0.058253, 0.0015684, -0.0431886, -0.0209517,
          -0.097558, 0.0191591, -0.000431375, -0.00686202, -0.0594855, 0.0716292, -0.0952797, 0.0536522,
          -0.063791, -0.0974441, 0.0173567, 0.0563725, 0.0596441} → SpikePositive_2, 0.328567, 2, 1],
       Cluster[Cluster[{0.971727, -0.0596889, 0.0474448, -0.0640848, -0.000744131, 0.0568001,
           0.0606394, -0.0352061, 0.0621654, 0.0802062, -0.0349508, 0.0319642, -0.00523245, 0.044493,
           0.0821664, 0.0731019, -0.0532013, -0.0455357, 0.0520489, 0.0585355} → SpikePositive_4,
         {0.966423, -0.0674757, 0.0554647, -0.0432617, 0.0597318, 0.0312359, -0.0146744,
           -0.101786, -0.0521611, 0.0758959, 0.0712873, 0.0182951, 0.0242038, 0.0207882, 0.102946,
           -0.0851805, 0.0231602, 0.0501532, 0.0735243, 0.0133773} → SpikePositive_9, 0.193079, 1, 1],
        {0.973177, -0.0143179, 0.017454, -0.0815008, 0.0640615, -0.0718526, -0.020035,
          0.0468446, -0.0351388, -0.026056, -0.0783309, -0.0574767, -0.0713074, 0.0296903,
          0.0391121, -0.0842894, -0.0214224, 0.0842498, -0.00426514, -0.0195874} → SpikePositive_6,
        0.257644, 2, 1], 0.332385, 3, 3], Cluster[Cluster[Cluster[
         Cluster[{-0.00634892, 0.0469787, 0.975649, 0.00800729, -0.0857652, -0.0733767, -0.0444004,
            0.0414565, -0.028985, -0.0509261, -0.0875459, -0.0151254, -0.0029478, -0.0152558,
            -0.0190962, -0.0716269, -0.0762463, 0.032735, 0.0303479, 0.0670751} → SpikePositive_17,
          {-0.0348226, 0.0207203, 0.973886, 0.102139, 0.0937659, 0.0986344, -0.0129664,
            0.0218629, 0.0236153, 0.0251701, 0.018967, 0.0269387, -0.02418, 0.024597, 0.00700588,
            0.0889882, 0.0672893, -0.0561361, 0.0182105, 0.0293179} → SpikePositive_15, 0.16385, 1, 1],
         {0.0844609, 0.0592278, 0.971989, -0.0221568, -0.0503454, -0.0670139, 0.0116156, 0.0450434,
           0.0504005, -0.0432833, 0.0256569, -0.0409855, -0.0319116, 0.0493455, 0.0487706, -0.0895384,
           -0.0911685, -0.0381602, -0.0419681, 0.0527794} → SpikePositive_20, 0.290051, 2, 1],
        Cluster[Cluster[{0.966576, 0.0396294, -0.0684005, 0.0197313, 0.0649133, -0.00424926,
            -0.0689057, -0.0837356, 0.0322856, -0.020455, -0.0225326, -0.0600544, 0.0082849, 0.0941703,
            -0.0974221, -0.0422418, -0.0263268, 0.0443156, 0.0974553, -0.0718231} → SpikePositive_3,
          {0.970565, 0.0563423, -0.0356883, -0.0918923, -0.0354868, 0.0814418, -0.0590716,
            0.0424911, -0.082389, -0.0730024, 0.0344587, -0.0578783, -0.0782079, 0.00597631, 0.00796937,
            -0.00564963, -0.0759616, -0.0188232, 0.0536684, 0.00422988} → SpikePositive_8, 0.220501,
          1, 1], {0.0558479, 0.0585074, 0.975087, 0.059428, 0.0865757, -0.0195558, 0.0437175,
           -0.0121055, -0.059396, 0.00279565, -0.00467662, -0.0163185, 0.0921236, -0.0810352,
           -0.00573544, 0.0107053, 0.0954525, -0.00134351, -0.000141434, 0.0325192} → SpikePositive_14,
         0.260663, 2, 1], 0.363707, 3, 3], {0.00840957, 0.0853478, 0.964152, -0.0619487,
         -0.0761645, -0.0371389, 0.0267932, 0.0773386, -0.000715143, -0.0403987, -0.00252004,
```

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```
            0.0520121, -0.0283832, -0.0640981, 0.0813266, -0.0655443, 0.0510528, -0.0833161,
            -0.0978328, 0.077786} → SpikePositive_11, 0.398224, 6, 1], 0.486106, 6, 7],
        Cluster[{0.0261203, -0.0459348, 0.960193, -0.0535144, -0.0796904, -0.0385966, 0.0668307,
           0.0443286, -0.0742133, 0.0352114, 0.0024666, 0.100321, 0.0775953, -0.0165483,
           -0.100866, -0.0889614, 0.063578, -0.00742959, 0.0912017, -0.0669753} → SpikePositive_18,
         {0.961868, -0.0121292, 0.0454807, -0.0987756, 0.00861658, 0.0563813, 0.0195099,
           0.0702466, -0.0892035, 0.0811513, -0.0577825, 0.0549826, -0.0791978,
           -0.0619687, 0.0176499, 0.0675396, 0.083561, -0.0549534, 0.0268929, 0.0874893} →
          SpikePositive_7, 0.342411, 1, 1], 0.538803, 13, 2],
       Cluster[{0.96379, -0.0948729, -0.0252853, 0.0827415, -0.0532786, 0.0877364,
          0.0347807, 0.0299562, 0.0698768, -0.0707597, 0.0516924,
          -0.0689011, 0.00595017, 0.0754929, -0.0433978, 0.0682848,
          0.0278066, -0.0330652, 0.0622196, -0.0815615} → SpikePositive_10,
        Cluster[Cluster[Cluster[{-0.0466938, 0.00775181, 0.973392, -0.026675, -0.0137985, 0.0653713,
             -0.0746897, -0.0288424, 0.0796465, -0.0156034, -0.0740683, -0.0604558, 0.0863012, -0.0237339,
             -0.0304634, 0.039449, 0.0785187, -0.0295269, 0.0659963, 0.0326474} → SpikePositive_16,
           {-0.00854676, 0.0858518, 0.965705, -0.0126694, -0.0605102, -0.0160961, 0.0455675,
             -0.073144, 0.0961231, 0.090109, -0.00755778, -0.0155226, 0.0525843, -0.0435363, 0.0950979,
             0.0628887, 0.0859513, 0.0399965, 0.0644759, -0.00107979} → SpikePositive_19, 0.232815, 1, 1],
          {0.0500355, -0.0685108, 0.975847, -0.0570955, -0.0412712, 0.0755937, 0.0204554,
            0.0170235, 0.0554969, 0.0920522, -0.0136969, -0.0725248, -0.0180233, 0.0342937, 0.01804,
            0.016408, -0.0746403, 0.054622, -0.00722388, 0.0378922} → SpikePositive_12, 0.303895, 2, 1],
         {-0.0432619, -0.0325615, 0.972197, 0.0255384, -0.0749987, 0.101228, -0.0550282,
           0.0577603, 0.0748688, -0.0624347, -0.0131491, -0.0213904, -0.0596143, 0.0307112,
           -0.0564378, 0.0196663, -0.0250186, 0.0728887, 0.0200498, -0.0668496} →
          SpikePositive_13, 0.329013, 3, 1], 0.405326, 1, 4], 0.605384, 15, 5]},
    GroupAssociations → <|G1 → {SpikePositive_1, SpikePositive_5, SpikePositive_2,
        SpikePositive_4, SpikePositive_9,
        SpikePositive_6, SpikePositive_17,
        SpikePositive_15, SpikePositive_20,
        SpikePositive_3, SpikePositive_8,
        SpikePositive_14, SpikePositive_11,
        SpikePositive_18, SpikePositive_7,
        SpikePositive_10, SpikePositive_16,
        SpikePositive_19, SpikePositive_12,
        SpikePositive_13}|>|>|>
```

Let' s now label the class manually "First Class":

```
In[4]:= clustersSingleClassLabel =
         TimeSeriesSingleClusters[classification1["SpikeMax"], SingleAssociationLabel → "First Class"]
```

Agglomerate::ties : 1 ties have been detected; reordering input may produce a different result. ≫

```
Out[4]= <|First Class →
          <|Cluster → Cluster[Cluster[Cluster[Cluster[Cluster[Cluster[{0.984595, 0.0426538, 0.0179441, -0.0228628,
                0.0250083, -0.0278621, -0.0652766, -0.0604749, 0.0729085, -0.0203339, 0.026914, 0.0384599,
                -0.00443374, 0.0214493, 0.0470012, 0.0542644, 0.000931502, -0.0266604, -0.0612261, 0.0237265} →
               SpikePositive_1, {0.957834, -0.0838027, -0.0202768, -0.0447831, 0.0898779, -0.0260558,
                -0.0909962, 0.0393741, 0.0762775, -0.0946617, -0.0849301, -0.0512037, -0.0799125, 0.0210224,
                -0.0376881, -0.0060933, -0.0535727, -0.0547708, -0.0976687, 0.07886} → SpikePositive_5,
              0.157065, 1, 1], {0.970907, -0.00593115, 0.0210836, -0.058253, 0.0015684, -0.0431886, -0.0209517,
               -0.097558, 0.0191591, -0.000431375, -0.00686202, -0.0594855, 0.0716292, -0.0952797, 0.0536522,
               -0.063791, -0.0974441, 0.0173567, 0.0563725, 0.0596441} → SpikePositive_2, 0.328567, 2, 1],
            Cluster[Cluster[{0.971727, -0.0596889, 0.0474448, -0.0640848, -0.000744131, 0.0568001,
                0.0606394, -0.0352061, 0.0621654, 0.0802062, -0.0349508, 0.0319642, -0.00523245, 0.044493,
                0.0821664, 0.0731019, -0.0532013, -0.0455357, 0.0520489, 0.0585355} → SpikePositive_4,
              {0.966423, -0.0674757, 0.0554647, -0.0432617, 0.0597318, 0.0312359, -0.0146744,
                -0.101786, -0.0521611, 0.0758959, 0.0712873, 0.0182951, 0.0242038, 0.0207882, 0.102946,
                -0.0851805, 0.0231602, 0.0501532, 0.0735243, 0.0133773} → SpikePositive_9, 0.193079, 1, 1],
             {0.973177, -0.0143179, 0.017454, -0.0815008, 0.0640615, -0.0718526, -0.020035,
               0.0468446, -0.0351388, -0.026056, -0.0783309, -0.0574767, -0.0713074, 0.0296903,
               0.0391121, -0.0842894, -0.0214224, 0.0842498, -0.00426514, -0.0195874} →
              SpikePositive_6, 0.257644, 2, 1], 0.332385, 3, 3], Cluster[
            Cluster[Cluster[Cluster[{-0.00634892, 0.0469787, 0.975649, 0.00800729, -0.0857652, -0.0733767,
```

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```
-0.0444004, 0.0414565, -0.028985, -0.0509261, -0.0875459, -0.0151254, -0.0029478, -0.0152558,
-0.0190962, -0.0716269, -0.0762463, 0.032735, 0.0303479, 0.0670751} → SpikePositive_17,
{-0.0348226, 0.0207203, 0.973886, 0.102139, 0.0937659, 0.0986344, -0.0129664, 0.0218629,
0.0236153, 0.0251701, 0.018967, 0.0269387, -0.02418, 0.024597, 0.00700588, 0.0889882,
0.0672893, -0.0561361, 0.0182105, 0.0293179} → SpikePositive_15, 0.16385, 1, 1],
{0.0844609, 0.0592278, 0.971989, -0.0221568, -0.0503454, -0.0670139, 0.0116156,
0.0450434, 0.0504005, -0.0432833, 0.0256569, -0.0409855, -0.0319116, 0.0493455, 0.0487706,
-0.0895384, -0.0911685, -0.0381602, -0.0419681, 0.0527794} → SpikePositive_20, 0.290051, 2, 1],
Cluster[Cluster[{0.966576, 0.0396294, -0.0684005, 0.0197313, 0.0649133, -0.00424926,
-0.0689057, -0.0837356, 0.0322856, -0.020455, -0.0225326, -0.0600544, 0.0082849, 0.0941703,
-0.0974221, -0.0422418, -0.0263268, 0.0443156, 0.0974553, -0.0718231} → SpikePositive_3,
{0.970565, 0.0563423, -0.0356883, -0.0918923, -0.0354868, 0.0814418, -0.0590716,
0.0424911, -0.082389, -0.0730024, 0.0344587, -0.0578783, -0.0782079, 0.00597631, 0.00796937,
-0.00564963, -0.0759616, -0.0188232, 0.0536684, 0.00422988} → SpikePositive_8, 0.220501, 1,
1], {0.0558479, 0.0585074, 0.975087, 0.059428, 0.0865757, -0.0195558, 0.0437175, -0.0121055,
-0.059396, 0.00279565, -0.00467662, -0.0163185, 0.0921236, -0.0810352, -0.00573544, 0.0107053,
0.0954525, -0.00134351, -0.000141434, 0.0325192} → SpikePositive_14, 0.260663, 2, 1],
0.363707, 3, 3], {0.00840957, 0.0853478, 0.964152, -0.0619487, -0.0761645, -0.0371389,
0.0267932, 0.0773386, -0.000715143, -0.0403987, -0.00252004, 0.0520121, -0.0283832,
-0.0640981, 0.0813266, -0.0655443, 0.0510528, -0.0833161, -0.0978328, 0.077786} →
SpikePositive_11, 0.398224, 6, 1], 0.486106, 6, 7],
Cluster[{0.0261203, -0.0459348, 0.960193, -0.0535144, -0.0796904, -0.0385966, 0.0668307,
0.0443286, -0.0742133, 0.0352114, 0.0024666, 0.100321, 0.0775953, -0.0165483,
-0.100866, -0.0889614, 0.063578, -0.00742959, 0.0912017, -0.0669753} → SpikePositive_18,
{0.961868, -0.0121292, 0.0454807, -0.0987756, 0.00861658, 0.0563813, 0.0195099,
0.0702466, -0.0892035, 0.0811513, -0.0577825, 0.0549826, -0.0791978,
-0.0619687, 0.0176499, 0.0675396, 0.083561, -0.0549534, 0.0268929, 0.0874893} →
SpikePositive_7, 0.342411, 1, 1], 0.538803, 13, 2],
Cluster[{0.96379, -0.0948729, -0.0252853, 0.0827415, -0.0532786, 0.0877364,
0.0347807, 0.0299562, 0.0698768, -0.0707597, 0.0516924,
-0.0689011, 0.00595017, 0.0754929, -0.0433978, 0.0682848,
0.0278066, -0.0330652, 0.0622196, -0.0815615} → SpikePositive_10,
Cluster[Cluster[Cluster[{-0.0466938, 0.00775181, 0.973392, -0.026675, -0.0137985, 0.0653713,
-0.0746897, -0.0288424, 0.0796465, -0.0156034, -0.0740683, -0.0604558, 0.0863012, -0.0237339,
-0.0304634, 0.039449, 0.0785187, -0.0295269, 0.0659963, 0.0326474} → SpikePositive_16,
{-0.00854676, 0.0858518, 0.965705, -0.0126694, -0.0605102, -0.0160961, 0.0455675,
-0.073144, 0.0961231, 0.090109, -0.00755778, -0.0155226, 0.0525843, -0.0435363, 0.0950979,
0.0628887, 0.0859513, 0.0399965, 0.0644759, -0.00107979} → SpikePositive_19, 0.232815, 1, 1],
{0.0500355, -0.0685108, 0.975847, -0.0570955, -0.0412712, 0.0755937, 0.0204554, 0.0170235,
0.0554969, 0.0920522, -0.0136969, -0.0725248, -0.0180233, 0.0342937, 0.01804, 0.016408,
-0.0746403, 0.054622, -0.00722388, 0.0378922} → SpikePositive_12, 0.303895, 2, 1],
{-0.0432619, -0.0325615, 0.972197, 0.0255384, -0.0749987, 0.101228, -0.0550282,
0.0577603, 0.0748688, -0.0624347, -0.0131491, -0.0213904, -0.0596143, 0.0307112,
-0.0564378, 0.0196663, -0.0250186, 0.0728887, 0.0200498, -0.0668496} →
SpikePositive_13, 0.329013, 3, 1], 0.405326, 1, 4], 0.605384, 15, 5],
InitialSplitCluster → {Cluster[Cluster[Cluster[Cluster[Cluster[
Cluster[{0.984595, 0.0426538, 0.0179441, -0.0228628, 0.0250083, -0.0278621, -0.0652766,
-0.0604749, 0.0729085, -0.0203339, 0.026914, 0.0384599, -0.00443374, 0.0214493,
0.0470012, 0.0542644, 0.000931502, -0.0266604, -0.0612261, 0.0237265} → SpikePositive_1,
{0.957834, -0.0838027, -0.0202768, -0.0447831, 0.0898779, -0.0260558, -0.0909962,
0.0393741, 0.0762775, -0.0946617, -0.0849301, -0.0512037, -0.0799125, 0.0210224, -0.0376881,
-0.0060933, -0.0535727, -0.0547708, -0.0976687, 0.07886} → SpikePositive_5, 0.157065, 1, 1],
{0.970907, -0.00593115, 0.0210836, -0.058253, 0.0015684, -0.0431886, -0.0209517,
-0.097558, 0.0191591, -0.000431375, -0.00686202, -0.0594855, 0.0716292, -0.0952797, 0.0536522,
-0.063791, -0.0974441, 0.0173567, 0.0563725, 0.0596441} → SpikePositive_2, 0.328567, 2, 1],
Cluster[Cluster[{0.971727, -0.0596889, 0.0474448, -0.0640848, -0.000744131, 0.0568001,
0.0606394, -0.0352061, 0.0621654, 0.0802062, -0.0349508, 0.0319642, -0.00523245, 0.044493,
0.0821664, 0.0731019, -0.0532013, -0.0455357, 0.0520489, 0.0585355} → SpikePositive_4,
{0.966423, -0.0674757, 0.0554647, -0.0432617, 0.0597318, 0.0312359, -0.0146744,
-0.101786, -0.0521611, 0.0758959, 0.0712873, 0.0182951, 0.0242038, 0.0207882, 0.102946,
-0.0851805, 0.0231602, 0.0501532, 0.0735243, 0.0133773} → SpikePositive_9, 0.193079, 1, 1],
{0.973177, -0.0143179, 0.017454, -0.0815008, 0.0640615, -0.0718526, -0.020035,
0.0468446, -0.0351388, -0.026056, -0.0783309, -0.0574767, -0.0713074, 0.0296903,
0.0391121, -0.0842894, -0.0214224, 0.0842498, -0.00426514, -0.0195874} → SpikePositive_6,
0.257644, 2, 1], 0.332385, 3, 3], Cluster[Cluster[Cluster[
Cluster[{-0.00634892, 0.0469787, 0.975649, 0.00800729, -0.0857652, -0.0733767, -0.0444004,
```

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```
                0.0414565, -0.028985, -0.0509261, -0.0875459, -0.0151254, -0.0029478, -0.0152558,
                -0.0190962, -0.0716269, -0.0762463, 0.032735, 0.0303479, 0.0670751} → SpikePositive_17,
              {-0.0348226, 0.0207203, 0.973886, 0.102139, 0.0937659, 0.0986344, -0.0129664,
                0.0218629, 0.0236153, 0.0251701, 0.018967, 0.0269387, -0.02418, 0.024597, 0.00700588,
                0.0889882, 0.0672893, -0.0561361, 0.0182105, 0.0293179} → SpikePositive_15, 0.16385, 1, 1],
            {0.0844609, 0.0592278, 0.971989, -0.0221568, -0.0503454, -0.0670139, 0.0116156, 0.0450434,
              0.0504005, -0.0432833, 0.0256569, -0.0409855, -0.0319116, 0.0493455, 0.0487706, -0.0895384,
              -0.0911685, -0.0381602, -0.0419681, 0.0527794} → SpikePositive_20, 0.290051, 2, 1],
          Cluster[Cluster[{0.966576, 0.0396294, -0.0684005, 0.0197313, 0.0649133, -0.00424926,
                -0.0689057, -0.0837356, 0.0322856, -0.020455, -0.0225326, -0.0600544, 0.0082849, 0.0941703,
                -0.0974221, -0.0422418, -0.0263268, 0.0443156, 0.0974553, -0.0718231} → SpikePositive_3,
              {0.970565, 0.0563423, -0.0356883, -0.0918923, -0.0354868, 0.0814418, -0.0590716,
                0.0424911, -0.082389, -0.0730024, 0.0344587, -0.0578783, -0.0782079, 0.00597631, 0.00796937,
                -0.00564963, -0.0759616, -0.0188232, 0.0536684, 0.00422988} → SpikePositive_8, 0.220501,
              1, 1], {0.0558479, 0.0585074, 0.975087, 0.059428, 0.0865757, -0.0195558, 0.0437175,
              -0.0121055, -0.059396, 0.00279565, -0.00467662, -0.0163185, 0.0921236, -0.0810352,
              -0.00573544, 0.0107053, 0.0954525, -0.00134351, -0.000141434, 0.0325192} → SpikePositive_14,
            0.260663, 2, 1], 0.363707, 3, 3], {0.00840957, 0.0853478, 0.964152, -0.0619487,
            -0.0761645, -0.0371389, 0.0267932, 0.0773386, -0.000715143, -0.0403987, -0.00252004,
            0.0520121, -0.0283832, -0.0640981, 0.0813266, -0.0655443, 0.0510528, -0.0833161,
            -0.0978328, 0.077786} → SpikePositive_11, 0.398224, 6, 1], 0.486106, 6, 7],
        Cluster[{0.0261203, -0.0459348, 0.960193, -0.0535144, -0.0796904, -0.0385966, 0.0668307,
            0.0443286, -0.0742133, 0.0352114, 0.0024666, 0.100321, 0.0775953, -0.0165483,
            -0.100866, -0.0889614, 0.063578, -0.00742959, 0.0912017, -0.0669753} → SpikePositive_18,
          {0.961868, -0.0121292, 0.0454807, -0.0987756, 0.00861658, 0.0563813, 0.0195099,
            0.0702466, -0.0892035, 0.0811513, -0.0577825, 0.0549826, -0.0791978,
            -0.0619687, 0.0176499, 0.0675396, 0.083561, -0.0549534, 0.0268929, 0.0874893} →
           SpikePositive_7, 0.342411, 1, 1], 0.538803, 13, 2],
       Cluster[{0.96379, -0.0948729, -0.0252853, 0.0827415, -0.0532786, 0.0877364,
           0.0347807, 0.0299562, 0.0698768, -0.0707597, 0.0516924,
           -0.0689011, 0.00595017, 0.0754929, -0.0433978, 0.0682848,
           0.0278066, -0.0330652, 0.0622196, -0.0815615} → SpikePositive_10,
        Cluster[Cluster[Cluster[{-0.0466938, 0.00775181, 0.973392, -0.026675, -0.0137985, 0.0653713,
              -0.0746897, -0.0288424, 0.0796465, -0.0156034, -0.0740683, -0.0604558, 0.0863012, -0.0237339,
              -0.0304634, 0.039449, 0.0785187, -0.0295269, 0.0659963, 0.0326474} → SpikePositive_16,
            {-0.00854676, 0.0858518, 0.965705, -0.0126694, -0.0605102, -0.0160961, 0.0455675,
              -0.073144, 0.0961231, 0.090109, -0.00755778, -0.0155226, 0.0525843, -0.0435363, 0.0950979,
              0.0628887, 0.0859513, 0.0399965, 0.0644759, -0.00107979} → SpikePositive_19, 0.232815, 1, 1],
           {0.0500355, -0.0685108, 0.975847, -0.0570955, -0.0412712, 0.0755937, 0.0204554,
             0.0170235, 0.0554969, 0.0920522, -0.0136969, -0.0725248, -0.0180233, 0.0342937, 0.01804,
             0.016408, -0.0746403, 0.054622, -0.00722388, 0.0378922} → SpikePositive_12, 0.303895, 2, 1],
          {-0.0432619, -0.0325615, 0.972197, 0.0255384, -0.0749987, 0.101228, -0.0550282,
            0.0577603, 0.0748688, -0.0624347, -0.0131491, -0.0213904, -0.0596143, 0.0307112,
            -0.0564378, 0.0196663, -0.0250186, 0.0728887, 0.0200498, -0.0668496} →
           SpikePositive_13, 0.329013, 3, 1], 0.405326, 1, 4], 0.605384, 15, 5]},
  GroupAssociations → <|G1 → {SpikePositive_1, SpikePositive_5, SpikePositive_2,
       SpikePositive_4, SpikePositive_9,
       SpikePositive_6, SpikePositive_17,
       SpikePositive_15, SpikePositive_20,
       SpikePositive_3, SpikePositive_8,
       SpikePositive_14, SpikePositive_11,
       SpikePositive_18, SpikePositive_7,
       SpikePositive_10, SpikePositive_16,
       SpikePositive_19, SpikePositive_12,
       SpikePositive_13}|>|>|>
```

See Also

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Autocorrelation ▪ **CreateTimeSeries** ▪ **LombScargle** ▪ **MatrixClusters** ▪ **SeriesApplier** ▪ **SeriesCompare** ▪ **SeriesInternalCompare** ▪ **TimeExtractor** ▪ **TimeSeriesClassification** ▪ **TimeSeriesModelFit** ▪ **TimeSeriesClusters**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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Tutorials ▾ See Also ▾ Related Guides ▾

URL ▾

TimeSeriesSingleDendrogramHeatmap

TimeSeriesSingleDendrogramHeatmap[*data*]
generates a dendrogram and heatmap plot for time series data without subgrouping for classified time series data.

Details

- TimeSeriesSingleDendrogramHeatmap[data] generates a single tier clustering dendrogram and heatmap plot for one set of time series data clusters, typically the output of a single class of TimeSeriesSingleClusters . The input has the form of an association:

-
```
data =
 <|"Cluster" → cluster object,
  "InitialSplitCluster" → {InitialSplitCluster1, InitialSplitCluster2 ...},
  "GroupAssociations" → <|"G1" → {member list G1},
    "G2" → {member list for G2},
    ...,
    "Gn" → {member list for Group n}|>
 |>
```

- The keys of the data correspond to the following properties related to the one tier clustering results generated by TimeSeriesSingleClusters for a single classification class:

"Cluster"	Cluster generated.
"InitialSplitCluster"	Clusters resulting from splitting the initial cluster (reported by key "Cluster") into groups using the SignificanceCriterion to determine the number of clusters.
"GroupAssociations"	Association denoting membership of each initial data label to groups generated by the single tier clustering.

- The data can also be provided as a list with the corresponding values from the TimeSeriesSingleClusters clustering for a single classification class:

-
```
data =
 {cluster object,
  {InitialSplitCluster1, InitialSplitCluster2 ...},
  <|"G1" → {member list G1},
   "G2" → {member list for G2},
   ...,
   "Gn" → {member list for Group n}|>
 }
```

- The following options can be given:

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ColorBlending	{CMYKColor[1, 0, 1, 0], CMYKColor[0, 1, 1, 0]}	Color scheme for the plot. The color list is passed to an internal Blend function to create a ColorFunction for an internal ArrayPlot function.
DendrogramColor	RGBColor[1, 1, 0]	Color to highlight the dendrograms.
FrameName	"Dendrogram and Heatmap"	Label for plot frame.
GroupSubSize	0.1	Relative size of group reference column in plot.
HorizontalAxisName	Time (arbitrary units)	Label for the horizontal heatmap axis.
HorizontalLabels	None	Labels for horizontal axis for each column.
IndexColor	"DeepSeaColors"	Choice of color for labeling the group index.
ImageSize	200	ImageSize is an option that specifies the overall size of an image to display for an object.
ScaleShift	None	Option to reset the blend of the colors used overall. The option is a real positive number, and is used as a multiplier for an internal Blend function's second argument.
VerticalLabels	None	Labels for vertical axis for each row.

Examples (13)

Basic Examples (1)

First we need to load the MathIOmica package.

In[1]:=
```
Needs["MathIOmica`"]
```

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

- We have multiple classes:

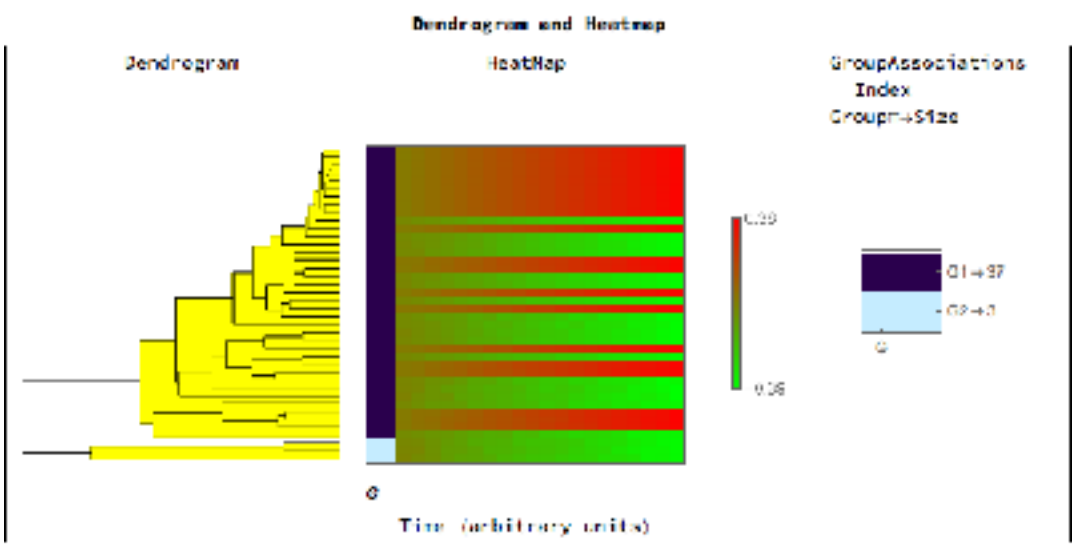
In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"]]
```

Out[4]=



The dendrogram is represented on the left, and is highlighted to represent the grouping level. The G column represents the groupings generated by the single tier clustering. The legend shows the corresponding groupings and the number of elements in each group. For example above, in group 1 (G1), we have 38 members. and in group 2 (G2) 2. We can extract the corresponding members from the input data:

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In[5]:=
```
clustersSingle["f1", "GroupAssociations", "G1"]
```

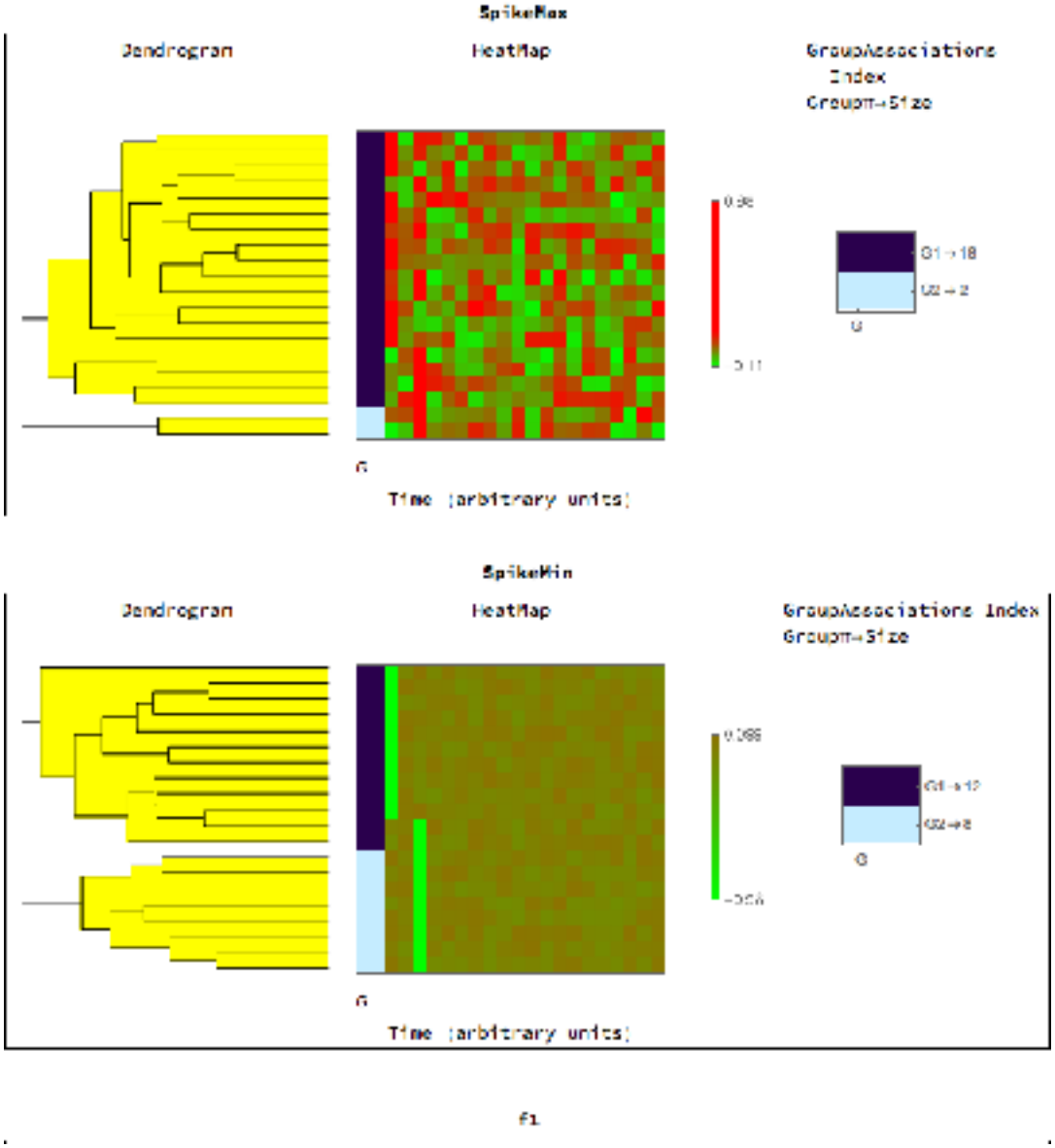
Out[5]=
```
{LinearPositive_1, LinearPositive_3, LinearPositive_6, LinearPositive_8,
 LinearPositive_10, LinearPositive_9, LinearPositive_7, LinearPositive_2, LinearPositive_5,
 LinearNegative_15, LinearPositive_11, LinearNegative_17, LinearNegative_11,
 LinearNegative_19, LinearPositive_13, LinearPositive_4, LinearNegative_20, LinearNegative_18,
 LinearPositive_16, LinearNegative_14, LinearPositive_15, LinearNegative_10,
 LinearNegative_2, LinearNegative_13, LinearNegative_12, LinearPositive_20, LinearNegative_16,
 LinearPositive_18, LinearPositive_12, LinearNegative_1, LinearNegative_9, LinearNegative_5,
 LinearNegative_4, LinearPositive_14, LinearPositive_17, LinearPositive_19, LinearNegative_8}
```

In[6]:=
```
clustersSingle["f1", "GroupAssociations", "G2"]
```

Out[6]=
```
{LinearNegative_3, LinearNegative_7, LinearNegative_6}
```

To plot all classes we can use TimeSeriesSingleDendrogramsHeatmaps:

In[7]:=
```
TimeSeriesSingleDendrogramsHeatmaps[clustersSingle]
```



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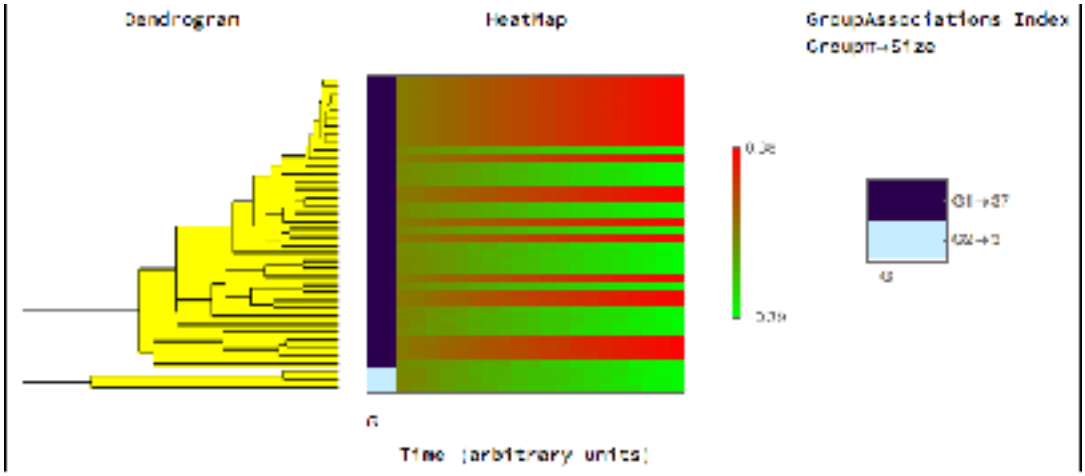
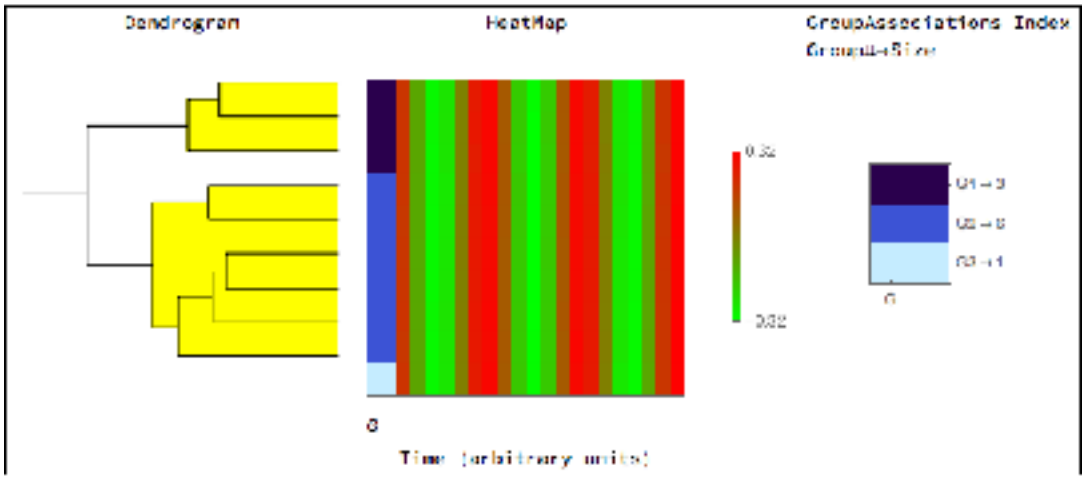
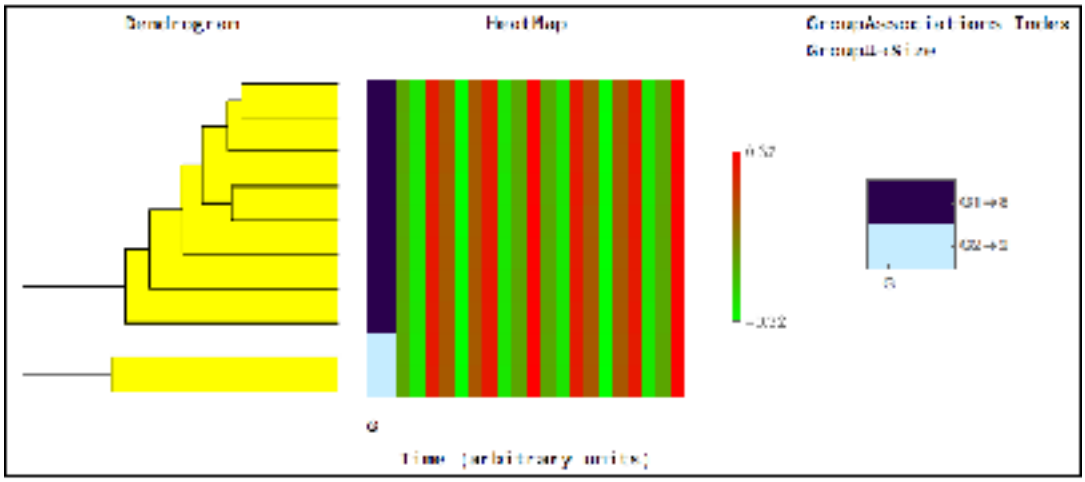


Out[7]=

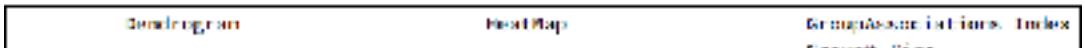
#3



#5



#6



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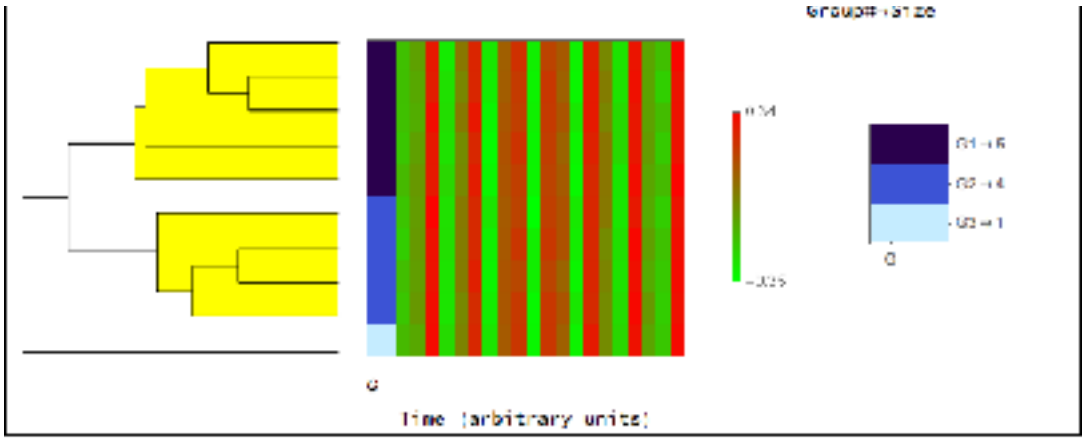

Generalizations & Extensions (11)

ColorBlending (2)

In[1]:=
```
Needs["MathIOmica`"]
```

ColorBlending provides a list of colors to be used in the plot to create gradient effects. Named colors can be used as well.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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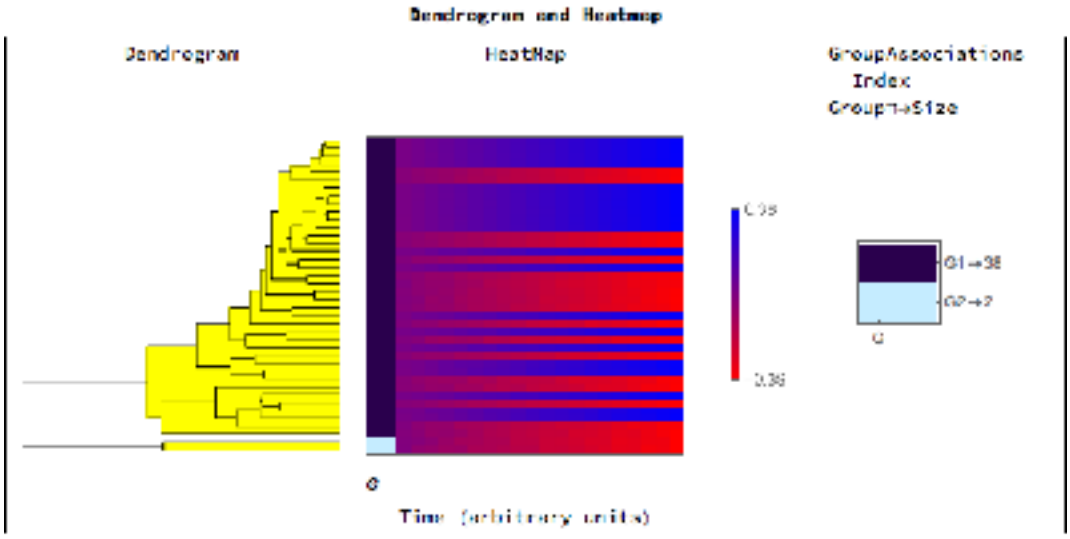
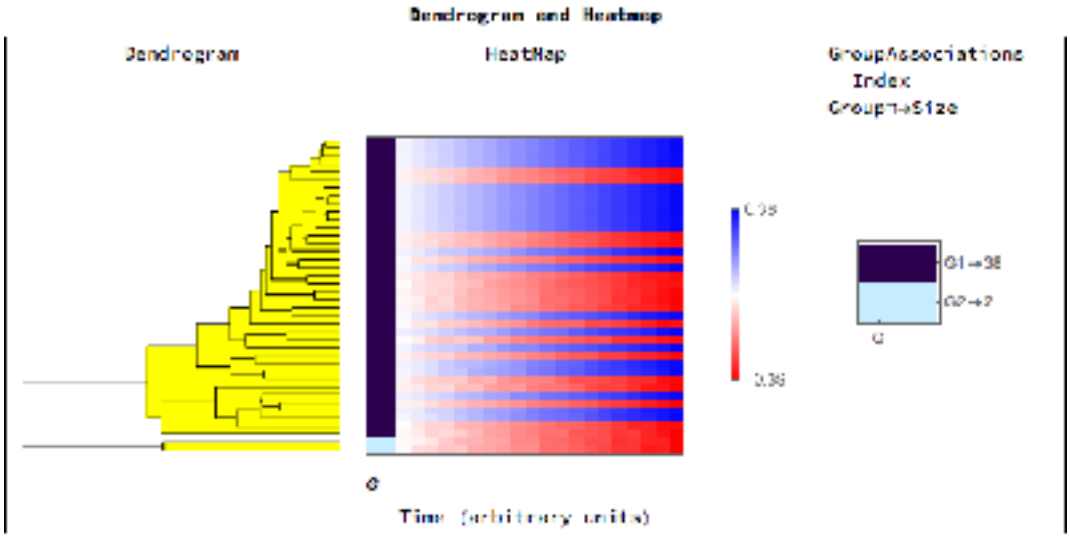
In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ColorBlending → {Red, Blue}]
```

Out[4]=



In[5]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ColorBlending → {Red, White, Blue}]
```

Out[5]=



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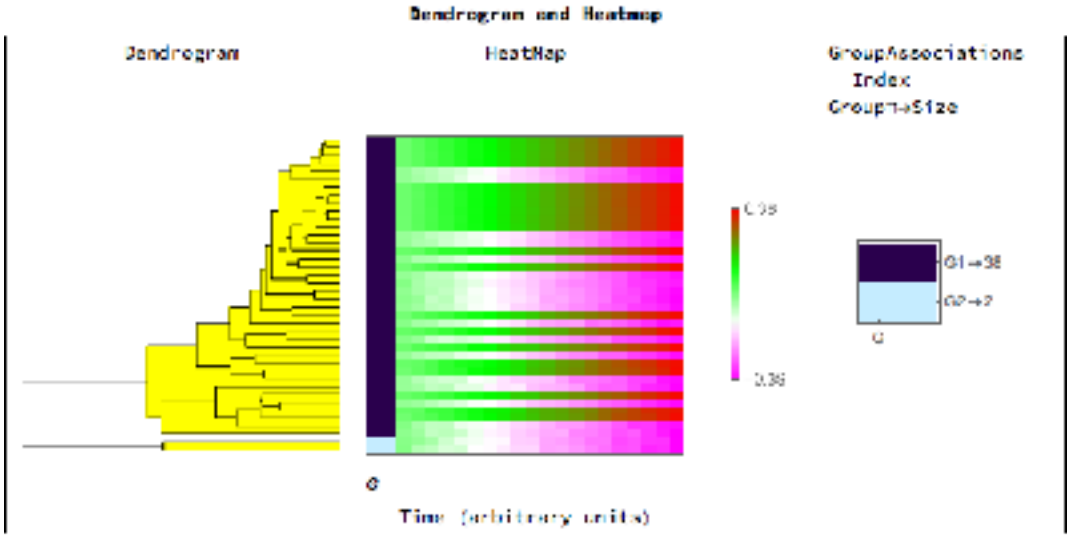
In[6]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"],
 ColorBlending → {RGBColor[1, 0, 1], White, CMYKColor[1, 0, 1, 0], CMYKColor[0, 1, 1, 0]}]
```

Out[6]=



In[1]:=
```
Needs["MathIOmica`"]
```

All of Mathematica's color gradients can be used instead of a list:

In[2]:=
```
ColorData["Gradients"]
```

Out[2]=
```
{AlpineColors, Aquamarine, ArmyColors, AtlanticColors, AuroraColors, AvocadoColors,
 BeachColors, BlueGreenYellow, BrassTones, BrightBands, BrownCyanTones, CandyColors, CherryTones,
 CMYKColors, CoffeeTones, DarkBands, DarkRainbow, DarkTerrain, DeepSeaColors, FallColors,
 FruitPunchColors, FuchsiaTones, GrayTones, GrayYellowTones, GreenBrownTerrain, GreenPinkTones,
 IslandColors, LakeColors, LightTemperatureMap, LightTerrain, MintColors, NeonColors, Pastel,
 PearlColors, PigeonTones, PlumColors, Rainbow, RedBlueTones, RedGreenSplit, RoseColors,
 RustTones, SandyTerrain, SiennaTones, SolarColors, SouthwestColors, StarryNightColors,
 SunsetColors, TemperatureMap, ThermometerColors, ValentineTones, WatermelonColors}
```

We consider the data which is classified and clustered:

In[3]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

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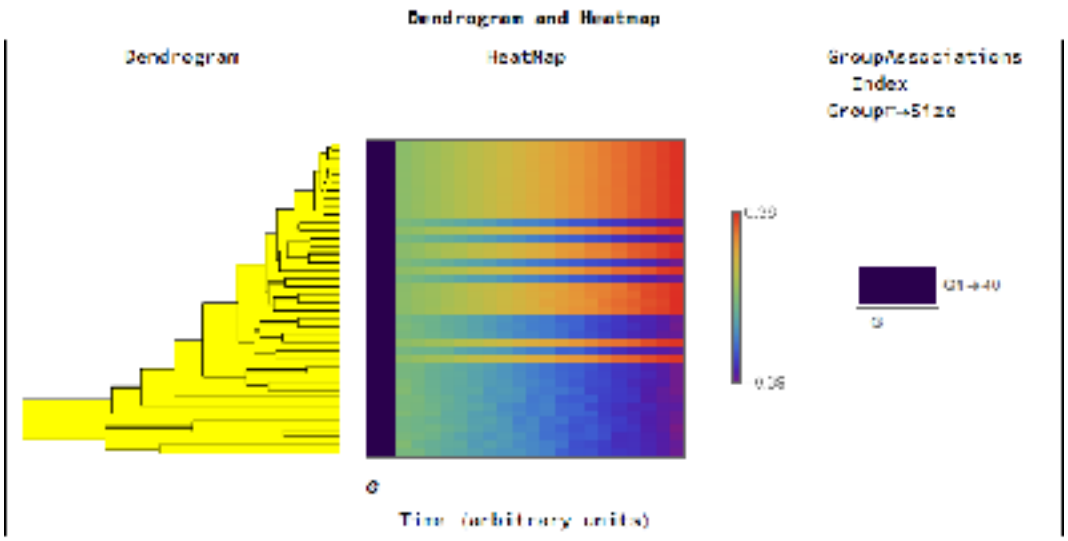
In[4]:=
```
Keys[clustersSingle]
```
Out[4]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

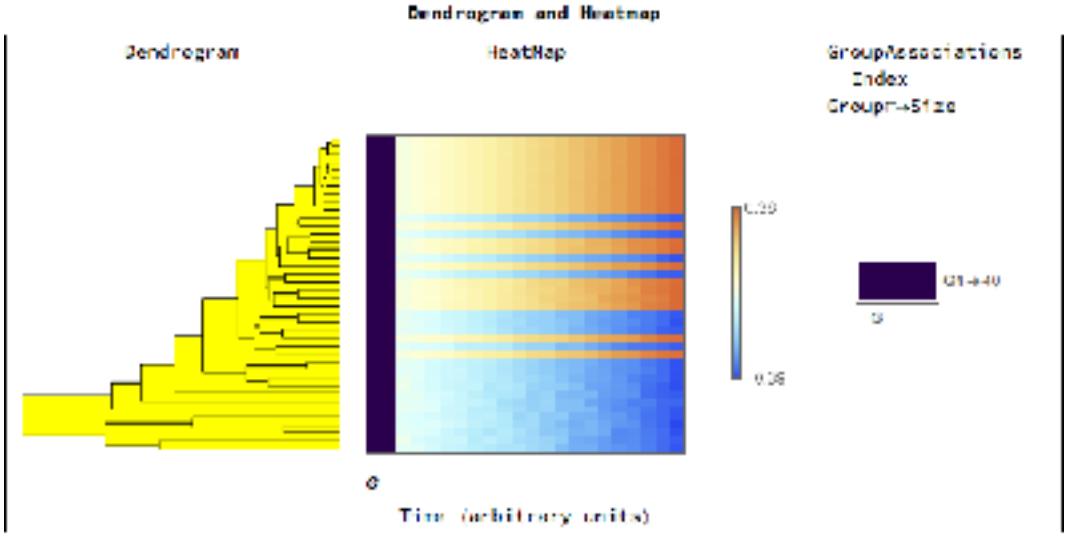
In[5]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ColorBlending → "Rainbow"]
```

Out[5]=



In[6]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ColorBlending → "LightTemperatureMap"]
```

Out[6]=



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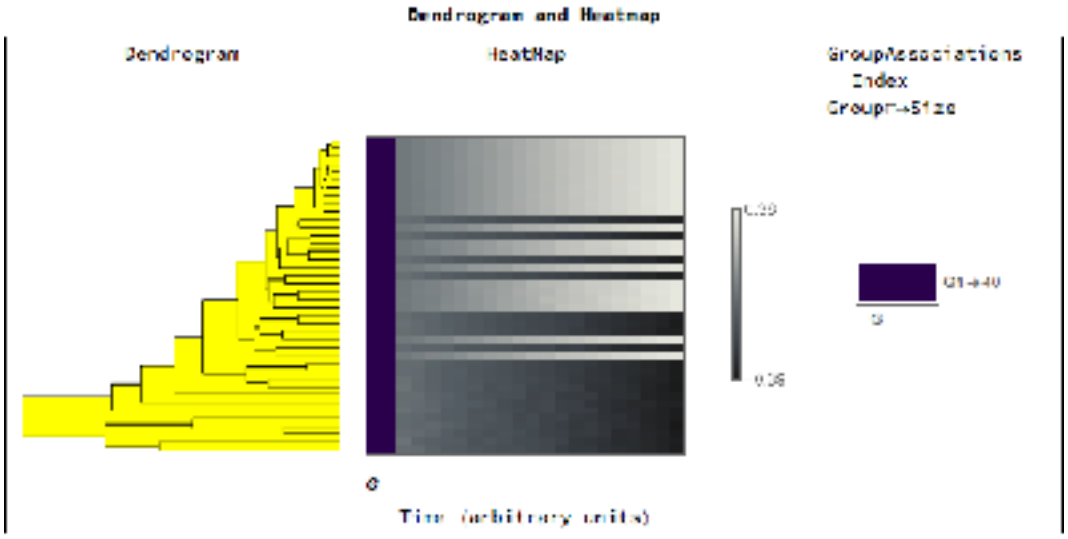
In[7]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ColorBlending → "GrayTones"]
```

Out[7]=



DendrogramColor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

DendrogramColor takes color values, for highlighting the dendrograms at the level where the groupings are called by the clustering.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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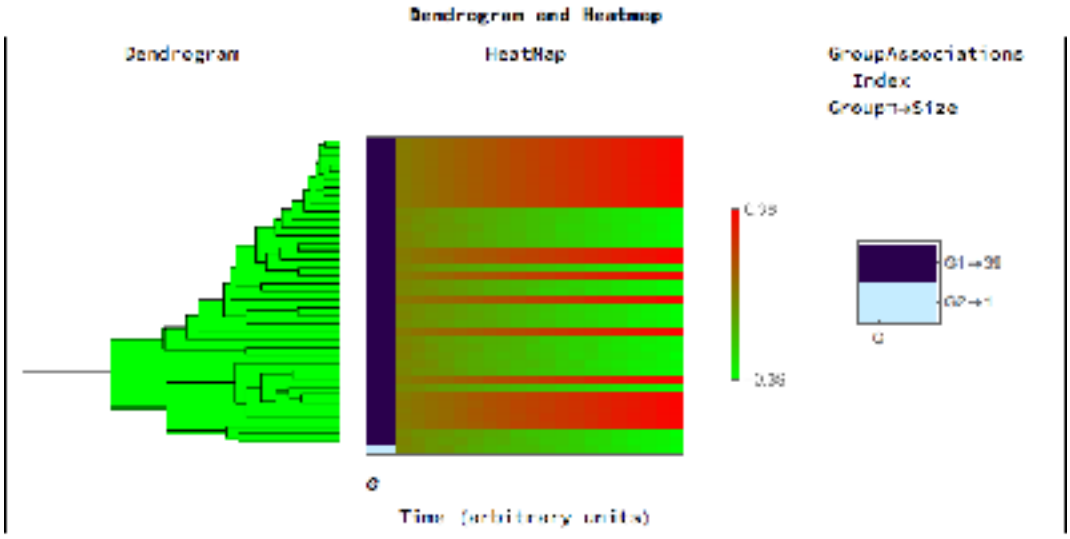
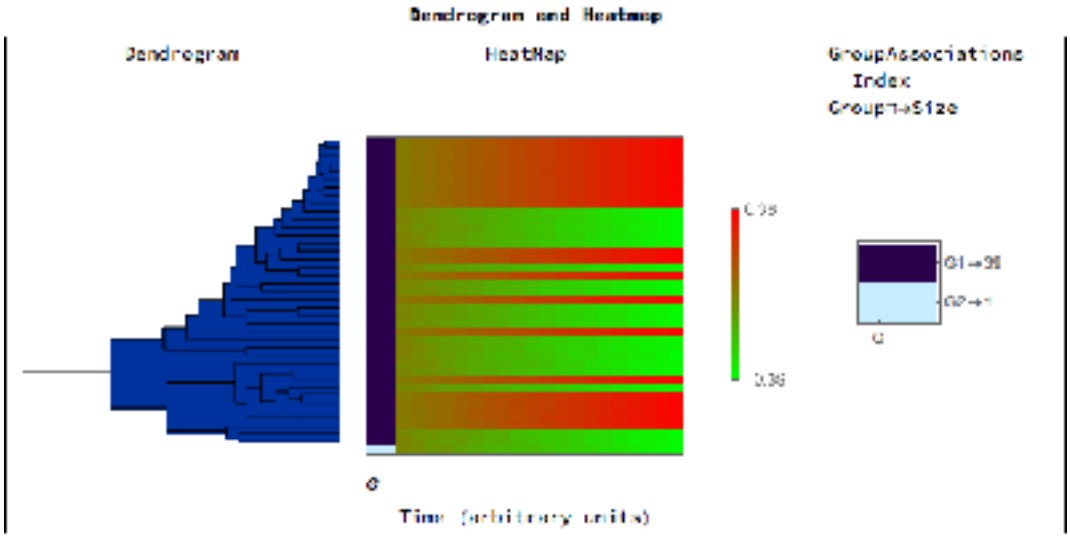
In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], DendrogramColor → RGBColor[0, 1, 0]]
```

Out[4]=



In[5]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], DendrogramColor → CMYKColor[1, .7, .05, .35]]
```

Out[5]=



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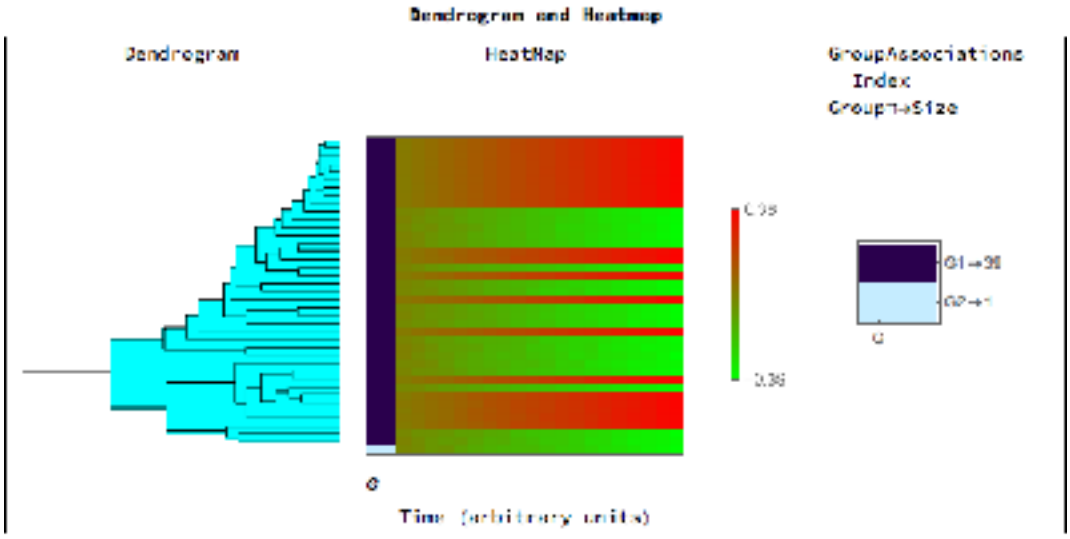
In[6]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], DendrogramColor → Cyan]
```

Out[6]=



FrameName (1)

In[1]:=
```
Needs["MathIOmica`"]
```

The FrameName option let's us create a label for plot frame.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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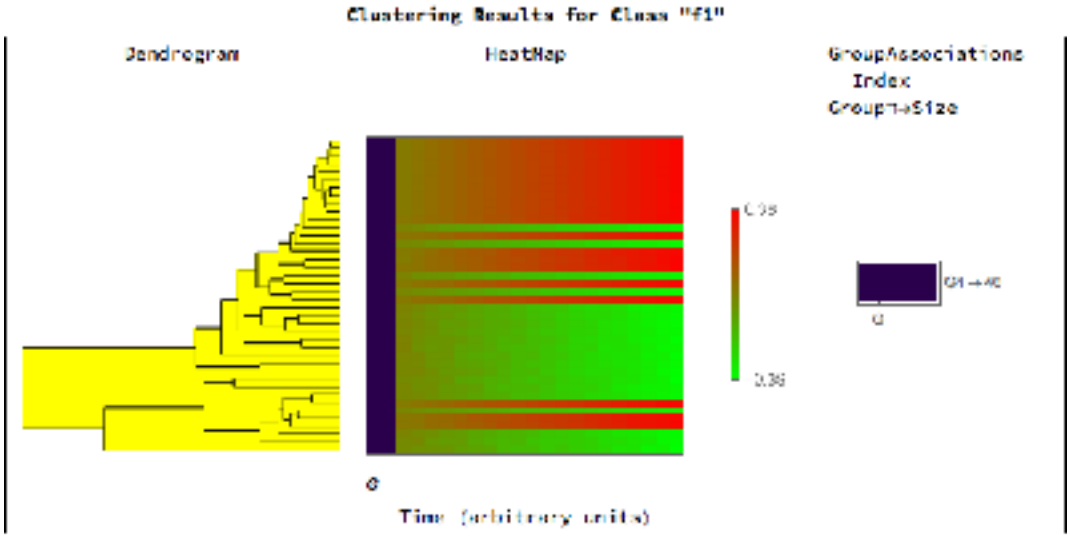
In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], FrameName → "Clustering Results for Class \"f1\""]
```

Out[4]=



GroupSubSize (1)

In[1]:=
```
Needs["MathIOmica`"]
```

GroupSubSize allows us to change the width (i.e. relative size as a fraction of the image) of the group reference column in the plots.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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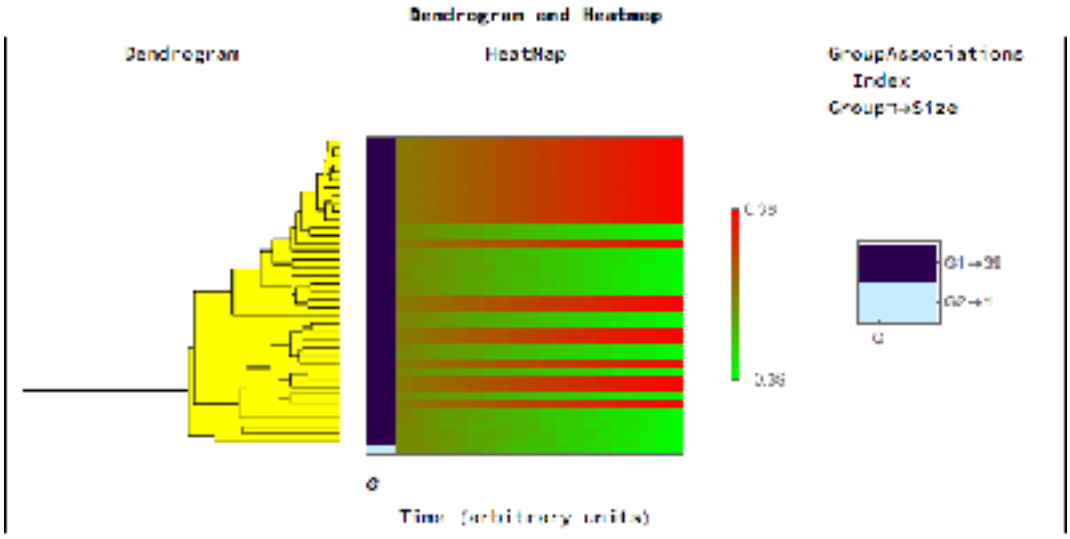
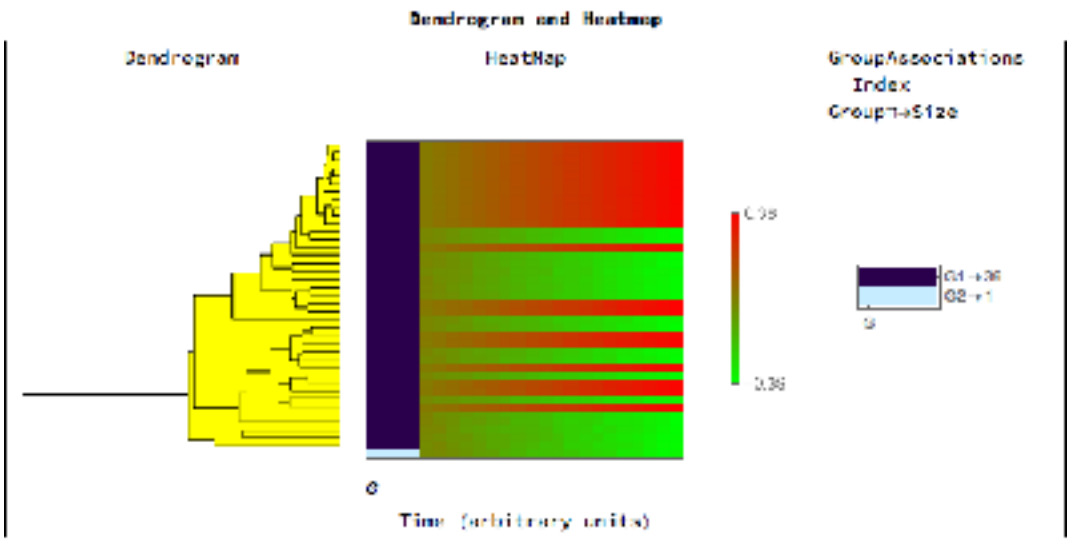
In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], GroupSubSize → 0.1]
```

Out[4]=



In[5]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], GroupSubSize → 0.2]
```

Out[5]=



HorizontalAxisName (1)

In[1]:=
```
Needs["MathIOmica`"]
```

HorizontalAxisName provides a label for the heatmap's horizontal axis.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

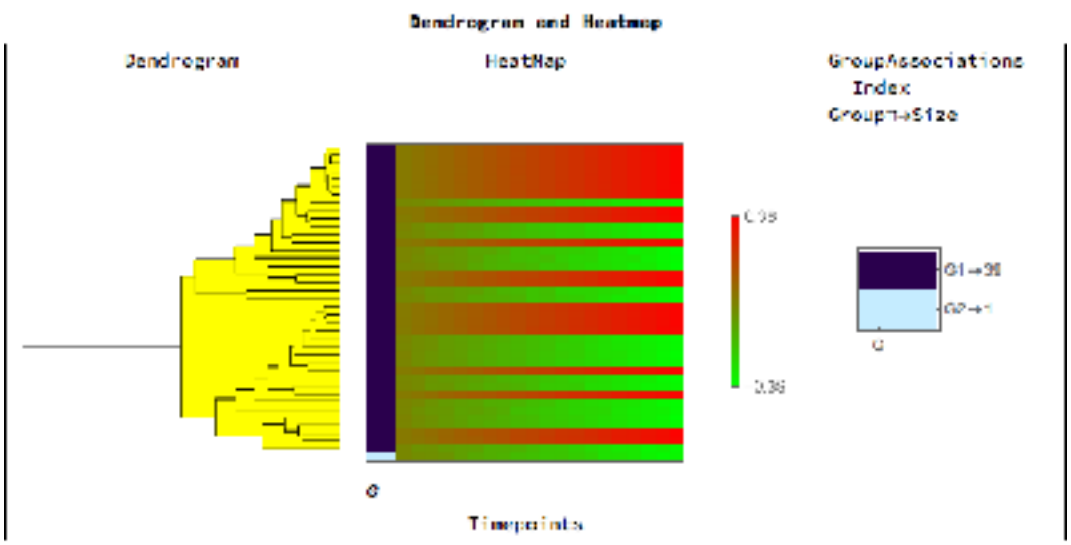
In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], HorizontalAxisName → "Timepoints"]
```

Out[4]=



HorizontalLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

HorizontalLabels provides labels for the horizontal heatmap axis.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

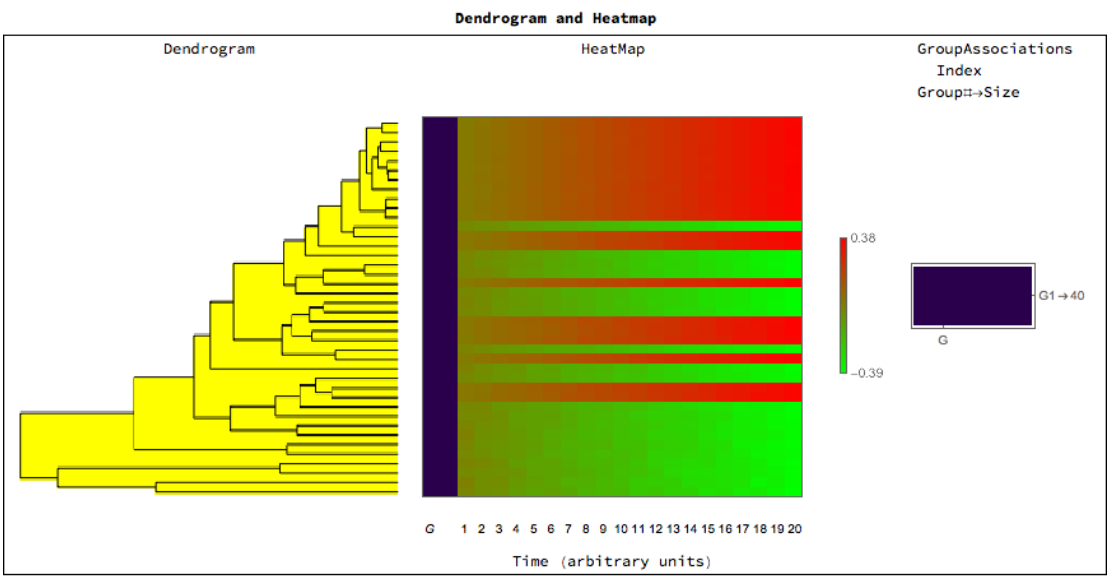
In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class (in this example we scale up the image as well to accomodate the extra labels):

In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ImageSize → 300, HorizontalLabels → Range[20]]
```

Out[4]=



IndexColor (1)

In[1]:=
```
Needs["MathIOmica`"]
```

IndexColor allows us to chose the color gradients for labeling the group index. Named Mathematica gradients can be used as well:

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In[2]:=
```
ColorData["Gradients"]
```

Out[2]=
```
{AlpineColors, Aquamarine, ArmyColors, AtlanticColors, AuroraColors, AvocadoColors,
 BeachColors, BlueGreenYellow, BrassTones, BrightBands, BrownCyanTones, CandyColors, CherryTones,
 CMYKColors, CoffeeTones, DarkBands, DarkRainbow, DarkTerrain, DeepSeaColors, FallColors,
 FruitPunchColors, FuchsiaTones, GrayTones, GrayYellowTones, GreenBrownTerrain, GreenPinkTones,
 IslandColors, LakeColors, LightTemperatureMap, LightTerrain, MintColors, NeonColors, Pastel,
 PearlColors, PigeonTones, PlumColors, Rainbow, RedBlueTones, RedGreenSplit, RoseColors,
 RustTones, SandyTerrain, SiennaTones, SolarColors, SouthwestColors, StarryNightColors,
 SunsetColors, TemperatureMap, ThermometerColors, ValentineTones, WatermelonColors}
```

We create, classify and cluster the following data for our example, for various trends and 20 time points:

In[3]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

In[4]:=
```
Keys[clustersSingle]
```

Out[4]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

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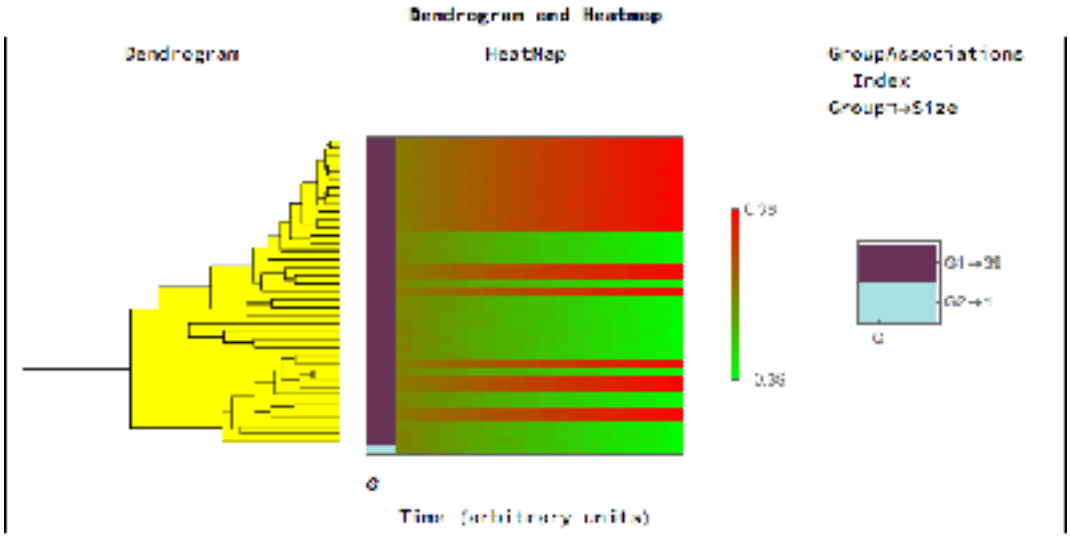
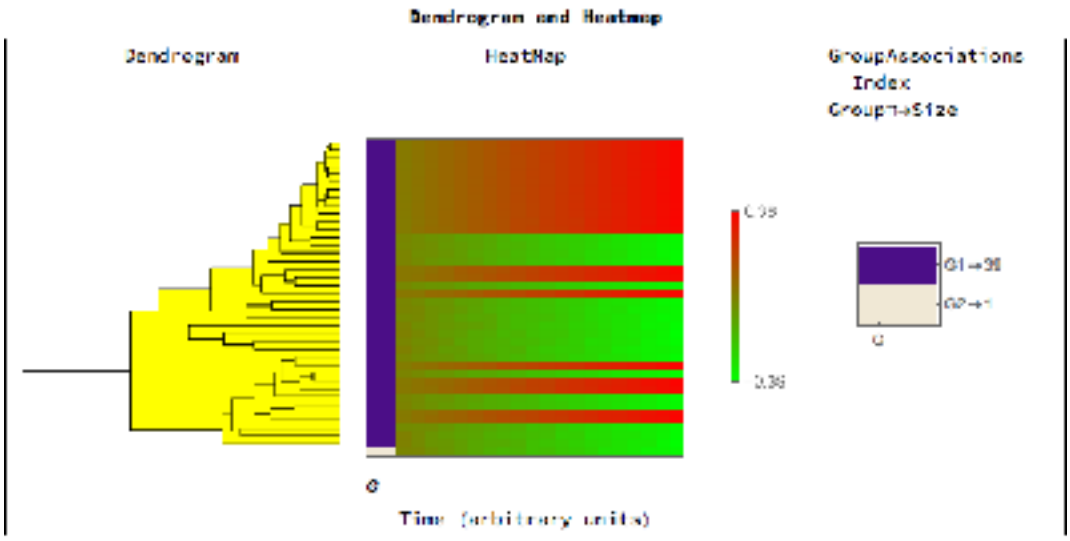
In[5]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], IndexColor → "CandyColors"]
```

Out[5]=



In[6]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], IndexColor → "LakeColors"]
```

Out[6]=



ImageSize (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ImageSize is an option that allows us to provide the overall size of the plots.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

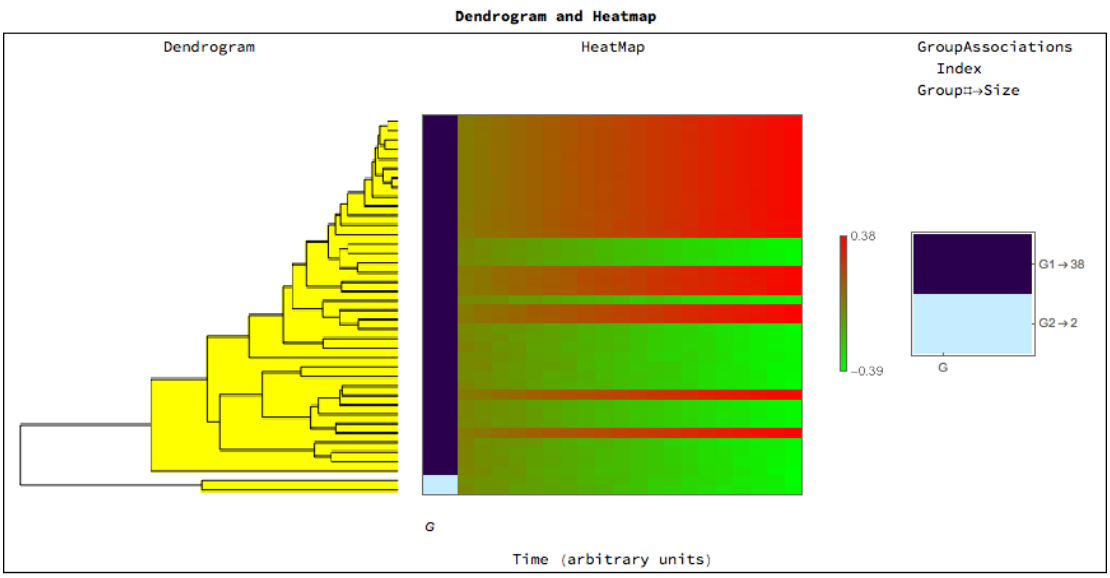
In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ImageSize → 300]
```

Out[4]=



ScaleShift (1)

In[1]:=
```
Needs["MathIOmica`"]
```

ScaleShift provides a shift of overall color in a heatmap, allowing for overall adjustments if necessary. We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

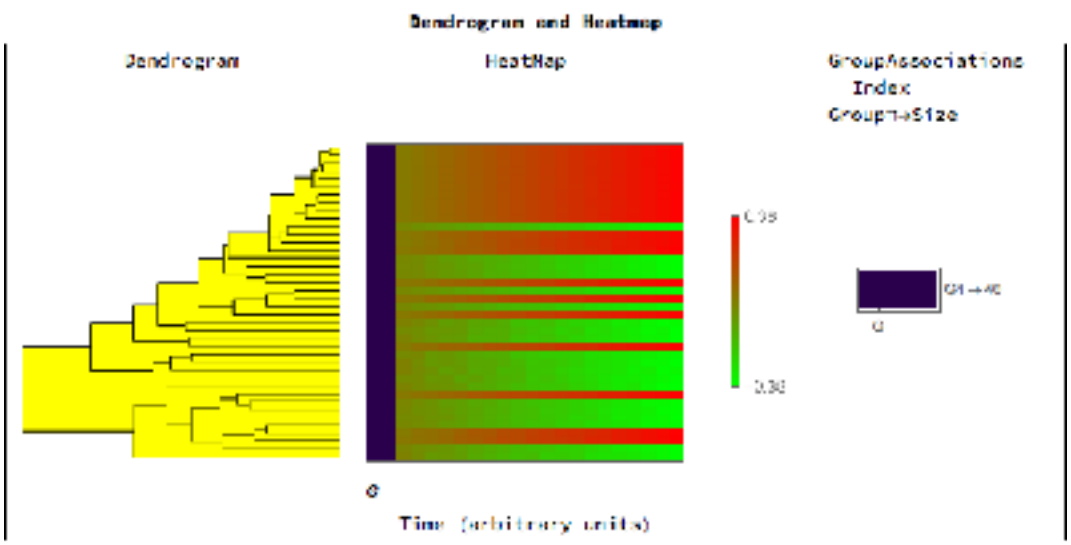
In[3]:=
```
Keys[clustersSingle]
```

Out[3]=
```
{SpikeMax, SpikeMin, f1, f3, f5, f6}
```

We can now plot the dendrogram for any given class:

In[4]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ScaleShift → 1]
```

Out[4]=



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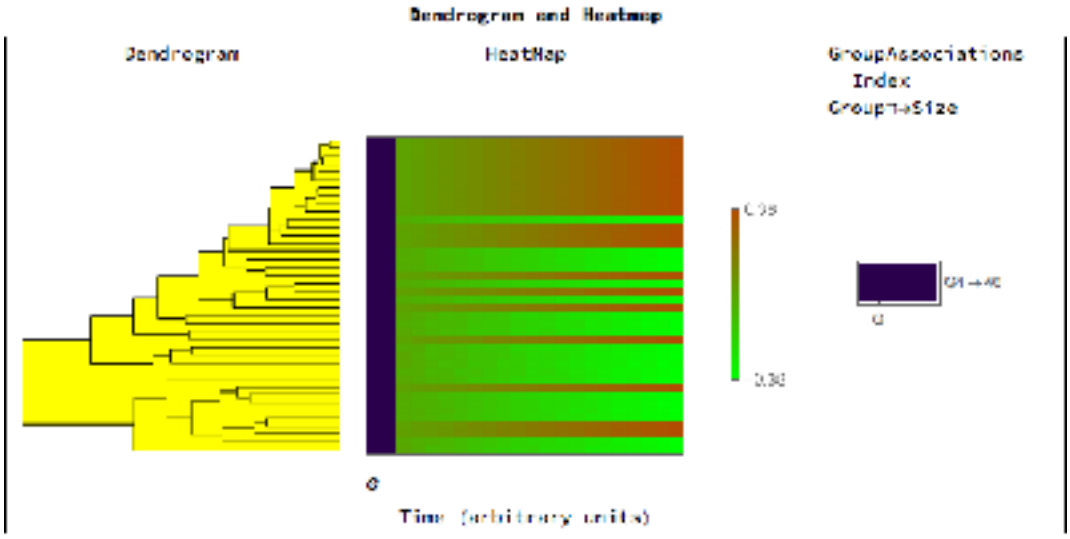
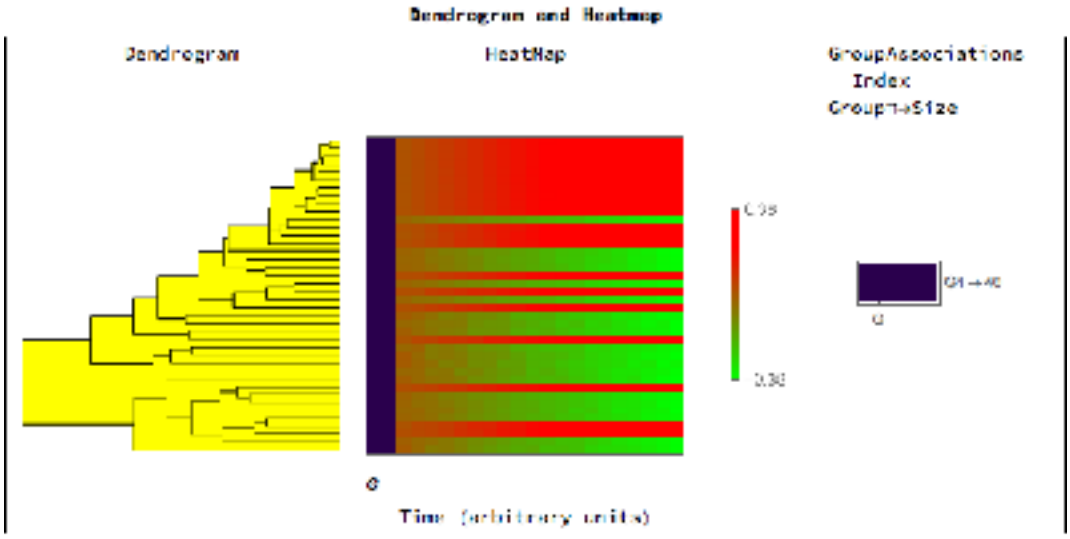
In[5]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ScaleShift → 0.7]
```

Out[5]=



In[6]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingle["f1"], ScaleShift → 1.3]
```

Out[6]=



VerticalLabels (1)

In[1]:=
```
Needs["MathIOmica`"]
```

VerticalLabels provides labels for the vertical heatmap axis (the default value is None). The labels are distributed evenly in the vertical direction.

We create, classify and cluster the following data for our example, for various trends and 20 time points:

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In[2]:=
```
classificationExampleSimple = Normalize[#] & /@
   Association[Join[Table["LP_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 5}],
     Table["LN_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 5}]]];
timePointsExample = Range[20];
classificationSimple = TimeSeriesClassification[classificationExampleSimple,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingleSimple = TimeSeriesSingleClusters[classificationSimple];
```

In[3]:=
```
Keys[clustersSingleSimple]
```

Out[3]=
```
{f1}
```

In[4]:=
```
Keys@Values@clustersSingleSimple
```

Out[4]=
```
{{Cluster, InitialSplitCluster, GroupAssociations}}
```

We can extract the labels for the clustering:

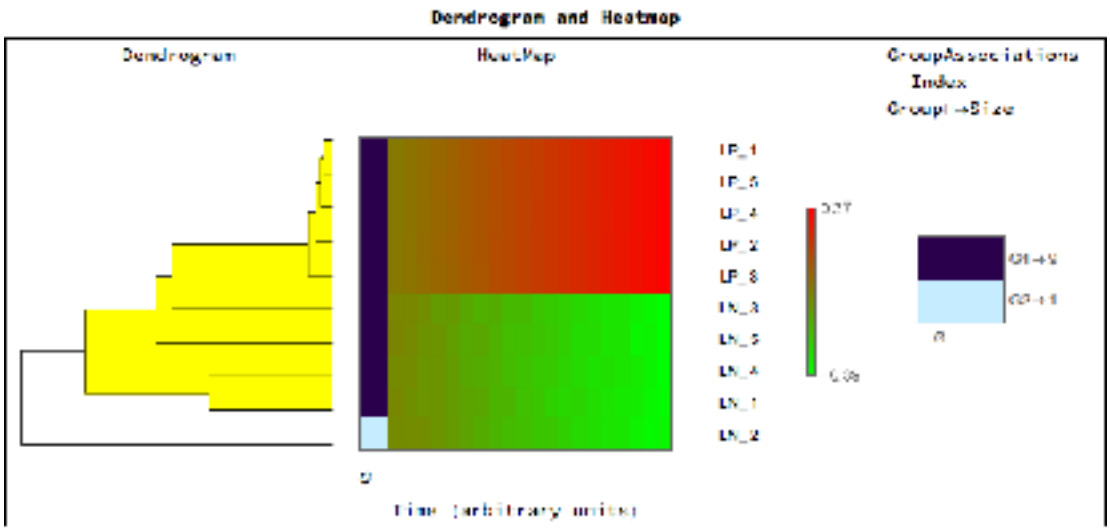
In[5]:=
```
Join @@ Query["f1", "GroupAssociations"]@clustersSingleSimple
```

Out[5]=
```
{LP_1, LP_5, LP_4, LP_2, LP_3, LN_3, LN_5, LN_4, LN_1, LN_2}
```

We can now plot the dendrogram for any given class:

In[6]:=
```
TimeSeriesSingleDendrogramHeatmap[clustersSingleSimple["f1"],
 VerticalLabels → Join @@ Query["f1", "GroupAssociations"]@clustersSingleSimple]
```

Out[6]=



Properties & Relations (1)

TimeSeriesSingleDendrogramsHeatmaps uses TimeSeriesSingleDendrogramHeatmap repeatedly to plot multiple classes generated from clustering (e.g. by TimeSeriesSingleClusters).

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See Also

Heatmapper ▪ **MatrixClusters** ▪ **MatrixDendrogramHeatmap** ▪ **MatrixDendrogramsHeatmaps** ▪ **TimeSeriesDendrogramHeatmap** ▪ **TimeSeriesDendrogramsHeatmaps** ▪ **TimeSeriesClusters** ▪ **TimeSeriesSingleClusters** ▪ **TimeSeriesSingleDendrogramsHeatmaps**

Tutorials

- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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URL ▾

TimeSeriesSingleDendrogramsHeatmaps

TimeSeriesSingleDendrogramsHeatmaps[*data*]
generate a dendrogram and heatmap plot for time series data without subgrouping for all classified time series data.

Details

- TimeSeriesSingleDendrogramsHeatmaps[*data*] generates dendrograms and associated heatmap plots for clustered time series data, typically the output of all classes generated by implementing TimeSeriesSingleClusters . The input has the form of an association:

- data =

```
<| Class1 → <|"Cluster" → cluster object1,
    "InitialSplitCluster" → {InitialSplitCluster11, InitialSplitCluster12 ...},
    "GroupAssociations" → <|"G1" → {member list G1},
      "G2" → {member list for G2},
      ...,
      "Gn1" → {member list for Gn1}|>|>,
  Class2 → <|"Cluster" → cluster object2,
    "InitialSplitCluster" → {InitialSplitCluster21, InitialSplitCluster22 ...},
    "GroupAssociations" → <|"G1" → {member list G1},
      "G2" → {member list for G2},
      ...,
      "Gn2" → {member list for Gn2}|>|>,
  ...,
  ClassM → <|"Cluster" → cluster objectM,
    "InitialSplitCluster" → {InitialSplitClusterM1, InitialSplitClusterM2 ...},
    "GroupAssociations" → <|"G1" → {member list G1},
      "G2" → {member list for G2},
      ...,
      "GnM" → {member list for GnM}|>|>
|>
```

- The keys of the data correspond to the following properties related to the single tier clustering results generated by TimeSeriesSingleClusters for each of the classification classes:

"Cluster"	Cluster generated.
"InitialSplitCluster"	Clusters resulting from splitting the initial cluster (reported by key "Cluster") into groups using the SignificanceCriterion to determine the number of clusters.
"GroupAssociations"	Association denoting membership of each initial data label to groups generated by the single tier clustering.

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- The following options can be given:

FunctionOptions	{ImageSize –> 200}	Options list passed to the internal TimeSeriesSingleDendrogramHeatmap function.

Examples (2)

Basic Examples (1)

First we need to load the MathIOmica package.

```
In[1]:= Needs["MathIOmica`"]
```

We create, classify and cluster the following data for our example, for various trends and 20 time points:

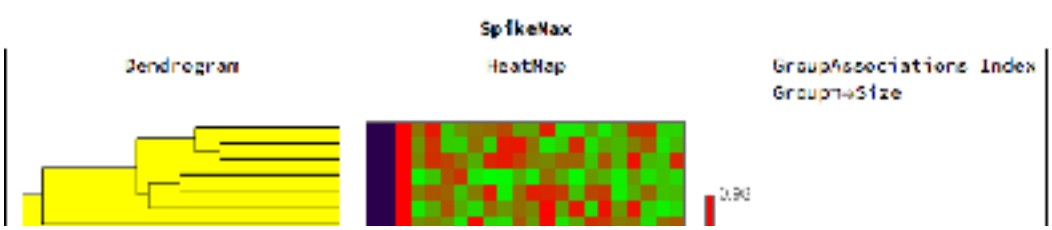
```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
          Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
           Table["Sinusoidal2_" <> ToString[i] →
             5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
           Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
            {i, 21, 30}]]];
        timePointsExample = Range[20];
        classification1 = TimeSeriesClassification[classificationExample1,
           timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
        clustersSingle = TimeSeriesSingleClusters[classification1];
```

- We have multiple classes:

```
In[3]:= Keys[clustersSingle]
Out[3]= {SpikeMax, SpikeMin, f1, f3, f5, f6}
```

- To plot all classes we use TimeSeriesSingleDendrogramsHeatmaps

```
In[4]:= TimeSeriesSingleDendrogramsHeatmaps[clustersSingle]
```



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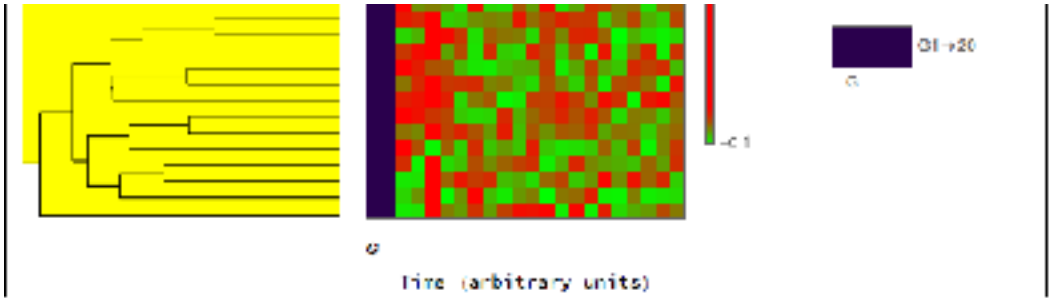
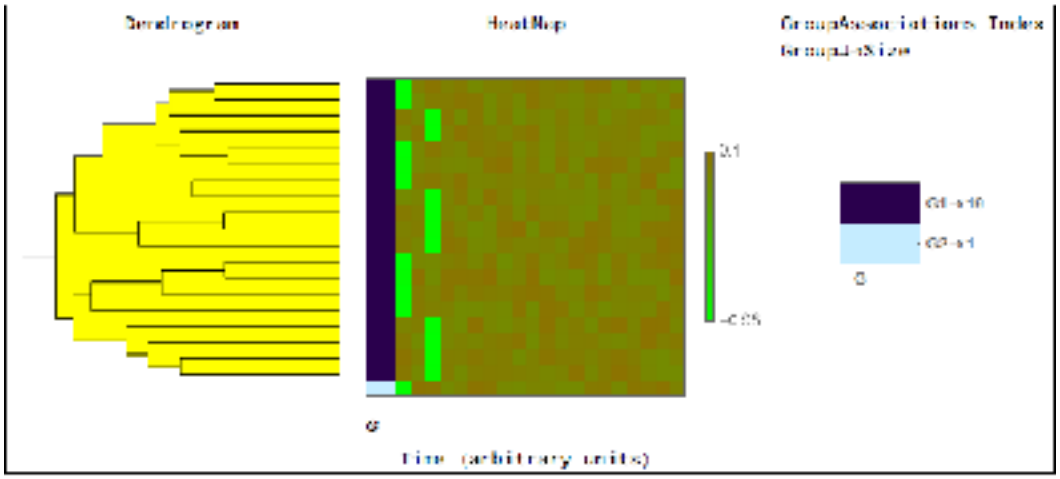
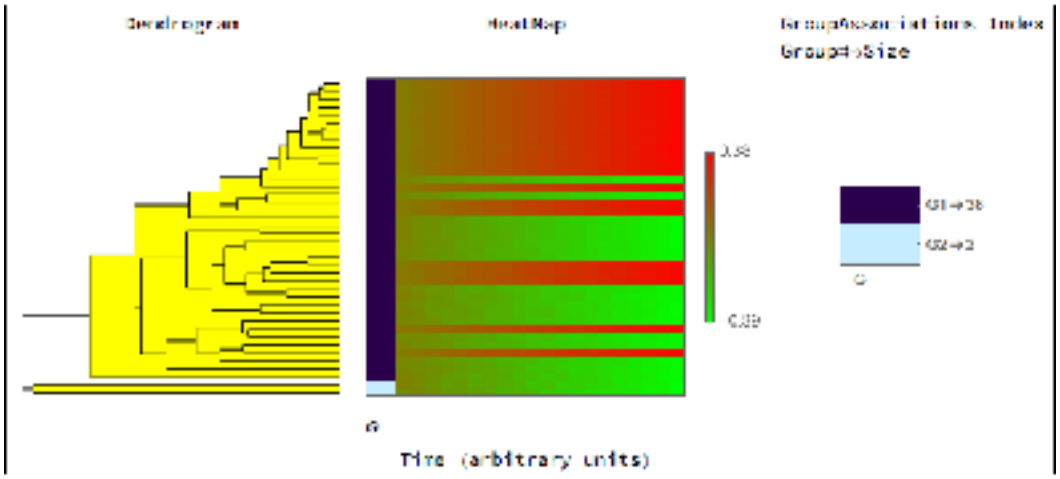


SpikeMin

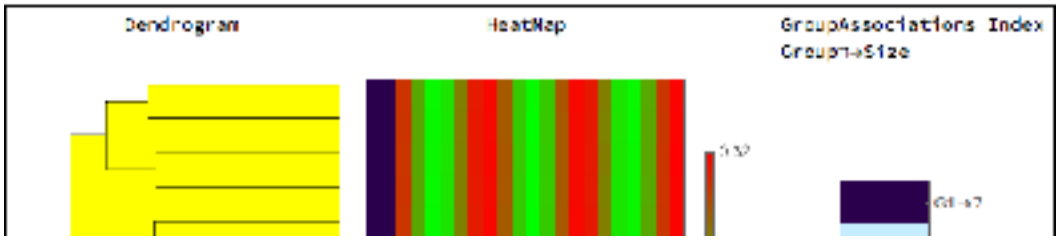


f1



Out[4]=

f2



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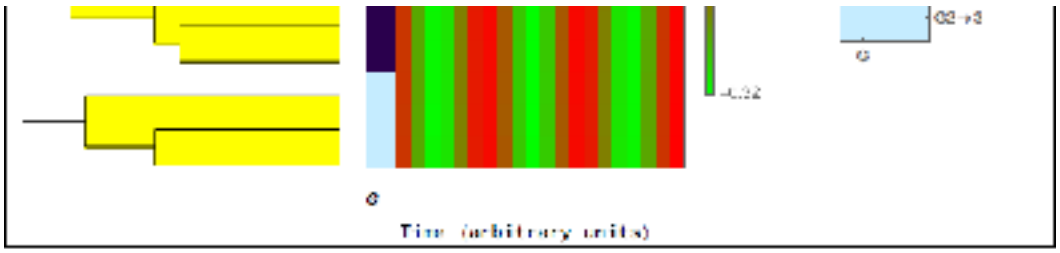

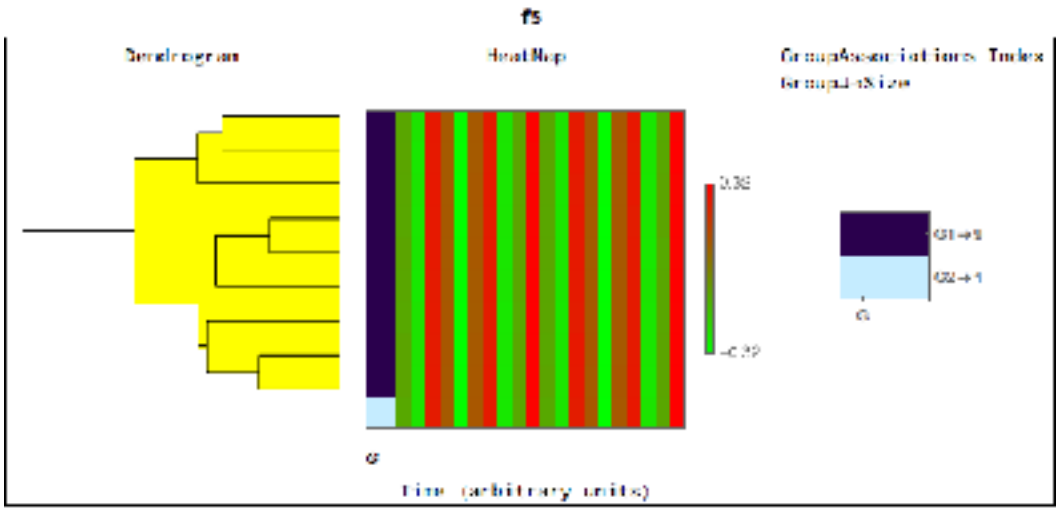

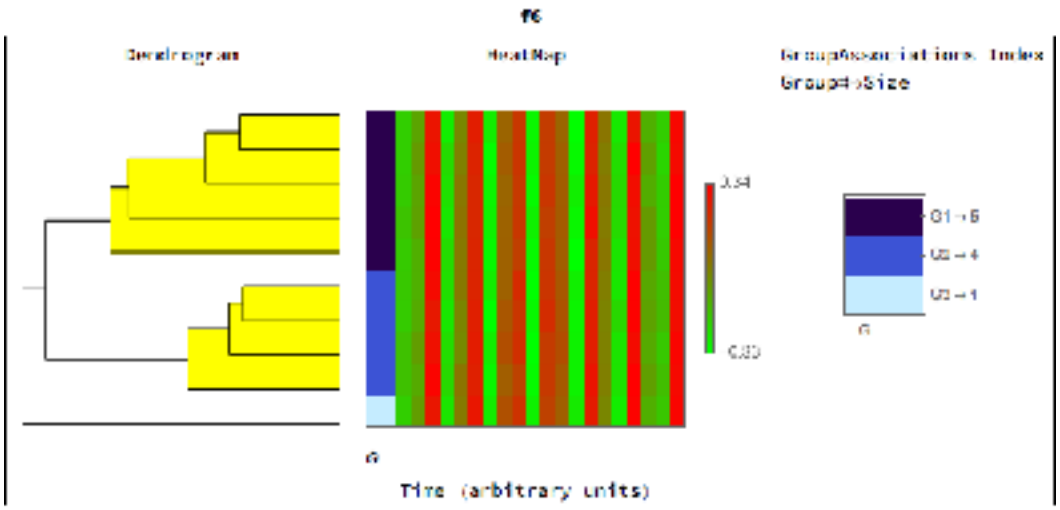

Options (1)

FunctionOptions (1)

In[1]:=
```
Needs["MathIOmica`"]
```

FunctionOptions provides a list of options that are used by an internal TimeSeriesSingleDendrogramHeatmap function that is used in the plots.

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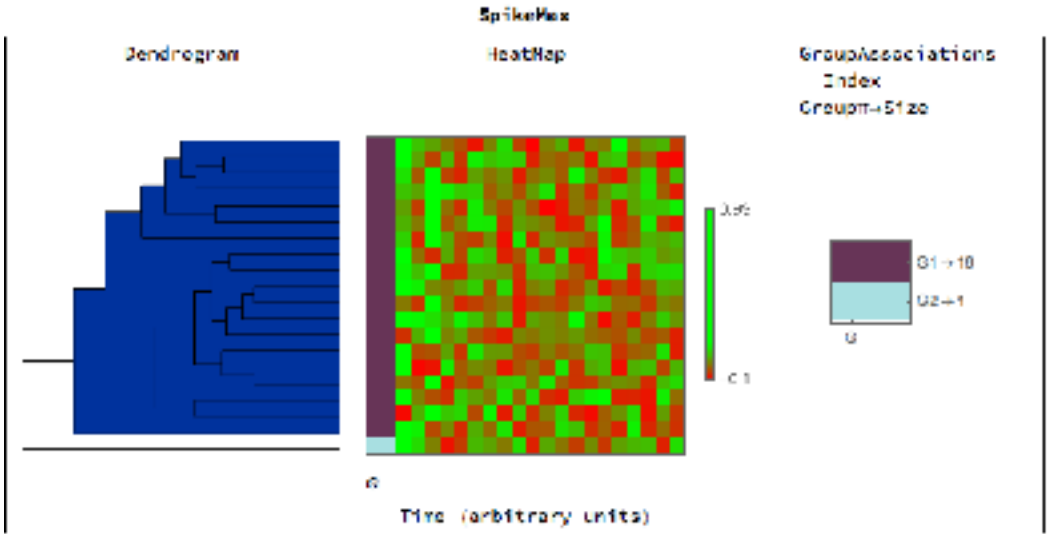
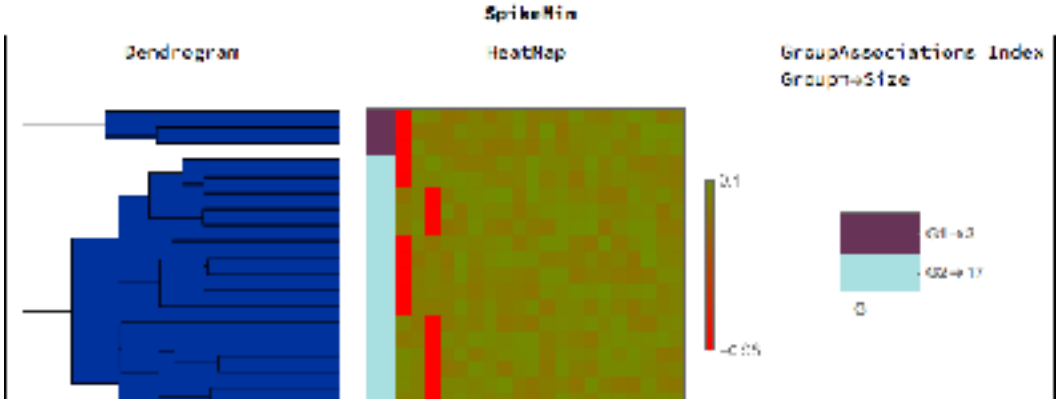
We create, classify and cluster the following data for our example, for various trends and 20 time points:

```
In[2]:= classificationExample1 = Normalize[#] & /@ Association[
    Join[Table["SpikePositive_" <> ToString[i] → UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikePositive_" <> ToString[i] → UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 1] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["SpikeNegative_" <> ToString[i] → -UnitVector[20, 3] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearPositive_" <> ToString[i] → Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearPositive_" <> ToString[i] → 0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["LinearNegative_" <> ToString[i] → -0.1 Range[20] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["LinearNegative_" <> ToString[i] → -0.2 Range[20] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal1_" <> ToString[i] → Cos[2 Pi * 0.65 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 1, 10}],
     Table["Sinusoidal2_" <> ToString[i] →
       5 Cos[2 Pi * 0.3 Range[20]] + RandomReal[{-.1, .1}, 20], {i, 11, 20}],
     Table["Sinusoidal3_" <> ToString[i] → 5 Cos[2 Pi * 0.15 * Range[20]] + RandomReal[{-.1, .1}, 20],
      {i, 21, 30}]]];
timePointsExample = Range[20];
classification1 = TimeSeriesClassification[classificationExample1,
   timePointsExample, LombScargleCutoff → 0.89, SpikeCutoffs → <|20 → {0.42, -0.42}|>];
clustersSingle = TimeSeriesSingleClusters[classification1];
```

```
In[3]:= TimeSeriesSingleDendrogramsHeatmaps[clustersSingle, FunctionOptions →
  {IndexColor → "CandyColors", ColorBlending → {Red, Green}, DendrogramColor → CMYKColor[1, .7, .05, .35]}]
```





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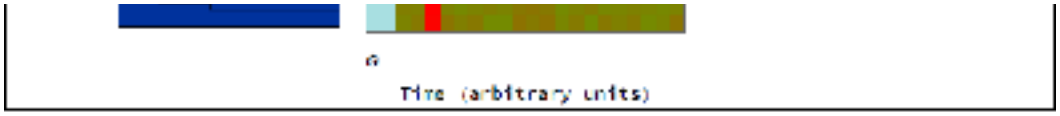
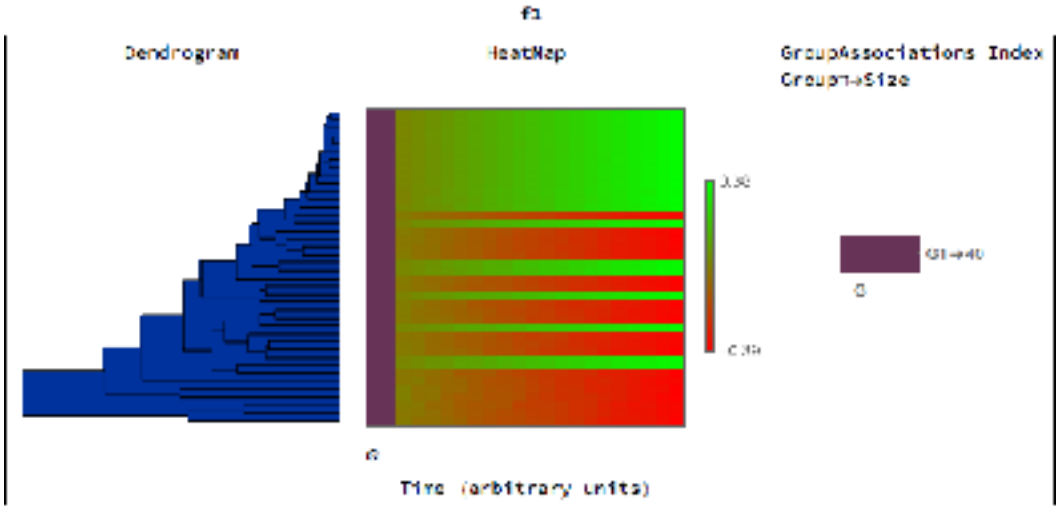
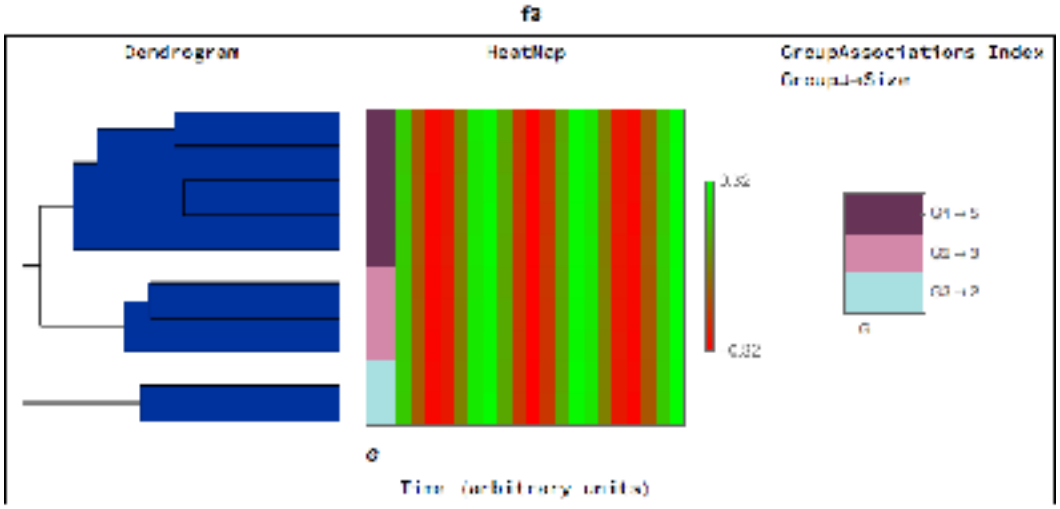
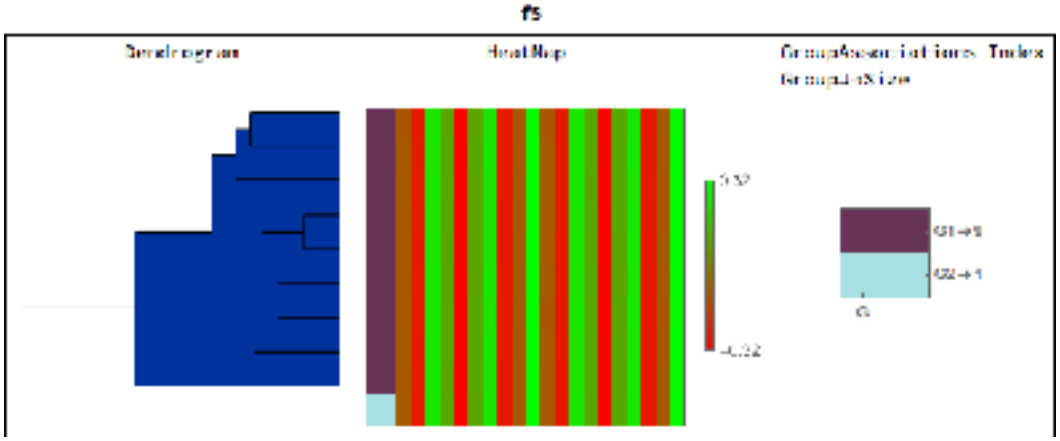




Out[3]=





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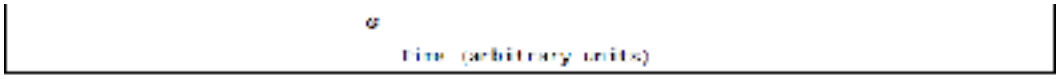

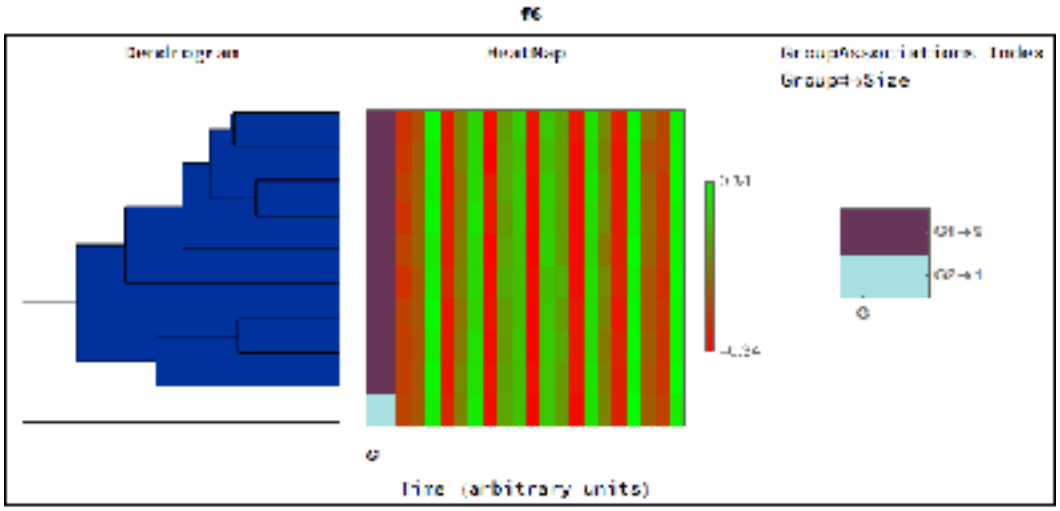

See Also

Heatmapper ▪ **MatrixClusters** ▪ **MatrixDendrogramHeatmap** ▪ **MatrixDendrogramsHeatmaps** ▪ **TimeSeriesClusters** ▪ **TimeSeriesDendrogramHeatmap** ▪ **TimeSeriesDendrogramsHeatmaps** ▪ **TimeSeriesSingleClusters** ▪ **TimeSeriesSingleDendrogramHeatmap**

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- MathIOmica Tutorial
- MathIOmica Dynamic Transcriptome

Related Guides

- MathIOmica Guide

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Related Links

- MathIOmicaGuide
- MathIOmicaOverview

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UCSCBrowserSQL

UCSCBrowserSQL[*query*]
performs a MySQL string query on the UCSC Genome Browser database tables.

Details

- UCSCBrowserSQL[query] performs a MySQL query string on the UCSC Genome Browser database tables.
- N.B. The function might have trouble connecting in case of firewalls, or other connectivity issues that may prevent it forming a MySQL connection to the UCSC Genome Browser.
- For table naming please consult the UCSC Genome Browser tables directly.

Examples (1)

Basic Examples (1)

First we need to load the MathIOmica package:

In[1]:=
```
Needs["MathIOmica`"]
```

We can carry out a MySQL query on the browser connection:

In[2]:=
```
UCSCBrowserSQL["SELECT hg19.kgXref.kgID FROM hg19.kgXref"]
```

Out[2]=
```
{{uc001aaa.3}, {uc001aac.4}, {uc001aae.4}, {uc001aah.4}, {uc001aai.1},
 {uc001aak.3}, {uc001aal.1}, {uc001aaq.2}, ··· 82 944 ···, {uc031tks.1}, {uc031tkt.1},
 {uc031tku.1}, {uc031tkv.1}, {uc031tkw.1}, {uc031tkx.1}, {uc031tky.1}, {uc031tkz.1}}
```

large output | show less | show more | show all | set size limit...

See Also

SQLExecute ▪ **GetGeneDictionary** ▪ **GOAnalysis** ▪ **GOAnalysisAssigner** ▪ **KEGGAnalysis** ▪ **KEGGAnalysisAssigner** ▪

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KEGGDictionary ▪ KEGGPathwayVisual ▪ MassDictionary ▪ OBOGODictionary

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Tutorials ▾ See Also ▾ URL ▾

UpperFrequencyFactor

`UpperFrequencyFactor`
is an option for LombScargle and InverseAutocovariance for scaling the upper Nyquist cutoff frequency.

Details

- UpperFrequencyFactor takes values ≥ 1, by which to scale the upper Nyquist cutoff frequency and increase spectral resolution.
- It is recommended to set `UpperFrequencyFactor` close to 1 unless one has an explicit reason to do otherwise.

See Also

Autocorrelation ▪ **InverseAutocovariance** ▪ **LombScargle**

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