Package ‘MAIT’
March 22, 2017

Type Package

Title Statistical Analysis of Metabolomic Data

Version 1.8.0

Date 10-3-2014

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Description The MAIT package contains functions to perform end-to-end statistical analysis of LC/MS Metabolomic Data. Special emphasis is put on peak annotation and in modular function design of the functions.

biocViews MassSpectrometry, Metabolomics, Software

License GPL-2

LazyLoad yes

Depends R (>= 2.10), CAMERA, Rcpp, pls

Imports gplots,e1071,class,MASS,plsgenomics,agricolae,xcms,methods,caret

Enhances rgl

NeedsCompilation no

R topics documented:

Biotransformations ......................................................... 2
biotransformationsTable .................................................. 3
classes ................................................................. 4
classifRatioClasses ....................................................... 5
classNum ............................................................... 5
Database .................................................................. 6
featureID .................................................................. 7
featureInfo .................................................................. 7
featureSigID ............................................................... 8
getScoresTable ................................................................ 9
identifyMetabolites ......................................................... 10
loadings .................................................................. 11
LSDResults .................................................................. 12
Biotransformations

Biotransformations of the significant data contained in a MAIT object are identified.

Description

This function takes a MAIT-class object having significant features already detected and looks up for biotransformations between them. MAIT has a default biotransformation table that will be used if no other table is specified via the bioTable input parameter.

Usage

Biotransformations(MAIT.object = NULL, peakPrecision = 0.005, bioTable = NULL, adductTable = NULL, adductAnnotation = FALSE)
**Arguments**

- **MAIT.object**
  A MAIT-class object where significant features have already been found.

- **peakPrecision**
  Maximum difference between the peak masses differences and the values shown in `bioTable` to be considered as a biotransformation. As default the value is 0.005 Da.

- **bioTable**
  Table containing the biotransformations to be looked for in the `signData` input. By default it is taken the MAIT-class biotransformations table.

- **adductTable**
  Table containing the adducts to be looked for in the `signData` input. By default it is taken the MAIT-class positive adducts table. If this argument is set to "negAdducts", then the default table for negative adducts is taken instead. It is possible to use a user-defined adduct table.

- **adductAnnotation**
  If it is set to TRUE, both adduct and Biotransformations annotation stages are performed.

**Value**

A MAIT-class object with the updated biotransformations slot.

**Author(s)**

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**

- spectralAnova
- spectralTStudent

**Examples**

```r
data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT<-Biotransformations(MAIT.object = MAIT, peakPrecision = 0.005)
MAIT@FeatureInfo@biotransformations; #Detected Biotransformations
```

---

**biotransformationsTable**

**Description**

This table contains the biotransformations to be looked up for.

**Value**

A table having the fields:

- NAME: The name of the biotransformation
- MASSDIFF: The mass difference of the fragment caused by the biotransformation
Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
Biotransformations

classes

Class names extractor from a MAIT object

Description
Function classes extracts the class names of a linkMAIT-class object as a vector.

Usage

classes(MAIT.object)

Arguments

MAIT.object A MAIT-class object

Value

A character vector containing the class names of the MAIT-class object

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

MAIT-class

Examples

data(MAIT_sample)
MAIT
classes(MAIT)
**classifRatioClasses**

*Class classification ratio extractor from a MAIT object*

**Description**

Function `classifRatioClasses` extracts the class classification ratio of a MAIT object as a matrix.

**Usage**

```r
classifRatioClasses(MAIT.object)
```

**Arguments**

- **MAIT.object**
  
  A MAIT-class object where function `Validation` has already been launched successfully.

**Value**

A matrix containing the classification ratio for each class, classifier and iteration.

**Author(s)**

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**

- `MAIT-class`

**Examples**

```r
data(MAIT_sample)
MAIT <- spectralSigFeatures(MAIT, p.adj="fdr", parametric=TRUE)
MAIT <- Validation(Iterations = 20, trainSamples= 15, MAIT.object = MAIT)
classifRatioClasses(MAIT)
```

---

**classNum**

*Sample number extractor for each class from a MAIT object*

**Description**

Function `classNum` extracts the number of samples belonging to each class of a MAIT object as a vector.

**Usage**

```r
classNum(MAIT.object)
```
Database

Arguments

MAIT.object  A MAIT-class object

Value

A numeric vector containing the number of samples for each class of the MAIT object. The order of the classes correspond to that of the output of function classes.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

MAIT-class

Examples

data(MAIT_sample)
MAIT
classNum(MAIT)

Database  Human Metabolome Database

Description

The Human Metabolome Database is saved in this dataframe.

Value

A table having the fields:

- ENTRY: HMDB entry
- NAME: The compound name
- FORMULA: The chemical formula of the compound
- MASS: Mass of the fragment
- Biofluid: Where the compound can be found

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

identifyMetabolites metaboliteTable
**featureID**

*Feature ID extractor from a MAIT object*

**Description**

Function `featureID` extracts the feature IDs of a MAIT object as a vector.

**Usage**

```r
featureID(MAIT.object)
```

**Arguments**

- `MAIT.object` A MAIT-class object

**Value**

A numeric vector containing the feature IDs of the MAIT object.

**Author(s)**

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**

- MAIT-class

**Examples**

```r
data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
featureID(MAIT)
```

---

**featureInfo**

*Feature Info extractor from a MAIT object*

**Description**

Function `featureInfo` extracts the slot MAIT.FeatureInfo of a MAIT object.

**Usage**

```r
featureInfo(MAIT.object)
```

**Arguments**

- `MAIT.object` A MAIT-class object
featureSigID

Value

An object of the class MAIT.FeatureInfo. More Info at MAIT-class.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

MAIT-class

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
featureInfo(MAIT)

featureSigID

Feature statistically significant ID extractor from a MAIT object

Description

Function featureSigID extracts the vector index of the feature IDs of a MAIT object that have been found significant through function spectralSigFeatures.

Usage

featureSigID(MAIT.object)

Arguments

MAIT.object A MAIT-class object

Value

A numeric vector containing the statistically significant feature IDs of the MAIT object.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

MAIT-class spectralSigFeatures

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
featureInfo(MAIT)
featureID(MAIT)[featureSigID(MAIT)] #Significant spectra IDs
getScoresTable

Description

Function getScoresTable takes an MAIT-class object and returns a list with the scores of the features in the samples. Additionally, it returns the spectral ID of the peak and (optionally) a table containing the peak information (mass, retention time and annotation).

Usage

getScoresTable(MAIT.object = NULL,
geticSpectra = TRUE,
geticExtendedTable = FALSE)

Arguments

MAIT.object A MAIT-class object where significant features have already been found.
geticSpectra If it is set to TRUE, an element of the returned list will contain the spectra ID of each feature.
geticExtendedTable If it is set to TRUE, an element of the returned list will contain a table with peak information (mass, retention time, annotation, intensity per sample).

Value

A list containing:

- scores: The intensity of each feature per sample
- spectralID: A numeric with the correspondence between peaks and spectral ID
- extendedTable: a data frame containing detailed peak information (mass, retention time, annotation, intensity per sample).

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

spectralTStudent spectralAnova

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
getScoresTable(MAIT,getExtendedTable=TRUE)
identifyMetabolites  

**Metabolite identifier**

**Description**
Takes a MAIT object and performs the metabolite search for the significant features

**Usage**

```r
identifyMetabolites(MAIT.object=NULL, peakTolerance=0.005, database=NULL, polarity="positive", printCSVfile=TRUE)
```

**Arguments**

- **MAIT.object** A MAIT-class object where significant features have already been found.
- **peakTolerance** Maximum difference between the peak masses differences and the values shown in the database to be considered as a match. As default the value is 0.005 Da.
- **database** User-defined input table. If it is set to NULL, the default MAIT database is selected to perform the metabolite identification.
- **polarity** Character parameter that can be set to "positive" or "negative" depending on the polarity in which the samples were taken.
- **printCSVfile** Set to TRUE if an output table has to be produced. The table should be found in (working directory)/Tables/SearchTable.csv.

**Value**
An output table is stored in the folder (working directory)/Tables/SearchTable.csv if `printCSVfile` is set to TRUE. More info at metaboliteTable

**Author(s)**
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**
Biotransformations spectralSigFeatures

**Examples**

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT<-Biotransformations(MAIT.object = MAIT, peakPrecision = 0.005)
MAIT <- identifyMetabolites(MAIT.object = MAIT, peakTolerance = 0.005,polarity="positive")
### loadings

**Loadings extractor for either PCA or PLS models**

#### Description

Function `loadings` returns the loading vectors for either the PCA, PLS models when functions `plotPCA` or `plotPLS` have been already respectively launched. It also can be used to retrieve the peak aggregation models.

#### Usage

```r
loadings(object, type = "none", ...)
```

#### Arguments

- **object**: A MAIT-class object
- **type**: A character whose value should be "PCA" or "PLS" depending on which loading vectors are wanted. If it is set to "none", the peak aggregation models are retrieved.
- **...**: Other input

#### Value

A matrix with the loading vectors.

#### Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

#### See Also

- `plotPCA`
- `plotPLS`

#### Examples

```r
data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
loadings(MAIT)

MAIT<-plotPCA(MAIT,plot3d=FALSE)
loadings(MAIT,type="PCA")

MAIT<-plotPLS(MAIT,plot3d=FALSE)
loadings(MAIT,type="PLS")
```
LSDResults  
Extractor of the Fisher's LSD tests from a MAIT object

Description
Function LSDResults extracts the results of the LSD tests of a MAIT object as a matrix.

Usage
LSDResults(MAIT.object)

Arguments
MAIT.object  A MAIT-class object

Value
A matrix containing the results of the Fisher's LSD tests. For each row, equal letters mean that the groups are found to be equal in the test.

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
MAIT-class FisherLSD spectralSigFeatures

Examples
data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
LSDResults(MAIT)

Description
A MAIT-class object containing simulated LC/MS data

Value
MAIT.object  A MAIT-class object

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>
MAIT-class

Class "MAIT"

Description

MAIT class objects are used in the MAIT package to perform the analysis and statistical calculus of LC/MS data. It has 5 main slots: FeatureInfo, RawData, Validation, PhenoData and FeatureData.

Slots

FeatureInfo: Object of class MAIT.FeatureInfo-class
RawData: Object of class MAIT.RawData-class
Validation: Object of class MAIT.Validation-class
PhenoData: Object of class MAIT.PhenoData-class
FeatureData: Object of class MAIT.FeatureData-class

Methods

summary signature(object = "MAIT"): This function show a summary of the workflow results performed so far including the classification results and the parameters used.
model signature(object = "MAIT"): returns the model for either the PCA, PLS models when functions plotPCA or plotPLS have been already respectively launched.
scores signature(object = "MAIT"): Retrieves the scores from a MAIT object
loadings signature(object = "MAIT"): Retrieves the loadings from a MAIT object

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

xsAnnotate

MAIT.FeatureData-class

Class "MAIT.FeatureData"

Description

MAIT.FeatureData objects are used in the MAIT package to save the feature data.
Slots

scores: Here it is saved the dataset obtained after applying the `peakAggregation` function.

featureID: The ID numbers of all features are saved here.

featureSigID: The ID numbers of the significant features are saved here.

LSDResults: The results of performing a Fisher LSD test on each significant variable are saved in this slot.

models: The model for each feature used to obtain the scores are saved in this slot.

pvalues: In this slot are saved the pvalues of the features.

pvaluesCorrection: The pvalues corrected by multiple test correction are saved here.

pcaModel: PCA model generated using the function `plotPCA`.

plsModel: PCA model generated using the function `plotPLS`.

masses: Masses used as an input for the function `MAITbuilder`.

rt: Retention time values used as an input for the function `MAITbuilder`.

extendedTable: Dataframe containing the information regarding masses, retention time values, intensity and spectra IDs passes as an input for the function `MAITbuilder`.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

`MAIT-class` `xsAnnotate`

Description

MAIT.FeatureInfo objects are used in the MAIT package to save the data related to the information of the features.

Slots

It stores information related to the features. It contains three extra slots:

biotransformations: Biotransformations found when function `Biotransformations` is launched.

peakAgMethod: In this slot is stored the table created by the function `identifyMetabolites`. It can be retrieved quickly in R by using the function `metaboliteTable`.

metaboliteTable: Peak Aggregation Method used when function `peakAggregation` is launched.

Methods

No methods defined with class "MAIT.FeatureInfo" in the signature.
Description

This class contains all the parameters used in the MAIT run.

Slots

- `sampleProcessing`: List containing the parameters of the function `sampleProcessing`
- `peakAnnotation`: List containing the parameters of the function `peakAnnotation`
- `peakAggregation`: List containing the parameters of the function `peakAggregation`
- `sigFeatures`: List containing the parameters of the function `spectralSigFeatures`
- `biotransformations`: List containing the parameters of the function `Biotransformations`
- `identifyMetabolites`: List containing the parameters of the function `identifyMetabolites`
- `classification`: List containing the parameters of the function `Validation`
- `plotPCA`: List containing the parameters of the function `plotPCA`
- `plotPLS`: List containing the parameters of the function `plotPLS`
- `plotHeatmap`: List containing the parameters of the function `plotHeatmap`

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

- MAIT-class
- `xsAnnotate`
MAIT.Phenodata-class  

Class "MAIT.Phenodata"

Description

MAIT.Phenodata objects are used in the MAIT package to save the phenotype data.

Objects from the Class

Objects can be created by calls of the form `new("MAIT.Phenodata", ...)`.

Slots

The information related to the classes present in the data is stored in this slot. It has three different extra slots:

- `classes`: It contains the name of the classes in the data. It can be quickly accessed by using the function `classes`.
- `classNum`: Vector showing the number of samples belonging to each class. It can be quickly accessed by using the function `classNum`.
- `resultsPath`: In this slot is saved the direction where the project is saved. This means that all the output tables and files of the MAIT object are going to be stored in that directory. It can be quickly accessed by using the function `resultsPath`.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

- MAIT-class xsAnnotate

MAIT.Rawdata-class  

Class "MAIT.Rawdata"

Description

MAIT.Rawdata objects are used in the MAIT package to save the data related to the information of the features.

Slots

This class contains information of the raw data and the parameters of the whole analysis. It has two slots:

- `parameters`: All the parameters of the analysis are saved in this slot. It can be obtained as a matrix in R by typing `summary(parameters(MAIT.object))`.
- `data`: This slot contains either the xcmsSet-class or the xsAnnotate object, depending if the function `peakAnnotation` has already been launched.
MAIT.Validation-class

Methods

No methods defined with class "MAIT.RawData" in the signature.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

MAIT-class xsAnnotate

MAIT.Validation-class  Class "MAIT.Validation"

Description

MAIT.Validation objects are used in the MAIT package to save the validation results obtained from the classification run.

Slots

The information related to the run of the function Validation is saved here. It contains three lots:

ovClassifRatioTable: Summary table showing the overall classification ratios for each of the three classifiers. It can be quickly gathered by using the function ovClassifRatioTable

ovClassifRatioData: All the data corresponding to the overall classification ratios. It can be quickly gathered by using the function ovClassifRatioData

classifRatioClasses: All the data corresponding to the classification ratios per class. It can be quickly gathered by using the function classifRatioClasses

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

MAIT-class xsAnnotate
Function MAITbuilder creates a MAIT-class object for a given external data. This process allows the user to analyse external peak data through all the MAIT processing steps.

**Usage**

```r
MAITbuilder(data = NULL,
             spectraID = NULL,
             masses = NULL,
             rt = NULL,
             classes = NULL,
             significantFeatures = FALSE,
             spectraEstimation = FALSE,
             rtRange = 0.2,
             corThresh = 0.7)
```

**Arguments**

- **data**: Matrix containing the peak intensity values for each sample. Each row should correspond to a peak and each column to a sample.
- **spectraID**: Numeric corresponding to the peak spectral grouping IDs. Two peaks having the same spectraID means that they correspond to the same spectrum.
- **masses**: Numeric that contains the masses of the peaks. It should be as long as the number of rows in the argument data.
- **rt**: Numeric that contains the retention time of the peaks. It should be as long as the number of rows in the argument data.
- **classes**: Character with the class labels for each sample. It should be as long as the number of columns in the argument data.
- **significantFeatures**: If it is set to TRUE, all the features set as an input are considered to be significant. Functions `Biotransformations`, `identifyMetabolites`, `Validation`, `plotPCA`, `plotPLS`, `plotHeatmap`, `plotBoxplot` are computed on the significant features only. If it is only wanted to perform an annotation process on the external peak data, this flag should be set to TRUE.
- **spectraEstimation**: If it is set to TRUE, an estimation of the peak grouping into spectra is performed. This computation is based on a retention time window (set by the argument `rtRange`) and a correlation threshold (defined by the parameter `corThresh`).
- **rtRange**: Retention time parameter used to build a window to perform an estimation of the peak grouping into spectra.
- **corThresh**: Peak correlation value used to define a threshold to perform an estimation of the peak grouping into spectra.
metaboliteTable

Value

All the input values are stored in a new MAIT object.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

Examples

data(MAIT_sample)
peaks<-scores(MAIT)
masses<-aux$extendedTable$mz
rt <- aux$extendedTable$rt
classFactor <- rep(classes(MAIT),classNum(MAIT))
importMAIT <- MAITbuilder (data=peaks,masses=masses,rt=rt,
significantFeatures=TRUE, spectraEstimation=TRUE, rtRange=0.2,
corThresh=0.7,classes=classFactor)

importMAIT

metaboliteTable

Metabolite table generator

Description

Takes a MAIT-class object and builds a table with the information related to the significant features and their possible identifications.

Usage

metaboliteTable(MAIT.object,
printCSVfile = FALSE)

Arguments

MAIT.object  A MAIT-class object where significant features have already been found.
printCSVfile  A boolean parameter. Set to TRUE if a csv file should be written with the metabolite table.

Value

An output table is stored in the folder (working directory)/Tables/SearchTable.csv having the fields:

- First column: search ID number.
- Second column (mz): Peak mass.
- Third column(rt): Peak retention time (in minutes).
- The columns from the third to the column labeled "p.adj" contain number of class samples where the peak has been detected and the intensities of the peak among samples.
- The P.adjust column contains the corrected peak p-value using bonferroni.
• The p column shows the peak p-value with no multiple test correction.
• The Fisher column shows the Fisher test results for the peak. Each of the letters separated by
  the character "_" corresponds to a class value. Classes having the same letters are indistin-
  guishable whereas those having different letters are statistically different classes.
• The isotopes column shows if the peak has been identified as a possible isotope.
• The adduct column shows which kind of adduct or biotransformation could the peak be.
• Column Name contains the name of the possible metabolite identification for the peak.
• The column labeled spectra contains the spectral ID of the peak.
• Column Biofluid shows if the identified search is stored as a biofluid in the input database or
  not.
• The column ENTRY shows the database name of the entry for the metabolite.

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
identifyMetabolites spectralAnova spectralTStudent

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT<-Biotransformations(MAIT.object = MAIT, peakPrecision = 0.005)
MAIT <- identifyMetabolites(MAIT.object = MAIT, peakTolerance = 0.005,polarity="positive")
head(metaboliteTable(MAIT))

model
Model extractor for either PCA or PLS models

Description
Function model returns the model for either the PCA, PLS models when functions plotPCA or
plotPLS have been already respectively launched.

Usage

model(x,type)

Arguments
  x
  A MAIT-class object
  type
  A character whose value should be "PCA" or "PLS" depending on which loading
  vectors are wanted.

Value
The PCA or PLS model
models

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
plotPCA or plotPLS

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT<-plotPCA(MAIT,plot3d=FALSE)
model(MAIT,type="PCA")

MAIT<-plotPLS(MAIT,plot3d=FALSE)
model(MAIT,type="PLS")

models

Model extractor from a MAIT object

Description
Function models extracts the models of a MAIT object as a list.

Usage
models(MAIT.object)

Arguments
MAIT.object  A MAIT-class object

Value
A list containing the models of the MAIT object.

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
MAIT-class

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
models(MAIT)
Negative adducts table

Description
This table contains the adducts to be looked up when the LC/MS polarisation mode was set to Negative. The layout of the table is that of the CAMERA adduct table.

Value
A table having the fields:
- ID: An ID number
- name: The adduct name
- nmol: Number of fragments in the adduct
- charge: Electric charge of the adduct
- massdiff: Mass difference in the fragment caused by the adduct
- oidscore: Numeric relating the related clusters of ions
- quasi: Binary value showing the validness of the annotation group
- ips: Four values are possible (0.25,0.5,0.75,1) depending on the likelihood of the rule

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
peakAnnotation

Overall classification ratio extractor for MAIT objects

Description
Function ovClassifRatioData extracts the overall classification ratio for a MAIT-class object

Usage

ovClassifRatioData(MAIT.object)

Arguments

MAIT.object A MAIT-class object

Value
A list containing the overall classification ratio of the MAIT-class object for each classifier.
### ovClassifRatioTable

**Author(s)**
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**
- MAIT-class Validation

**Examples**
```r
data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT <- Validation(Iterations = 20, trainSamples= 15, MAIT.object = MAIT)
```

---

**ovClassifRatioTable**  
*Overall classification table extractor for MAIT objects*

**Description**
Function `ovClassifRatioTable` extracts the overall classification table for a MAIT-class object.

**Usage**

```r
ovClassifRatioTable(MAIT.object)
```

**Arguments**

- `MAIT.object`  
  A MAIT-class object

**Value**
A list containing the overall classification table of the MAIT object for each classifier showing the mean value and their standard error.

**Author(s)**
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**
- MAIT-class Validation

**Examples**
```r
data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT <- Validation(Iterations = 20, trainSamples= 15, MAIT.object = MAIT)
```

---

**ovClassifRatioData**  
*Overall classification table extractor for MAIT objects*

**Description**
Function `ovClassifRatioData` extracts the overall classification table for a MAIT-class object.

**Usage**

```r
ovClassifRatioData(MAIT.object)
```

**Arguments**

- `MAIT.object`  
  A MAIT-class object

**Value**
A list containing the overall classification table of the MAIT object for each classifier showing the mean value and their standard error.
parameters  

Extractor of the parameters used in the whole run from a MAIT object

Description
Function parameters extracts the slot linkMAIT.Parameters-class of a MAIT-class object. This class contains all the parameters that have been used in the previous functions. Typing a summary of this object, a matrix version of the parameters is obtained.

Usage

parameters(MAIT.object)

Arguments

MAIT.object  A MAIT-class object

Value
An object of the class MAIT.Parameters.

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
MAIT-class

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT <- Validation(Iterations = 20, trainSamples= 15, MAIT.object = MAIT)
parameters(MAIT)

peakAnnotation  

Spectra constructor and peak annotator

Description
peakAnnotation function performs spectra building and peak annotation using the CAMERA package on a MAIT-class object, after applying the sampleProcessing function. The resultant xsAnnotate object is stored in a MAIT-class object.
peakAnnotation

Usage

peakAnnotation(MAIT.object = NULL,
corrWithSamp = 0.7,
perfwhm = 0.6,
sigma = 6,
adductTable = NULL,
printSpectraTable = TRUE,
corrBetSamp = 0.75,
pval = 0.05,
calcIso = TRUE,
calcCis = TRUE,
calcCaS = TRUE,
graphMethod = "hcs",
annotateAdducts = TRUE)

Arguments

MAIT.object  A MAIT-class object where function sampleProcessing has already been applied. The output of the function is going to be an update of the same MAIT-class object.
corrWithSamp  Correlation threshold value within samples
perfwhm  This parameter is used to group two peaks depending on their retention time. Two peaks are considered to be coeluted if their retention time falls in a range defined as Rt_med +/- FWHM * perfwhm. Where Rt_med is the retention time median and FWHM is the Full Width at Half Maximum. Defined this way, perfwhm is the percentage of the width of the FWHM (Full Width at Half Maximum)
sigma  Defining the coelution range as defined in the perfwhm variable, the FWHM is obtained by the expression FWHM=SD*sigma, where SD is calculated considering the peak as normally distributed.
adductTable  User-defined input table to annotate the peaks. If it is set to NULL, the default MAIT table for adducts in positive polarization is selected. If its value is "negAdducts", the default MAIT table for fragments in negative polarization is chosen. By default it is set to NULL.
printSpectraTable  If it is set to TRUE, a three-column table is build as a csv file, where the first column shows the peak mass, the second column its retention time and the third one shows its spectral ID number. This file is saved under the project directory, in the subfolder named Tables.
corrBetSamp  Correlation threshold value between samples
pval  See groupCorr function in the CAMERA package
calcIso  See groupCorr function in the CAMERA package
calcCis  See groupCorr function in the CAMERA package
calcCaS  See groupCorr function in the CAMERA package
graphMethod  See groupCorr function in the CAMERA package
annotateAdducts  If it is set to TRUE, the function will perform an adduct annotation stage.
Value

A MAIT-class object containing the xsAnnotate-class in the rawData slot.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

xsAnnotate, xsAnnotate-class

Examples

#Provided that the data files are saved accordingly
#in subfolders under a folder named "data" (see vignette):
#MAIT<-sampleProcessing(dataDir = "data", project = "Results", snThres=2,rtStep=0.02)
#MAIT<-peakAnnotation(MAIT.object = MAIT,corrWithSamp = 0.7, corrBetSamp = 0.7,perfwhm = 0.6)

plotBoxplot(MAIT.object=NULL)

Description

This function takes a MAIT-class object containing information related to the significant features and plots a boxplot for each significant feature (peak or spectra).

Usage

plotBoxplot(MAIT.object=NULL)

Arguments

MAIT.object A MAIT-class object where significant features have already been found.

Value

A boxplot is stored as a png file for each of the significant features (peak or spectra). The files will be stored in the directory (working directory)/Boxplots

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

spectralAnova, spectralTStudent

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT<-plotBoxplot(MAIT)
**plotHeatmap**

Builds ten heatmaps with different p-values and clustering distances

**Description**

This function takes a MAIT object containing information of the significant features in the data and plots 10 heatmaps. 5 different p-values (0.05, 0.01, 0.001, 1e-4 and 1e-5) and two clustering distances (euclidean and pearson) are used.

**Usage**

```r
plotHeatmap(MAIT.object=NULL)
```

**Arguments**

- **MAIT.object** A MAIT-class object where significant features have already been found.

**Value**

10 different heatmaps using 5 p-values (0.05, 0.01, 0.001, 1e-4 and 1e-5) and two clustering distances (euclidean and pearson) are created. The plots will be stored as png files in a folder called (working directory)/Heatmaps.

**Author(s)**

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**

- `spectralAnova`
- `spectralTStudent`

**Examples**

```r
data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT<-plotHeatmap(MAIT)
```

---

**plotPCA**

2D and 3D PCA scoreplots from a MAIT object

**Description**

This function takes a MAIT-class object containing information of the significant features in the data and performs 2D scoreplots (PC1 vs PC2, PC2 vs PC3 and PC1 vs PC3) saved as png files. Additionally it also performs an interactive 3D PCA scoreplot.
Usage

plotPCA (MAIT.object=NULL, Log=FALSE, center=TRUE, scale=TRUE, plot3d=TRUE)

Arguments

MAIT.object A MAIT-class object where significant features have already been found.
Log Set to TRUE if the data should be plotted using the logarithm of the intensity.
center Set to TRUE if the data should be centered around its mean. See scale.
scale Set to TRUE if the data should be scaled. See scale.
plot3d Boolean set to TRUE if a 3D PCA scoreplot should be plot.

Value

Three different PCA scoreplots are printed in three png files. One using PC1 vs PC2, another with PC1 vs PC3 and the last one with PC2 vs PC3. The files will be stored in the directory (working directory)/PCA_Scoreplots. Moreover, an interactive 3D PCA scoreplot is also generated through function PCAplot3d.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

spectralAnova spectralTStudent

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT<-plotPCA(MAIT,plot3d=FALSE)

Description

This function takes a MAIT-class object containing information of the significant features in the data and performs 2D scoreplots (PC1 vs PC2, PC2 vs PC3 and PC1 vs PC3) saved as png files. Additionally it also performs an interactive 3D PLS scoreplot.
posAdducts

Usage

plotPLS (MAIT.object=NULL, Log=FALSE, center=TRUE, scale=TRUE, plot3d=TRUE)

Arguments

MAIT.object A MAIT-class object where significant features have already been found.
Log Set to TRUE if the data should be plotted using the logarithm of the intensity.
center Set to TRUE if the data should be centered around its mean. See scale.
scale Set to TRUE if the data should be scaled. See scale.
plot3d Boolean set to TRUE if a 3D PCA scoreplot should be plot.

Value

If the number of components in the PLS is found to be three or more, three different PLS scoreplots are printed in three png files. One using PC1 vs PC2, another with PC1 vs PC3 and the last one with PC2 vs PC3. If the number of components is less than three, all the possible plots of these three are created. The files will be stored in the directory (working directory)/PLS_Scoreplots. Moreover, an interactive 3D PLS scoreplot is also generated through function PCAplot3d.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

spectralAnova spectralTStudent

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT<-plotPLS(MAIT,plot3d=FALSE)

<table>
<thead>
<tr>
<th>posAdducts</th>
<th>Positive adducts table</th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>This table contains the adducts to be looked up for when the LC/MS polarisation mode was set to positive. The layout of the table is that of the CAMERA adduct table.</td>
</tr>
</tbody>
</table>
Value
A table having the fields:

- ID: An ID number
- name: The adduct name
- nmol: Number of fragments in the adduct
- charge: Electric charge of the adduct
- massdiff: Mass difference in the fragment caused by the adduct
- oidscore: Numeric relating the related clusters of ions
- quasi: Binary value showing the validness of the annotation group
- ips: Four values are possible (0.25,0.5,0.75,1) depending on the likelihood of the rule

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
peakAnnotation

---

pvalues  
_Pvalues extractor from a MAIT object_

Description
Function pvalues extracts the pvalues contained in a MAIT-class object.

Usage

pvalues(MAIT.object)

Arguments

- MAIT.object  
  A MAIT-class object

Value
A numeric vector containing the pvalues of a MAIT-class object.

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

MAIT-class spectralSigFeatures
**pvaluesCorrection**

**Examples**

```r
data(MAIT_sample)
MAIT <- spectralSigFeatures(MAIT, p.adj="fdr", parametric=TRUE)
pvalues(MAIT)
```

---

**pvaluesCorrection**  
*P-values correction extractor from a MAIT object*

**Description**

Function `pvaluesCorrection` returns a character showing whether some multiple testing correction has been performed on the p-values.

**Usage**

```r
pvaluesCorrection(MAIT.object)
```

**Arguments**

- **MAIT.object**  
  A MAIT-class object

**Value**

The output is a character whose values could be "None" if no p-value correction has been performed or "Bonferroni" if Bonferroni multiple test correction was selected when function `spectralSigFeatures` was applied.

**Author(s)**

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**

- MAIT-class `spectralSigFeatures`

**Examples**

```r
data(MAIT_sample)
MAIT <- spectralSigFeatures(MAIT, p.adj="fdr", parametric=TRUE)
pvaluesCorrection(MAIT)
```
### rawData

**Raw data extractor from a MAIT object**

**Description**

Function `rawData` extracts the raw data used to build the `MAIT-class` object.

**Usage**

```r
rawData(MAIT.object)
```

**Arguments**

- `MAIT.object` A `MAIT-class` object

**Value**

A list containing either a `xcmsSet` or a `xsAnnotate` object.

**Author(s)**

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**

- `xsAnnotate-class`

**Examples**

```r
data(MAIT_sample)
MAIT
rawData(MAIT)
```

---

### resultsPath

**Retrieves the folder where the results are saved for a MAIT object**

**Description**

Function `resultsPath` returns the folder where the plots and tables are saved for a `MAIT-class` object.

**Usage**

```r
resultsPath(MAIT.object)
```
sampleProcessing

Arguments
MAIT.object A MAIT-class object

Value
A character showing where the plots and tables have been stored.

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
MAIT-class

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
resultsPath(MAIT)

Description

sampleProcessing takes a set of netCDF files containing LC/MS sample data and performs a peak detection, retention time correction and peak grouping steps using the package xcms. A MAIT-class object is created and all the information is saved in it.

Usage

sampleProcessing(dataDir = NULL,
 snThres = 2,
 Sigma = 5/2.3548,
 mzSlices = 0.3,
 retcorrMethod = "loess",
 groupMethod = "density",
 bwGroup = 3,
 mzWidGroup = 0.25,
 filterMethod = "matchedFilter",
 rtStep = 0.03,
 nSlaves = 0,
 minfrac = 0.5,
 minsamp = 1,
 peakwidth = c(5, 20),
 project = NULL,
 ppm = 10,
 family = c("gaussian", "symmetric"),
 span = 0.2,
 fwhm = 30)
sampleProcessing

Arguments

- **dataDir**: Folder where the netCDF files are stored. The samples files must be classified in subdirectories according to their classes.
- **snThres**: Signal to noise ratio. Setting a high value of this parameter will lead to a higher number of features although they will be more noisy.
- **Sigma**: Standard deviation (width) of matched filtration model peak.
- **mzSlices**: Minimum difference in m/z for peaks with overlapping retention times.
- **retcorrMethod**: Method used to correct the retention times values of the variables.
- **groupMethod**: Method used to build the group peaks of variables.
- **bwGroup**: Bandwidth (standard deviation or half width at half maximum) of gaussian smoothing kernel to apply to the peak density chromatogram.
- **mzWidGroup**: Width of overlapping m/z slices to use for creating peak density chromatograms and grouping peaks across samples.
- **filterMethod**: Filtering method applied in the peak detection step.
- **rtStep**: Step size to use for profile generation.
- **nSlaves**: Number of slaves for parallel calculus.
- **project**: Project folder name under which the results will be saved. This folder will be created in the working directory.
- **minfrac**: minimum fraction of samples necessary in at least one of the sample groups for it to be a valid group. See group.density in package xcms for details.
- **minsamp**: Minimum number of samples necessary in at least one of the sample groups for it to be a valid group. See group.density in package xcms for details.
- **ppm**: maximal tolerated m/z deviation in consecutive scans, in ppm (parts per million). See findPeaks.centWave in package xcms for details.
- **peakwidth**: Chromatographic peak width, given as range (min,max) in seconds.
- **fwhm**: See fwhm argument in xcmsSet function.
- **span**: See span argument in xcmsSet function.
- **family**: See family argument in xcmsSet function.

Value

A MAIT-class object containing the data of the netCDF files. The xcmsSet-class object can be retrieved using the function `rawData`.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

Examples

#Provided that the data files are saved accordingly
#in subfolders under a folder named "data" (see vignette):
#MAIT<-sampleProcessing(dataDir = "data", project = "Results", snThres=2, rtStep=0.02)
scores

Retrieves the scores from a MAIT object

Description
Function scores extracts the scores MAIT object

Usage

scores(object, 
   type,...)

Arguments

object A MAIT-class object
type If it is set to "none", the peak aggregation models are returned. If it is set to "PCA", the PCA model is returned. If it is set to "PLS", the PCA model is returned.
...
   Other input

Value
A numeric matrix containing the scores saved in the MAIT object

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
MAIT-class

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
scores(MAIT)

MAIT<-plotPCA(MAIT,plot3d=FALSE)
scores(MAIT,type="PCA")

MAIT<-plotPLS(MAIT,plot3d=FALSE)
scores(MAIT,type="PLS")
**sigPeaksTable**

*Build a table of the information related to the significant features contained in a MAIT object*

**Description**

Function `sigPeaksTable` takes an **MAIT-class** object containing significant feature information and builds a table with the information related to these features.

**Usage**

```r
sigPeaksTable(MAIT.object=NULL,
              printCSVfile=FALSE,
              extendedTable = TRUE,
              printAnnotation=TRUE)
```

**Arguments**

- **MAIT.object** A **MAIT-class** object where significant features have already been found.
- **printCSVfile** Set to TRUE if an output table has to be produced. The table should be found in (working directory)/(project directory)/Tables/significativeFeatures.csv.
- **extendedTable** Set to TRUE if the table created by the peak external data is used.
- **printAnnotation** Set to TRUE if the peak annotation is provided in the output table.

**Value**

A table containing:

- First column (mz): Peak mass
- Second column (mzmin): Minimum peak mass of the peak group.
- Third column (mzmax): Maximum peak mass of the peak group.
- Fourth column (rt): Peak retention time (in minutes).
- Fifth column (rtmin): Minimum peak retention time of the peak group.
- Sixth column (rtmax): Maximum peak retention time of the peak group.
- Seventh column (npeaks): Number of samples where the peak has been detected.
- The columns from the ninth to the column labeled “isotopes” contain number of class samples where the peak has been detected and the intensities of the peak among samples.
- The isotopes column shows if the peak has been identified as a possible isotope.
- The adduct column shows which kind of adduct could the peak be.
- The column labeled pcgroup contains the spectral ID of the peak.
- The P.adjust column contains the corrected peak p-value using post-hoc methods.
- The p column shows the peak p-value with no multiple test correction.
- The Fisher column shows the Fisher test results for the peak. Each of the letters separated by the character "_" corresponds to a class value. Classes having the same letters are indistinguishable whereas those having different letters are statistically different classes.
- The last columns contain the mean and median values for each feature.
spectralSigFeatures

Author(s)
Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also
spectralTStudent spectralAnova

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
head(sigPeaksTable(MAIT))

spectralSigFeatures  Extract significant features from a MAIT object

Description
Function spectralSigFeatures takes a MAIT-class object and obtains which of the variables are
significant given a p-value threshold. The parameters of the significant features can ve printed to
an output table (TRUE by default). Depending on the number of classes in the data, the function
chooses between using ANOVA tests through function spectralAnova, or T-Student tests by using
function spectralTStudent.

Usage

spectralSigFeatures(MAIT.object = NULL,
pvalue = 0.05,
p.adj = "none",
printCSVfile = FALSE,
scale = FALSE,
parametric = TRUE,
var.equal = FALSE,
test.fun = NULL,
jitter = FALSE,
jitter.factor = 1,
jitter.amount = 0,
namefun = NULL)

Arguments

MAIT.object  A MAIT-class object where function peakAggregation has already been applied.
The output of the function is going to be an update of the same MAIT-class
object.
pvalue  P-value threshold. Variables having a p-value lower than this value is considered
as a significant variable.
p.adj  Character with the name of the posthoc method to be applied to correct the
pvalues. The supported methods are that of the p.adjust function
printCSVfile  Set to TRUE if an output table has to be produced. See function sigPeaksTable
for more information.
**Value**

A MAIT-class object containing the significant features of the scores slot of MAIT-class object used as an input.

**Author(s)**

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

**See Also**

MAIT-class spectralTStudent spectralAnova sigPeaksTable

**Examples**

```r
data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
```

---

**Description**

Function Validation performs a cross-validated classification using three different classifiers: KNN, PLSDA and SVM. The output comes in a table with the classification ratio and its standard error. The classification ratio is weighted to take into account the different sample number of each class.
Validation

Usage

Validation(Iterations=NULL,
    MAIT.object=NULL,
    trainSamples=NULL,
    PCAscale=FALSE,
    PCAcenter=TRUE,
    RemoveOnePeakSpectra=FALSE,
    tuneSVM=FALSE,
    scale=TRUE)

Arguments

<table>
<thead>
<tr>
<th>Arguments</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Iterations</td>
<td>Number of iterations to be performed in the classifications. For each iteration a new training group is randomly chosen.</td>
</tr>
<tr>
<td>MAIT.object</td>
<td>A MAIT-class object where significant features have already been found.</td>
</tr>
<tr>
<td>trainSamples</td>
<td>Number of samples per class to construct the train dataset.</td>
</tr>
<tr>
<td>PCAscale</td>
<td>If method=&quot;PCA&quot; and PCAscale is set to TRUE, then the data is scaled following the prcomp function. If it is set to TRUE, scale input is ignored.</td>
</tr>
<tr>
<td>PCAcenter</td>
<td>If method=&quot;PCA&quot; and PCAscale is set to TRUE, then the data is centered following the prcomp function. If it is set to TRUE, scale input is ignored.</td>
</tr>
<tr>
<td>RemoveOnePeakSpectra</td>
<td>If it is set to TRUE, all the one-peak spectra are deleted from the dataSet and the resulting spectralData object will only contain spectra with more than one peak.</td>
</tr>
<tr>
<td>tuneSVM</td>
<td>If it is set to TRUE, a tune of parameters is performed before the SVM calculus.</td>
</tr>
<tr>
<td>scale</td>
<td>If it is set to TRUE, the data is scaled through the spectral mean value. Set to TRUE by default.</td>
</tr>
</tbody>
</table>

Value

The numerical results of the classification per class and per classifier are saved in a MAIT-class object. Additionally, a table is also included in the output both in the list (field table) and printed as a csv file in the folder (working directory)/Validation. A boxplot is also printed as a png in the same folder showing the differences between classifiers. The confusion matrices of each iteration and classifier are also stored as csv files.

Author(s)

Francesc Fernandez, <francesc.fernandez.albert@upc.edu>

See Also

peakAggregation spectralAnova spectralTStudent spectralSigFeatures

Examples

data(MAIT_sample)
MAIT<-spectralSigFeatures(MAIT,p.adj="fdr",parametric=TRUE)
MAIT <- Validation(Iterations = 20, trainSamples= 15, MAIT.object = MAIT)
Index

*Topic classes
- MAIT-class, 13
- MAIT.FeatureData-class, 13
- MAIT.FeatureInfo-class, 14
- MAIT.Parameters-class, 15
- MAIT.PhenoData-class, 16
- MAIT.RawData-class, 16
- MAIT.Validation-class, 17

*Topic file
- Biotransformations, 2
- biotransformationsTable, 3
- Database, 6
- identifyMetabolites, 10
- MAIT, 12
- metaboliteTable, 19
- negAdducts, 22
- peakAnnotation, 24
- plotPCA, 27
- plotPLS, 28
- posAdducts, 29
- sigPeaksTable, 36
- spectralSigFeatures, 37

*Topic function
- plotBoxplot, 26
- plotHeatmap, 27
- sampleProcessing, 33

- Biotransformations, 2, 4, 10, 14, 15, 18
- biotransformationsTable, 3
- classes, 4, 6, 16
- classifRatioClasses, 5, 17
- classNum, 5, 16

- Database, 6
- featureID, 7
- featureInfo, 7
- featureSigID, 8
- FisherLSD, 12
- getScoresTable, 9
- groupCorr, 25
- identifyMetabolites, 6, 10, 14, 15, 18, 20

- jitter, 38
- loadings, 11
- loadings, MAIT-method (MAIT-class), 13
- LSDResults, 12

- MAIT, 12
- MAIT-class, 2–12, 13, 19–39
- MAIT.FeatureData-class, 13
- MAIT.FeatureInfo-class, 14
- MAIT.Parameters-class, 15
- MAIT.PhenoData-class, 16
- MAIT.RawData-class, 16
- MAIT.Validation-class, 17
- MAITbuilder, 14, 18
- metaboliteTable, 6, 10, 14, 19
- model, 20
- model, MAIT-method (MAIT-class), 13
- models, 21

- negAdducts, 22
- ovClassifRatioData, 17, 22
- ovClassifRatioTable, 23
- p.adjust, 37
- parameters, 24
- PCAplot3d, 28, 29
- peakAggregation, 14, 15, 17, 39
- peakAnnotation, 15, 16, 22, 24, 30
- plotBoxplot, 18, 26
- plotHeatmap, 15, 18, 27
- plotPCA, 11, 13–15, 18, 20, 21, 27
- plotPLS, 11, 13–15, 18, 20, 21, 28
- posAdducts, 29
- pvalues, 30
- pvaluesCorrection, 31

- rawData, 32, 34
- resultsPath, 16, 32

- sampleProcessing, 15, 24, 25, 33
- scale, 28, 29
- scores, 35
- scores, MAIT-method (MAIT-class), 13
INDEX

sigPeaksTable, 36, 37, 38
spectralAnova, 3, 9, 20, 26–29, 37–39
spectralSigFeatures, 8, 10, 12, 15, 30, 31, 37, 39
spectralTStudent, 3, 9, 20, 26–29, 37–39
summary, MAIT-method (MAIT-class), 13

Validation, 5, 15, 17, 18, 23, 38

xsAnnotate, 13–17, 24, 26, 32
xsAnnotate-class, 26