

Package ‘MAIT’

March 30, 2021

Type Package

Title Statistical Analysis of Metabolomic Data

Version 1.24.0

Date 09-06-2020

Author Francesc Fernandez-Albert,
Rafael Llorach, Cristina
Andres-LaCueva, Alexandre Perera

Maintainer Pol Sola-Santos
<pol.soladelossantos@gmail.com>

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 ImmunoOncology, 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

Suggests faahKO

Enhances rgl

git_url <https://git.bioconductor.org/packages/MAIT>

git_branch RELEASE_3_12

git_last_commit 6469a14

git_last_commit_date 2020-10-27

Date/Publication 2021-03-29

R topics documented:

Biotransformations	2
biotransformationsTable	4
classes	4
classifRatioClasses	5
classNum	6

Database	6
featureID	7
featureInfo	8
featureSigID	8
getScoresTable	9
identifyMetabolites	10
loadings	11
LSDResults	12
MAIT	13
MAIT-class	13
MAIT.FeatureData-class	14
MAIT.FeatureInfo-class	14
MAIT.Parameters-class	15
MAIT.PhenoData-class	16
MAIT.RawData-class	16
MAIT.Validation-class	17
MAITbuilder	18
metaboliteTable	19
model	20
models	21
negAdducts	22
ovClassifRatioData	22
ovClassifRatioTable	23
parameters	24
peakAnnotation	24
plotBoxplot	26
plotHeatmap	27
plotPCA	27
plotPLS	28
posAdducts	29
pvalues	30
pvaluesCorrection	31
rawData	32
resultsPath	32
sampleProcessing	33
scores	35
sigPeaksTable	36
spectralSigFeatures	37
Validation	38

Index 40

Biotransformations	<i>Biotransformations of the significant data contained in a MAIT object are identified.</i>
--------------------	--

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

<code>MAIT.object</code>	A MAIT-class object where significant features have already been found.
<code>peakPrecision</code>	Maximum difference between the peak masses differences and the values shown in <code>bioTable</code> to be considered as a biotransformation. As default the value is 0.005 Da.
<code>bioTable</code>	Table containing the biotransformations to be looked for in the <code>signData</code> input. By default it is taken the MAIT-class biotransformations table.
<code>adductTable</code>	Table containing the adducts to be looked for in the <code>signData</code> 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
<code>adductAnnotation</code>	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

```
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
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

```
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

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

classNum	<i>Sample number extractor for each class from a MAIT object</i>
----------	--

Description

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

Usage

```
classNum(MAIT.object)
```

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	<i>Human Metabolome Database</i>
----------	----------------------------------

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

```
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

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

featureInfo	<i>Feature Info extractor from a MAIT object</i>
-------------	--

Description

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

Usage

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

Arguments

MAIT.object A [MAIT-class](#) object

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	<i>Feature statistically significant ID extractor from a MAIT object</i>
--------------	--

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)
featureSigID(MAIT)
featureID(MAIT)[featureSigID(MAIT)] #Significant spectra IDs
```

getScoresTable	<i>Returns a list with the peak scores, masses, retention time and other information</i>
----------------	--

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,
               getSpectra = TRUE,
               getExtendedTable = FALSE)
```

Arguments

MAIT.object A [MAIT-class](#) object where significant features have already been found.

getSpectra If it is set to TRUE, an element of the returned list will contain the spectra ID of each feature.

getExtendedTable 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

```
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

```
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](#) or [plotPLS](#)

Examples

```
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)
```

MAIT	<i>MAIT</i>
------	-------------

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	<i>Class "MAIT"</i>
------------	---------------------

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](#)

MAIT.FeatureInfo-class

Class "MAIT.FeatureInfo"

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.

Author(s)

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

See Also

[MAIT-class xsAnnotate](#)

MAIT.Parameters-class *Class* "MAIT.Parameters"

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](#)

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

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](#)

MAITbuilder

*MAIT constructor function when using external peak data***Description**

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

```
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.

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)
aux<-getScoresTable(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	<i>Metabolite table generator</i>
-----------------	-----------------------------------

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 indistinguishable 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

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)
```

negAdducts	<i>Negative adducts table</i>
------------	-------------------------------

Description

This table contains the adducts to be looked up for 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](#)

ovClassifRatioData	<i>Overall classification ratio extractor for MAIT objects</i>
--------------------	--

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.

Author(s)

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

See Also

[MAIT-class Validation](#)

Examples

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

ovClassifRatioTable *Overall classification table extractor for MAIT objects*

Description

Function ovClassifRatioData extracts the overall classification table for a [MAIT-class](#) object

Usage

```
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

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

parameters	<i>Extractor of the parameters used in the whole run from a MAIT object</i>
------------	---

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	<i>Spectra constructor and peak annotator</i>
----------------	---

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.

Usage

```
peakAnnotation(MAIT.object = NULL,
               corrWithSamp = 0.7,
               perfw hm = 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
perfw hm	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 $Rt_med \pm FWHM * perfw hm$. Where Rt_med is the retention time median and FWHM is the Full Width at Half Maximum. Defined this way, perfw hm is the percentage of the width of the FWHM (Full Width at Half Maximum)
sigma	Defining the coelution range as defined in the perfw hm 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	<i>Prints a png file for each of the significant peak/spectra present in the input</i>
-------------	--

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	<i>Builds ten heatmaps with different p-values and clustering distances</i>
-------------	---

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

```
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

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

plotPCA	<i>2D and 3D PCA scoreplots from a MAIT object</i>
---------	--

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)
```

plotPLS

2D and 3D PLS 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 PLS scoreplot.

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)
```

posAdducts

Positive adducts table

Description

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.

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](#)

Examples

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

pvaluesCorrection	<i>P-values correction extractor from a MAIT object</i>
-------------------	---

Description

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

Usage

```
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

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

rawData	<i>Raw data extractor from a MAIT object</i>
---------	--

Description

Function rawData extracts the raw data used to build the [MAIT-class](#) object

Usage

```
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

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

resultsPath	<i>Retrieves the folder where the results are saved for a MAIT object</i>
-------------	---

Description

Function resultsPath returns the folder where the plots and tables are saved for a [MAIT-class](#) object

Usage

```
resultsPath(MAIT.object)
```

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)
```

sampleProcessing *Peak detector of netCDF samples using xcms package*

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 = 5,
                 Sigma = 5/2.3548,
                 mzSlices = 0.3,
                 retcorrMethod = "loess",
                 groupMethod = "density",
                 bwGroup = 3,
                 mzWidGroup = 0.25,
                 filterMethod = "centWave",
                 prefilter = c(3,3000),
                 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)
```

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.
prefilter	$c(k, I)$ specifying the prefilter step for the first analysis step (ROI detection). Mass traces are only retained if they contain at least k peaks with intensity $\geq I$.
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 <code>group.density</code> 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 <code>group.density</code> in package xcms for details.
ppm	maximal tolerated m/z deviation in consecutive scans, in ppm (parts per million). See <code>findPeaks.centWave</code> in package xcms for details.
peakwidth	Chromatographic peak width, given as range (min,max) in seconds.
fwhm	See <code>fwhm</code> argument in <code>xcmsSet</code> function.
span	See <code>span</code> argument in <code>xcmsSet</code> function.
family	See <code>family</code> argument in <code>xcmsSet</code> 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	<i>Retrieves the scores from a MAIT object</i>
--------	--

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	<i>Build a table of the information related to the significant features contained in a MAIT object</i>
---------------	--

Description

Function sigPeaksTable takes an [MAIT-class](#) object containing significant feature information and builds a table with the information related to these features.

Usage

```
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 the table created by the peak external data is used.
printAnnotation	Set to TRUE 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

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 be 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

<code>MAIT.object</code>	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.
<code>pvalue</code>	P-value threshold. Variables having a p-value lower than this value is considered as a significant variable.
<code>p.adj</code>	Character with the name of the posthoc method to be applied to correct the p-values. The supported methods are that of the p.adjust function
<code>printCSVfile</code>	Set to TRUE if an output table has to be produced. See function sigPeaksTable for more information.

<code>scale</code>	Set to FALSE by default. When set to TRUE, a unit variance scaling of the data when no peak aggregation is performed. If a peak aggregation method is applied, this parameter is ignored.
<code>parametric</code>	If it is set to TRUE, the statistical tests to be applied will be parametrical tests (e.g. ANOVA, TStudent or Welch's tests). Non-parametrical tests (e.g. Kruskal-Wallis, Mann-Whitney tests) are applied otherwise.
<code>var.equal</code>	Set to FALSE by default. When set to TRUE, a Student's T-Test is applied when having 2 classes in the data. If it is set to FALSE, a Welch's test is applied instead.
<code>test.fun</code>	Function of the user-defined posthoc method to be applied.
<code>jitter</code>	If it is set to TRUE, a jitter noise is added to the data. This is useful when applying Mann-Whitney tests with ties.
<code>jitter.factor</code>	See argument factor of the function jitter .
<code>jitter.amount</code>	See argument amount of the function jitter .
<code>namefun</code>	Name of the user-defined posthoc test in the argument test.fun.

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

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

Validation

*Cross validated classification over the output of the function
signPeaksAnova or function TStudent2Clases*

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.

Usage

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

Arguments

Iterations	Number of iterations to be performed in the classifications. For each iteration a new training group is randomly chosen.
MAIT.object	A MAIT-class object where significant features have already been found.
trainSamples	Number of samples per class to construct the train dataset.
PCAscale	If method="PCA" 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.
PCAcenter	If method="PCA" 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.
RemoveOnePeakSpectra	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.
tuneSVM	If it is set to TRUE, a tune of parameters is performed before the SVM calculus.
scale	If it is set to TRUE, the data is scaled through the spectral mean value. Set to TRUE by default.

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

* classes

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

* file

Biotransformations, 2
biotransformationsTable, 4
Database, 6
identifyMetabolites, 10
MAIT, 13
metaboliteTable, 19
negAdducts, 22
peakAnnotation, 24
plotPCA, 27
plotPLS, 28
posAdducts, 29
sigPeaksTable, 36
spectralSigFeatures, 37

* function

plotBoxplot, 26
plotHeatmap, 27
sampleProcessing, 33

Biotransformations, 2, 4, 11, 15, 18
biotransformationsTable, 4

classes, 4, 6, 16
classifRatioClasses, 5, 17
classNum, 6, 16

Database, 6

featureID, 7
featureInfo, 8
featureSigID, 8
FisherLSD, 12

getScoresTable, 9
groupCorr, 25

identifyMetabolites, 7, 10, 15, 18, 20

jitter, 38

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

MAIT, 13
MAIT-class, 2–13, 13, 19–39
MAIT.FeatureData-class, 14
MAIT.FeatureInfo-class, 14
MAIT.Parameters-class, 15
MAIT.PhenoData-class, 16
MAIT.RawData-class, 16
MAIT.Validation-class, 17
MAITbuilder, 14, 18
metaboliteTable, 7, 11, 15, 19
model, 20
model,MAIT-method (MAIT-class), 13
models, 21

negAdducts, 22

ovClassifRatioData, 17, 22
ovClassifRatioTable, 23

p.adjust, 37
parameters, 24
PCAp3d, 28, 29
peakAggregation, 14, 15, 37, 39
peakAnnotation, 15, 16, 22, 24, 30
plotBoxplot, 18, 26
plotHeatmap, 15, 18, 27
plotPCA, 11–15, 18, 20, 21, 27
plotPLS, 11–15, 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

sigPeaksTable, [36](#), [37](#), [38](#)
spectralAnova, [3](#), [10](#), [20](#), [26–29](#), [37–39](#)
spectralSigFeatures, [8](#), [9](#), [11](#), [12](#), [15](#), [30](#),
[31](#), [37](#), [39](#)
spectralTStudent, [3](#), [10](#), [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](#)