Package 'specmine'

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Type Package

Title Metabolomics and Spectral Data Analysis and Mining

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nmrglue.

Imports caret, e1071, ggplot2, impute, ellipse, GGally, pcaPP,
compare, baseline, MASS, pls, readJDX, speaq, genefilter,
RColorBrewer, grDevices, graphics, methods, stats, utils,
Metrics, imputeTS, specmine.datasets, mrbin, plotly, narray

Suggests ggdendro, reticulate, qdap, qpdf, scatterplot3d, MAIT, xcms,
KEGGgraph, KEGGREST, rcytoscapejs, rgl, grid, curl, RCurl,
pins, knitr, rmarkdown

LazyData true

VignetteBuilder knitr

URL https://github.com/BioSystemsUM/specmine

BugReports https://github.com/BioSystemsUM/specmine/issues

Description Provides a set of methods for metabolomics
data analysis, including data loading in different formats,
pre-processing, metabolite identification, univariate and multivariate
data analysis, machine learning, feature selection and pathway analysis. Case studies

can be found on the website: <http://bio.di.uminho.pt/metabolomicspackage/index.html>.
This package suggests 'rcytoscapejs', a package not in mainstream repositories. If you need to install it,
use: devtools::install_github('cytoscape/r-cytoscape.js@v0.0.7').

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

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R topics documented:

`absorbance_to_transmittance`

Convert absorbance to transmittance

Description

Converts absorbance values to transmittance values.

Usage

```
absorbance_to_transmittance(dataset)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.

Value

Returns the dataset with the data points converted to transmittance values.

aggregate_samples *Aggregate samples*

Description

Aggregate samples according to an aggregate function like mean, median, etc.

Usage

```
aggregate_samples(dataset, indexes, aggreg.fn = "mean",
meta.to.remove = c())
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
indexes	index vector with the samples that are going to be aggregated (e.g. c(1,1,2,2), this index vector will aggregate the first two samples and the last two samples).
aggreg.fn	aggregation function (e.g. "mean", "median", etc).
meta.to.remove	metadata's variables to be removed.

Value

Returns the dataset with the samples aggregated.

Examples

```
## Example of aggregating samples
library(specmine.datasets)
data(propolis)
propolis_proc = missingvalues_imputation(propolis)
dataset = aggregate_samples(propolis_proc, as.integer(propolis$metadata$seasons), "mean")
```

aov_all_vars *Analysis of variance*

Description

Perform analysis of variance of all variables in the dataset.

Usage

```
aov_all_vars(dataset, column.class, doTukey = TRUE, write.file = FALSE,
file.out = "anova-res.csv")
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
column.class	string or index indicating what metadata to use.
doTukey	boolean value for do or do not TukeyHSD.
write.file	boolean value indicating if a file with the results is written or not.
file.out	name of the file if write.file is TRUE.

Value

Data frame with the results of ANOVA, with p-value, logarithm of p-value, false discovery rate (fdr) and tukey is doTukey is TRUE. The result is ordered by p-value.

Examples

```
  ## Example of ANOVA with TukeyHSD
  library(specmine.datasets)
  data(propolis)
  propolis_proc = missingvalues_imputation(propolis)
  propolis_proc = flat_pattern_filter(propolis_proc, "iqr", by.percent = TRUE,
red.value = 75)
  result = aov_all_vars(propolis_proc, "seasons", doTukey = FALSE)
```

---

apply_by_group *Apply by group*

Description

Apply a function to samples from a given metadata's group.

Usage

```
apply_by_group(dataset, fn.to.apply, metadata.var, var.value)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
fn.to.apply	function to apply (e.g. mean, max, min).
metadata.var	name of the metadata's variable.
var.value	value of the metadata's variable.

Value

Returns a vector with the variables and the value of the applied function.

Examples

```
    ## Example of applying a function to a group
library(specmine.datasets)
    data(cachexia)
    apply.group.result = apply_by_group(cachexia, mean, "Muscle.loss",
 "control")
```

`apply_by_groups` *Apply by groups*

Description

Apply a function to samples from a metadata's variable.

Usage

```
apply_by_groups(dataset, metadata.var, fn.to.apply = "mean",
variables = NULL, variable.bounds = NULL)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`metadata.var`	name of the metadata's variable.
`fn.to.apply`	function to apply (e.g. mean, max, min).
`variables`	allows to define which variables to calculate the stats (if numbers, indexes are assumed).
`variable.bounds`	allow to define an interval of variables (if numeric).

Value

Returns a vector with the variables and the value of the applied function on the metadata's groups.

Examples

```
    ## Example of applying a function to groups
library(specmine.datasets)
    data(cachexia)
    apply.groups.result = apply_by_groups(cachexia, "Muscle.loss", mean)
```

apply_by_sample *Apply function to samples*

Description

Applies a function to the values of each sample

Usage

```
apply_by_sample(dataset, fn.to.apply, samples = NULL, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
fn.to.apply	function to apply (e.g. mean, max, min).
samples	if defined restricts the application to a given set of samples.
...	additional parameters to apply function.

Value

Returns a vector with the samples and the value of the applied function.

Examples

```
    ## Example of applying a function to variables
library(specmine.datasets)
    data(cachexia)
    apply.samples.result = apply_by_sample(cachexia, mean)
```

apply_by_variable *Apply function to variables*

Description

Applies a function to the values of each variable

Usage

```
apply_by_variable(dataset, fn.to.apply, variables = NULL,
variable.bounds = NULL, samples = NULL, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
fn.to.apply	function to apply (e.g. mean, max, min).
variables	allows to define which variables to calculate the stats (if numbers, indexes are assumed).
variable.bounds	allow to define an interval of variables (if numeric).
samples	if defined restricts the application to a given set of samples.
...	additional parameters to apply function.

Value

Returns a vector with the variables and the value of the applied function.

Examples

```
    ## Example of applying a function to variables
library(specmine.datasets)
    data(cachexia)
    apply.variables.result = apply_by_variable(cachexia, mean)
```

---

background_correction *Background correction*

Description

Perform background correction on the spectra.

Usage

```
background_correction(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns the dataset with background correction performed on the data.

Examples

```
## Example of background correction
library(specmine.datasets)
data(cachexia)
cachexia.corrected = background_correction(cachexia)
```

`baseline_correction` *Baseline correction*

Description

Performs baseline correction on the dataset.

Usage

```
baseline_correction(dataset, method = "modpolyfit", ...)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`method`	string representing the baseline correction method. It can be one of these methods: • "als" Asymmetric Least Squares, baseline correction by 2nd derivative constrained weighted regression • "fillPeaks" An iterative algorithm using suppression of baseline by means in local windows • "irls" Iterative Restricted Least Squares, an algorithm with primary smoothing and repeated baseline suppressions and regressions with 2nd derivative constraint • "lowpass" Low-pass filter, an algorithm for removing baselines based on Fast Fourier Transform filtering • "medianWindow" an implementation and extension of Mark S. Friedrichs' model-free algorithm • "modpolyfit" Modified polynomial fitting, an implementation of Chad A. Lieber and Anita Mahadevan-Jansen's algorithm for polynomial fitting • "peakDetection" A translation from Kevin R. Coombes et al.'s MATLAB code for detecting peaks and removing baselines • "rfbaseline" Robust Baseline Estimation, Wrapper for Andreas F. Ruckstuhl, Matthew P. Jacobson, Robert W. Field, James A. Dodd's algorithm based on LOWESS and weighted regression • "rollingBall" Ideas from Rolling Ball algorithm for X-ray spectra by M. A. Kneen and H. J. Annegarn. Variable window width has been left out
...	Additional parameters of the baseline correction method.

Value

Returns the dataset with the data's baseline corrected.

boxplot_variables *Boxplot of variables*

Description

Boxplot of each variable of the dataset.

Usage

```
boxplot_variables(dataset, variables = NULL, samples = NULL,
horizontal = TRUE, col = "lightblue", nchar.label = 10,
cex.axis = 0.8, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variables	vector with the variables names or a NULL value indicating all variables.
samples	vector with the samples names or a NULL value indicating all samples.
horizontal	boolean value indicating if the boxplots should be horizontal.
col	string that represents the color of the bodies of the boxplots.
nchar.label	number of characters to display the variables' names.
cex.axis	numeric value that indicates the amount by which the axis is magnified relative to the default.
...	additional parameters of boxplot function.

Examples

```
## Example of showing the boxplot of a few variables
library(specmine.datasets)
data(cachexia)
boxplot_variables(cachexia, variables = c("Creatine","Serine","Lactate"))
```

boxplot_vars_factor *Boxplot of variables with metadata's variable factors*

Description

Boxplot of variables with metadata's variable factors from the dataset.

Usage

```
boxplot_vars_factor(dataset, meta.var, variables = NULL,
samples = NULL, horizontal = FALSE, nchar.label = 10, col = NULL,
vec.par = NULL, cex.axis = 0.8, ylabs = NULL, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
meta.var	metadata's variable.
variables	vector with the variables names or a NULL value indicating all variables.
samples	vector with the samples names or a NULL value indicating all samples.
horizontal	boolean value indicating if the boxplots should be horizontal.
nchar.label	number of characters to display the variables' names.
col	string that represents the color of the bodies of the boxplots.
vec.par	vector with the disposition of the boxplots (rows, columns).
cex.axis	numeric value that indicates the amount by which the axis is magnified relative to the default.
ylabs	y-axis labels.
...	additional parameters of boxplot function.

Examples

```
## Example of showing the boxplot factors of a few variables
library(specmine.datasets)
data(cachexia)
boxplot_vars_factor(cachexia, "Muscle.loss", variables = c("Creatine","Serine",
"Lactate"))
```

---

check_2d_dataset *Check 2D dataset.*

Description

Check if the dataset is valid and if not give the proper error message.

Usage

```
check_2d_dataset(dataset_2d)
```

Arguments

dataset_2d	List representing the 2D dataset from a 2D metabolomics experiment.

Value

Message saying if the 2D dataset is valid or invalid, in the last case also gives the reason.

check_dataset *Check dataset*

Description

Check if the dataset is valid and if not give the proper error message.

Usage

```
check_dataset(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Message saying if the dataset is valid or invalid, in the last case also gives the reason.

Examples

```
## Example checking a dataset
library(specmine.datasets)
data(cachexia)
check_dataset(cachexia)
```

clustering *Perform cluster analysis*

Description

Perform cluster analysis on the dataset.

Usage

```
clustering(dataset, method = "hc", distance = "euclidean",
type = "samples", num.clusters = 5, clustMethod = "complete")
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
method	a string describing the method of clustering. Possible types are: • "hc" perform hierarchical clustering. • "kmeans" perform kmeans clustering.

distance	the distance measure to be used to compute the distances between the rows of a data matrix. Possible types are "euclidean", "manhattan", "pearson" or "spearman". Only for hierarchical clustering.
type	a string indicating if cluster analysis will be performed on samples ("samples") or on variables ("variables").
num.clusters	the number of clusters in k-means cluster analysis.
clustMethod	Cluster method for hierarchical clustering.

Value

An object of class kmeans or hclust with the clustering results.

Examples

```
## Example of kmeans and hierarchical clustering
library(specmine.datasets)
data(cachexia)
hc.result = clustering(cachexia, method = "hc",
    distance = "euclidean")
kmeans.result = clustering(cachexia, method = "kmeans",
num.clusters = 4)
```

---

compare_regions_by_sample

Compare regions by sample

Description

Compare two regions of a dataset by samples.

Usage

```
compare_regions_by_sample(dataset1, dataset2, fn.to.apply,
samples = NULL, ...)
```

Arguments

dataset1	list representing the dataset from a metabolomics experiment.
dataset2	list representing the dataset from a metabolomics experiment.
fn.to.apply	function to apply (e.g. mean, max, min).
samples	if defined restricts the application to a given set of samples.
...	additional parameters to apply.by.sample function.

Value

Returns a data.frame with the results of the function applied to the samples and the ration between the two datasets.

Examples

```
    ## Example of comparing regions by sample
library(specmine.datasets)
    data(cachexia)
    subset1 = subset_x_values(cachexia, 1:31, by.index = TRUE)
    subset2 = subset_x_values(cachexia, 32:63, by.index = TRUE)
    comp.regions.result = compare_regions_by_sample(subset1, subset2,
  mean)
```

---

convert_chebi_to_kegg *Convert CHEBI codes to KEGG codes.*

Description

Converts a vector of CHEBI codes into a vector of the corresponding KEGG codes. This is performed by using our internal library used in NMR identification, it will not have all chebi codes.

Usage

```
convert_chebi_to_kegg(chebi_codes)
```

Arguments

chebi_codes	Vector with the CHEBI codes (each chebi must be structured like: CHEBI:<number>)

Value

Named vector with kegg codes and respective names. Vector names are the compound names and the vector elements the kegg codes.

Examples

```
keggs=convert_hmdb_to_kegg(c("CHEBI:15377", "CHEBI:26078", "CHEBI:30168"))
keggs
```

---

convert_from_chemospec *Convert from ChemoSpec*

Description

Convert the dataset in the ChemoSpec format to a dataset of this package.

Usage

```
convert_from_chemospec(csobj, type = "undefined",
description = "")
```

Arguments

csobj	ChemoSpec object representing the dataset.
type	string representing the type of the data.
description	string representing the description of the dataset.

Value

Returns a list representing the dataset converted.

---

convert_hmdb_to_kegg *Convert HMDB codes to KEGG codes.*

Description

Converts a vector of HMDB codes into a vector of the corresponding KEGG codes. This is performed by using our internal library used in NMR identification, it will not have all chebi codes.

Usage

```
convert_hmdb_to_kegg(hmdb_codes)
```

Arguments

hmdb_codes	Vector with the HMDB codes (each hmdb code must have 7 digits, e.g., HMDB0000001)

Value

Named vector with kegg codes and respective names. Vector names are the compound names and the vector elements the kegg codes.

Examples

```
keggs=convert_hmdb_to_kegg(c("HMDB0000001", "HMDB0000008", "HMDB0000246"))
keggs
```

convert_keggpathway_2_reactiongraph

Convert KEGGPathway object to graph object.

Description

Converts KEGGPathway object into a graph object.

Usage

```
convert_keggpathway_2_reactiongraph(pathObj)
```

Arguments

pathObj	KEGGPathway object.

Value

Kegg reaction graph.

convert_multiple_spcmnm_to_kegg

Convert specmine metabolite codes to KEGG codes.

Description

Converts a vector of specmine metabolite codes into a vector of the corresponding KEGG codes. This is performed by using our internal library used in NMR identification, it will not have all chebi codes.

Usage

```
convert_multiple_spcmnm_to_kegg(spcmnm_codes)
```

Arguments

spcmnm_codes	Vector with the SPCMNM codes (each chebi must be structured like: SPCMNM<number>)

Value

Named vector with kegg codes and respective names. Vector names are the compound names and the vector elements the kegg codes.

Examples

```
keggs=convert_multiple_spcmnm_to_kegg(c("SPCMNM2111", "SPCMNM2142", "SPCMNM069774"))
keggs
```

convert_to_factor *Convert metadata to factor*

Description

Convert a metadata's variable to factor.

Usage

```
convert_to_factor(dataset, metadata.var)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.var	name of the metadata's variable.

Value

Returns the dataset with the metadata's variable converted to factor.

correlations_dataset *Dataset correlations*

Description

Calculate the correlations of all variables or samples in the dataset.

Usage

```
correlations_dataset(dataset, method = "pearson", by.var = TRUE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
method	correlation method, it can be "pearson", "kendall" or "spearman".
by.var	if TRUE then the correlations of the variables will be calculated, if not then the correlations of the samples will be calculated.

Value

Returns the correlation matrix

Examples

```
  ## Example of correlations of variables
  library(specmine.datasets)
  data(cachexia)
  corr.result = correlations_dataset(cachexia,
method = "pearson", by.var = TRUE)
```

`correlations_test` *Correlations test*

Description

Performs correlations test to the whole dataset.

Usage

```
correlations_test(dataset, method = "pearson", by.var = TRUE,
alternative = "two.sided")
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`method`	correlation method, it can be "pearson", "kendall" or "spearman".
`by.var`	if TRUE then the correlations of the variables will be calculated, if not then the correlations of the samples will be calculated.
`alternative`	alternative argument from cor.test of stats package. Can be "two.sided", "less" or "greater".

Value

Returns a matrix with the correlation values and the p-values

Examples

```
  ## Example of correlations test of variables
  library(specmine.datasets)
  data(cachexia)
  corr.result = correlations_test(cachexia,
method = "pearson", by.var = FALSE)
```

correlation_test *Correlation test of two variables or samples*

Description

Performs correlations test of two variables or samples from the dataset.

Usage

```
correlation_test(dataset, x, y, method = "pearson",
alternative = "two.sided", by.var = TRUE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
x	first variable or sample.
y	second variable or sample.
method	correlation method, it can be "pearson", "kendall" or "spearman".
alternative	alternative argument from cor.test of stats package. Can be "two.sided", "less" or "greater".
by.var	if TRUE then the correlations of the variables will be calculated, if not then the correlations of the samples will be calculated.

Value

Returns the correlation result from cor.test function of stats package.

Examples

```
  ## Example of correlations test of variables
  library(specmine.datasets)
  data(cachexia)
  corr.result = correlation_test(cachexia, "Serine", "Creatine", method = "pearson",
by.var = TRUE)
```

count_missing_values *Count missing values*

Description

Counts the missing values on the dataset.

Usage

```
count_missing_values(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns the number of missing values on the dataset.

Examples

```
## Example of counting the missing values
library(specmine.datasets)
data(cachexia)
count_missing_values(cachexia)
```

---

count_missing_values_per_sample
Count missing values per sample

Description

Counts the missing values on each sample of the dataset.

Usage

```
count_missing_values_per_sample(dataset, remove.zero = TRUE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
remove.zero	boolean value indicating if the results of samples with no missing value are removed.

Value

Returns a vector with the number of missing values on each sample.

Examples

```
## Example of counting the missing values on each sample
library(specmine.datasets)
data(cachexia)
cachexia$data[10,10] = NA
count_missing_values_per_sample(cachexia)
```

count_missing_values_per_variable *Count missing values per variable*

Description

Counts the missing values on each variable of the dataset.

Usage

```
count_missing_values_per_variable(dataset, remove.zero = TRUE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
remove.zero	boolean value indicating if the results of variables with no missing value are removed.

Value

Returns a vector with the number of missing values on each sample.

Examples

```
## Example of counting the missing values on each variable
library(specmine.datasets)
data(cachexia)
cachexia$data[10,10] = NA
count_missing_values_per_variable(cachexia)
```

create_2d_dataset *Create 2D dataset*

Description

Creates a 2D dataset from existing objects.

Usage

```
create_2d_dataset(list_2d, type = "undefined", metadata = NULL, description = "",
                  sample.names = NULL, F1 = NULL, F2 = NULL, label.x = NULL,
                  label.y = NULL, label.values = NULL)
```

Arguments

list_2d	A list of matrices where each matrix represents a 2D spectra from one sample.
type	Type of data: string that can be one of the following: • 2d-nmr
metadata	Data frame with the dataset's metadata: columns represent each metadata variable and rows represent the value of the metadata for the sample.
description	String with a short description of the dataset.
sample.names	Vector with sample names, if NULL then the names of the 2D list or sequential numbers will be used.
F1	Vector of the indirect dimension' ppm values.
F2	Vector of the diret dimension' ppm values.
label.x	Label for the x axis.
label.y	Label for the y axis.
label.values	Label for the variable represented by a pair (x,y).

Value

List representing the 2D dataset:

data	A list of matrices where each matrix matches one 2D spectra.
type	The type of the data in the dataset.
description	A short text describing the dataset.
metadata	A dataframe with the metadata variables.
F1_ppm	The ppm values regarding indirect dimension.
F2_ppm	The ppm values regarding direct dimension.
labels	A list of labels for the x, y and pairs'(x,y) values.

---

create_dataset *Create dataset*

Description

Create a dataset from existing objects

Usage

```
create_dataset(datamatrix, type = "undefined", metadata = NULL,
description = "", sample.names = NULL, x.axis.values = NULL,
label.x = NULL, label.values = NULL, xSet = NULL)
```

Arguments

`datamatrix`	matrix with numerical data: rows are assumed to be variables and columns assumed to be samples.
`type`	type of data: string that can be one of the following: • nmr-spectra • nmr-peaks • ir-spectra • uvv-spectra • raman-spectra • fluor-spectra • ms-spectra • lcms-peaks • gcms-peaks • integrated-data • concentrations • undefined
`metadata`	data frame with the dataset's metadata: columns represent each metadata variable and rows represent the value of the metadata for the sample.
`description`	string with a short description of the dataset.
`sample.names`	vector with sample names, if NULL then the column names of datamatrix or sequential numbers will be used.
`x.axis.values`	vector with the x axis values, if NULL then the row names of datamatrix or sequential numbers will be used.
`label.x`	x axis label.
`label.values`	values label.
`xSet`	xcmsSet object from xcms package to store the reading and preprocessing results from MS spectra. Used for metabolite identification purposes.

Value

list representing the dataset:

`data`	matrix with the data
`type`	type of the data
`description`	short description of the dataset
`metadata`	data frame with the metadata variables
`labels`	list with labels of x axis and values
`xSet`	xcmsSet object

create_pathway_with_reactions *Creates the pathway, with reactions included in the nodes.*

Description

Creates a cytoscape pathway, where the reactions between compounds are also included in the nodes.

Usage

```
create_pathway_with_reactions(path, path.name, identified_cpds,
                              nodeNames="kegg", nodeTooltip=FALSE,
                              map.zoom=FALSE, map.layout="preset",
                              map.width=NULL, map.height=NULL)
```

Arguments

path	KEGGPathway object.
path.name	Name of the pathway.
identified_cpds	Vector of kegg codes to color differently in the map.
nodeNames	How the nodes should be named. If "kegg", nodes are named with kegg codes. If "names", nodes are named with the common names.
nodeTooltip	Boolean value indicating if tooltips of nodes should appear when hovering with the mouse. Does not work for all environments (e.g. can be used in shiny apps).
map.zoom	Boolean value indicating if a zoom widget should appear or not. Does not work for all environments (e.g. can be used in shiny apps).
map.layout	Layout of the map, available values are the ones of cytoscape ("breadthfirst", "preset", "cose", ...)
map.width	width of the map, in percentage (e.g. "80%"). May not work as expected in some environments.
map.height	Height of the map, in px (e.g. "500px"). May not work as expected in some environments.

cubic_root_transform *Cubic root transformation*

Description

Performs cubic root transformation on the data matrix.

Usage

```
cubic_root_transform(datamat)
```

Arguments

datamat	data matrix.

Value

Returns the data matrix with the cubic root transformation applied.

Examples

```
## Example of cubic root transformation
library(specmine.datasets)
data(cachexia)
datamat.cubic = cubic_root_transform(cachexia$data)
```

---

dataset_from_peaks *Dataset from peaks*

Description

Converts a peak list to a dataset.

Usage

```
dataset_from_peaks(sample.list, metadata = NULL,
description = "", type = "nmr-peaks")
```

Arguments

sample.list	list with the peaks from each sample.
metadata	data frame with the associated metadata.
description	string with the description of the dataset.
type	string that represents the type of the data.

Value

Returns the dataset from the peak list.

Examples

```
    ## Example of converting a peak list to a dataset (computationally heavy)
library(specmine.datasets)
data(propolisSampleList)
    dataset = dataset_from_peaks(propolisSampleList, metadata = NULL,
      description = "some text", type = "nmr-peaks")
```

`data_correction` *Data correction*

Description

Perform spectra corrections with 3 different methods.

Usage

```
data_correction(dataset, type = "background",
method = "modpolyfit", ...)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`type`	string that represents the type of correction that will be applied to the spectra. The three possible types are: "background", to perform background correction; "offset", to perform offset correction; and "baseline", to perform baseline correction.
`method`	string parameter of baseline correction indicating the correction method.
`...`	additional parameters of baseline correction.

Value

Returns the dataset with the spectra corrected.

`dendrogram_plot` *Plot dendrogram*

Description

Plot dendrogram of hierarchical clustering results.

Usage

```
dendrogram_plot(dataset, hc.result, column.metadata = 1,
labels = NULL, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
hc.result	object of class hclust with the clustering results.
column.metadata	string or index indicating what metadata to use to name the leafs.
labels	vector with the leaf names (optional).
...	other parameters for plotting.

Examples

```
### Example of a dendrogram
library(specmine.datasets)
data(cachexia)
hc.result = hierarchical_clustering(cachexia)
dendrogram_plot(cachexia, hc.result)
```

---

dendrogram_plot_col *Plot dendrogram*

Description

Plot dendrogram of hierarchical clustering results with different colors

Usage

```
dendrogram_plot_col(dataset, hc.result, classes.col, colors = NULL, title = "",
lab.cex = 1, leg.pos = "topright", label_samples=NULL,...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
hc.result	object of class hclust with the clustering results.
classes.col	string or index indicating what metadata to use to color the leafs.
colors	vector with the corresponding colors of the metadata classes.
title	title of dendrogram.
lab.cex	the magnification to be used for x and y labels relative to the current setting of cex.
leg.pos	position of the legend.
label_samples	string or index indicating what metadata to use to name the leafs. If not provided the name of the leafs will remain the samples names.
...	other parameters for plotting.

Examples

```
## Example of colored dendrogram
library(specmine.datasets)
data(cachexia)
hc.result = hierarchical_clustering(cachexia)
dendrogram_plot_col(cachexia, hc.result, "Muscle.loss",
title = "Example")
```

`detect_nmr_peaks_from_dataset` *Detection of the peaks in an NMR spectra dataset.*

Description

This function detects the peaks, that have a minimum intensity of `baseline_tresh`, and performs alignment of those peaks.

Usage

```
detect_nmr_peaks_from_dataset(dataset, baseline_tresh=50000,
                              ap.method="own", ap.samp.classes=1, ap.step=0.03)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`baseline_tresh`	Minimum intensity value that peaks must have. Peaks with intensity smaller than baseline_tresh will not be considered as detected peaks.
`ap.method`	Method to used in the alignment of peaks, after they are identified. Can be "own" or "metaboanalyst", which the later is for using the peak alignment used in MetaboAnalyst software.
`ap.samp.classes`	the metadata's variable to be used in the MetaboAnalyst method.
`ap.step`	step value for the peak alignment process

Value

Returns a dataset with the peaks detected and aligned.

`feature_selection` *Perform feature selection*

Description

Perform feature selection on the dataset.

Usage

```
feature_selection(dataset, column.class, method = "rfe",
functions, validation = "cv", repeats = 5, number = 10,
subsets = 2^(2:4))
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`column.class`	string or index indicating what metadata to use.
`method`	method used for feature selection. Possible values are "rfe" (recursive feature elimination) and "filter" (Selection by filter - sbf) from caret's package.
`functions`	a list of functions for model fitting, prediction and variable importance/filtering.
`validation`	the external resampling method: boot, cv, LOOCV or LGOCV (for repeated training/test splits.
`repeats`	for repeated k-fold cross-validation only: the number of complete sets of folds to compute.
`number`	either the number of folds or number of resampling iterations.
`subsets`	a numeric vector of integers corresponding to the number of features that should be retained (rfe only).

Value

caret's result from rfe or sbf.

Examples

```
## Example of feature selection using rfe and sbf
library(caret)
library(specmine.datasets)
data(cachexia)
rfe.result = feature_selection(cachexia, "Muscle.loss",
             method="rfe", functions = caret::rfFuncs,
             validation = "cv", number = 3,
             subsets = 2^(1:6))
sbf.result = feature_selection(cachexia, "Muscle.loss",
     method="filter", functions = caret::rfSBF,
     validation = "cv")
```

`filter_feature_selection` *Perform selection by filter*

Description

Perform selection by filter using univariate filters, from caret's package.

Usage

```
filter_feature_selection(datamat, samples.class,
functions = caret::rfSBF, method = "cv", repeats = 5)
```

Arguments

`datamat`	data matrix from dataset.
`samples.class`	string or index indicating what metadata to use.
`functions`	a list of functions for model fitting, prediction and variable filtering.
`method`	the external resampling method: boot, cv, LOOCV or LGOCV (for repeated training/test splits.
`repeats`	for repeated k-fold cross-validation only: the number of complete sets of folds to compute.

Value

A caret's sbf object with the result of selection by filter.

Examples

```
## Example of selection by filter
library(caret)
library(specmine.datasets)
data(cachexia)
rfe.result = filter_feature_selection(cachexia$data,
     cachexia$metadata$Muscle.loss, functions = caret::rfSBF,
     method = "cv")
```

find_equal_samples *Find equal samples*

Description

Finds samples that have the same peak values - x and y (equal data frames)

Usage

```
find_equal_samples(sample.list)
```

Arguments

sample.list	list of data frames with the samples' peaks.

Value

Returns a dataframe with two columns indicating which pair of samples are equal.

Examples

```
    ## Example of finding equal samples
library(specmine.datasets)
    data(propolisSampleList)
    equal.samples = find_equal_samples(propolisSampleList)
```

first_derivative *First derivative*

Description

Calculates the first derivative of the data.

Usage

```
first_derivative(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Return the dataset with the first derivative of the data calculated.

`flat_pattern_filter` *Flat pattern filter*

Description

Performs a flat pattern filter over the dataset.

Usage

```
flat_pattern_filter(dataset, filter.function = "iqr",
by.percent = TRUE, by.threshold = FALSE, red.value = 0)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`filter.function`	filter function. It can be: • **"iqr"** - Interquantile Range • **"rsd"** - Relative Standard Deviation • **"sd"** - Standard Deviation • **"mad"** - Median Absolute Deviation • **"mean"** - Mean • **"median"** - Median
`by.percent`	boolean value, if TRUE the number of variables to filter will be a percentage of the number of variables in the dataset; percentage is given by the "red.value" parameter
`by.threshold`	boolean value, if TRUE, defines filtering will select variables where values of filtering function are below a given threshold. Threshold is defined by red.value that defines the minimum value of the function needed to keep the variable.
`red.value`	it can be the percentage or the threshold number. If red.value = "auto", will calculate number of variables to remove automatically

Value

Returns the dataset with the data filtered.

Examples

```
## Example of flat pattern filter
library(specmine.datasets)
data(propolis)
dataset.filtered = flat_pattern_filter(propolis, "iqr", by.percent = TRUE,
   red.value = 20)
```

fold_change *Fold change analysis*

Description

Perform fold change analysis on the dataset.

Usage

```
fold_change(dataset, metadata.var, ref.value,
threshold.min.fc = NULL, write.file = FALSE,
file.out = "fold_change.csv")
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.var	metadata to use to calculate the fold change.
ref.value	class name to indicate the initial value.
threshold.min.fc	minimum threshold of the fold change value.
write.file	boolean value to write or not a file with the results.
file.out	name of the file.

Value

Table of results with fold change and log2 of fold change.

Examples

```
  ## Example of fold change
  library(specmine.datasets)
  data(cachexia)
  fold.change.results = fold_change(cachexia, "Muscle.loss",
"control", write.file = FALSE)
```

fold_change_var *Fold change applied on two variables*

Description

Fold change applied on two variables. Instead of having the difference of the variables on two groups, we have the difference of the groups on two variables.

Usage

```
fold_change_var(dataset, metadata.var, variables,
threshold.min.fc = NULL, write.file = FALSE,
file.out = "fold_change_reverse.csv")
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.var	metadata to use to calculate the fold change.
variables	vector with two positions containing the name of the variables.
threshold.min.fc	minimum threshold of the fold change value.
write.file	boolean value to write or not a file with the results.
file.out	name of the file.

Value

Table of results with fold change and log2 of fold change.

Examples

```
  ## Example of fold change reverse
  library(specmine.datasets)
  data(cachexia)
  fold.change.results = fold_change_var(cachexia, "Muscle.loss",
c("Creatine", "Serine"))
```

---

get_cpd_names — *Get the names of the compounds that correspond to the kegg codes given.*

Description

Gets the common name of the compounds of the kegg codes given.

Usage

```
get_cpd_names(kegg_codes)
```

Arguments

kegg_codes	Character vector with kegg codes.

Value

Named vector with the names of the compounds. The names of the vector are the compounds' names and the vector elements the kegg codes.

Examples

```
get_cpd_names(c("cpd:C00001", "cpd:C00008", "gl:G13099"))
```

`get_data` *Get data*

Description

Get the data matrix from dataset

Usage

```
get_data(dataset)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.

Value

Returns the data matrix

Examples

```
## Example of getting the data matrix
library(specmine.datasets)
data(cachexia)
cachexia.dm = get_data(cachexia)
```

`get_data_as_df` *Get data as data frame*

Description

Get the data matrix from the dataset as a data frame.

Usage

```
get_data_as_df(dataset)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.

Value

Returns the data matrix from the dataset as a data.frame object.

Examples

```
## Example of getting the data matrix as data frame
library(specmine.datasets)
data(cachexia)
cachexia.dt = get_data_as_df(cachexia)
```

`get_data_value` *Get data value*

Description

Get a data value given the x-axis labels and the sample

Usage

```
get_data_value(dataset, x.axis.val, sample, by.index = FALSE)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`x.axis.val`	index or name of the x-axis value.
`sample`	index or name of the sample.
`by.index`	boolean value indicating if the x-axis value and sample are represented as index or not.

Value

Returns a numeric with the data point value.

Examples

```
## Example of getting a data value from the dataset
library(specmine.datasets)
data(cachexia)
data.value = get_data_value(cachexia, "Creatine", "PIF_178",
     by.index = FALSE)
```

get_data_values *Get data values*

Description

Gets the values of all samples in the dataset given a set of x axis names or indexes.

Usage

```
get_data_values(dataset, x.axis.val, by.index = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
x.axis.val	vector with the values of the x axis (could be names or indexes).
by.index	boolean value indicating if the x.axis.val is a vector of indexes or not.

Value

Returns a matrix with the values of all samples in the specified x axis.

Examples

```
  ## Example of getting a metadata value
  library(specmine.datasets)
  data(cachexia)
  data.values = get_data_values(cachexia, c("Creatine","Serine","Lactate"),
by.index = FALSE)
```

get_files_list_per_assay *Get list of files per assay for MetaboLights study.*

Description

Returns a list of the data files in each assay of a MetaboLights study.

Usage

```
get_files_list_per_assay(studyID)
```

Arguments

studyID	ID of the metabolights study

Value

A list with one or more item. Each item corresponds to an assay of the MetaboLights study. Each item contains a data frame with the names of the samples (column 'Samples') and respective file names (column 'Files').

References

MetaboLights database: https://www.ebi.ac.uk/metabolights/

---

get_metabolights_study

Download MetaboLights study files.

Description

Download data and metadata files for each assay from the specified MetaboLights database study.

Usage

```
get_metabolights_study(studyID, directory)
```

Arguments

`studyID`	ID of the metabolights study to download. For example, 'MTBLS100'
`directory`	Directory where to download the data.

Note

Study's files are stored by assay. Data files from assay 1 of the study will be stored in folder '1'.

Be aware that the study's files may not be structured in the right way to be readily imported with a specmine read function.

Specmine takes into consideration that the names of the data files/folders correspond to the names of the samples. In some studies, data file names do not correspond to the samples' names in the metadata. To overcome this, we create a file called 'samples_files.csv' matching the sample name to the respective data file/zipped folder.

In some cases, one downloaded zipped data folder may contain more than one sample / replicates, but metabolights information only associates the overall folder as one sample. So manual naming of the folder samples and further changing the metadata file (metadata.csv) may be necessary.

Also, some data formats of some metabolights studies are not yet readable by specmine.

The metadata file(s) are csv file(s) with the metadata information on each sample. There is one metadata file per assay. Metadata file from assay 1 will be named 'metadata1.csv'.

References

MetaboLights database: https://www.ebi.ac.uk/metabolights/

`get_metabolights_study_files_assay` *Download data files from an assay of MetaboLights study*

Description

Downloads the data files from the assay specified in 'assay' of the MetaboLights study ('studyID')

Usage

```
get_metabolights_study_files_assay(studyID, assay, directory)
```

Arguments

`studyID`	ID of the metabolights study to download.
`assay`	Number of the assay.
`directory`	Directory where to download the data.

Details

This function should be used together with `get_metabolights_study_metadata_assay`. See example below.

Be aware that the study's files may not be structured in the right way to be readily imported with a specmine read function.

Specmine takes into consideration that the names of the data files/folders correspond to the names of the samples. In some studies, data file names do not correspond to the samples' names in the metadata. To overcome this, we create a file called 'samples_files.csv' matching the sample name to the respective data file/zipped folder.

In some cases, one downloaded zipped data folder may contain more than one sample / replicates, but metabolights information only associates the overall folder as one sample. So manual naming of the folder samples and further changing the metadata file (metadata.csv) may be necessary.

Also, some data formats of some metabolights studies are not yet readable by specmine.

References

MetaboLights database: https://www.ebi.ac.uk/metabolights/

`get_metabolights_study_metadata_assay`
Download metadata file from an assay of MetaboLights study

Description

Downloads the metadata file from the assay specified in 'assay' of the MetaboLights study ('studyID').

Usage

```
get_metabolights_study_metadata_assay(studyID, assay, directory)
```

Arguments

`studyID`	ID of the metabolights study to download.
`assay`	Number of the assay.
`directory`	Directory where to download the data.

Details

This function should be used together with `get_metabolights_study_files_assay`. See example below.

The metadata file is a csv file with the metadata information on each sample of the study's assay.

References

MetaboLights database: https://www.ebi.ac.uk/metabolights/

`get_metabolights_study_samples_files`
Get list of files from an assay of the MetaboLights study and saves it in a csv file.

Description

Get list of files from an assay of the MetaboLights study and saves it in a csv file.

Usage

```
get_metabolights_study_samples_files(studyID, assay, directory)
```

Arguments

`studyID`	ID of the metabolights study
`assay`	Number of the assay
`directory`	Directory path where the file will be saved.

References

MetaboLights database: https://www.ebi.ac.uk/metabolights/

`get_MetabolitePath` *Returns an object of KEGGPathway of the pathway especified in pathcode.*

Description

Returns an object of KEGGPathway of the pathway specified in pathcode (e.g. "hsa00010").

Usage

```
get_MetabolitePath(pathcode)
```

Arguments

`pathcode`	Pathway code of the path wanted.

Value

KEGGPathway object.

`get_metabPaths_org` *Get the metabolic pathways present in given organism.*

Description

Get vector with paths numbers that occur in the given organism, named with the full paths names.

Usage

```
get_metabPaths_org(org_code)
```

Arguments

`org_code`	Organism code. The correct code for an organism can be consulted using function `get_OrganismsCodes`.

get_metadata *Get metadata*

Description

Get the metadata from the dataset

Usage

```
get_metadata(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

returns a data frame with the metadata.

Examples

```
## Example of getting the metadata
library(specmine.datasets)
data(cachexia)
cachexia.mt = get_metadata(cachexia)
```

get_metadata_value *Get metadata value*

Description

Get the metadata value

Usage

```
get_metadata_value(dataset, variable, sample)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variable	index or name of the metadata variable.
sample	index or name of the sample.

Value

Return the corresponding metadata value of the sample.

Examples

```
## Example of getting a metadata value
library(specmine.datasets)
data(cachexia)
metadata.value = get_metadata_value(cachexia, "Muscle.loss", "PIF_178")
```

`get_metadata_var` *Get metadata variable*

Description

Get the values of a metadata variable from the dataset.

Usage

```
get_metadata_var(dataset, var)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`var`	index or name of the metadata variable.

Value

Returns a vector with the values of the metadata variable.

Examples

```
## Example of getting a metadata variable
library(specmine.datasets)
data(cachexia)
metadata.variable = get_metadata_var(cachexia, "Muscle.loss")
```

`get_OrganismsCodes` *Get all organisms in KEGG.*

Description

Get code, t number, full name and phylogeny of all organisms in KEGG.

Usage

```
get_OrganismsCodes()
```

Value

Data frame with t number, organism code, full name and phylogeny for each kegg organism.

Examples

```
get_OrganismsCodes()
```

`get_paths_with_cpds_org` *Get only the paths of the organism that contain one or more of the given compounds.*

Description

Gives only the metabolic paths of the mentioned organism that contain one or more of the given compounds.

Usage

```
get_paths_with_cpds_org(organism_code, compounds, full.result=TRUE)
```

Arguments

`organism_code`	Organism code. The correct code for an organism can be consulted using function `get_OrganismsCodes`.
`compounds`	Named vector with kegg codes of compounds and respective names. This vector can be obtained by using the function `get_cpd_names` or the function `convert_hmdb_to_kegg`.
`full.result`	If the full result is to be given. Defaults to TRUE.

Value

Data frame.

If full result is chosen, the data frame contains information on the pathways of the organism that contains one or more of the given compounds and, for each pathway, the kegg codes (and their names) of the compounds given that are present in that path. The ratio between the number of compounds given compounds present in each pathway and the total number of compounds in each pathway is also given, full result or not.

If full result is not wanted, only the pathways will be given.

Examples

```
#Get human metabolic paths that have one or more of the three following compounds
keggs=get_cpd_names(c("cpd:C00033", "cpd:C00147", "gl:G13099"))
paths_org_cpds=get_paths_with_cpds_org("hsa", keggs)
paths_org_cpds
```

get_peak_values *Get peak values*

Description

Gets the peak values from a data frame of samples' peaks.

Usage

```
get_peak_values(samples.df, peak.val)
```

Arguments

samples.df	data frame with the samples' peaks.
peak.val	peak name.

Value

Returns a vector with the peak values.

Examples

```
## Example of getting the peak values
library(specmine.datasets)
data(propolis)
peak.values = get_peak_values(propolis$data, 2.11)
```

get_samples_names_dx *Get sample's names from DX files*

Description

Function to get the names of the DX files from a folder.

Usage

```
get_samples_names_dx(foldername)
```

Arguments

foldername	string with the path of the data folder.

Value

Returns a vector with the sample's names.

get_samples_names_spc *Get sample's names from SPC files*

Description

Function to get the names of the SPC files from a folder.

Usage

```
get_samples_names_spc(foldername)
```

Arguments

foldername	string with the path of the data folder.

Value

Returns a vector with the sample's names.

get_sample_2d_data *Get data*

Description

Get the data matrix of a specific sample from a 2D dataset.

Usage

```
get_sample_2d_data(dataset_2d, sample)
```

Arguments

dataset_2d	List representing the 2D dataset from a 2D metabolomics experiment.
sample	A string or integer, representing a sample from a 2D metabolomics experiment.

Value

Returns the sample's data matrix.

get_sample_names *Get sample names*

Description

Get the sample names from the dataset.

Usage

```
get_sample_names(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns a vector with the sample names.

Examples

```
## Example of getting the sample names
library(specmine.datasets)
data(cachexia)
sample.names = get_sample_names(cachexia)
```

get_type *Get type of data*

Description

Get the type of the data from the dataset

Usage

```
get_type(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns a string with the type of the data.

Examples

```
## Example of getting the type of the data
library(specmine.datasets)
data(cachexia)
type = get_type(cachexia)
```

`get_value_label` *Get value label*

Description

Get the value label from the dataset

Usage

```
get_value_label(dataset)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.

Value

Returns a string with the value label.

Examples

```
## Example of getting the value label
library(specmine.datasets)
data(cassavaPPD)
value.label = get_value_label(propolis)
```

`get_x_label` *Get x-axis label*

Description

Get the x-axis label from the dataset.

Usage

```
get_x_label(dataset)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.

Value

Returns a string with the x-axis label.

Examples

```
## Example of getting the x-axis label
library(specmine.datasets)
data(cassavaPPD)
x.label = get_x_label(propolis)
```

`get_x_values_as_num` *Get x-axis values as numbers*

Description

Get the x-axis values from the dataset as numbers.

Usage

```
get_x_values_as_num(dataset)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.

Value

Returns a numeric vector with the x-axis values, if the variable labels are not all numeric then an error message is shown.

Examples

```
## Example of getting the x-axis values as numbers
library(specmine.datasets)
data(propolis)
xvalues.numeric = get_x_values_as_num(propolis)
```

get_x_values_as_text *Get x-axis values as text*

Description

Get the x-axis values from the dataset as text.

Usage

```
get_x_values_as_text(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns a character vector with the x-axis values.

Examples

```
## Example of getting the x-axis values as text
library(specmine.datasets)
data(propolis)
xvalues.text = get_x_values_as_text(propolis)
```

group_peaks *Group peaks*

Description

Group peaks with peak alignment.

Usage

```
group_peaks(sample.list, type, method = "own", metadata = NULL,
samp.classes = 1, description = "", label.x = NULL,
label.values = NULL, step = 0.03)
```

Arguments

sample.list	list containing the sample's data.
type	type of the data.
method	method of peak alignment. Can be "own" or "metaboanalyst", which the later is for using the peak alignment used in MetaboAnalyst software.
metadata	data frame containing the metadata.
samp.classes	the metadata's variable to be used in the MetaboAnalyst method.
description	short description of the data.
label.x	the label for the x values.
label.values	the label for the y values.
step	step value for the peak alignment process.

Value

Returns a dataset with the peaks of the data aligned.

Examples

```
   ## Example of grouping peaks (computationally heavy)
   library(specmine.datasets)
   data(propolisSampleList)
   peaks.ds = group_peaks(propolisSampleList, "nmr-peaks", method = "own",
    metadata = NULL, description = "short description",
label.x = "ppm", label.values = "intensity", step = 0.03)
```

---

heatmap_correlations *Correlations heatmap*

Description

Plots a heatmap with the correlations.

Usage

```
heatmap_correlations(correlations, col = NULL, ...)
```

Arguments

correlations	correlation matrix
col	colors to be used on heatmap.
...	extra parameters to visual purposes.

Examples

```
## Example of correlations heatmap
library(specmine.datasets)
data(cachexia)
correlations = correlations_dataset(cachexia)
heatmap_correlations(correlations)
```

`hierarchical_clustering` *Perform hierarchical clustering analysis*

Description

Perform hierarchical clustering analysis on the dataset.

Usage

```
hierarchical_clustering(dataset, distance = "euclidean",
clustMethod = "complete", hc.type = "samples")
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`distance`	the distance measure to be used to compute the distances between the rows of a data matrix. Possible types are "euclidean", "manhattan", "pearson" or "spearman".
`clustMethod`	the agglomeration method to be used. Possible values are "ward", "single", "complete", "average", "mcquitty", "median" or "centroid".
`hc.type`	a string indicating if hierarchical cluster analysis will be performed on samples ("samples") or on variables ("variables")

Value

An object of class hclust with the clustering results.

Examples

```
## Example of hierarchical clustering
library(specmine.datasets)
data(cachexia)
hc.result = hierarchical_clustering(cachexia,
    distance = "euclidean", clustMethod = "complete",
    hc.type = "samples")
```

impute_nas_knn *Impute missing values with KNN*

Description

Impute missing values with KNN

Usage

```
impute_nas_knn(dataset, k = 10, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
k	the number of nearest neighbors.
...	additional values to impute.knn function.

Value

Returns the dataset with no missing values.

Examples

```
## Example of NA imputation with knn
library(specmine.datasets)
data(propolis)
dataset = impute_nas_knn(propolis, k=10)
```

impute_nas_linapprox *Impute missing values with linear approximation*

Description

Impute missing values with linear approximation.

Usage

```
impute_nas_linapprox(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns the dataset with no missing values.

Examples

```
## Example of NA imputation with linear approximation
library(specmine.datasets)
data(propolis)
dataset = impute_nas_linapprox(propolis)
```

---

impute_nas_mean *Impute missing values with mean*

Description

Impute missing values with mean

Usage

```
impute_nas_mean(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns the dataset with no missing values.

Examples

```
## Example of NA imputation with mean
library(specmine.datasets)
data(propolis)
propolis = impute_nas_mean(propolis)
```

---

impute_nas_median *Impute missing values with median*

Description

Impute missing values with median

Usage

```
impute_nas_median(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns the dataset with no missing values.

Examples

```
## Example of NA imputation with median
library(specmine.datasets)
data(propolis)
propolis = impute_nas_median(propolis)
```

`impute_nas_value` *Impute missing values with value replacement*

Description

Impute missing values with value replacement.

Usage

```
impute_nas_value(dataset, value)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`value`	value to replace the missing values.

Value

Returns the dataset with no missing values.

Examples

```
## Example of NA imputation with value replacing
library(specmine.datasets)
data(propolis)
propolis = impute_nas_value(propolis, 0.0005)
```

indexes_to_xvalue_interval *Get the x-values of a vector of indexes*

Description

Returns x-values corresponding to a vector of indexes (only to numerical values - spectra)

Usage

```
indexes_to_xvalue_interval(dataset, indexes)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
indexes	numeric vector containing the indexes.

Value

Returns a numeric vector with the interval of x-values from the indexes vector

Examples

```
## Example of getting the interval of x-values from indexes
library(specmine.datasets)
data(propolis)
xvalue.interval = indexes_to_xvalue_interval(propolis, c(10,50))
```

is_spectra *Check type of data*

Description

Check if the dataset is from spectral data where x.values are numeric.

Usage

```
is_spectra(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns a boolean indicating if the dataset is from spectral data or not.

Examples

```
## Example of checking if the dataset is from spectral data
library(specmine.datasets)
data(propolis)
is_spectra(propolis)
```

`kmeans_clustering` *Perform k-means clustering analysis*

Description

Perform k-means clustering analysis on the dataset.

Usage

```
kmeans_clustering(dataset, num.clusters, type = "samples")
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`num.clusters`	the number of clusters.
`type`	a string indicating if k-means will be performed on samples ("samples") or on variables ("variables")

Value

An object of class kmeans with the clustering results.

Examples

```
## Example of kmeans clustering
library(specmine.datasets)
data(cachexia)
kmeans.result = kmeans_clustering(cachexia,
num.clusters = 4, type = "samples")
```

kmeans_plot *Plot kmeans clusters*

Description

Plot for each formed cluster, in grey the values of all samples of that cluster and in blue the median of that samples.

Usage

```
kmeans_plot(dataset, kmeans.result)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
kmeans.result	object of class kmeans with the clustering results.

Examples

```
## Example of kmeans plot - dataset filtered for performance purposes
library(specmine.datasets)
data(cachexia)
kmeans.result = kmeans_clustering(cachexia,
num.clusters = 4, type = "samples")
kmeans_plot(cachexia, kmeans.result)
```

kmeans_result_df *Show cluster's members*

Description

Show for each cluster from kmeans analysis the sample names belonging to them.

Usage

```
kmeans_result_df(kmeans.result)
```

Arguments

kmeans.result	object of class kmeans with the clustering results.

Value

Data frame with the clusters and the samples' names that belong to each one.

Examples

```
## Example of showing kmeans cluster's members
library(specmine.datasets)
data(cachexia)
kmeans.result = kmeans_clustering(cachexia,
num.clusters = 4, type = "samples")
kmeans_result_df(kmeans.result)
```

`kruskalTest_dataset` *Kruskal-Wallis tests on dataset*

Description

Run Kruskal-Wallis Tests for each row of the data from the dataset.

Usage

```
kruskalTest_dataset(dataset, metadata.var, threshold = NULL,
write.file = FALSE, file.out = "kruskal.csv")
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`metadata.var`	metadata variable to use in the t-tests.
`threshold`	threshold value of the p-value.
`write.file`	boolean value to write or not a file with the results.
`file.out`	name of the file.

Value

Table with the results of the Kruskal-Wallis tests, with p-value, -log10(p-value) and false discovery rate (fdr).

Examples

```
## Example of ks-Tests on dataset
library(specmine.datasets)
data(cachexia)
kruskaltests.result = kruskalTest_dataset(cachexia, "Muscle.loss",
write.file = FALSE)
```

ksTest_dataset *Kolmogorov-Smirnov tests on dataset*

Description

Run Kolmogorov-Smirnov Tests for each row of the data from the dataset.

Usage

```
ksTest_dataset(dataset, metadata.var, threshold = NULL,
write.file = FALSE, file.out = "ks.csv")
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.var	metadata variable to use in the t-tests.
threshold	threshold value of the p-value.
write.file	boolean value to write or not a file with the results.
file.out	name of the file.

Value

Table with the results of the Kolmogorov-Smirnov tests, with p-value, -log10(p-value) and false discovery rate (fdr).

Examples

```
## Example of ks-Tests on dataset
library(specmine.datasets)
data(cachexia)
kstests.result = ksTest_dataset(cachexia, "Muscle.loss",
write.file = FALSE)
```

linregression_onevar *Linear regression on one variable*

Description

Performs linear regression on one variable of the dataset.

Usage

```
linregression_onevar(dataset, x.val, metadata.vars, combination)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
x.val	the x-value to be tested.
metadata.vars	metadata variables to use in linear regression. For example, c('variable1','variable2').
combination	a formula specifying the model. For example, 'variable1+variable2'.

Value

Returns a summary of the result from the lm function from stats package.

---

linreg_all_vars *Linear Regression*

Description

Performs linear regression analysis over the dataset with the selected metadata's variables.

Usage

```
linreg_all_vars(dataset, metadata.vars, combination)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.vars	metadata variables to use in linear regression. For example, c('variable1','variable2').
combination	a formula specifying the model. For example, 'variable1+variable2'.

Value

Returns a list where each element is the linear regression result of a variable on the dataset.

---

linreg_coef_table *Linear regression coefficient table*

Description

Gets a data.frame with the coefficient values.

Usage

```
linreg_coef_table(linreg.results, write.file = FALSE,
file.out = "linreg-coefs.csv")
```

Arguments

linreg.results	Linear regression results from linreg.all.vars function.
write.file	boolean value to indicate if a file should be written with the results.
file.out	name of the file.

Value

Returns a data.frame with the coefficient values.

---

linreg_pvalue_table *Linear regression p-values table*

Description

Gets the p-values table from the linear regression analysis.

Usage

```
linreg_pvalue_table(linreg.results, write.file = FALSE,
file.out = "linreg-pvalues.csv")
```

Arguments

linreg.results	Linear regression results from linreg.all.vars function.
write.file	boolean value to indicate if a file should be written with the results.
file.out	name of the file.

Value

Returns a data.frame with the p-values.

---

linreg_rsquared *Linear regression r-squared*

Description

Gets the linear regression r-squared values.

Usage

```
linreg_rsquared(linreg.results, write.file = FALSE,
file.out = "linreg-rsquared.csv")
```

Arguments

linreg.results	Linear regression results from linreg.all.vars function.
write.file	boolean value to indicate if a file should be written with the results.
file.out	name of the file.

Value

Returns a data.frame with the r-squared values.

---

log_transform *Logarithmic transformation.*

Description

Performs logarithmic transformation on the data matrix.

Usage

```
log_transform(datamat)
```

Arguments

datamat	data matrix.

Value

Returns the data matrix with the logarithmic transformation applied.

Examples

```
## Example of logarithmic transformation
library(specmine.datasets)
data(propolis)
propolis_proc = missingvalues_imputation(propolis)
datamat.log = log_transform(propolis_proc$data)
```

low_level_fusion *Low level fusion*

Description

Low level fusion method for integrate different datasets (only samples with the same name on all datasets will be merged)

Usage

```
low_level_fusion(datasets)
```

Arguments

datasets	list containing the datasets to be fused (each dataset is a list from the pre defined format for the dataset).

Value

Return a single dataset with all the datasets merged.

MAIT_identify_metabolites *MAIT metabolite identification*

Description

Performs metabolite identification using MAIT.

Usage

```
MAIT_identify_metabolites(dataset, metadata.variable,
xSet = NULL, data.folder = NULL, features = NULL,
mass.tolerance = 0.5)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.variable	metadata's variable.
xSet	xcmsSet object that can be passed. Stored in dataset$xSet.
data.folder	string indicating the data folder.
features	features that can be used to help to identify the metabolites.
mass.tolerance	mass tolerance.

Details

After runing the MAIT_identify_metabolites function, the results table can be aaccessed by:

mait.metab.table = mait.metabolites@FeatureInfo@metaboliteTable

where 'mait.metabolites' is the result obtained from runing MAIT_identify_metabolites.

Value

Returns an object resulted from identifyMetabolites function from MAIT package.

References

http://www.bioconductor.org/packages/release/bioc/html/MAIT.html

---

mean_centering *Mean centering*

Description

Performs mean centering on the dataset.

Usage

```
mean_centering(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns the dataset with mean centering applied.

---

merge_datasets *Merge two datasets*

Description

Merges two datasets with the same variables and metadata's variables.

Usage

```
merge_datasets(dataset1, dataset2)
```

Arguments

dataset1	list representing the first dataset from a metabolomics experiment.
dataset2	list representing the second dataset from a metabolomics experiment.

Value

Returns one dataset with the data from the two datasets merged.

---

merge_data_metadata *Merge data and metadata*

Description

Merges the data and metadata from the dataset into a single data.frame.

Usage

```
merge_data_metadata(dataset, samples = NULL,
metadata.vars = NULL, x.values = NULL, by.index = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
samples	vector with indexes or names of the samples to select
metadata.vars	metadata's variables.
x.values	vector with the desired x-values to get from the dataset.
by.index	if TRUE, the values of the x.values argument are indexes.

Value

Returns a data.frame with the data and metadata from the dataset merged.

Examples

```
## Example of merging data and metadata
library(specmine.datasets)
data(cachexia)
dt.merged = merge_data_metadata(cachexia)
```

metabolights_studies_list

List the study IDs available in the MetaboLights database.

Description

Gives the IDs of the studies available in the MetaboLights database.

Usage

```
metabolights_studies_list()
```

Value

Vector with the different study IDs available in the MetaboLights database.

References

MetaboLights database: https://www.ebi.ac.uk/metabolights/

Examples

```
## metabolights_studies_list()
```

metadata_as_variables *Metadata as variables*

Description

Use one or more metadata variables as variables.

Usage

```
metadata_as_variables(dataset, metadata.vars, by.index = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.vars	name or index of the metadata variables that are going to be used as data variables.
by.index	boolean value indicating if the metadata variables are indexes or names

Value

Returns the dataset with the metadata variables removed from the metadata and added on the data matrix.

Examples

```
## Example of using a metadata variable as data variable
library(specmine.datasets)
data(propolis)
propolis = metadata_as_variables(propolis, "seasons", by.index = FALSE)
```

`missingvalues_imputation` *Missing values imputation*

Description

Treats the missing values of a dataset according to a specific method.

Usage

```
missingvalues_imputation(dataset, method = "value",
value = 5e-04, k = 5)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`method`	imputation method. It can be: • **"value"** - replaces the missing values with a specific value • **"mean"** - replaces the missing values with the mean of the variables' values • **"median"** - replaces the missing values with the median of the variables' values • **"knn"** - replaces the missing values with k nearest neighbor averaging • **"linapprox"** - replaces the missing values with linear approximation
`value`	the value to replace the missing values if the method is "value".
`k`	the number of neighbors if the method is "knn".

Value

Returns the dataset with no missing values.

Examples

```
## Example of impute missing values
library(specmine.datasets)
data(propolis)
dataset = missingvalues_imputation(propolis, method = "value",
  value = 0.0005)
```

msc_correction *Multiplicative scatter correction*

Description

Perform multiplicative scatter correction on the spectra.

Usage

```
msc_correction(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Return the dataset with the multiplicative scatter correction employed on the data.

multiClassSummary *Multi Class Summary*

Description

Summary function for caret to compute AUC.

Usage

```
multiClassSummary(data, lev = NULL, model = NULL)
```

Arguments

data	data parameter.
lev	lev parameter.
model	model parameter.

References

www.r-bloggers.com/error-metrics-for-multi-class-problems-in-r-beyond-accuracy-and-kappa/

multifactor_aov_all_vars *Multifactor ANOVA*

Description

Perform multi-factor ANOVA on all variables with the selected metadata variables.

Usage

```
multifactor_aov_all_vars(dataset, metadata.vars, combination)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.vars	metadata variables to use in ANOVA.
combination	a formula specifying the model.

Value

List where each element is the multifactor anova result of a variable on the dataset.

Examples

```
## Example of multifactor ANOVA on all variables
library(specmine.datasets)
data(propolis)
propolis = missingvalues_imputation(propolis, "value", value = 0.00005)
m.aov.results = multifactor_aov_all_vars(propolis,
c("seasons","agroregions"), "seasons*agroregions")
```

multifactor_aov_pvalues_table *Multifactor ANOVA p-values table*

Description

Gets the p-values table from the multifactor ANOVA results.

Usage

```
multifactor_aov_pvalues_table(multifactor.aov.results,
write.file = FALSE, file.out = "multi-anova-pvalues.csv")
```

Arguments

multifactor.aov.results	multifactor anova results.
write.file	boolean value to indicate if a file is written.
file.out	name of the file.

Value

Returns a data.frame with the p-values.

Examples

```
## Example of multifactor ANOVA p-values table
library(specmine.datasets)
data(propolis)
propolis = missingvalues_imputation(propolis, "value", value = 0.00005)
m.aov.results = multifactor_aov_all_vars(propolis,
c("seasons","agroregions"), "seasons*agroregions")
m.aov.pvalues = multifactor_aov_pvalues_table(m.aov.results)
```

---

multifactor_aov_varexp_table

Multifactor ANOVA variability explained table

Description

Gets the variability explained table from the multifactor ANOVA results.

Usage

```
multifactor_aov_varexp_table(multifactor.aov.results,
write.file = FALSE, file.out = "multi-anova-varexp.csv")
```

Arguments

multifactor.aov.results	multifactor anova results.
write.file	boolean value to indicate if a file is written.
file.out	name of the file.

Value

Returns a data.frame with the variability explained.

Examples

```
## Example of multifactor ANOVA variability explained table
library(specmine.datasets)
data(propolis)
propolis = missingvalues_imputation(propolis, "value", value = 0.00005)
m.aov.results = multifactor_aov_all_vars(propolis,
c("seasons","agroregions"), "seasons*agroregions")
m.aov.varepx = multifactor_aov_varexp_table(m.aov.results)
```

`multiplot` *Multiplot*

Description

Multiplot from ggplot2 - function taken from (see references).

Usage

```
multiplot(plots, plotlist = NULL, file, cols = 1, layout = NULL)
```

Arguments

`plots`	list with the plots to display.
`plotlist`	plot list.
`file`	file.
`cols`	number of columns.
`layout`	layout of the plot.

References

http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_

Examples

```
    ## Example of multiplot
 library(specmine.datasets)
    data(cachexia)
    pca.result = pca_analysis_dataset(cachexia)
    plot1 = pca_scoresplot2D(cachexia, pca.result, "Muscle.loss",
ellipses = TRUE)
    plot2 = pca_scoresplot2D(cachexia, pca.result, "Muscle.loss",
ellipses = FALSE, labels = TRUE)
    plts = list(plot1,plot2)
    multiplot(plts, cols = 2)
```

`nmr_identification` *NMR metabolite identification*

Description

This function performs metabolite identification on a dataset of nmr peaks.

Usage

```
nmr_identification(dataset, ppm.tol, frequency_scores, solvent_scores, organism_scores,
                method='Match_uniq', per.sample=FALSE, tresh_zero=0, alpha=10e-4)
```

Arguments

`dataset`	List representing the dataset from an nmr peaks metabolomics experiment.
`ppm.tol`	ppm tolerance when matching reference peaks to the dataset peaks.
`per.sample`	Logical indicating wether identification should be done for each sample (for each sample, only the peaks present in that sample will be used in the identification) or for all samples together (all peaks will be used together in the identification).
`tresh_zero`	Intensity value above which peaks are considered present. Only necessary if per.sample=TRUE
`method`	Identification method to use. There are three: 'Match_uniq' (default), 'Hyper' or 'Hyper_uniq'. For more information, see details below.
`alpha`	A metabolite with a corrected p.value above alpha will not be considered identified. Only necessary if method is either 'Hyper' or 'Hyper_uniq'.
`frequency_scores`	Each frequency in the library should be given a score from 0 to 1, according to the frequency in which the samples were acquired. A score of 1 should be given to the frequency under which the samples were acquired. Argument should be in the form of a list, like: list('400'=0, '500'=1, '600'=0, '700'=0). For more information, see details below.
`solvent_scores`	Each solvent in the library should be given a score from 0 to 1, according to the solvent with which the samples were acquired. A score of 1 should be given to the solvent with which the samples were acquired. Argument should be in the form of a list, like: list(CD3OD=0, D2O=1, Water=1, CDCl3=0, 'Acetone-d6'=0, 'Acetone'=0, "DMSO-d6"=0, "100%_DMSO"=0, "5%_DMSO"=0, C=0, C6D6=0, CD3CN=0, C2D2Cl4=0, CD2Cl2=0, CDC3OD=0, Ethanol=0). For more information, see details below.
`organism_scores`	This gives the opportunity to score each reference according to the presence or not of the respective metabolite in the organism(s) or group(s) of organisms under study, so that metabolites not present in an organism/group of interest will have a lower score and thus be less likely to be identified. The presence of a metabolite in an organism/group is evaluated using the information

in the KEGG database. Thus, all organism/group codes should be present in KEGG. Argument should be in the form of a list, like: list('hsa'=1, 'other'=0, 'not_in_kegg'=0). For more information, see details below.

Details

There are three methods implemented to perform metabolite identification. The default one is Matched Ratio with uniqueness score ('Match_uniq'):

- Hypergeometric Test: it calculates the probability of a group of k peaks matching to a certain reference spectrum not being caused by chance. A p-value over alpha denotes that the metabolite corresponding to the reference spectrum in question is not present in the sample. After all reference metabolites are matched to the samples, the p-values are adjusted for multiple testing using the False Discovery Rate (FDR) method. For those with p.value under alpha, the score is transformed into a scale of 0 to 1, by applying the following: 1-(p.value/alpha).

- Hypergeometric Test with Uniqueness score ('Hyper_uniq'): the final score of a reference spectrum is obtained by calculating the average between the hypergeometric test score and the uniqueness score, if the hypergeometric test score is not null. The uniqueness score of a reference is the average of the uniqueness rate of all peaks in that reference. The uniqueness rate of a peak is calculated by dividing 1 by the number of reference spectra that peak is in, based on the reference library used.

- Matched ratio scores with uniqueness score ('Match_uniq'): the final score of a reference spectrum is obtained by calculating the average between the matched ratio score and the uniqueness score, if the matched ratio score is not null. The matched ratio score gives the ratio of peaks from a reference that matched the sample. It is calculated by dividing the number of different peaks matched between the reference and the sample by the total number of different peaks in such reference.

After scoring a match between a reference and a sample, the reference is further scored regarding the conditions under which it was acquired. To do so, each frequency and solvent represented in the library must be given a score by the user. The user also has the possibility to score each reference according to the presence or not of the respective metabolite in the organism(s) or group(s) of organisms under study, so that metabolites not present in an organism/group of interest will have a lower score and thus be less likely to be identified. The presence of a metabolite in an organism/group is evaluated using the information in the KEGG database.

Value

If per.sample=FALSE, it gives a list with two items: results_table and more_results. If per.sample=TRUE, it gives a list with as many items as the number of samples. Each sample contains a list with the two items results_table and more_results.

results_table is a data.frame with the information on the metabolites matched. Each row corresponds to a spectrum from the library that matched the dataset:

SPCMNM ID of the metabolite in our library.

Name Name of the metabolite.

SPCMNS ID of the respective spectrum in our library.

Final_Score Final score.

match_score Matching score.

hypergeometric_score Hypergeometric score, if method='Hyper' or 'Hyper_uniq'.

ratio matched ratio score, if method='Match_uniq'

uniqueness_score uniqueness_score, if method = 'Hyper_uniq' or 'Match_uniq'

score_frequency Score given to the frequency of that spectrum.

score_solvents Score given to the solvent of that spectrum.

score_organisms The organism score, according to the metabolite's presence in one of the organisms/groups given by the user in organism_scores argument.

n.peaks.matched Number of peaks from the metabolite's spectrum that matched the sample.

detailed_results_id ID to access the more detailed results in the item more_results.

more_results is a list whose items are identified by an ID that is specified in the detailed_results_ID column of the results_table. Each item is a list with the following information:

matched_peaks_ref Vector with the peaks from the reference spectrum that matched the sample. Reference peak in the ith position matched the sample peak in the ith position of the vector matched_peaks_samp.

matched_peaks_samp Vector with the peaks from the sample that matched the reference spectrum. Sample peak in the ith position matched the reference peak in the ith position of the vector matched_peaks_ref.

reference_peaks Vector with all the peaks in the reference spectrum.

Examples

```
library(specmine.datasets)
data(propolis)
propolis_mv=missingvalues_imputation(propolis)
freq_scores = list('400'=0, '500'=0, '600'=1, '700'=0)
solv_scores = list(CD3OD=0, D2O=.8, Water=.8, CDCl3=0, 'Acetone-d6'=0, 'Acetone'=0,"DMSO-d6"=0,
                   '100%_DMSO'=0,
                   '5%_DMSO'=0, C=0, C6D6=0, CD3CN=0, C2D2Cl4=0, CD2Cl2=0,
                   CDC3OD=1, Ethanol=0)
org_scores = list('Eudicots'=1, 'Monocots'=1, 'ame'=.9, 'other'=0, 'not_in_kegg'=0)
id_res=nmr_identification(propolis_mv, ppm.tol=0.03, freq_scores, solv_scores, org_scores)
```

---

normalize *Normalize data*

Description

Normalize the data from the dataset with a specific method.

Usage

```
normalize(dataset, method, ref = NULL, constant = 1000)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
method	string specifying the normalization method. The possible values are: • **"sum"** normalization by sum. • **"median"** normalization by median. • **"ref.sample"** normalization by reference sample. • **"ref.feature"** normalization by reference feature.
ref	the reference if method is "ref.sample" or "ref.feature".
constant	the constant value if method is "sum".

Value

Returns the dataset with the data normalized.

---

normalize_samples *Normalize samples*

Description

Normalize the data from a datamatrix with a specific method.

Usage

```
normalize_samples(datamat, method, ref = NULL, constant = 1000)
```

Arguments

datamat	data matrix.
method	string specifying the normalization method. The possible values are: • **"sum"** normalization by sum. • **"median"** normalization by median. • **"ref.sample"** normalization by reference sample. • **"ref.feature"** normalization by reference feature.
ref	the reference if method is "ref.sample" or "ref.feature".
constant	the constant value if method is "sum".

Value

Returns the data matrix normalized.

num_samples *Get number of samples*

Description

Get the number of samples from a dataset.

Usage

```
num_samples(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns an integer with the number of samples in the dataset.

Examples

```
## Example of getting the number of samples
library(specmine.datasets)
data(cachexia)
number.of.samples = num_samples(cachexia)
```

num_x_values *Get number of x values*

Description

Get the number of x-axis values.

Usage

```
num_x_values(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns an integer with the number of x-axis values.

Examples

```
## Example of getting the number of x-axis values
library(specmine.datasets)
data(propolis)
number.x.values = num_x_values(propolis)
```

`offset_correction` *Offset correction*

Description

Perform offset correction on the data.

Usage

```
offset_correction(dataset)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.

Value

Returns the dataset

`pathway_analysis` *Creates the metabolic pathway wanted. If any of the given compounds is present in the pathway, it is coloured differently.*

Description

The pathway created contains the compounds, reactions and other paths that it connects to as nodes.

The compounds given in `compounds` are colored in blue, while the rest of the compounds are colored in grey.

The other paths that it may connect to are colored in orange.

Reversive reactions are colored in green and the irreversible ones in red.

Usage

```
pathway_analysis(compounds, pathway,
                 nodeNames="kegg", nodeTooltip=FALSE,
           map.zoom=FALSE, map.layout="preset", map.width=NULL, map.height=NULL)
```

Arguments

compounds	Vector of compounds of interest, in kegg codes.
pathway	KEGG code (e.g., "hsa00010") of the path wanted.
nodeNames	How the nodes should be named. If "kegg", nodes are named with kegg codes. If "names", nodes are named with the common names.
nodeTooltip	If a tooltip should appear when hovering a node.
map.zoom	If the map should have the zoom in and out option.
map.layout	Layout of the map, available values are the ones of cytoscape ("breadthfirst", "preset", "cose", ...)
map.width	Width of the map, in percentage
map.height	Width of the map, in px (e.g. "500px")

Value

Shows the pathway created.

---

pca_analysis_dataset *PCA analysis (classical)*

Description

Performs a classical PCA analysis over the dataset.

Usage

```
pca_analysis_dataset(dataset, scale = TRUE, center = TRUE,
write.file = FALSE, file.out = "pca", ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
scale	boolean value indicating if the variables are going to be scaled or not.
center	booleam value indicating if the variables are going to be centered or not.
write.file	boolean value that indicates if the results from PCA analysis are going to be written on a file.
file.out	name of the file that will store the results.
...	additional parameters to ggplot function.

Value

object of class 'prcomp' with the results from the PCA analysis.

Examples

```
## Example of performing a classical PCA analysis
library(specmine.datasets)
data(cachexia)
pca.results = pca_analysis_dataset(cachexia)
```

`pca_biplot` *PCA biplot*

Description

Shows a PCA biplot.

Usage

```
pca_biplot(dataset, pca.result, cex = 0.8, legend.cex = 0.8,
x.colors = 1, inset = c(0, 0), legend.place = "topright", ...)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`pca.result`	prcomp object with the PCA results.
`cex`	cex value.
`legend.cex`	cex value of the legend.
`x.colors`	colors of a metadata's variable.
`inset`	inset parameter of legend function.
`legend.place`	legend place.
`...`	additional parameters passed to biplot function.

Examples

```
## Example of a PCA biplot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_biplot(cachexia, pca.result, cex = 0.8)
```

pca_biplot3D *3D PCA biplot (interactive)*

Description

Shows a interactive 3D PCA biplot.

Usage

```
pca_biplot3D(dataset, pca.result, column.class = NULL,
pcas = c(1, 2, 3))
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
pca.result	prcomp object with the PCA results.
column.class	metadata's variable.
pcas	the three principal components.

Examples

```
### Example of a 3D PCA biplot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_biplot3D(cachexia, pca.result, "Muscle.loss", pcas = c(1,2,3))
```

pca_importance *PCA importance*

Description

Gets the importance from the PCs.

Usage

```
pca_importance(pca.res, pcs = 1:length(pca.res$sdev), sd = TRUE,
prop = TRUE, cumul = TRUE, min.cum = NULL)
```

Arguments

pca.res	prcomp object with the PCA results.
pcs	vector with the PCs to get.
sd	boolean value indicating if standard deviation will be returned or not.
prop	boolean value that indicates if the proportion of variance is returned or not.
cumul	boolean value that indicates if the cumulative variance is returned or not.
min.cum	allows to define minimum cumulative % of variance

Value

Returns the information about the importance of the PCs.

Examples

```
## Example of performing a classical PCA analysis
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_importance(pca.result, pcs = 1:5)
```

---

pca_kmeans_plot2D *2D PCA k-means plot*

Description

Groups the points with the clusters given by k-means in a 2D PCA scores plot.

Usage

```
pca_kmeans_plot2D(dataset, pca.result, num.clusters = 3,
pcas = c(1, 2), kmeans.result = NULL, labels = FALSE, bw=FALSE,
ellipses = FALSE, leg.pos = "right", xlim = NULL, ylim = NULL)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
pca.result	prcomp object with the PCA results.
num.clusters	number of clusters of k-means.
pcas	vector with the principal components to be plotted.
kmeans.result	result from k-means. If null k-means is performed in the function.
labels	boolean value indicating if the samples' labels will be shown.
ellipses	boolean value that indicates if an ellipse will be drawn on each group of the metadata's variable. Ellipses will not be drawn if bw=TRUE.
bw	if TRUE, it will be displayed a black and white plot. It defaults to FALSE.

leg.pos	legend position.
xlim	vector with two positions with the x-axis limits.
ylim	vector with two positions with the y-axis limits.

Examples

```
## Example of a 2D PCA k-means plot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_kmeans_plot2D(cachexia, pca.result, num.clusters = 3, pcas = c(1,2))
```

---

pca_kmeans_plot3D *3D PCA k-means plot (interactive)*

Description

Groups the points with the clusters given by k-means in a interactive 3D PCA scores plot.

Usage

```
pca_kmeans_plot3D(dataset, pca.result, num.clusters = 3,
pcas = c(1, 2, 3), kmeans.result = NULL, labels = FALSE,
size = 1, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
pca.result	prcomp object with the PCA results.
num.clusters	number of clusters of k-means.
pcas	vector with the principal components to be plotted.
kmeans.result	result from k-means. If null k-means is performed in the function.
labels	boolean value indicating if the samples' labels will be shown.
size	parameter of plot3d from rgl package.
...	additional parameters of plot3d function from rgl package.

Examples

```
### Example of a 3D PCA k-means plot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_kmeans_plot3D(cachexia, pca.result, num.clusters = 3,
       pcas = c(1,2,3))
```

pca_pairs_kmeans_plot *PCA k-means pairs plot*

Description

Groups the points with the clusters from k-means in a PCA pairs plot.

Usage

```
pca_pairs_kmeans_plot(dataset, pca.result, num.clusters = 3,
kmeans.result = NULL, pcas = c(1, 2, 3, 4, 5))
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
pca.result	prcomp object with the PCA results.
num.clusters	number of clusters of k-means.
kmeans.result	result from k-means. If null k-means is performed in the function.
pcas	vector with the principal components to be plotted.

Examples

```
## Example of a PCA k-means pairs plot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
kmeans.res = kmeans_clustering(cachexia, 3)
pca_pairs_kmeans_plot(cachexia, pca.result, num.clusters = 3,
 kmeans.result = kmeans.res, pcas = c(1,2,3,4,5))
```

pca_pairs_plot *PCA pairs plot*

Description

Shows a PCA pairs plot.

Usage

```
pca_pairs_plot(dataset, pca.result, column.class = NULL,
pcas = c(1, 2, 3, 4, 5), ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
pca.result	prcomp object with the PCA results.
column.class	metadata's variable.
pcas	the principal components to be shown.
...	additional parameters to ggpairs function from GGally package.

Examples

```
## Example of a PCA pairs plot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_pairs_plot(cachexia, pca.result, "Muscle.loss", pcas = c(1,2,3))
```

---

pca_plot_3d *3D pca plot*

Description

3D plot from 3 components

Usage

```
pca_plot_3d(dataset, model, var.class, pcas = 1:3, colors = NULL,
legend.place = "topright", ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
model	model with pca scores (pls model).
var.class	metadata column class.
pcas	the components to be plotted.
colors	colors of the groups.
legend.place	legend place.
...	additional parameters to legend function.

Examples

```
### Example of a 3d pca plot
library(specmine.datasets)
data("cachexia")
train.result = train_models_performance(cachexia, "pls",
"Muscle.loss", "cv")
pca_plot_3d(cachexia, train.result$final.models$pls, "Muscle.loss")
```

pca_robust *PCA analysis (robust)*

Description

Performs a robust PCA analysis.

Usage

```
pca_robust(dataset, center = "median", scale = "mad", k = 10,
write.file = FALSE, file.out = "robpca", ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
center	indicates how the data is to be centered. Can be a function or a vector with the center values of each column.
scale	indicates how the data is to be rescaled. Can be a function or a vector with the scale value of each column.
k	the desired number of components to compute
write.file	boolean value that indicates if the results from PCA analysis are going to be written on a file.
file.out	name of the file that will store the results.
...	additional parameters pass to or from other functions.

Value

Returns an object of class 'princomp' with the PCA results.

Examples

```
  ## Example of performing a robust PCA analysis
  library(specmine.datasets)
  data(cachexia)
  pca.results = pca_robust(cachexia, center = "mean", scale = "mad",
k = 10)
```

`pca_scoresplot2D` *2D PCA scores plot*

Description

Shows a 2D PCA scores plot of two principal componets.

Usage

```
pca_scoresplot2D(dataset, pca.result, column.class,
pcas = c(1, 2), labels = FALSE, ellipses = FALSE, bw=FALSE,
pallette = 2, leg.pos = "right", xlim = NULL, ylim = NULL)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`pca.result`	prcomp object with the PCA results.
`column.class`	metadata's variable.
`pcas`	vector of two elements with the PCs that will be plotted.
`labels`	boolean value indicating if the sample's labels will be displayed.
`ellipses`	boolean value that indicates if an ellipse will be drawn on each group of the metadata's variable. Ellipses will not be drawn if bw=TRUE.
`bw`	if TRUE, it will be displayed a black and white plot. It defaults to FALSE.
`pallette`	parameter of scale_colour_brewer from ggplot2.
`leg.pos`	position of the legend.
`xlim`	vector with two numeric values indicating the limits of the x axis.
`ylim`	vector with two numeric values indicating the limits of the y axis.

Examples

```
## Example of a 2D PCA scores plot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_scoresplot2D(cachexia, pca.result, "Muscle.loss", pcas = c(1,2),
      ellipses = TRUE)
```

pca_scoresplot3D *3D PCA scores plot*

Description

Shows a 3D PCA scores plot of three principal componets.

Usage

```
pca_scoresplot3D(dataset, pca.result, column.class,
pcas = c(1, 2, 3))
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
pca.result	prcomp object with the PCA results.
column.class	metadata's variable.
pcas	vector with the principal components to be plotted.

Examples

```
### Example of a 3D PCA scores plot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_scoresplot3D(cachexia, pca.result, "Muscle.loss", pcas = c(1,2,3))
```

pca_scoresplot3D_rgl *3D PCA scores plot (interactive)*

Description

Shows a interactive 3D PCA scores plot of three principal components.

Usage

```
pca_scoresplot3D_rgl(dataset, pca.result, column.class,
pcas = c(1, 2, 3), size = 1, labels = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
pca.result	prcomp object with the PCA results.
column.class	metadata's variable.
pcas	vector with the principal components to be plotted.
size	parameter of plot3d from rgl package.
labels	boolean value indicating if the samples' labels will be shown.

Examples

```
### Example of a 3D PCA scores plot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_scoresplot3D_rgl(cachexia, pca.result, "Muscle.loss",
          pcas = c(1,2,3), labels = TRUE)
```

---

pca_screeplot *PCA scree plot*

Description

PCA scree plot with the proportion and cumulative variance of the PCs.

Usage

```
pca_screeplot(pca.result, num.pcs = NULL, cex.leg = 0.8,
leg.pos = "right", lab.text = c("individual percent",
"cumulative percent"), fill.col = c("blue", "red"),
ylab = "Percentage", xlab = "Principal components", ...)
```

Arguments

pca.result	prcomp object with the PCA results.
num.pcs	number of principal components.
cex.leg	cex value of legend.
leg.pos	legend position.
lab.text	legend's labels.
fill.col	color of the legend's boxes.
ylab	y-axis label.
xlab	x-axis label
...	additional parameters to matplot.

Examples

```
## Example of a scree plot
library(specmine.datasets)
data(cachexia)
pca.result = pca_analysis_dataset(cachexia)
pca_screeplot(pca.result)
```

`peaks_per_sample` *Peaks per sample*

Description

Counts number of peaks in a sample (given its index).

Usage

```
peaks_per_sample(sample.list, sample.index)
```

Arguments

`sample.list`	list of data frames with the samples' peaks.
`sample.index`	sample index.

Value

Return a integer value with the number of peaks in the sample.

Examples

```
    ## Example of counting the peaks in a sample
library(specmine.datasets)
    data(propolisSampleList)
    num.peaks.sample = peaks_per_sample(propolisSampleList, 4)
```

`peaks_per_samples` *Peaks per samples*

Description

Calculates the number of peaks on each sample.

Usage

```
peaks_per_samples(sample.list)
```

Arguments

sample.list	list of data frames with the samples' peaks.

Value

Returns a numeric vector with the number of peaks on each sample.

Examples

```
    ## Example of counting the peaks in each sample
library(specmine.datasets)
    data(propolisSampleList)
    num.peaks.samples = peaks_per_samples(propolisSampleList)
```

---

peak_detection2d *Detection of the peaks in an 2D NMR spectra dataset.*

Description

This function detects the peaks across samples, reducing the dimensionality of the 2D spectra. If baseline_thresh is not provided it will be calculated a signal-to-noise ratio (SNR) for each spectra that will serve as threshold.

Usage

```
peak_detection2d(specmine_2d_dataset, baseline_thresh=NULL, noiseFilt=0, negatives=F)
```

Arguments

specmine_2d_dataset	List representing a 2D dataset from a 2D metabolomics experiment.
baseline_thresh	Minimum intensity value that peaks must have. Peaks with intensity smaller than baseline_thresh will not be considered as detected peaks.
noiseFilt	Integer argument that applies a noise filter when searching for peaks. Can be one of the following: • 0 Does not apply a noise filter. • 1 Applies a mild filter (adjacent points in the direct dimension must be above the noise threshold). • 2 Applies a strong filter (all adjacent points must be above the noise threshold). Defaults to 0.
negatives	Boolean value that decides if negative ppm values should be considered or not. Default to FALSE.

Value

Returns a 1D specmine dataset where the rows are combinations of ppms (indirect dimension x direct dimension) and the columns are the samples. The combinations of ppms represent peaks detected.

`plotvar_twofactor` *Plot variable distribution on two factors*

Description

Plot variable distribution on two factors from the dataset.

Usage

```
plotvar_twofactor(dataset, variable, meta.var1, meta.var2,
colour = "darkblue", title = "", xlabel = NULL, ylabel = NULL)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`variable`	variable's name.
`meta.var1`	first metadata's variable.
`meta.var2`	second metadata's variable.
`colour`	colours of the bodies of the boxplots.
`title`	title of the plot.
`xlabel`	x-axis label.
`ylabel`	y-axis label.

Value

Returns the plot object from ggplot function.

Examples

```
## Example of plotting a variable's distribution with 2 factors
library(specmine.datasets)
data(propolis)
propolis_proc = missingvalues_imputation(propolis)
plotvar_twofactor(propolis_proc, "0.46", "seasons", "agroregions")
```

plot_2d_spectra *Plot of 2D spectra*

Description

Plot spectra from 2D specmine dataset.

Usage

```
plot_2d_spectra(specmine_2d_dataset, title_spectra = "", meta = NULL, spec_samples = NULL)
```

Arguments

specmine_2d_dataset	List representing the 2D dataset from a 2D metabolomics experiment.
title_spectra	The title of the plot.
meta	String indicating the metadata's variable.
spec_samples	Vector with samples' names or numbers, if NULL only four samples are plotted. The two with highest and lowest signal-to-noise ratio (SNR).

plot_anova *Plot ANOVA results*

Description

Function for plotting the results from ANOVA.

Usage

```
plot_anova(dataset, anova.results, anova.threshold = 0.01,
reverse.x = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
anova.results	ANOVA results.
anova.threshold	ANOVA threshold for the p-value.
reverse.x	boolean value to indicate if the x-axis is plotted in reverse.

Examples

```
    ## Example of plotting the ANOVA results - first filter the
    ## dataset to reduce computation time
library(specmine.datasets)
data(propolis)
    propolis_proc = missingvalues_imputation(propolis)
    propolis_proc = flat_pattern_filter(propolis_proc, "iqr", by.percent = TRUE,
red.value = 75)
    anova.results = aov_all_vars(propolis_proc, "seasons", doTukey = FALSE)
    plot_anova(propolis_proc, anova.results)
```

---

plot_fold_change *Plot fold change results*

Description

Function for plotting the results from fold change.

Usage

```
plot_fold_change(dataset, fc.results, fc.threshold, plot.log = TRUE,
var = FALSE, xlab = "")
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
fc.results	fold change results.
fc.threshold	fold change threshold for the p-value.
plot.log	boolean value to determine if the fold change values are transformed logarithmically or not.
var	boolean value, if TRUE it uses the xlab argument to represent the xlabel of the plot.
xlab	string with the x axis description.

Examples

```
    ## Example of plotting the fold change results
library(specmine.datasets)
    data(cachexia)
    fc.results = fold_change(cachexia, "Muscle.loss",
"control")
    plot_fold_change(cachexia, fc.results, 2)
```

plot_kruskaltest *Plot Kruskal-Wallis tests results*

Description

Function for plotting the results from Kruskal-Wallis tests.

Usage

```
plot_kruskaltest(dataset, kr.results, kr.threshold = 0.01)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
kr.results	Kruskal-Wallis tests results.
kr.threshold	Kruskal-Wallis test threshold for the p-value.

Examples

```
    ## Example of plotting the Kolmogorov-Smirnov tests results
library(specmine.datasets)
    data(cachexia)
    kr.results = kruskalTest_dataset(cachexia, "Muscle.loss",
write.file = FALSE)
    plot_kruskaltest(cachexia, kr.results, 0.05)
```

plot_kstest *Plot Kolmogorov-Smirnov tests results*

Description

Function for plotting the results from Kolmogorov-Smirnov tests.

Usage

```
plot_kstest(dataset, ks.results, ks.threshold = 0.01)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
ks.results	Kolmogorov-Smirnov tests results.
ks.threshold	Kolmogorov-Smirnov test threshold for the p-value.

Examples

```
    ## Example of plotting the Kolmogorov-Smirnov tests results
library(specmine.datasets)
    data(cachexia)
    ks.results = ksTest_dataset(cachexia, "Muscle.loss",
write.file = FALSE)
    plot_kstest(cachexia, ks.results, 0.05)
```

`plot_peaks` *Plot the peaks of a MS or NMR dataset.*

Description

Function returns a plot where each point represents the intensity of a peak in a sample. Peaks are coloured according to a metadata class.

Usage

```
plot_peaks(dataset, column.class, samples = NULL, variable.bounds = NULL,
xlab = NULL, ylab = NULL, legend.place = "topright", cex = 0.8,
reverse.x = FALSE, p.size=0.5, ...)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`column.class`	string indicating the metadata's variable.
`samples`	vector with samples' names, if NULL all the samples will be considered.
`variable.bounds`	numeric vector with two elements indicating the interval of x-values to plot.
`xlab`	x-axis label.
`ylab`	y-axis label.
`legend.place`	string indicating the place that the legend's box will be placed.
`cex`	numeric value that indicates the amount by which the legend is magnified relative to the default.
`reverse.x`	boolean value indicating if the x-axis will be shown reversed or not.
`p.size`	numeric value indicating the amount by which the plot points are magnified relative to the default.
`...`	additional parameters to matplot.

Examples

```
 library(specmine.datasets)
 data(propolis)
plot_peaks(propolis, "seasons", variable.bounds = c(0,3), samples=c("XX_au", "XX_sm", "XX_wi"))
```

plot_regression_coefs_pvalues *Plot regression coefficient and p-values*

Description

Plots the linear regression coefficient and the p-values.

Usage

```
plot_regression_coefs_pvalues(linreg.results, bar.col = NULL,
coef.size = 5, ...)
```

Arguments

linreg.results	linear regression results.
bar.col	color of the bars.
coef.size	coefficient font size.
...	additional parameters to geom_text and geom_bar from ggplot.

plot_spectra *Plot spectra*

Description

Plot spectra from dataset.

Usage

```
plot_spectra(dataset, column.class, func = NULL, samples = NULL,
variable.bounds = NULL, xlab = NULL, ylab = NULL, lty = 1,
legend.place = "topright", cex = 0.8, reverse.x = FALSE, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
column.class	string indicating the metadata's variable.
func	function to compute the summary statistics to apply to the data.
samples	vector with samples' names, if NULL all the samples will be considered.
variable.bounds	numeric vector with two elements indicating the interval of x-values to plot.
xlab	x-axis label.
ylab	y-axis label.

lty	parameter of matplot.
legend.place	string indicating the place that the legend's box will be placed.
cex	numeric value that indicates the amount by which the legend is magnified relative to the default.
reverse.x	boolean value indicating if the x-axis will be shown reversed or not.
...	additional parameters to matplot.

---

plot_spectra_simple *Plot spectra (simple)*

Description

Plot spectra from dataset (simple version).

Usage

```
plot_spectra_simple(dataset, samples = NULL,
variable.bounds = NULL, xlab = NULL, ylab = NULL,
lty = 1, lwd = 1, col = 1, reverse.x = FALSE, ...)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
samples	vector with samples' names, if NULL all the samples will be considered.
variable.bounds	numeric vector with two elements indicating the interval of x-values to plot.
xlab	x-axis label.
ylab	y-axis label
lty	parameter of matplot.
lwd	parameter of matplot.
col	parameter of matplot.
reverse.x	boolean value indicating if the x-axis will be shown reversed or not.
...	additional parameters to pass to matplot.

plot_ttests *Plot t-tests results*

Description

Function for plotting the results from t-tests.

Usage

```
plot_ttests(dataset, tt.results, tt.threshold = 0.01)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
tt.results	t-tests results.
tt.threshold	t-test threshold for the p-value.

Examples

```
    ## Example of plotting the t-tests results
library(specmine.datasets)
    data(cachexia)
    ttests.results = tTests_dataset(cachexia, "Muscle.loss")
    plot_ttests(cachexia, ttests.results, 0.05)
```

predict_samples *Predict samples*

Description

Predict new samples.

Usage

```
predict_samples(train.result, new.samples)
```

Arguments

train.result	result from training a classifier.
new.samples	dataframe with new samples.

Value

Returns a data frame with the samples and the predicted class.

Examples

```
## Example of predicting samples
library(specmine.datasets)
data(cachexia)
training.result = train_models_performance(cachexia, "pls",
 "Muscle.loss", "cv")
result = predict_samples(training.result$final.models$pls, cachexia$data)
```

`read_Bruker_files` *Read Bruker processed spectra.*

Description

This functions read a directory containing directories where each one corresponds to a bruker spectrum directory.

A CSV file with the names of the samples and to which bruker spectrum directory (directory name) they correspond to should be given, unless directories' names correspond to the samples names.

Usage

```
read_Bruker_files(bruker_directory, metadata_file=NULL,
                  m.header_col=TRUE, m.header_row=TRUE, m.sep=",",
                  samples.names=NULL, zipped=TRUE,
                  description="", label.x="ppm", label.values="intensity")
```

Arguments

`bruker_directory`	Path of the directory with all the directories of the bruker spectra.
`metadata_file`	Path of the metadata file.
`m.header_col`	Boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.
`m.header_row`	Boolean value indicating if the metadata CSV file contains a header row with the name of the samples.
`m.sep`	The separator character of the metadata file.
`samples.names`	CSV file where the first column represents the samples names and in the second column the names of the spectra directories to which they correspond. If NULL, it will be considered that the directories names are the samples names (it has to be the same names that appear in the metadata file).
`zipped`	Boolean value indicating if the spectra directories are zipped or not.
`description`	A short text describing the dataset.
`label.x`	The label for the x values.
`label.values`	The label for the y values.

Value

Returns a list representing a dataset for specmine.

`read_Bruker_files_2d` *Read Bruker processed 2D spectra.*

Description

This functions reads a directory containing directories where each one corresponds to a bruker 2D spectrum directory. A CSV file with the names of the samples and to which bruker 2D spectrum directory (directory name) they correspond to should be given, unless directories' names correspond to the samples names.

Usage

```
read_Bruker_files_2d(bruker_directory, metadata_file=NULL,
                     m.header_col=T, m.header_row=T, m.sep=",",
                     samples.names=NULL, zipped=T,
                     description="", label.x="ppm",
                     label.y = "ppm", label.values="intensity")
```

Arguments

`bruker_directory`	Path of the directory with all the directories of the bruker 2D spectra.
`metadata_file`	Path of the metadata file.
`m.header_col`	Boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.
`m.header_row`	Boolean value indicating if the metadata CSV file contains a header row with the name of the samples.
`m.sep`	The separator character of the metadata file.
`samples.names`	CSV file where the first column represents the samples names and in the second column the names of the spectra directories to which they correspond. If NULL, it will be considered that the directories names are the samples names (it has to be the same names that appear in the metadata file).
`zipped`	Boolean value indicating if the spectra directories are zipped or not.
`description`	A short text describing the dataset.
`label.x`	The label for the x values.
`label.y`	The label for the y values.
`label.values`	The label for the pairs' (x,y) variables.

Value

Returns a list representing a 2D dataset for specmine:

data	A list of matrices where each matrix matches one 2D spectra.
type	The type of the data in the dataset.
description	A short text describing the dataset.
metadata	A dataframe with the metadata variables.
F1_ppm	The ppm values regarding indirect dimension.
F2_ppm	The ppm values regarding direct dimension.
labels	A list of vectors for the x, y and pairs'(x,y) values.

---

read_csvs_folder *Read CSVs from folder*

Description

Reads multiple CSV files in a given folder.

Usage

```
read_csvs_folder(foldername, ...)
```

Arguments

foldername	string with the name of the folder.
...	additional parameters to read.csv function.

Value

Returns a list of data frames.

---

read_dataset_csv *Read dataset from CSV*

Description

Reads the data from a CSV file and creates the dataset.

Usage

```
read_dataset_csv(filename.data, filename.meta = NULL,
type = "undefined", description = "", label.x = NULL,
label.values = NULL, sample.names = NULL, format = "row",
header.col = TRUE, header.row = TRUE, sep = ",",
header.col.meta = TRUE, header.row.meta = TRUE, sep.meta = ",")
```

Arguments

filename.data	name of the data file.
filename.meta	name of the metadata file.
type	type of the data.
description	a short text describing the dataset.
label.x	the label for the x values.
label.values	the label for the y values.
sample.names	the names of the samples.
format	format which the data are in the CSV file. It can be "row" if the samples are in the rows or "col" if the samples are in the columns.
header.col	boolean value indicating if the CSV contains a header column with the names of the samples or variables.
header.row	boolean value indicating if the CSV contains a header row with the names of the samples or variables.
sep	the separator character.
header.col.meta	boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.
header.row.meta	boolean value indicating if the metadata CSV file contains a header row with the name of the samples.
sep.meta	the separator character of the metadata file.

Value

Returns the dataset from the CSV file.

---

read_dataset_dx *Read dataset from (J)DX files*

Description

Reads the data from the (J)DX files and creates the dataset.

Usage

```
read_dataset_dx(folder.data, filename.meta = NULL,
type = "undefined", description = "", label.x = NULL,
label.values = NULL, header.col.meta = TRUE,
header.row.meta = TRUE, sep.meta = ",")
```

Arguments

folder.data	string containing the path of the data folder.
filename.meta	name of the metadata file.
type	type of the data.
description	a short text describing the dataset.
label.x	the label for the x values.
label.values	the label for the y values.
header.col.meta	boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.
header.row.meta	boolean value indicating if the metadata CSV file contains a header row with the name of the samples.
sep.meta	the separator character of the metadata file.

Value

Returns the dataset from the (J)DX files.

---

read_dataset_spc *Read dataset from SPC files*

Description

Reads the data from the SPC files and creates the dataset.

Usage

```
read_dataset_spc(folder.data, filename.meta = NULL,
type = "undefined", description = "", nosubhdr = FALSE,
label.x = NULL, label.values = NULL, header.col.meta = TRUE,
header.row.meta = TRUE, sep.meta = ",")
```

Arguments

folder.data	string containing the path of the data folder.
filename.meta	name of the metadata file.
type	type of the data.
description	a short text describing the dataset.
nosubhdr	if TRUE, it won't read the subheader.
label.x	the label for the x values.
label.values	the label for the y values.

header.col.meta
: boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.

header.row.meta
: boolean value indicating if the metadata CSV file contains a header row with the name of the samples.

sep.meta
: the separator character of the metadata file.

Value

Returns the dataset from the SPC files.

`read_data_csv` *Read CSV data*

Description

Reads the data from the CSV file.

Usage

```
read_data_csv(filename, format = "row", header.col = TRUE,
header.row = TRUE, sep = ",")
```

Arguments

filename
: name of the file with the data.

format
: format which the data are in the CSV file. It can be "row" if the samples are in the rows or "col" if the samples are in the columns.

header.col
: boolean value indicating if the CSV contains a header column with the names of the samples or variables.

header.row
: boolean value indicating if the CSV contains a header row with the names of the samples or variables.

sep
: the separator character.

Value

Returns a numeric matrix with the data.

read_data_dx *Read data from (J)DX files*

Description

Reads the data from the (J)DX files.

Usage

```
read_data_dx(foldername, debug = 0)
```

Arguments

foldername	string with the path of the data folder.
debug	debug option for readJDX's readJDX function.

Value

Returns a list with the samples and the respective data points.

read_data_spc *Read data from SPC files*

Description

Reads the data from the SPC files.

Usage

```
read_data_spc(foldername, nosubhdr = FALSE)
```

Arguments

foldername	string with the path of the data folder.
nosubhdr	if TRUE, it won't read the subheader.

Value

Returns a list with the samples and the respective data points.

read_metadata *Read metadata*

Description

Read the metadata from a file.

Usage

```
read_metadata(filename, header.col = TRUE, header.row = TRUE,
sep = ",")
```

Arguments

filename	name of the file with the metadata.
header.col	boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.
header.row	boolean value indicating if the metadata CSV file contains a header row with the name of the samples.
sep	the separator character.

Value

Returns a data frame with the metadata.

read_ms_spectra *Read MS spectra*

Description

Read the data from the MS files and creates the dataset.

Usage

```
read_ms_spectra(folder.name, type = "undefined",
filename.meta = NULL, description = "", prof.method = "bin",
fwhm = 30, bw = 30, intvalue = "into", header.col.meta = TRUE,
header.row.meta = TRUE, sep.meta = ",")
```

Arguments

folder.name	string containing the path of the data folder.
type	type of the data.
filename.meta	name of the metadata file.
description	a short text describing the dataset.
prof.method	profmethod parameter from xcmsSet function from xcms package.
fwhm	fwhm parameter from xcmsSet function from xcms package. A commonly used value is 30 (seconds) for LC-MS and 4 (seconds) for GC-MS spectra.
bw	bw parameter from group function from xcms package.
intvalue	value parameter from groupval function from xcms package. It can be: • **"into"** - integrated area of original (raw) peak • **"intf"** - integrated area of filtered peak. • **"maxo"** - maximum intensity of original (raw) peak. • **"maxf"** - maximum intensity of filtered peak.
header.col.meta	boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.
header.row.meta	boolean value indicating if the metadata CSV file contains a header row with the name of the samples.
sep.meta	the separator character of the metadata file.

Value

Returns a dataset from the MS files.

---

read_multiple_csvs *Read multiple CSVs*

Description

Reads multiple CSVs, each one with a sample.

Usage

```
read_multiple_csvs(filenames, ext = ".csv", ...)
```

Arguments

filenames	list of file names of the files to read.
ext	extension name.
...	additional parameters to read.csv function.

Value

returns a list of dataframes.

read_spc_nosubhdr *Import for Thermo Galactic's spc file format These functions allow to import .spc files.*

Description

Import for Thermo Galactic's spc file format These functions allow to import .spc files.

Usage

```
read_spc_nosubhdr(filename, keys.hdr2data = c("fexper", "fres", "fsource"),
  keys.hdr2log = c("fdate", "fpeakpt"), keys.log2data = FALSE,
  keys.log2log = TRUE, log.txt = TRUE, log.bin = FALSE,
  log.disk = FALSE, hdr = list(), nosubhdr = TRUE, no.object = FALSE)
```

Arguments

`filename`	The complete file name of the .spc file.
`keys.hdr2data, keys.hdr2log, keys.log2data, keys.log2log`	character vectors with the names of parameters in the .spc file's log block (log2xxx) or header (hdr2xxx) that should go into the extra data (yyy2data) or into the `long.description` field of the returned hyperSpec object's log (yyy2log). All header fields specified in the .spc file format specification (see below) are imported and can be referred to by their de-capitalized names.
`log.txt`	Should the text part of the .spc file's log block be read?
`log.bin, log.disk`	Should the normal and on-disk binary parts of the .spc file's log block be read? If so, they will be put as raw vectors into the hyperSpec object's log.
`hdr`	A list with fileheader fields that overwrite the settings of actual file's header. Use with care, and look into the source code for detailed insight on the elements of this list.
`nosubhdr`	Boolean value to decide if the header should be read or not. Default to TRUE.
`no.object`	If `TRUE`, a list with wavelengths, spectra, labels, log and data are returned instead of a hyperSpec object. This parameter will likely be subject to change in future - use with care.

Value

If the file contains multiple spectra with individual wavelength axes, `read.spc` returns a list of hyperSpec objects. Otherwise the result is a hyperSpec object.

`read.spc.KaiserMap` returns a hyperSpec object with data columns x, y, and z containing the stage position as recorded in the .spc files' log.

Note

Only a restricted set of test files was available for development. Particularly, the w-planes feature could not be tested.

If you have .spc files that cannot be read with these function, don't hesitate to contact the package maintainer with your code patch or asking advice.

Author(s)

C. Beleites

See Also

textio

`read_varian_2dspectra_raw`

Function that reads raw 2D spectra (intensity over time spectra) from the varian format and processes them to ppm spectra.

Description

This function read raw 2D spectra (i.e. intensity over time spectra) from the varian format and processess them to intensity over ppm spectra. For this function to work, in each spectrum directory should be present a fid and procpar files.

Python 3 with module nmrglue must be installed.

Usage

```
read_varian_2dspectra_raw(varian_spectra_directory,
                  metadata_file=NULL, m.header_col=T, m.header_row=T, m.sep=",",
                    samples.names=NULL, zero_filling=T, apodization=T, zipped=T,
                          description="", label.x="ppm",
                          label.y="ppm", label.values="intensity")
```

Arguments

`varian_spectra_directory`	Path of the directory with all the directories of the varian 2D spectra.
`metadata_file`	Path of the metadata file.
`m.header_col`	Boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.
`m.header_row`	Boolean value indicating if the metadata CSV file contains a header row with the name of the samples.
`m.sep`	The separator character of the metadata file.

samples.names	CSV file where the first column represents the samples names and in the second column the names of the spectra directories to which they correspond. If NULL, it will be considered that the directories names are the samples names (it has to be the same names that appear in the metadata file).
zero_filling	Boolean value indicating whether zero-filling should be performed or not when processing the fid of the 2D spectra. Defaults to TRUE.
apodization	Boolean value indicating whether **exponential** apodization should be performed or not when processing the fid of the 2D spectra. Defaults to TRUE.
zipped	Boolean value indicating if the spectra directories are zipped or not. Defaults to TRUE.
description	A short text describing the dataset.
label.x	The label for the x values (indirect dimension).
label.y	The label for the y values (direct dimension).
label.values	The label for the pair'(x,y) values.

Value

Returns a list representing a 2D dataset for specmine:

data	A list of matrices where each matrix matches one 2D spectra.
type	The type of the data in the dataset.
description	A short text describing the dataset.
metadata	A dataframe with the metadata variables.
F1_ppm	The ppm values regarding indirect dimension.
F2_ppm	The ppm values regarding direct dimension.
labels	A list of vectors for the x, y and pairs'(x,y) values.

Warning

You must not call this function unless you have Python (>=3.5.2) installed in your machine and the module nmrglue.

---

read_varian_spectra_raw

Function that reads raw spectra (intensity over time spectra) from the varian format and processes them to ppm spectra.

Description

This function read raw spectra (i.e. intensity over time spectra) from the varian format and processess them to intensity over ppm spectra. For this function to work, in each spectrum directory should be present a fid and procpar files.

Python 3 with modules nmrglue must be installed.

Usage

```
read_varian_spectra_raw(varian_spectra_directory,
metadata_file=NULL, m.header_col=TRUE, m.header_row=TRUE, m.sep=",",
samples.names=NULL, zero_filling=TRUE, apodization=TRUE, zipped=TRUE,
description="", label.x="ppm", label.values="intensity")
```

Arguments

varian_spectra_directory	Path of the directory with all the directories of the varian spectra.
metadata_file	Path of the metadata file.
m.header_col	Boolean value indicating if the metadata CSV file contains a header column with the name of the metadata variables.
m.header_row	Boolean value indicating if the metadata CSV file contains a header row with the name of the samples.
m.sep	The separator character of the metadata file.
samples.names	CSV file where the first column represents the samples names and in the second column the names of the spectra directories to which they correspond. If NULL, it will be considered that the directories names are the samples names (it has to be the same names that appear in the metadata file).
zero_filling	boolean value indicating whether zero-filling should be performed or not when processing the fid spectra. Defaults to TRUE.
apodization	boolean value indicating whether apodization should be performed or not when processing the fid spectra. Defaults to TRUE.
zipped	Boolean value indicating if the spectra directories are zipped or not.
description	A short text describing the dataset.
label.x	The label for the x values.
label.values	The label for the y values.

Value

Returns a list representing a dataset for specmine.

Warning

You must not call this function unless you have Python (>=3.5.2) installed in your machine and the module nmrglue.

recursive_feature_elimination *Perform recursive feature elimination*

Description

Perform recursive feature elimination on the dataset using caret's package.

Usage

```
recursive_feature_elimination(datamat, samples.class,
functions = caret::rfFuncs, method = "cv", repeats = 5,
number = 10, subsets = 2^(2:4))
```

Arguments

datamat	data matrix from dataset.
samples.class	string or index indicating what metadata to use.
functions	a list of functions for model fitting, prediction and variable importance.
method	the external resampling method: boot, cv, LOOCV or LGOCV (for repeated training/test splits.
repeats	for repeated k-fold cross-validation only: the number of complete sets of folds to compute.
number	either the number of folds or number of resampling iterations.
subsets	a numeric vector of integers corresponding to the number of features that should be retained.

Value

A caret's rfe object with the result of recursive feature selection.

Examples

```
## Example of recursive feature elimination
library(specmine.datasets)
data(cachexia)
library(caret)
rfe.result = recursive_feature_elimination(cachexia$data,
     cachexia$metadata$Muscle.loss, functions = caret::rfFuncs,
     method = "cv", number = 3, subsets = 2^(1:6))
```

remove_data *Remove data*

Description

Remove data from the dataset.

Usage

```
remove_data(dataset, data.to.remove, type = "sample",
by.index = FALSE, rebuild.factors = TRUE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
data.to.remove	vector with the elements' names to remove
type	type of the element to remove. It can be: • **"sample"** to remove samples. • **"data"** to remove variables. • **"metadata"** to remove metadata's variables.
by.index	if TRUE, the values of the data.to.remove argument are indexes in case the type is "data".
rebuild.factors	if TRUE, rebuilds the factors from metadata.

Value

Returns the dataset with the specified data removed.

Examples

```
## Example of removing data
library(specmine.datasets)
data(cachexia)
dataset = remove_data(cachexia, c("Creatine","Serine"), type = "data",
  by.index = FALSE)
```

remove_data_variables *Remove data variables*

Description

Remove data variables from the dataset.

Usage

```
remove_data_variables(dataset, variables.to.remove,
by.index = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variables.to.remove	vector with the variables' names to remove.
by.index	if TRUE, the values of the variables.to.remove argument are indexes.

Value

Returns the dataset with the specified data variables removed.

Examples

```
## Example of removing data variables
library(specmine.datasets)
data(cachexia)
dataset = remove_data_variables(cachexia, c("Creatine","Serine"),
  by.index = FALSE)
```

remove_metadata_variables *Remove metadata's variables*

Description

Remove metadata's variables from the dataset

Usage

```
remove_metadata_variables(dataset, variables.to.remove)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variables.to.remove	vector with the metadata's variables to remove.

Value

Returns the dataset with the selected metadata's variables removed.

Examples

```
## Example of removing metadata's variables
library(specmine.datasets)
data(propolis)
dataset = remove_metadata_variables(propolis, c("seasons"))
```

---

remove_peaks_interval *Remove interval of peaks*

Description

Removes peaks from a given interval.

Usage

```
remove_peaks_interval(sample.df, peak.val.min, peak.val.max)
```

Arguments

sample.df	data frame with the samples' peaks.
peak.val.min	minimum peak value.
peak.val.max	maximum peak value.

Value

Returns a data frame with the filtered samples' peaks.

Examples

```
## Example of removing a interval of peaks
library(specmine.datasets)
data(propolisSampleList)
samples.df = remove_peaks_interval(propolisSampleList[[1]], 2, 8.05)
```

remove_peaks_interval_sample_list *Remove interval of peaks (sample list)*

Description

Removes peaks on a sample list given a peak interval.

Usage

```
remove_peaks_interval_sample_list(sample.list, peak.val.min,
peak.val.max)
```

Arguments

sample.list	list of data frames with the samples' peaks.
peak.val.min	minimum peak value.
peak.val.max	maximum peak value.

Value

Returns the sample list with the filtered peaks.

Examples

```
## Example of removing a interval of peaks in a sample list
library(specmine.datasets)
data(propolisSampleList)
samples.list = remove_peaks_interval_sample_list(propolisSampleList, 2, 8.05)
```

remove_samples *Remove samples*

Description

Remove samples from the dataset.

Usage

```
remove_samples(dataset, samples.to.remove, rebuild.factors = TRUE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
samples.to.remove	vector with the sample's names to remove.
rebuild.factors	if TRUE, rebuilds the factors from metadata.

Value

Returns the dataset with the specified samples removed.

Examples

```
## Example of removing samples
library(specmine.datasets)
data(cachexia)
cachexia = remove_samples(cachexia, c("PIF_178","PIF_090"))
```

---

remove_samples_by_nas *Remove samples by NAs*

Description

Remove samples from the dataset by the number of NAs

Usage

```
remove_samples_by_nas(dataset, max.nas = 0, by.percent = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
max.nas	number of NAs (or percentage) to which samples with more NAs will be removed.
by.percent	if TRUE the max.nas argument is a percentage.

Value

Returns the dataset with the samples with more NAs than the limit removed.

Examples

```
## Example of removing samples by NAs
library(specmine.datasets)
data(propolis)
propolis = remove_samples_by_nas(propolis, 40, by.percent = TRUE)
```

remove_samples_by_na_metadata

Remove samples by NA on metadata

Description

Remove samples from the dataset with the metadata's variable value with NAs.

Usage

```
remove_samples_by_na_metadata(dataset, metadata.var)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.var	metadata's variable.

Value

Returns the dataset with the samples with NA on metadata's variable removed.

Examples

```
## Example of removing samples that have NAs on metadata's variable
library(specmine.datasets)
data(cachexia)
cachexia$metadata$Muscle.loss[10] = NA
cachexia = remove_samples_by_na_metadata(cachexia, "Muscle.loss")
```

remove_variables_by_nas

Remove variables by NAs

Description

Remove variables from the dataset by the number of NAs

Usage

```
remove_variables_by_nas(dataset, max.nas = 0, by.percent = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
max.nas	number of NAs (or percentage) to which samples with more NAs will be removed.
by.percent	if TRUE the max.nas argument is a percentage.

Value

Returns the dataset with the variables with more NAs than the limit removed.

Examples

```
## Example of removing variables by NAs
library(specmine.datasets)
data(propolis)
propolis = remove_variables_by_nas(propolis, 40, by.percent = TRUE)
```

`remove_x_values_by_interval` *Remove x-values by interval*

Description

Remove an interval of x-values from the dataset.

Usage

```
remove_x_values_by_interval(dataset, min.value, max.value)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`min.value`	minimum value of the interval.
`max.value`	maximum value of the interval.

Value

Returns the dataset with the specified interval of x-values removed.

`replace_data_value` *Replace data value*

Description

Replace a data value for a new value on the dataset.

Usage

```
replace_data_value(dataset, x.axis.val, sample, new.value,
by.index = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
x.axis.val	variable index or name.
sample	sample name.
new.value	new value to replace the old value.
by.index	boolean value to indicate if the x.axis.val is an index or not.

Value

Returns the dataset with the data value replaced.

Examples

```
## Example of replacing a data value from the dataset
library(specmine.datasets)
data(cachexia)
dataset = replace_data_value(cachexia, "Creatine", "PIF_178", 10.3,
  by.index = FALSE)
```

---

replace_metadata_value

Replace metadata's value

Description

Replace a metadata's variable value of a sample.

Usage

```
replace_metadata_value(dataset, variable, sample, new.value)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variable	metadata's variable.
sample	name of the sample.
new.value	new value of the metadata's variable.

Value

Returns the dataset with the metadata updated.

Examples

```
## Example of replacing metadata's variable value of a sample
library(specmine.datasets)
data(cachexia)
dataset = replace_metadata_value(cachexia, "Muscle.loss", "PIF_178",
  "control")
```

`savitzky_golay` *Savitzky-golay transformation*

Description

Smoothing and derivative of the data using Savitzky-Golay.

Usage

```
savitzky_golay(dataset, p.order, window, deriv = 0)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`p.order`	integer value representing the polynomial order.
`window`	odd number indicating the window size.
`deriv`	integer value indicating the differentiation order.

Value

Returns the dataset with the spectra smoothed using Savitzky-Golay.

`scaling` *Scale dataset*

Description

Performs scaling according to a method.

Usage

```
scaling(dataset, method = "auto")
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
method	string specifying the scaling method. The possible values are: • **"auto"** auto scaling. • **"range"** range scaling. • **"pareto"** pareto scaling. • **"tointerval"** scaling to an interval.

Value

Returns the dataset scaled.

---

scaling_samples *Scale data matrix*

Description

Performs scaling according to a method.

Usage

```
scaling_samples(datamat, method = "auto")
```

Arguments

datamat	data matrix.
method	string specifying the scaling method. The possible values are: • **"auto"** auto scaling. • **"range"** range scaling. • **"pareto"** pareto scaling. • **"tointerval"** scaling to an interval.

Value

Returns the data matrix scaled.

set_metadata *Set new metadata*

Description

Updates the dataset's metadata with a new one.

Usage

```
set_metadata(dataset, new.metadata)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
new.metadata	matrix or dataframe with the new metadata.

Value

Returns the dataset with the updated metadata.

Examples

```
## Example of setting a new metadata to the dataset
library(specmine.datasets)
data(cachexia)
new.metadata = c(rep("meta1", 39), rep("meta2", 38))
new.metadata = data.frame(var_meta = new.metadata)
rownames(new.metadata) = get_sample_names(cachexia)
cachexia = set_metadata(cachexia, new.metadata)
```

set_sample_names *Set samples names*

Description

Set new samples names to the dataset.

Usage

```
set_sample_names(dataset, new.sample.names)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
new.sample.names	vector with the new samples names.

Value

Returns the dataset with the updated samples names.

Examples

```
## Example of setting a new value label to the dataset
library(specmine.datasets)
data(cachexia)
new.samples.names = as.character(1:77)
cachexia = set_sample_names(cachexia, new.samples.names)
```

---

set_value_label *Set value label*

Description

Set a new value label for the dataset.

Usage

```
set_value_label(dataset, new.val.label)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
new.val.label	string with the new value label.

Value

Returns the dataset with the updated value label.

Examples

```
## Example of setting a new value label to the dataset
library(specmine.datasets)
data(cachexia)
cachexia = set_value_label(cachexia, "new value label")
```

set_x_label *Set x-label*

Description

Set a new x-label to the dataset.

Usage

```
set_x_label(dataset, new.x.label)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
new.x.label	string with the x-label.

Value

Returns the dataset with the updated x-label.

Examples

```
## Example of setting a new x-label to the dataset
library(specmine.datasets)
data(cachexia)
cachexia = set_x_label(cachexia, "new x-label")
```

set_x_values *Set new x-values*

Description

Set new x-values to the dataset

Usage

```
set_x_values(dataset, new.x.values, new.x.label = NULL)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
new.x.values	vector with the new x-values.
new.x.label	string with the new x-label (can be NULL).

Value

Returns the dataset with the updated x-values.

Examples

```
## Example of setting new x-values to the dataset
library(specmine.datasets)
data(cachexia)
new.xvalues = 1:63
cachexia = set_x_values(cachexia, new.xvalues, new.x.label = NULL)
```

---

shift_correction *Shift correction*

Description

Shifts the spectra according to a specific method.

Usage

```
shift_correction(dataset, method = "constant", shift.val = 0,
interp.function = "linear", ref.limits = NULL)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
method	string that indicates the shifting method. It can be: • "constant" uses a constant shift that is added to the x-values • "interpolation" uses interpolation according to "interp.function"
shift.val	value of the shift (for constant and interpolation methods); can be a single value for all spectra, can be the string "auto", the shifts are automatically determined or a vector with the size of the number of samples with the shifts for each spectra.
interp.function	string that represents the interpolation function, can be "linear" or "spline".
ref.limits	vector with 2 elements that represents the reference limits to calculate the shifts.

Value

Returns the dataset with the spectras shifted.

smoothing_interpolation *Smoothing interpolation*

Description

Performs smoothing interpolation according to a specific method.

Usage

```
smoothing_interpolation(dataset, method = "bin",
reducing.factor = 2, x.axis = NULL, p.order = 3,
window = 11, deriv = 0, na.rm = TRUE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
method	string specifying the smoothing method. The three possible methods are: "bin", "loess" and "savitzky.golay".
reducing.factor	numeric value indicating the reducing factor for bin method.
x.axis	numeric vector representing the new x-axis for loess method.
p.order	numeric value representing the polynomial order for savitzky-golay method.
window	numeric value indicating the size of the window for savitzky-golay method. (must be an odd number)
deriv	numeric value indicating the differentiation order for savitzky-golay method.
na.rm	boolean value indicating if NAs should be removed. Defaults to TRUE.

Value

Returns the dataset with the spectra smoothed.

snv_dataset *Standard Normal Variate*

Description

Performs Standard Normal Variate on the dataset.

Usage

```
snv_dataset(dataset)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.

Value

Returns the dataset with the data normalized by SNV.

---

spectra_options *Information on the library of NMR reference spectra in our package.*

Description

This dataset provides all the information on the library of NMR spectra used as references in NMR metabolite identification.

Usage

```
data("spectra_options")
```

Format

A data frame with 1816 observations on the following 9 variables. Each observation corresponds to a spectrum in our library.

SPCMNS a character vector with the spetcra IDs.

SPCMNM a character vector with the metabolite IDs of the corresponding spectra.

FREQUENCY a character vector with the frequencies under which the spectra were obtained.

NUCLEUS a character vector mentioned the nucleus examined. All observations are '1H'.

PH a character vector with the pH of the samples from which the spectra were obtained. May contain missing values.

TEMPERATURE a character vector with the temperature under which the spectra were obtained. May contain missing values.

SOLVENT a character vector with the solvent of the samples from which the spectra were obtained.

ORIGINAL_DATABASE_ID whenever available, a character vector with the ID of the corresponding spectra from the database it was originally acquired from.

DATABASE a character vector specifying from which database the spectra were taken from.

References

The spectra were taken from the following databases: HMDB (https://hmdb.ca), BMRB (http://www.bmrb.wisc.edu) and SDBS (https://sdbs.db.aist.go.jp). Some spectra were internally acquired and are mentioned as OUR in the DATABASE variable.

Examples

```
data(spectra_options)
```

stats_by_sample *Statistics of samples*

Description

Get a summary of statistics of the samples.

Usage

```
stats_by_sample(dataset, samples = NULL)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
samples	if defined restricts the application to a given set of samples.

Value

Returns a vector with the a summary of statistics of the samples.

Examples

```
    ## Example of getting stats of samples
library(specmine.datasets)
    data(cachexia)
    samples.stats.result = stats_by_sample(cachexia)
```

stats_by_variable *Statistics of variables*

Description

Get a summary of statistics of the variables.

Usage

```
stats_by_variable(dataset, variables = NULL,
variable.bounds = NULL)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variables	allows to define which variables to calculate the stats (if numbers, indexes are assumed).
variable.bounds	allow to define an interval of variables (if numeric).

Value

Returns a vector with the a summary of statistics of the variables.

Examples

```
    ## Example of getting stats of variables
 library(specmine.datasets)
    data(cachexia)
    variable.stats.result = stats_by_variable(cachexia)
```

`subset_by_samples_and_xvalues` *Subset by samples and x-values*

Description

Gets a subset of specific samples and x-values.

Usage

```
subset_by_samples_and_xvalues(dataset, samples, variables = NULL,
by.index = FALSE, variable.bounds = NULL, rebuild.factors = TRUE)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`samples`	vector with indexes or names of the samples to select
`variables`	vector with the desired variables to get from the dataset.
`by.index`	if TRUE, the values of the variables argument are indexes.
`variable.bounds`	variable bounds used if by.index is FALSE and variables are NULL.
`rebuild.factors`	if TRUE the metadata factors are rebuilded.

Value

Returns the dataset with the selected samples and x-values.

Examples

```
## Example of subsetting samples and x-values
library(specmine.datasets)
data(cachexia)
subset = subset_by_samples_and_xvalues(cachexia, c("PIF_178","NETL_022_V1"),
 variables = c("Creatine","Serine"))
```

subset_metadata *Subset metadata*

Description

Subsets the metadata according to the specified metadata's variables.

Usage

```
subset_metadata(dataset, variables)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variables	metadata's variables.

Value

Returns the dataset with the metadata subsetted.

Examples

```
## Example of subsetting samples
library(specmine.datasets)
data(propolis)
subset = subset_metadata(propolis, c("seasons"))
```

subset_random_samples *Subset random samples*

Description

Gets a subset of random samples from the dataset.

Usage

```
subset_random_samples(dataset, nsamples)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
nsamples	integer representing the number of samples that we want to get.

Value

Returns the dataset with a number of random samples.

Examples

```
## Example of subsetting random samples
library(specmine.datasets)
data(cachexia)
subset = subset_random_samples(cachexia, 15)
```

`subset_samples` *Subset samples*

Description

Gets a subset of specific samples from the dataset.

Usage

```
subset_samples(dataset, samples, rebuild.factors = TRUE)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`samples`	vector with indexes or names of the samples to select
`rebuild.factors`	if TRUE the metadata factors are rebuilded.

Value

Returns the dataset with the selected set of samples.

Examples

```
## Example of subsetting samples
library(specmine.datasets)
data(cachexia)
subset = subset_samples(cachexia, c("PIF_178","PIF_132"))
```

subset_samples_by_metadata_values *Subset samples by metadata values*

Description

Gets a subset of specific samples according to metadata's values from the dataset.

Usage

```
subset_samples_by_metadata_values(dataset, metadata.varname,
values)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.varname	name of the metadata's variable.
values	values of the metadata's variable.

Value

Returns the dataset with the set of samples according to the metadata's values.

Examples

```
## Example of subsetting samples by metadata's values
library(specmine.datasets)
data(propolis)
subset_samples_by_metadata_values(propolis, "seasons",
                                  c("sm","au"))
```

subset_x_values *Subset x-values*

Description

Gets a subset of specific x-values from the dataset.

Usage

```
subset_x_values(dataset, variables, by.index = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variables	vector with the desired variables to get from the dataset.
by.index	if TRUE, the values of the variables argument are indexes.

Value

Returns the dataset with the selected set of x-values.

Examples

```
## Example of subsetting x-values
library(specmine.datasets)
data(cachexia)
subset = subset_x_values(cachexia, c(1,2,10,20), by.index = TRUE)
```

---

subset_x_values_by_interval

Subset x-values by interval

Description

Gets a subset of a specific interval of x-values.

Usage

```
subset_x_values_by_interval(dataset, min.value, max.value)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
min.value	the minimum value of the interval.
max.value	the maximum value of the interval.

Value

Returns the dataset with the selected interval of x-values.

Examples

```
## Example of subsetting x-values by an interval
library(specmine.datasets)
data(propolis)
subset = subset_x_values_by_interval(propolis, 1, 3)
```

summary_var_importance *Summary of variables importance*

Description

Summary of variables importance of the models

Usage

```
summary_var_importance(performances, number.rows)
```

Arguments

performances	the result from training the models.
number.rows	number of variables to display.

Value

Returns list with the variables importance of each model.

Examples

```
## Example of getting a summary of variables importance
library(specmine.datasets)
data(cachexia)
training.result = train_models_performance(cachexia, "pls",
 "Muscle.loss", "cv")
result = summary_var_importance(training.result, 10)
```

sum_2d_dataset *2D Dataset summary*

Description

Returns a summary with its main features

Usage

```
sum_2d_dataset(dataset_2d, stats = TRUE)
```

Arguments

dataset_2d	List representing the 2D dataset from a 2D metabolomics experiment.
stats	If TRUE prints some global statistics for each 2D spectra.

Value

Returns the summary of the 2D dataset containing:

- Description
- Type of data
- Number of samples
- Number of data points
- Number of metadata variables if metadata not null
- Labels of x axis, y axis and pair'(x,y) values if labels not null

If the parameter 'stats' is TRUE then returns also:

- Number of missing values in each spectra
- Mean of data values in each spectra
- Median of data values in each spectra
- Standard deviation in each spectra
- Range of values in each spectra
- Quantiles for each spectra

`sum_dataset` *Dataset summary*

Description

Returns a summary with its main features.

Usage

```
sum_dataset(dataset, stats = TRUE)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`stats`	if TRUE prints some global statistics of the data values.

Value

Returns the summary of the dataset containing:

- Description
- Type of data
- Number of samples
- Number of datapoints
- Number of metadata variables if metadata not null

- Labels of x axis values and data points if labels not null

If the parameter 'stats' is TRUE then returns also:

- Number of missing values in data
- Mean of data values
- Median of data values
- Standard deviation
- Range of values
- Quantiles

Examples

`train_and_predict` *Train and predict*

Description

Train a model and predict new unlabeled samples with that model.

Usage

```
train_and_predict(dataset, new.samples, column.class, model,
validation, num.folds = 10, num.repeats = 10, tunelength = 10,
tunegrid = NULL, metric = NULL, summary.function =
defaultSummary)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`new.samples`	dataframe with new samples to predict the class label.
`column.class`	metadata column class.
`model`	model to be used in training.
`validation`	validation method.
`num.folds`	number of folds in cross validation.
`num.repeats`	number of repeats.
`tunelength`	number of levels for each tuning parameters.
`tunegrid`	dataframe with possible tuning values.
`metric`	metric used to evaluate the model's performance. Can be "Accuracy" or "ROC".
`summary.function`	summary function. For "ROC" the multiClassSummary function must be used.

Value

Returns a list with the training result and the predictions result.

Examples

```
## Example of training and predicting
library(specmine.datasets)
data(cachexia)
result = train_and_predict(cachexia, new.samples = cachexia$data,
"Muscle.loss", "pls", "cv")
```

`train_classifier` *Train classifier*

Description

Train a specific classifier.

Usage

```
train_classifier(dataset, column.class, model, validation,
num.folds = 10, num.repeats = 10, tunelength = 10,
tunegrid = NULL, metric = NULL,
summary.function = defaultSummary, class.in.metadata = TRUE)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`column.class`	metadata column class.
`model`	model to be used in training.
`validation`	validation method.
`num.folds`	number of folds in cross validation.
`num.repeats`	number of repeats.
`tunelength`	number of levels for each tuning parameters.
`tunegrid`	dataframe with possible tuning values.
`metric`	metric used to evaluate the model's performance. Can be "Accuracy" or "ROC".
`summary.function`	summary function. For "ROC" the multiClassSummary function must be used.
`class.in.metadata`	boolean value to indicate if the class is in metadata.

Value

Returns the train result object from caret.

Examples

```
## Example of training a classifier
library(specmine.datasets)
data(cachexia)
result = train_classifier(cachexia, "Muscle.loss", "pls", "cv")
```

`train_models_performance` *Train models*

Description

Train various models.

Usage

```
train_models_performance(dataset, models, column.class,
validation, num.folds = 10, num.repeats = 10, tunelength = 10,
tunegrid = NULL, metric = NULL, summary.function = "default",
class.in.metadata = TRUE, compute.varimp = TRUE)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`models`	models to be used in training.
`column.class`	metadata column class.
`validation`	validation method.
`num.folds`	number of folds in cross validation.
`num.repeats`	number of repeats.
`tunelength`	number of levels for each tuning parameters.
`tunegrid`	dataframe with possible tuning values.
`metric`	metric used to evaluate the model's performance. Can be "Accuracy" or "ROC".
`summary.function`	summary function. For "ROC" the multiClassSummary function must be used.
`class.in.metadata`	boolean value to indicate if the class is in metadata.
`compute.varimp`	boolean value to indicate if the var importance is calculated.

Value

Returns a list with the results from training

`performance`	The results from the best tunes of the models
`vips`	The variable importance from the models
`full.results`	The full results from the tuning parameters of each model
`best.tunes`	The best tune of each model
`confusion.matrices`	The confusion matrices of the models (only in classification)
`final.models`	The final models

Examples

```
## Example of training models
library(specmine.datasets)
data(cachexia)
result = train_models_performance(cachexia, "pls",
    "Muscle.loss", "cv")
```

`transform_data` *Transform data*

Description

Performs data transformation according to a method.

Usage

```
transform_data(dataset, method = "log")
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`method`	string specifying the transformation method. The possible values are: • **"log"** logarithmic transformation. • **"cubicroot"** cubic root transformation.

Value

Returns the dataset with the data transformation applied.

Examples

```
## Example of logarithmic transformation
library(specmine.datasets)
data(cachexia)
dataset.log = transform_data(cachexia, "log")
```

`transmittance_to_absorbance` *Convert transmittance to absorbance*

Description

Converts transmittance values to absorbance values.

Usage

```
transmittance_to_absorbance(dataset, percent = TRUE)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`percent`	boolean value to indicate if the absorbance values are in a percentage or not.

Value

Returns the dataset with the data points converted to absorbance values.

`tTests_dataset` *t-Tests on dataset*

Description

Run t-Tests for each row of the data from the dataset.

Usage

```
tTests_dataset(dataset, metadata.var, threshold = NULL,
write.file = FALSE, file.out = "ttests.csv")
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
metadata.var	metadata variable to use in the t-tests.
threshold	threshold value of the p-value.
write.file	boolean value to write or not a file with the results.
file.out	name of the file.

Value

Table with the results of the t-tests, with p-value, -log10(p-value) and false discovery rate (fdr).

Examples

```
## Example of t-Tests on dataset
library(specmine.datasets)
data(cachexia)
ttests.result = tTests_dataset(cachexia, "Muscle.loss",
write.file = FALSE)
```

---

values_per_peak *Values per peak*

Description

Gets the number of values on each peak.

Usage

```
values_per_peak(samples.df)
```

Arguments

samples.df	data frame with the samples' peaks.

Value

Returns a vector with the number of values for each peak.

Examples

```
## Example of getting the number of values for each peak
library(specmine.datasets)
data(propolis)
num.peaks = values_per_peak(propolis$data)
```

values_per_sample *Values per peak*

Description

Gets the number of values on each sample.

Usage

```
values_per_sample(samples.df)
```

Arguments

samples.df	data frame with the samples' peaks.

Value

Returns a vector with the number of values for each sample.

Examples

```
## Example of getting the number of values for each sample
library(specmine.datasets)
data(propolis)
num.values.samples = values_per_sample(propolis$data)
```

variables_as_metadata *Variables as metadata*

Description

Use one or more data variables as metadata variables.

Usage

```
variables_as_metadata(dataset, variables, by.index = FALSE)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
variables	name or index of the variables that are going to be used as metadata variables.
by.index	boolean value indicating if the variables are indexes or names

Value

Returns the dataset with the variables removed from the data and added on the metadata.

Examples

```
## Example of using a variable as metadata variable
library(specmine.datasets)
data(cachexia)
dataset = variables_as_metadata(cachexia, "Creatine", by.index = FALSE)
```

`volcano_plot_fc_tt` *Volcano plot*

Description

Volcano plot to intersect the results from t-tests and fold change.

Usage

```
volcano_plot_fc_tt(dataset, fc.results, tt.results,
fc.threshold = 2, tt.threshold = 0.01)
```

Arguments

`dataset`	list representing the dataset from a metabolomics experiment.
`fc.results`	fold change results.
`tt.results`	t-tests results.
`fc.threshold`	fold change threshold value.
`tt.threshold`	t-test p-value threshold.

Value

Returns the name of the samples which intersects both fold change and t-tests results above the given thresholds.

Examples

```
    ## Example of a volcano plot
library(specmine.datasets)
    data(cachexia)
    foldchange.results = fold_change(cachexia, "Muscle.loss", "control")
    ttests.results = tTests_dataset(cachexia, "Muscle.loss")
    volcano_plot_fc_tt(cachexia, foldchange.results, ttests.results,
       fc.threshold = 2, tt.threshold = 0.01)
```

xvalue_interval_to_indexes *Get indexes of an interval of x-values*

Description

Returns indexes corresponding to an interval of x-values (only to numerical values - spectra)

Usage

```
xvalue_interval_to_indexes(dataset, min.value, max.value)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
min.value	mininum x-value of the interval.
max.value	maximum x-value of the interval.

Value

Returns a numeric vector with the indexes of the x-values interval

Examples

```
## Example of getting the indexes of an interval of x-values
library(specmine.datasets)
data(propolis)
indexes.interval = xvalue_interval_to_indexes(propolis, 2.0, 5.5)
```

x_values_to_indexes *Get x-values indexes*

Description

Returns the indexes corresponding to a vector of x-values (only to numerical values - spectra)

Usage

```
x_values_to_indexes(dataset, x.values)
```

Arguments

dataset	list representing the dataset from a metabolomics experiment.
x.values	vector of x-values.

Value

Returns a numeric vector with the indexes of the x-values.

Examples

```
## Example of getting the indexes of the x-values
library(specmine.datasets)
data(propolis)
indexes = x_values_to_indexes(propolis, c(1.3, 3.51, 6.03))
```

Index