Package ‘DAPAR’

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Type Package

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Description This package contains a collection of functions for the visualisation and the statistical analysis of proteomic data.

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**boxPlotD**

Builds a boxplot from a dataframe

**Description**

Boxplot for quantitative proteomics data

**Usage**

```r
boxPlotD(qData, dataForXAxis = NULL, labels = NULL,
         group2Color = "Condition")
```

**Arguments**

- `qData`: A dataframe that contains quantitative data.
- `labels`: A vector of the conditions (labels) (one label per sample).
- `group2Color`: A string that indicates how to color the replicates: one color per condition (value "Condition") or one color per replicate (value "Replicate"). Default value is by Condition.

**Value**

A boxplot

**Author(s)**

Florence Combes, Samuel Wieczorek

**See Also**

densityPlotD

**Examples**

```r
data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
types <- c("Label","Analyt.Rep")
dataForXAxis <- Biobase::pData(UPSpep25)[,types]
labels <- Biobase::pData(UPSpep25)[,"Label"]
boxPlotD(qData, dataForXAxis, labels)
```
**BuildAdjacencyMatrix**  
*Function matrix of appartenence group*

**Description**

Method to create a binary matrix with proteins in columns and peptides in lines on a MSnSet object (peptides)

**Usage**

`BuildAdjacencyMatrix(obj.pep, protID, unique = TRUE)`

**Arguments**

- `obj.pep`: An object (peptides) of class `MSnSet`.
- `protID`: The name of proteins ID column
- `unique`: A boolean to indicate whether only the unique peptides must be considered (TRUE) or if the shared peptides have to be integrated (FALSE).

**Value**

A binary matrix

**Author(s)**

Florence Combes, Samuel Wieczorek, Alexia Dorffer

**Examples**

```r
data(UPSpep25)
BuildAdjacencyMatrix(UPSpep25, "Protein.group.IDs", TRUE)
```

---

**BuildColumnToProteinDataset**  
*creates a column for the protein dataset after aggregation by using the previous peptide dataset.*

**Description**

This function creates a column for the protein dataset after aggregation by using the previous peptide dataset.

**Usage**

`BuildColumnToProteinDataset(peptideData, matAdj, columnName)`
compareNormalizationD

Arguments

- `peptideData`: A data.frame of meta data of peptides. It is the fData of the MSnset object.
- `matAdj`: The adjacency matrix used to aggregate the peptides data.
- `columnName`: The name of the column in fData(peptides_MSnset) that the user wants to keep in the new protein data.frame.

Value

A vector

Author(s)

Samuel Wieczorek

Examples

data(UPSrep25)
protID <- "Protein.group.IDs"
M <- BuildAdjacencyMatrix(UPSrep25, protID, FALSE)
data <- Biobase::fData(UPSrep25)
name <- "organism"
BuildColumnToProteinDataset(data, M, name )

cmpareNormalizationD  Builds a plot from a dataframe

Description

Plot to compare the quantitative proteomics data before and after normalization

Usage

```
compareNormalizationD(qDataBefore, qDataAfter, labelsForLegend = NULL,
indData2Show = NULL, group2Color = "Condition")
```

Arguments

- `qDataBefore`: A dataframe that contains quantitative data before normalization.
- `qDataAfter`: A dataframe that contains quantitative data after normalization.
- `labelsForLegend`: A vector of the conditions (labels) (one label per sample).
- `indData2Show`: A vector of the indices of the columns to show in the plot. The indices are those of indices of the columns in the dataframe qDataBefore.
- `group2Color`: A string that indicates how to color the replicates: one color per condition (value "Condition") or one color per replicate (value "Replicate"). Default value is by Condition.

Value

A plot
corrMatrixD

Displays a correlation matrix of the quantitative data of the exprs() table.

Description

Correlation matrix based on a MSnSet object

Usage

corrMatrixD(qData, samplesData, gradientRate = 5)

Arguments

qData A dataframe of quantitative data.
samplesData A dataframe where lines correspond to samples and columns to the meta-data for those samples.
gradienRate The rate parameter to control the exponential law for the gradient of colors

Value

A colored correlation matrix

Author(s)

Florence Combes, Samuel Wieczorek

Examples

data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
samplesData <- Biobase::pData(UPSpep25)
corrMatrixD(qData, samplesData)
**CountPep**

**Compute the number of peptides used to aggregate proteins**

**Description**

This function computes the number of peptides used to aggregate proteins.

**Usage**

```r
CountPep(M)
```

**Arguments**

- `M`: A "valued" adjacency matrix in which lines and columns correspond respectively to peptides and proteins.

**Value**

A vector of boolean which is the adjacency matrix but with NA values if they exist in the intensity matrix.

**Author(s)**

Alexia Dorffer

**Examples**

```r
data(UPSpep25)
protID <- "Protein.group.IDs"
M <- BuildAdjacencyMatrix(UPSpep25, protID, FALSE)
CountPep(M)
```

---

**createMSnset**

**Creates an object of class MSnSet from text file**

**Description**

Builds an object of class MSnSet from a single tabulated-like file for quantitative and meta-data and a dataframe for the samples description. It differs from the original MSnSet builder which requires three separated files tabulated-like quantitative proteomic data into a MSnSet object, including metadata.

**Usage**

```r
createMSnset(file, metadata = NULL, indExpData, indFData, indiceID = NULL, logData = FALSE, replaceZeros = FALSE, pep_prot_data = NULL)
```
deleteLinesFromIndices

Arguments

file  
The name of a tab-separated file that contains the data.
metadata  
A dataframe describing the samples (in lines).
indExpData  
A vector of string where each element is the name of a column in designTable that have to be integrated in the fData() table of the MSnSet object.
indFData  
The name of column in file that will be the name of rows for the exprs() and fData() tables
indiceID  
The indice of the column containing the ID of entities (peptides or proteins)
logData  
A boolean value to indicate if the data have to be log-transformed (Default is FALSE)
replaceZeros  
A boolean value to indicate if the 0 and NaN values of intensity have to be replaced by NA (Default is FALSE)
pep_prot_data  
A string that indicates whether the dataset is about peptides or proteins.

Value

An instance of class MSnSet.

Author(s)

Florence Combes, Samuel Wieczorek

Examples

exprsFile <- system.file("extdata", "UPSpep25.txt", package="DAPAR")
metadataFile <- system.file("extdata", "samples.txt", package="DAPAR")
metadata = read.table(metadataFile, header=TRUE, sep="\t", as.is=TRUE)
indExpData <- c(56:61)
indFData <- c(1:55,62:71)
indiceID <- 64
createMSnset(exprsFile, metadata,indExpData, indFData, indiceID,
  pep_prot_data = "peptide")
deleteLinesFromIndices

Delete the lines in the matrix of intensities and the metadata table given their indice.

Description

Delete the lines of exprs() table identified by their indice.

Usage

deleteLinesFromIndices(obj, deleteThat = NULL, processText = NULL)

Arguments

obj  
An object of class MSnSet containing quantitative data.
deleteThat  
A vector of integers which are the indices of lines to delete.
processText  
A string to be included in the MSnSet object for log.
Density plot of quantitative proteomics data over samples.

Usage

densityPlotD(qData, labelsForLegend = NULL, indData2Show = NULL, group2Color = "Condition")

Arguments

- **qData**: A dataframe that contains quantitative data.
- **labelsForLegend**: A vector of the conditions (labels) (one label per sample).
- **indData2Show**: A vector of indices to show in densityplot. If NULL, then all labels are displayed.
- **group2Color**: A string that indicates how to color the replicates: one color per condition (value "Condition") or one color per replicate (value "Replicate"). Default value is by Condition.

Value

A density plot

Author(s)

Florence Combes, Samuel Wieczorek

See Also

boxPlotD, varianceDistD

Examples

data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
labels <- lab2Show <- Biobase::pData(UPSpep25)[,"Label"]
densityPlotD(qData, labels)
diffAna  This function performs a differential analysis on an MSnSet object (adapted from limma)

Description

Performs a differential analysis on an MSnSet object, based on limma functions.

Usage

diffAna(qData, design)

Arguments

qData A dataframe that contains quantitative data.

design The design matrix as described in the limma package documentation

Value

A dataframe with the p-value and log(Fold Change) associated to each element (peptide/protein)

Author(s)

Florence Combes, SamuelWieczorek

Examples

data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
design <- cbind(cond1=1, cond2=rep(0,nrow(Biobase::pData(UPSpep25))))
rownames(design) <- rownames(Biobase::pData(UPSpep25))
labels <- Biobase::pData(UPSpep25)[,"Label"]
indices <- getIndicesConditions(labels, "25fmol", "10fmol")
design[indices$iCond2,2] <- 1
diffAna(qData, design)

diffAnaComputeFDR  Computes the FDR corresponding to the p-values of the differential analysis using

Description

This function is a wrapper to the function adjust.p from the cp4p package. It returns the FDR corresponding to the p-values of the differential analysis. The FDR is computed with the function p.adjust from stats.

Usage

diffAnaComputeFDR(data, threshold_PVal = 0, threshold_LogFC = 0, pi0Method = 1)
**Arguments**

- **data**
  - The result of the differential analysis processed by `diffAna`
- **threshold_PVal**
  - The threshold on p-value to distinguish between differential and non-differential data
- **threshold_LogFC**
  - The threshold on log(Fold Change) to distinguish between differential and non-differential data
- **pi0Method**
  - The parameter pi0.method of the method adjust.p in the package `cp4p`

**Value**

The computed FDR value (floating number)

**Author(s)**

Samuel Wieczorek

**Examples**

```r
data(UPSpep25)
obj <- wrapper.mvImputation(UPSpep25, "QRILC")
condition1 <- '25fmol'
condition2 <- '10fmol'
qData <- Biobase::exprs(obj)
samplesData <- Biobase::pData(obj)
labels <- Biobase::pData(obj)[,"Label"]
limma <- diffAnaLimma(qData, samplesData, labels, condition1, condition2)
diffAnaComputeFDR(limma)
```

`diffAnaGetSignificant`  
*Returns a MSnSet object with only proteins significant after differential analysis.*

**Description**

Returns a MSnSet object with only proteins significant after differential analysis.

**Usage**

```r
diffAnaGetSignificant(obj)
```

**Arguments**

- **obj**
  - An object of class `MSnSet`.

**Value**

A MSnSet

**Author(s)**

Alexia Dorffer
**Examples**

```r
data(UPSpep25)
condition1 <- "25fmol"
condition2 <- "10fmol"
resLimma <- wrapper.diffAnaLimma(UPSpep25, condition1, condition2)
obj <- diffAnaSave(UPSpep25, resLimma, "limma", condition1, condition2)
signif <- diffAnaGetSignificant(obj)
```

**diffAnaLimma**

Performs differential analysis on an MSnSet object, calling the limma package functions

**Description**

Method to perform differential analysis on an MSnSet object (calls the limma package function).

**Usage**

```r
diffAnaLimma(qData, samplesData, labels, condition1, condition2)
```

**Arguments**

- **qData**
  A dataframe that contains quantitative data.

- **samplesData**
  A dataframe where lines correspond to samples and columns to the meta-data for those samples.

- **labels**
  A vector of the conditions (labels) (one label per sample).

- **condition1**
  A vector that contains the names of the conditions considered as condition 1

- **condition2**
  A vector that contains the names of the conditions considered as condition 2

**Value**

A dataframe as returned by the limma package

**Author(s)**

Florence Combes, Samuel Wieczorek

**Examples**

```r
data(UPSpep25)
condition1 <- '25fmol'
condition2 <- '10fmol'
qData <- Biobase::exprs(UPSpep25)
samplesData <- Biobase::pData(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
diffAnaLimma(qData, samplesData, labels, condition1, condition2)
```
diffAnaSave

Returns a MSnSet object with the results of the differential analysis performed with limma package.

Description

This method returns a MSnSet object with the results of differential analysis.

Usage

diffAnaSave(obj, data, method = "limma", condition1, condition2,
            threshold_pVal = 1e-60, threshold_logFC = 0, fdr = 0,
            calibrationMethod = "pounds")

Arguments

obj  An object of class MSnSet.
data  The result of the differential analysis processed by diffAna
method  The method used for differential analysis. Available choices are: "limma", "Welch"
condition1  A vector containing the names (some values of the slot "Label" of pData()) of
             the first condition.
condition2  A vector containing the names (some values of the slot "Label" of pData()) of
             the second condition.
threshold_pVal  A float that indicates the threshold on p-value choosen to discriminate differential proteins.
threshold_logFC  A float that indicates the threshold on log(Fold Change) to discriminated differential proteins.
fdr  The FDR based on the values of threshold_pVal and threshold_logFC
 calibrationMethod  The calibration method used to compute the calibration plot

Value

A MSnSet

Author(s)

Alexia Dorffer, Samuel Wieczorek

Examples

data(UPSpep25)
condition1 <- '25fmol'
condition2 <- '10fmol'
limma <- wrapper.diffAnaLimma(UPSpep25, condition1, condition2)
obj <- diffAnaSave(UPSpep25, limma, "limma", condition1, condition2)
Description

Plots a volcanoplot after the differential analysis. Typically, the log of Fold Change is represented on the X-axis and the log10 of the p-value is drawn on the Y-axis. When the threshold_pVal and the threshold_logFC are set, two lines are drawn respectively on the y-axis and the X-axis to visually distinguish between differential and non differential data.

Usage

diffAnaVolcanoplot(logFC = NULL, pVal = NULL, threshold_pVal = 1e-60, threshold_logFC = 0, conditions = NULL)

Arguments

logFC A vector of the log(fold change) values of the differential analysis.
pVal A vector of the p-value values returned by the differential analysis.
threshold_pVal A floating number which represents the p-value that separates differential and non-differential data.
threshold_logFC A floating number which represents the log of the Fold Change that separates differential and non-differential data.
conditions A list of the names of condition 1 and 2 used for the differential analysis.

Value

A volcanoplot

Author(s)

Florence Combes, Samuel Wieczorek

Examples

data(UPSpep25)
condition1 <- '25fmol'
condition2 <- '10fmol'
data <- wrapper.diffAnaLimma(UPSpep25, condition1, condition2)
diffAnaVolcanoplot(data$logFC, data$P.Value)
**diffAnaWelch**

*Performs a differential analysis on a MSnSet object using the Welch t-test*

**Description**

Computes differential analysis on an MSnSet object, using the Welch t-test (`t.test`{stats}).

**Usage**

```r
diffAnaWelch(qData, labels, condition1, condition2)
```

**Arguments**

- `qData` A dataframe that contains quantitative data.
- `labels` A vector of the conditions (labels) (one label per sample).
- `condition1` A vector containing the names of the conditions qData as condition 1
- `condition2` A vector containing the names of the conditions considered as condition 2

**Value**

A dataframe with two slots: P.Value (for the p-value) and logFC (the log of the Fold Change).

**Author(s)**

Florence Combes, Samuel Wieczorek

**Examples**

```r
data(UPSpep25)
condition1 <- '25fmol'
condition2 <- '10fmol'
qData <- Biobase::exprs(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
diffAnaWelch(qData, labels, condition1, condition2)
```

---

**getIndicesConditions**

*Gets the conditions indices.*

**Description**

Returns a list for the two conditions where each slot is a vector of indices for the samples.

**Usage**

```r
getIndicesConditions(labels, cond1, cond2)
```
getIndicesOfLinesToRemove

**Arguments**

labels A vector of strings containing the column "Label" of the pData().
cond1 A vector of Labels (a slot in the pData() table) for the condition 1.
cond2 A vector of Labels (a slot in the pData() table) for the condition 2.

**Value**

A list with two slots iCond1 and iCond2 containing respectively the indices of samples in the pData() table of the dataset.

**Author(s)**

Florence Combes, Samuel Wieczorek

**Examples**

data(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
getIndicesConditions(labels, "25fmol", "10fmol")

getIndicesOfLinesToRemove

Get the indices of the lines to delete, based on a prefix string

**Description**

This function returns the indice of the lines to delete, based on a prefix string

**Usage**

getIndicesOfLinesToRemove(obj, idLine2Delete = NULL, prefix = NULL)

**Arguments**

obj An object of class MSnSet.

idLine2Delete The name of the column that correspond to the data to filter

prefix A character string that is the prefix to find in the data

**Value**

A vector of integers.

**Author(s)**

Samuel Wieczorek

**Examples**

data(UPSpep25)
getIndicesOfLinesToRemove(UPSpep25, "Potential.contaminant", prefix="+")
**getNumberOf**  
*Number of lines with prefix*

**Description**  
Returns the number of lines, in a given column, where content matches the prefix.

**Usage**  
`getNumberOf(obj, name = NULL, prefix = NULL)`

**Arguments**
- `obj` An object of class `MSnSet`.
- `name` The name of a column.
- `prefix` A string

**Value**  
An integer

**Author(s)**  
Samuel Wieczorek

**Examples**
```r
data(UPSppep25)
getNumberOf(UPSppep25, "Potential.contaminant", "+")
```

**getNumberOfEmptyLines**  
*Returns the number of empty lines in the data*

**Description**  
Returns the number of empty lines in a matrix.

**Usage**  
`getNumberOfEmptyLines(qData)`

**Arguments**
- `qData` A matrix corresponding to the quantitative data.

**Value**  
An integer
getPaletteForLabels

Author(s)

Samuel Wieczorek

Examples

data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
getNumberOfEmptyLines(qData)

Description

Selects colors for the plots in DAPAR based on the different conditions in the dataset. The palette is derived from the brewer palette "Dark2" (see RColorBrewer).

Usage

getPaletteForLabels(labels)

Arguments

labels A vector of labels (strings).

Value

A palette designed for the data manipulated in DAPAR

Author(s)

Florence Combes, Samuel Wieczorek

Examples

data(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
getPaletteForLabels(labels)
getPaletteForReplicates

Palette for plot the replicates in DAPAR

Description
Selects colors for the plots in DAPAR based on the replicates in the dataset. The palette is derived from the brewer palette "Dark2" (see RColorBrewer).

Usage
getPaletteForReplicates(nColors)

Arguments
nColors The desired number of colors

Value
A palette designed for the data manipulated in DAPAR

Author(s)
Samuel Wieczorek

Examples
data(UPSpep25)
n <- nrow(Biobase::pData(UPSpep25))
getPaletteForLabels(5)

getPourcentageOfMV
Percentage of missing values

Description
Returns the percentage of missing values in the quantitative data (exprs() table of the dataset).

Usage
getPourcentageOfMV(obj)

Arguments
obj An object of class MSnSet.

Value
A floating number
getProteinsStats

Author(s)
Florence Combes, Samuel Wieczorek

Examples

data(UPSpep25)
getPourcentageOfMV(UPSpep25)

getProteinsStats
computes the number of proteins that are only defined by specific peptides, shared peptides or a mixture of two.

Description
This function computes the number of proteins that are only defined by specific peptides, shared peptides or a mixture of two.

Usage
getProteinsStats(matUnique, matShared)

getProcessingInfo

Returns the contains of the slot processing of an object of class MSnSet

Description
Returns the contains of the slot processing of an object of class MSnSet.

Usage
getProcessingInfo(obj)

Arguments

obj
An object (peptides) of class MSnbase.

Value
The slot processing of obj@processingData

Author(s)
Samuel Wieczorek

Examples

data(UPSpep25)
getProcessingInfo(UPSpep25)
GraphPepProt

Arguments

matUnique The adjacency matrix with only specific peptides.
matShared The adjacency matrix with both specific and shared peptides.

Value

A list

Author(s)

Samuel Wieczorek

Examples

data(UPSpep25)
protID <- "Protein.group.IDs"
MShared <- BuildAdjacencyMatrix(UPSpep25, protID, FALSE)
MUnique <- BuildAdjacencyMatrix(UPSpep25, protID, TRUE)
getProteinsStats(MUnique, MShared)

---

GraphPepProt  
*Function to create a histogram that shows the repartition of peptides w.r.t. the proteins*

Description

Method to create a plot with proteins and peptides on a MSnSet object (peptides)

Usage

GraphPepProt(mat)

Arguments

mat An adjacency matrix.

Value

A histogram

Author(s)

Alexia Dorffer, Samuel Wieczorek

Examples

data(UPSpep25)
mat <- BuildAdjacencyMatrix(UPSpep25, "Protein.group.IDs")
GraphPepProt(mat)
heatmap.DAPAR

This function is inspired from the function `heatmap.2` that displays quantitative data in the `exprs()` table of an object of class `MSnSet`. For more information, please refer to the help of the `heatmap.2` function.

Description

Heatmap inspired by the heatmap.2 function.

Usage

```r
heatmap.DAPAR(x, col = heat.colors(100), srtCol = NULL, labCol = NULL, 
labRow = NULL, key = TRUE, key.title = NULL, main = NULL, 
ylab = NULL)
```

Arguments

- `x` A dataframe that contains quantiative data.
- `col` colors used for the image. Defaults to heat colors (heat.colors).
- `srtCol` angle of column labels, in degrees from horizontal
- `labCol` character vectors with column labels to use.
- `labRow` character vectors with row labels to use.
- `key` logical indicating whether a color-key should be shown.
- `key.title` main title of the color key. If set to NA no title will be plotted.
- `main` main title; default to none.
- `ylab` y-axis title; default to none.

Value

A heatmap

Author(s)

Samuel Wieczorek

Examples

```r
data(testWithoutNA)
qData <- Biobase::exprs(testWithoutNA)
heatmapD(qData)
```
This function is a wrapper to heatmap.2 that displays quantitative data in the exprs() table of an object of class MSnSet

Description

Heatmap of the quantitative proteomic data of a MSnSet object

Usage

heatmapD(qData, distance = "euclidean", cluster = "average", dendro = FALSE)

Arguments

- qData: A dataframe that contains quantitative data.
- distance: The distance used by the clustering algorithm to compute the dendrogram. See help(heatmap.2).
- cluster: the clustering algorithm used to build the dendrogram. See help(heatmap.2).
- dendro: A boolean to indicate if the dendrogram has to be displayed

Value

A heatmap

Author(s)

Florence Combes, Samuel Wieczorek

Examples

data(testWithoutNA)
qData <- Biobase::exprs(testWithoutNA)
heatmapD(qData)

limmaCompleteTest

Computes a hierarchical differential analysis

Description

This function is a limmaCompleteTest

Usage

limmaCompleteTest(qData, Conditions, RepBio, RepTech, Contrast = 1)
### MeanPeptides

**Arguments**

- `qData` A matrix of quantitative data, without any missing values.
- `Conditions` A vector of factor which indicates the name of the biological condition for each replicate.
- `RepBio` A vector of factor which indicates the number of the bio rep for each replicate.
- `RepTech` A vector of factor which indicates the number of the tech rep for each replicate.
- `Contrast` Indicates if the test consists of the comparison of each biological condition versus each of the other ones (Contrast=1; for example H0:”C1=C2” vs H1:”C1!=C2”, etc.) or each condition versus all others (Contrast=2; e.g. H0:”C1=(C2+C3)/2” vs H1:”C1!=(C2+C3)/2”, etc. if there are three conditions).

**Value**

fdsfdgfdg

**Author(s)**

Quentin Giai-Gianetto

**Examples**

```r
data(UPSpep25)
obj <- wrapper.mvImputation(UPSpep25, "QRILC")
condition1 <- '25fmol'
condition2 <- '10fmol'
qData <- Biobase::exprs(obj)
RepBio <- RepTech <- factor(1:6)
conds <- factor(c(rep(condition1, 3), (rep(condition2, 3))))
limma <- limmaCompleteTest(qData, conds, RepBio, RepTech)
```

---

**MeanPeptides**

*Compute the intensity of proteins as the mean of the intensities of their peptides.*

**Description**

This function computes the intensity of proteins as the mean of the intensities of their peptides.

**Usage**

`MeanPeptides(matAdj, expr)`

**Arguments**

- `matAdj` An adjacency matrix in which lines and columns correspond respectively to peptides and proteins.
- `expr` A matrix of intensities of peptides

**Value**

A matrix of intensities of proteins
**mvFilter**

**Author(s)**
Alexia Dorffer

**Examples**
```
data(UPSpep25)
protID <- "Protein.group.IDs"
matAdj <- BuildAdjacencyMatrix(UPSpep25, protID, FALSE)
MeanPeptides(matAdj, Biobase::exprs(UPSpep25))
```

---

**Description**
Filters the lines of `exprs()` table with conditions on the number of missing values. The user chooses the minimum amount of intensities that is acceptable and the filter delete lines that do not respect this condition. The condition may be on the whole line or condition by condition.

**Usage**
```
mvFilter(obj, type, th, processText = NULL)
```

**Arguments**
- `obj` An object of class `MSnSet` containing quantitative data.
- `type` Method used to choose the lines to delete. Values are: "none", "wholeMatrix", "allCond", "atLeastOneCond"
- `th` An integer value of the threshold
- `processText` A string to be included in the `MSnSet` object for log.

**Details**
The different methods are: "wholeMatrix": given a threshold `th`, only the lines that contain at least `th` values are kept. "allCond": given a threshold `th`, only the lines which contain at least `th` values for each of the conditions are kept. "atLeastOneCond": given a threshold `th`, only the lines that contain at least `th` values, and for at least one condition, are kept.

**Value**
An instance of class `MSnSet` that have been filtered.

**Author(s)**
Florence Combes, Samuel Wieczorek

**Examples**
```
data(UPSpep25)
mvFilter(UPSpep25, "wholeMatrix", 2)
```
mvFilterFromIndices  Filter lines in the matrix of intensities w.r.t. some criteria

Description
Filters the lines of `exprs()` table with conditions on the number of missing values. The user chooses the minimum amount of intensities that is acceptable and the filter delete lines that do not respect this condition. The condition may be on the whole line or condition by condition.

Usage
```r
mvFilterFromIndices(obj, keepThat = NULL, processText = NULL)
```

Arguments
- `obj` An object of class `MSnSet` containing quantitative data.
- `keepThat` A vector of integers which are the indices of lines to keep.
- `processText` A string to be included in the `MSnSet` object for log.

Details
The different methods are: "wholeMatrix": given a threshold \( th \), only the lines that contain at least \( th \) values are kept. "allCond": given a threshold \( th \), only the lines which contain at least \( th \) values for each of the conditions are kept. "atLeastOneCond": given a threshold \( th \), only the lines that contain at least \( th \) values, and for at least one condition, are kept.

Value
An instance of class `MSnSet` that have been filtered.

Author(s)
Florence Combes, Samuel Wieczorek

Examples
```r
data(UPSpep25)
mvFilter(UPSpep25, c(1:10))
```

mvFilterGetIndices  Filter lines in the matrix of intensities w.r.t. some criteria

Description
Returns the indices of the lines of `exprs()` table to delete w.r.t. the conditions on the number of missing values. The user chooses the minimum amount of intensities that is acceptable and the filter delete lines that do not respect this condition. The condition may be on the whole line or condition by condition.
Usage

`mvFilterGetIndices(obj, type, th)`

Arguments

- **obj**: An object of class `MSnSet` containing quantitative data.
- **type**: Method used to choose the lines to delete. Values are: "none", "wholeMatrix", "allCond", "atLeastOneCond"
- **th**: An integer value of the threshold

Details

The different methods are: "wholeMatrix": given a threshold `th`, only the lines that contain at least `th` values are kept. "allCond": given a threshold `th`, only the lines which contain at least `th` values for each of the conditions are kept. "atLeastOneCond": given a threshold `th`, only the lines that contain at least `th` values, and for at least one condition, are kept.

Value

An vector of indices that correspond to the lines to keep.

Author(s)

Florence Combes, Samuel Wieczorek

Examples

```r
data(UPSpep25)
mvFilterGetIndices(UPSpep25, "wholeMatrix", 2)
```

---

**mvHisto**

Histogram of missing values

Description

This method plots a histogram of missing values.

Usage

`mvHisto(qData, samplesData, labels, indLegend = "auto", showValues = FALSE)`

Arguments

- **qData**: A dataframe that contains quantitative data.
- **samplesData**: A dataframe where lines correspond to samples and columns to the meta-data for those samples.
- **labels**: A vector of the conditions (labels) (one label per sample).
- **indLegend**: The indices of the column name's in `pData()` tab
- **showValues**: A logical that indicates whether numeric values should be drawn above the bars.
mvImage

Value
A histogram

Author(s)
Florence Combes, Samuel Wieczorek

Examples
data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
samplesData <- Biobase::pData(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]

mvHisto(qData, samplesData, labels, indLegend="auto", showValues=TRUE)

Description
Plots a heatmap of the quantitative data. Each column represents one of the conditions in the object of class MSnSet and the color is proportional to the mean of intensity for each line of the dataset. The lines have been sorted in order to visualize easily the different number of missing values. A white square is plotted for missing values.

Usage
mvImage(qData, labels)

Arguments
qData A dataframe that contains quantitative data.
labels A vector of the conditions (labels) (one label per sample).

Value
A heatmap

Author(s)
Samuel Wieczorek, Thomas Burger

Examples
data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]

mvImage(qData, labels)
mvImputation  

**Missing values imputation from a matrix**

**Description**

This method is a wrapper to the `imputeLCMD` package adapted to a matrix.

**Usage**

```r
mvImputation(qData, method)
```

**Arguments**

- **qData**
  A dataframe that contains quantitative data.
- **method**
  The imputation method to be used. Choices are QRILC, KNN, BPCA and MLE.

**Value**

The matrix imputed

**Author(s)**

Samuel Wieczorek

**Examples**

```r
data(UPSpec25)
qData <- Biobase::exprs(UPSpec25)
mvImputation(qData, "QRILC")
```

---

mvPerLinesHisto  

**Bar plot of missing values per lines**

**Description**

This method plots a bar plot which represents the distribution of the number of missing values (NA) per lines (ie proteins).

**Usage**

```r
mvPerLinesHisto(qData, samplesData, indLegend = "auto", showValues = FALSE)
```

**Arguments**

- **qData**
  A dataframe that contains the data to plot.
- **samplesData**
  A dataframe which contains informations about the replicates.
- **indLegend**
  The indice of the column name’s in `pData()` tab
- **showValues**
  A logical that indicates wether numeric values should be drawn above the bars.
mvPerLinesHistoPerCondition

Description

This method plots a bar plot which represents the distribution of the number of missing values (NA) per lines (ie proteins) and per conditions.

Usage

mvPerLinesHistoPerCondition(qData, samplesData, indLegend = "auto",
                               showValues = FALSE)

Arguments

qData A dataframe that contains quantitative data.
samplesData A dataframe where lines correspond to samples and columns to the meta-data for those samples.
indLegend The indice of the column name’s in pData() tab
showValues A logical that indicates wether numeric values should be drawn above the bars.

Value

A bar plot

Author(s)

Samuel Wieczorek

Examples

data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
samplesData <- Biobase::pData(UPSpep25)
mvPerLinesHisto(qData, samplesData)
**mvTypePlot**

*Distribution of missing values with respect to intensity values*

**Description**

This method plots a scatter plot which represents the distribution of missing values. The colors correspond to the different conditions (slot Label in in the dataset of class `MSnSet`). The x-axis represents the mean of intensity for one condition and one entity in the dataset (i.e. a protein) whereas the y-axis counts the number of missing values for this entity and the considered condition. The data have been jittered for an easier visualization.

**Usage**

```r
mvTypePlot(qData, labels, threshold = 0)
```

**Arguments**

- `qData`: A dataframe that contains quantitative data.
- `labels`: A vector of the conditions (labels) (one label per sample).
- `threshold`: An integer for the intensity that delimits MNAR and MCAR missing values.

**Value**

A scatter plot

**Author(s)**

Florence Combes, Samuel Wieczorek

**Examples**

```r
data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
mvTypePlot(qData, labels, threshold=0)
```

---

**normalizeD**

*Normalisation*

**Description**

Provides several methods to normalize data from a matrix. They are organized in four main families: Strong Rescaling, Median Centering, Mean Centering, Mean Centering Scaling. For the first family, two sub-categories are available: the sum by columns and the quantiles method. For the three other families, two categories are available: "Overall" which means that the value for each protein (i.e. line in the expression data tab) is computed over all the samples; "within conditions" which means that the value for each protein (i.e. line in the matrix) is computed condition by condition.

**Usage**

```r
normalizeD(qData, labels, family, method)
```
pepAgregate

Arguments

- **qData**: A dataframe that contains quantitative data.
- **labels**: A vector of strings containing the column "Label" of the pData().
- **family**: One of the following: Global Rescaling, Median Centering, Mean Centering, Mean Centering Scaling.
- **method**: "Overall" or "within conditions".

Value

A matrix normalized

Author(s)

Florence Combes, Samuel Wieczorek

Examples

data(UPSpep25)
qData <- Biobase::exprs(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
normalizeD(qData, labels, "Median Centering", "within conditions")

pepAgregate

Function aggregate peptides to proteins

Description

Method to aggregate with a method peptides to proteins on a MSnSet object (peptides)

Usage

pepAgregate(obj.pep, protID, method = "sum overall", matAdj = NULL, n = NULL)

Arguments

- **obj.pep**: An object (peptides) of class MSnbase.
- **protID**: The name of proteins ID column
- **method**: The method used to aggregate the peptides into proteins. Values are "sum", "mean" or "sum on top n": do the sum / mean of intensity on all peptides belonging to proteins. Default is "sum"
- **matAdj**: An adjacency matrix
- **n**: The number of peptides considered for the aggregation.

Value

An object of class MSnbase with proteins
proportionConRev

Author(s)
Alexia Dorffer, Samuel Wieczorek

Examples
data(UPSpep25)
protID <- "Protein.group.IDs"
mat <- BuildAdjacencyMatrix(UPSpep25, protID, TRUE)
pepAggragate(UPSpep25, protID, "sum overall", mat)

---

proportionConRev  Barplot of proportion of contaminants and reverse

Description
Plots a barplot of proportion of contaminants and reverse

Usage
proportionConRev(obj, idContaminants = NULL, prefixContaminants = NULL,
idReverse = NULL, prefixReverse = NULL)

Arguments
obj  An object of class MSnSet.
idContaminants  The name of a column of Contaminants
prefixContaminants  The prefix to identify contaminants
idReverse  The name of a column of Reverse
prefixReverse  The prefix to identify Reverse

Value
A barplot

Author(s)
Samuel Wieczorek

Examples
data(UPSpep25)
pref <- "+
proportionConRev(UPSpep25, "Potential.contaminant", pref, "Reverse", pref)
sumPeptides

removeLines

Remove lines in the dataset based on a prefix string.

Description
This function removes lines in the dataset based on a prefix string.

Usage
removeLines(obj, idLine2Delete = NULL, prefix = NULL)

Arguments

obj An object of class MSnSet.

idLine2Delete The name of the column that correspond to the data to filter

prefix A character string that is the prefix to find in the data

Value
An object of class MSnSet.

Author(s)
Samuel Wieczorek

Examples

data(UPSpep25)
removeLines(UPSpep25, "Potential.contaminant")
removeLines(UPSpep25, "Reverse")

SumPeptides

Compute the intensity of proteins with the sum of the intensities of their peptides.

Description
This function computes the intensity of proteins based on the sum of the intensities of their peptides.

Usage

SumPeptides(matAdj, expr)

Arguments

matAdj An adjacency matrix in which lines and columns correspond respectively to peptides and proteins.

expr A matrix of intensities of peptides
Value

A matrix of intensities of proteins

Author(s)

Alexia Dorffler

Examples

data(UPSpep25)
protID <- "Protein.group.IDs"
M <- BuildAdjacencyMatrix(UPSpep25, protID, FALSE)
SumPeptides(M, Biobase::exprs(UPSpep25))

test  Test dataset

description

Partial (small) dataset for unit tests containing missing values.

Format

An object of class MSnSet

testWithoutNA  Test dataset

description

Partial (small) dataset for unit tests without any missing values.

Format

An object of class MSnSet
**Description**

This function computes the intensity of proteins as the sum of the intensities of their \( n \) best peptides.

**Usage**

\[
\text{TopnPeptides}(\text{matAdj}, \text{expr}, n)
\]

**Arguments**

- \( \text{matAdj} \): An adjacency matrix in which lines and columns correspond respectively to peptides and proteins.
- \( \text{expr} \): A matrix of intensities of peptides.
- \( n \): The maximum number of peptides used to aggregate a protein.

**Value**

A matrix of intensities of proteins.

**Author(s)**

Alexia Dorffer

**Examples**

```r
data(UPSpep25)
protID <- "Protein.group.IDs"
matAdj <- BuildAdjacencyMatrix(UPSpep25, protID, FALSE)
TopnPeptides(matAdj, Biobase::exprs(UPSpep25), 3)
```

---

**UPSpep25**

**UPSpep25 dataset**

This dataset is the final outcome of a quantitative mass spectrometry-based proteomic analysis of two samples containing different concentrations of 48 human proteins (UPS1 standard from Sigma-Aldrich) within a constant yeast background (see Giai Gianetto et al. (2016) for details). It contains the abundance values of the different human and yeast peptides identified and quantified in these two conditions. The two conditions represent the measured abundances of peptides when respectively 25fmol and 10fmol of UPS1 human proteins were mixed with the yeast extract before mass spectrometry analyses. Three technical replicates were acquired for each condition.

To identify and quantify peptides, spectra were searched using MaxQuant (version 1.5.1.2) against the Uniprot database, the UPS database and the frequently observed contaminants database. Maximum false discovery rates were set to 0.01 by employing a reverse database strategy.

The dataset is either available as a CSV file (see inst/extdata/UPSpep25.txt), or as a MSnSet structure (UPSpep25). In the latter case, the quantitative data are those of the raw intensities.
**Usage**

```r
data(UPSpep25)
```

**Format**

An object of class `MSnSet` related to peptide quantification. It contains 6 samples divided into two conditions (25fmol and 10fmol) and 13918 peptides.

The data frame `exprs(UPSpep25)` contains six columns that are the quantitation of peptides for the six replicates.

The data frame `fData(UPSpep25)` contains the meta data about the peptides.

The data frame `pData(UPSpep25)` contains the experimental design and gives few informations about the samples.

**Value**

An object of class `MSnSet`.

**References**


**Description**

Builds a densityplot of the variance of entities in the `exprs()` table of a object. The variance is calculated for each condition (Label) present in the dataset (see the slot ‘Label’ in the `pData()` table)

**Usage**

```r
varianceDistD(qData, labels = NULL)
```

**Arguments**

- `qData` A dataframe that contains quantitative data.
- `labels` A vector of the conditions (labels) (one label per sample).

**Value**

A density plot

**Author(s)**

Florence Combes, Samuel Wieczorek
violinPlotD

See Also
densityPlotD.

Examples

```r
data(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
varianceDistD(UPSpep25)
```

---

**violinPlotD**

*Builds a violinplot from a dataframe*

**Description**

ViolinPlot for quantitative proteomics data

**Usage**

```r
violinPlotD(qData, dataForXAxis = NULL, labels = NULL, 
group2Color = "Condition")
```

**Arguments**

- `qData` A dataframe that contains quantitative data.
- `dataForXAxis` A vector containing the types of replicates to use as X-axis. Available values are: Label, Analyt.Rep, Bio.Rep and Tech.Rep. Default is "Label".
- `labels` A vector of the conditions (labels) (one label per sample).
- `group2Color` A string that indicates how to color the replicates: one color per condition (value "Condition") or one color per replicate (value "Replicate"). Default value is by Condition.

**Value**

A violinplot

**Author(s)**

Florence Combes, Samuel Wieczorek

**See Also**

densityPlotD

**Examples**

```r
data(UPSpep25)
library(vioplot)
qData <- Biobase::exprs(UPSpep25)
types <- c("Label","Analyt.Rep")
dataForXAxis <- Biobase::pData(UPSpep25)[,types]
labels <- Biobase::pData(UPSpep25)[,"Label"]
violinPlotD(qData, dataForXAxis, labels)
```
wrapper.boxPlotD

Wrapper to the boxplotD function on an object MSnSet

Description
This function is a wrapper for using the boxPlotD function with objects of class MSnSet.

Usage

wrapper.boxPlotD(obj, dataForXAxis = "Label", group2Color = "Condition")

Arguments

obj
An object of class MSnSet.
dataForXAxis
A vector of strings containing the names of columns in pData() to print labels on X-axis (Default is "Label").

group2Color
A string that indicates how to color the replicates: one color per condition (value "Condition") or one color per replicate (value "Replicate"). Default value is by Condition.

Value
A boxplot

Author(s)
Florence Combes, Samuel Wieczorek

See Also

wrapper.densityPlotD

Examples

data(UPSpep25)
types <- c("Label","Analyt.Rep")
wrapper.boxPlotD(UPSpep25, types)

wrapper.compareNormalizationD

Builds a plot from a dataframe

Description
Wrapper to the function that plot to compare the quantitative proteomics data before and after normalization.

Usage

wrapper.compareNormalizationD(objBefore, objAfter, labelsForLegend = NULL, indData2Show = NULL, group2Color = "Condition")
wrapper.corrMatrixD

### Arguments

- **objBefore**: A dataframe that contains quantitative data before normalization.
- **objAfter**: A dataframe that contains quantitative data after normalization.
- **labelsForLegend**: A vector of the conditions (labels) (one label per sample).
- **indData2Show**: A vector of the indices of the columns to show in the plot. The indices are those of indices of the columns int the data.frame qDataBefore.
- **group2Color**: A string that indicates how to color the replicates: one color per condition (value "Condition") or one color per replicate (value "Replicate"). Default value is by Condition.

### Value

A plot

### Author(s)

Samuel Wieczorek

### Examples

```r
data(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
objAfter <- wrapper.normalizeD(UPSpep25, "Median Centering", "within conditions")
wrapper.compareNormalizationD(UPSpep25, objAfter, labels)
```

---

**wrapper.corrMatrixD**

Displays a correlation matrix of the quantitative data of the exprs()
table

### Description

Builds a correlation matrix based on a **MSnSet** object.

### Usage

```r
wrapper.corrMatrixD(obj, rate = 5)
```

### Arguments

- **obj**: An object of class **MSnSet**.
- **rate**: A float that defines the gradient of colors.

### Value

A colored correlation matrix

### Author(s)

Alexia Dorffer
Examples

data(UPSpep25)
wrapper.corrMatrixD(UPSpep25)

wrapper.densityPlotD Builds a densityplot from an object of class MSnSet

Description

This function is a wrapper for using the densityPlotD function with objects of class MSnSet.

Usage

wrapper.densityPlotD(obj, labelsForLegend = NULL, indData2Show = NULL, group2Color = "Condition")

Arguments

obj An object of class MSnSet.
labelsForLegend A vector of labels to show in densityplot.
indData2Show A vector of the indices of the columns to show in the plot. The indices are those of indices of the columns int the data frame qDataBefore in the density plot.
group2Color A string that indicates how to color the replicates: one color per condition (value "Condition") or one color per replicate (value "Replicate"). Default value is by Condition.

Value

A density plot

Author(s)

Alexia Dorffer

See Also

wrapper.boxPlotD, wrapper.varianceDistD

Examples

data(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
wrapper.densityPlotD(UPSpep25, labels)
**wrapper.diffAnaLimma**  
*Performs differential analysis on an MSnSet object, calling the limma package functions*

**Description**  
Method to perform differential analysis on a MSnSet object (calls the limma package function).

**Usage**  
`wrapper.diffAnaLimma(obj, condition1, condition2)`

**Arguments**
- `obj` : An object of class MSnSet.
- `condition1` : A vector that contains the names of the conditions considered as condition 1.
- `condition2` : A vector that contains the names of the conditions considered as condition 2.

**Value**
A dataframe as returned by the limma package

**Author(s)**
Alexia Dorffer

**Examples**
```
data(UPSpep25)
condition1 <- c('25fmol', '10fmol')
condition2 <- c('25fmol', '10fmol')
wrapper.diffAnaLimma(UPSpep25, condition1, condition2)
```

---

**wrapper.diffAnaWelch**  
*Performs a differential analysis on a MSnSet object using the Welch t-test*

**Description**  
Computes differential analysis on a MSnSet object, using the Welch t-test (t.test(stats)).

**Usage**  
`wrapper.diffAnaWelch(obj, condition1, condition2)`

**Arguments**
- `obj` : An object of class MSnSet.
- `condition1` : A vector containing the names of the conditions considered as condition 1.
- `condition2` : A vector containing the names of the conditions considered as condition 2.
Value

A dataframe with two slots: `P.Value` (for the p-value) and `logFC` (the log of the Fold Change).

Author(s)

Alexia Dorffer

Examples

data(UPSpep25)
condition1 <- '25fmol'
condition2 <- '10fmol'
wrapper.diffAnaWelch(UPSpep25, condition1, condition2)

wrapper.heatmapD

This function is a wrapper to `heatmap.2` that displays quantitative data in the `exprs()` table of an object of class `MSnSet`

Description

Builds a heatmap of the quantitative proteomic data of a `MSnSet` object.

Usage

wrapper.heatmapD(obj, distance = "euclidean", cluster = "average", dendro = FALSE)

Arguments

obj An object of class `MSnSet`.
distance The distance used by the clustering algorithm to compute the dendrogram. See `help(heatmap.2)`.
cluster the clustering algorithm used to build the dendrogram. See `help(heatmap.2)`
dendro A boolean to indicate if the dendrogram has to be displayed

Value

A heatmap

Author(s)

Alexia Dorffer

Examples

data(testWithoutNA)
wrapper.heatmapD(testWithoutNA)
wrapper.mvHisto  Histogram of missing values from a MSnSet object

Description
This method plots from a MSnSet object a histogram of missing values.

Usage
wrapper.mvHisto(obj, indLegend = "auto", showValues = FALSE)

Arguments
- obj: An object of class MSnSet.
- indLegend: The indices of the column name's in pData() tab.
- showValues: A logical that indicates whether numeric values should be drawn above the bars.

Value
A histogram

Author(s)
Alexia Dorffer

Examples
data(UPSpep25)
wrapper.mvHisto(UPSpep25, showValues=TRUE)

wrapper.mvImage  Heatmap of missing values from a MSnSet object

Description
Plots a heatmap of the quantitative data. Each column represent one of the conditions in the object of class MSnSet and the color is proportional to the mean of intensity for each line of the dataset. The lines have been sorted in order to visualize easily the different number of missing values. A white square is plotted for missing values.

Usage
wrapper.mvImage(obj)

Arguments
- obj: An object of class MSnSet.

Value
A heatmap
 Author(s)  
Alexia Dorffer

Examples  
data(UPSpep25)  
wrapper.mvImage(UPSpep25)

wrapper.mvImputation  
Missing values imputation from a MSnSet object

Description  
This method is a wrapper to the imputeLCMD package adapted to objects of class MSnSet.

Usage  
wrapper.mvImputation(obj, method)

Arguments  

  obj  
  An object of class MSnSet.

  method  
  The imputation method to be used. Choices are QRILC, KNN, BPCA and MLE.

Value  
The object obj which has been imputed

Author(s)  
Alexia Dorffer

Examples  
data(UPSpep25)  
wrapper.mvImputation(UPSpep25, "QRILC")

wrapper.mvPerLinesHisto  
Histogram of missing values per lines from an object MSnSet

Description  
This method is a wrapper to plots from a MSnSet object a histogram which represents the distribution of the number of missing values (NA) per lines (ie proteins).

Usage  
wrapper.mvPerLinesHisto(obj, indLegend = "auto", showValues = FALSE)
wrapper.mvPerLinesHistoPerCondition

Arguments

obj          An object of class MSnSet.
indLegend    The indice of the column name’s in pData() tab.
showValues   A logical that indicates wether numeric values should be drawn above the bars.

Value

A histogram

Author(s)

Alexia Dorffer

Examples

data(UPSpep25)
wrapper.mvPerLinesHisto(UPSpep25)

Description

This method is a wrapper to plots from a MSnSet object a bar plot which represents the distribution of the number of missing values (NA) per lines (ie proteins) and per conditions.

Usage

wrapper.mvPerLinesHistoPerCondition(obj, indLegend = "auto",
                                      showValues = FALSE)

Arguments

obj          An object of class MSnSet.
indLegend    The indice of the column name’s in pData() tab.
showValues   A logical that indicates wether numeric values should be drawn above the bars.

Value

A bar plot

Author(s)

Samuel Wieczorek

Examples

data(UPSpep25)
wrapper.mvPerLinesHistoPerCondition(UPSpep25)
wrapper.mvTypePlot

Distribution of missing values with respect to intensity values from a MSnSet object

Description
This method plots a scatter plot which represents the distribution of missing values. The colors correspond to the different conditions (slot Label in in the dataset of class MSnSet). The x-axis represent the mean of intensity for one condition and one entity in the dataset (i.e., a protein) whereas the y-axis count the number of missing values for this entity and the considered condition. The data have been jittered for an easier visualization.

Usage
wrapper.mvTypePlot(obj, threshold = 0)

Arguments
obj An object of class MSnSet.
threshold An integer for the intensity that delimits MNAR and MCAR missing values.

Value
A scatter plot

Author(s)
Florence Combes, Samuel Wieczorek

Examples
data(UPSpep25)
wrapper.mvTypePlot(UPSpep25)

wrapper.normalizeD Normalisation

Description
Provides several methods to normalize quantitative data from a MSnSet object. They are organized in four main families: Strong Rescaling, Median Centering, Mean Centering, Mean Centering Scaling. For the first family, two sub-categories are available: the sum by columns and the quantiles method. For the three other families, two categories are available: "Overall" which means that the value for each protein (i.e., line in the expression data tab) is computed over all the samples; "within conditions" which means that the value for each protein (i.e., line in the exprs() data tab) is computed condition by condition.

Usage
wrapper.normalizeD(obj, family, method)
Arguments

- **obj**: An object of class `MSnSet`.
- **family**: One of the following: Global Rescaling, Median Centering, Mean Centering, Mean Centering Scaling.
- **method**: "Overall" or "within conditions".

Value

An instance of class `MSnSet` where the quantitative data in the `exprs()` tab has been normalized.

Author(s)

Alexia Dorffer

Examples

```r
data(UPSpep25)
wrapper.normalizeD(UPSpep25, "Median Centering", "within conditions")
```

---

**wrapper.varianceDistD**

*Distribution of variance of proteins*

Description

Builds a densityplot of the variance of entities in the `exprs()` table of an object `MSnSet`. The variance is calculated for each condition (Label) present in the dataset (see the slot 'Label' in the `pData()` table).

Usage

```r
wrapper.varianceDistD(obj)
```

Arguments

- **obj**: An object of class `MSnSet`.

Value

A density plot

Author(s)

Alexia Dorffer

See Also

`wrapper.densityPlotD`

Examples

```r
data(UPSpep25)
wrapper.varianceDistD(UPSpep25)
```
**wrapper.violinPlotD**  
*Wrapper to the violinPlotD function on an object MSnSet*

**Description**
This function is a wrapper for using the violinPlotD function with objects of class MSnSet.

**Usage**

```r
wrapper.violinPlotD(obj, dataForXAxis = "Label", group2Color = "Condition")
```

**Arguments**

- `obj`  
  An object of class MSnSet.

- `dataForXAxis`  
  A vector of strings containing the names of columns in pData() to print labels on X-axis (Default is "Label").

- `group2Color`  
  A string that indicates how to color the replicates: one color per condition (value "Condition") or one color per replicate (value "Replicate"). Default value is by Condition.

**Value**
A violin plot

**Author(s)**
Samuel Wieczorek

**See Also**

- `wrapper.densityPlotD`, `wrapper.boxPlotD`

**Examples**

```r
data(UPSpep25)
library(vioplot)
types <- c("Label","Analyt.Rep")
wrapper.violinPlotD(UPSpep25, types)
```

---

**wrapperCalibrationPlot**

*Performs a calibration plot on an MSnSet object, calling the cp4p package functions.*

**Description**
This function is a wrapper to the calibration.plot method of the cp4p package for use with MSnSet objects.
Usage

wrapperCalibrationPlot(vPVal, pi0Method = "pounds")

Arguments

vPVal  A dataframe that contains quantitative data.
pi0Method  A vector of the conditions (labels) (one label per sample).

Value

A plot

Author(s)

Samuel Wieczorek

Examples

data(UPSpep25)
condition1 <- '25fmol'
condition2 <- '10fmol'
qData <- Biobase::exprs(UPSpep25)
labels <- Biobase::pData(UPSpep25)[,"Label"]
diffAnaWelch(qData, labels, condition1, condition2)

writeMSnsetToExcel  This function exports a MSnSet object to a Excel file.

Description

This function exports a MSnSet data object to a Excel file. Each of the three data.frames in the MSnSet object (i.e. experimental data, phenoData and metaData are respectively integrated into separate sheets in the Excel file).

Usage

writeMSnsetToExcel(obj, filename)

Arguments

obj  An object of class MSnSet.
filename  A character string for the name of the Excel file.

Value

A Excel file (.xlsx)

Author(s)

Samuel Wieczorek
Examples

data(UPS pep25)
writeMSnsetToExcel(UPS pep25, "foo")
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