

# Package ‘DAPAR’

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**Type** Package

**Title** Tools for the Differential Analysis of Proteins Abundance with R

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**Author** Samuel Wieczorek [cre,aut],  
Florence Combes [aut],  
Thomas Burger [aut],  
Cosmin Lazar [ctb],  
Alexia Dorffer [ctb]

**Maintainer** Samuel Wieczorek <samuel.wieczorek@cea.fr>

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

**License** Artistic-2.0

**VignetteBuilder** knitr

**Depends** R (>= 3.5), foreach, parallel, doParallel

**Suggests** BiocGenerics, Biobase, testthat, BiocStyle

**Imports** MSnbase, RColorBrewer, stats, preprocessCore, Cairo, png, lattice, reshape2, gplots, pcaMethods, ggplot2, limma, knitr, tmvtnorm, norm, impute, stringr, grDevices, graphics, openxlsx, utils, cp4p (>= 0.3.5), scales, Matrix, vioplot, imp4p (>= 0.8), highcharter (>= 0.5.0), DAPARdata (>= 1.15.9), siggenes, graph, lme4, readxl, clusterProfiler, dplyr, tidy, AnnotationDbi, tidyverse, vsn, FactoMineR, factoextra, visNetwork, igraph

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*addOriginOfValue*

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---

<code>addOriginOfValue</code>	<i>Sets the OriginOfValues dataframe</i>
-------------------------------	--

---

### Description

Sets the OriginOfValues dataframe in the fData table

### Usage

```
addOriginOfValue(obj, index = NULL)
```

### Arguments

<code>obj</code>	An object of class MSnSet
<code>index</code>	A list of integer xxxxxxx

### Value

An instance of class MSnSet.

### Author(s)

Samuel Wieczorek

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
addOriginOfValue(Exp1_R25_pept)
```

---

<code>aggregateIter</code>	<code>xxxx</code>
----------------------------	-------------------

---

### Description

Method to xxxxx

### Usage

```
aggregateIter(obj.pep, X, init.method = "Sum", method = "Mean",
n = NULL)
```

**Arguments**

obj.pep	xxxxx
X	xxxx
init.method	xxxxx
method	xxxxx
n	xxxx

**Value**

A protein object of class MSnset

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(Exp1_R25_pept[1:1000], protID, FALSE)
aggregateIter(Exp1_R25_pept[1:1000],X=X)
```

---

aggregateIterParallel xxxx

---

**Description**

Method to xxxxx

**Usage**

```
aggregateIterParallel(obj.pep, X, init.method = "Sum", method = "Mean",
  n = NULL)
```

**Arguments**

obj.pep	xxxxx
X	xxxx
init.method	xxxxx
method	xxxxx
n	xxxx

**Value**

xxxxxx

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
protID <- "Protein_group_IDs"
obj.pep <- Exp1_R25_pept[1:1000]
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
aggregateIterParallel(obj.pep, X)
```

---

aggregateMean	<i>Compute the intensity of proteins as the mean of the intensities of their peptides.</i>
---------------	--

---

**Description**

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

**Usage**

```
aggregateMean(obj.pep, X)
```

**Arguments**

obj.pep	A peptide object of class MSnset
X	An adjacency matrix in which lines and columns correspond respectively to peptides and proteins.

**Value**

A matrix of intensities of proteins

**Author(s)**

Alexia Dorffer

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj.pep <- Exp1_R25_pept[1:1000]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
aggregateMean(obj.pep, X)
```

---

aggregateSum	<i>Compute the intensity of proteins with the sum of the intensities of their peptides.</i>
--------------	---

---

### Description

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

### Usage

```
aggregateSum(obj.pep, X)
```

### Arguments

obj.pep	A matrix of intensities of peptides
X	An adjacency matrix in which lines and columns correspond respectively to peptides and proteins.

### Value

A matrix of intensities of proteins

### Author(s)

Alexia Dorffer

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
protID <- "Protein_group_IDs"
obj.pep <- Exp1_R25_pept[1:1000]
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
DAPAR::aggregateSum(obj.pep, X)
```

---

aggregateTopn	<i>Compute the intensity of proteins as the sum of the intensities of their n best peptides.</i>
---------------	--

---

### Description

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

### Usage

```
aggregateTopn(obj.pep, X, method = "Mean", n = 10)
```



**Arguments**

obj.pep	A matrix of intensities of peptides
X	An adjacency matrix in which lines and columns correspond respectively to peptides and proteins.
method	xxx
n	The maximum number of peptides used to aggregate a protein.

**Value**

A matrix of intensities of proteins

**Author(s)**

Alexia Dorffer, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj.pep <- Exp1_R25_pept[1:1000]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
DAPAR::aggregateTopn(obj.pep, X, n=3)
```

---

barplotEnrichGO\_HC     *A barplot that shows the result of a GO enrichment, using the package highcharter*

---

**Description**

A barplot of GO enrichment analysis

**Usage**

```
barplotEnrichGO_HC(ego, maxRes = 5, title = NULL)
```

**Arguments**

ego	The result of the GO enrichment, provides either by the function <code>enrichGO</code> in the package <code>DAPAR</code> or the function <code>enrichGO</code> of the package <code>clusterProfiler</code>
maxRes	The maximum number of categories to display in the plot
title	The title of the plot

**Value**

A barplot

**Author(s)**

Samuel Wiczorek

---

barplotGroupGO_HC	<i>A barplot which shows the result of a GO classification, using the package highcharter</i>
-------------------	---

---

**Description**

A barplot of GO classification analysis

**Usage**

```
barplotGroupGO_HC(ggo, maxRes = 5, title = "")
```

**Arguments**

ggo	The result of the GO classification, provides either by the function group_GO in the package DAPAR or the function groupGO in the package <a href="#">clusterProfiler</a>
maxRes	An integer which is the maximum number of classes to display in the plot
title	The title of the plot

**Value**

A barplot

**Author(s)**

Samuel Wiczorek

---

boxPlotD	<i>Builds a boxplot from a dataframe</i>
----------	--

---

**Description**

Boxplot for quantitative proteomics data

**Usage**

```
boxPlotD(obj, legend = NULL, palette = NULL)
```

**Arguments**

obj	xxx
legend	A vector of the conditions (one string per sample).
palette	xxx

**Value**

A boxplot

**Author(s)**

Florence Combes, Samuel Wiczorek

**See Also**

[densityPlotD](#)

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
boxPlotD(Exp1_R25_pept)
```

---

boxPlotD\_HC

*Builds a boxplot from a dataframe using the library highcharter*

---

**Description**

Boxplot for quantitative proteomics data using the library highcharter

**Usage**

```
boxPlotD_HC(obj, legend = NULL, palette = NULL)
```

**Arguments**

obj	xxx
legend	A vector of the conditions (one condition per sample).
palette	xxx

**Value**

A boxplot

**Author(s)**

Samuel Wiczorek

**See Also**

[densityPlotD\\_HC](#)

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
legend <- Biobase::pData(Exp1_R25_pept)[,"Sample.name"]
boxPlotD_HC(Exp1_R25_pept, legend)
```

---

BuildAdjacencyMatrix *Function matrix of appartenance 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 Wiczorek, Alexia Dorffer

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
BuildAdjacencyMatrix(Exp1_R25_pept[1:1000], "Protein_group_IDs", TRUE)
```

---

BuildColumnToProteinDataset

*creates a column for the protein dataset after agregation 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, proteinNames)
```

**Arguments**

peptideData	A data.frame of meta data of peptides. It is the fData of the MSnset object.
matAdj	The adjacency matrix used to agregate 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.
proteinNames	The names of the protein in the new dataset (i.e. rownames)

**Value**

A vector

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
protID <- "Protein_group_IDs"
obj.pep <- Exp1_R25_pept[1:1000]
M <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
data <- Biobase::fData(obj.pep)
protData <- DAPAR::aggregateMean(obj.pep, M)
name <- "Protein_group_IDs"
proteinNames <- rownames(Biobase::fData(protData))
BuildColumnToProteinDataset(data, M, name,proteinNames )
```

---

BuildColumnToProteinDataset\_par

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

---

**Description**

This function creates a column for the protein dataset after agregation by using the previous peptide dataset. It is a parallel version of the function BuildColumnToProteinDataset

**Usage**

```
BuildColumnToProteinDataset_par(peptideData, matAdj, columnName,
  proteinNames)
```

**Arguments**

peptideData	A data.frame of meta data of peptides. It is the fData of the MSnset object.
matAdj	The adjacency matrix used to agregate 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.
proteinNames	The names of the protein in the new dataset (i.e. rownames)

**Value**

A vector

**Author(s)**

Samuel Wieczorek

**Examples**

```
## Not run:
require(DAPARdata)
data(Exp1_R25_pept)
protID <- "Protein_group_IDs"
obj.pep <- Exp1_R25_pept[1:1000]
M <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
data <- Biobase::fData(obj.pep)
protData <- DAPAR::aggregateSum(obj.pep, M)
name <- "Protein_group_IDs"
proteinNames <- rownames(Biobase::fData(protData))
BuildColumnToProteinDataset_par(data, M, name,proteinNames )

## End(Not run)
```

---

buildGraph

*Display a CC*

---

**Description**

Display a CC

**Usage**

```
buildGraph(The.CC, X)
```

**Arguments**

The.CC	A cc (a list)
X	xxxxx

**Value**

A plot

**Author(s)**

Thomas Burger, Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
X <- BuildAdjacencyMatrix(Exp1_R25_pept, "Protein_group_IDs", FALSE)
ll <- get.pep.prot.cc(X)
g <- buildGraph(ll[[1]], X)
```

---

check.conditions	<i>Check if the design is valid</i>
------------------	-------------------------------------

---

**Description**

This function check the validity of the conditions

**Usage**

```
## S3 method for class 'conditions'  
check(conds)
```

**Arguments**

conds            A vector

**Value**

A list

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)  
data(Exp1_R25_pept)  
check.conditions(Biobase::pData(Exp1_R25_pept)$Condition)
```

---

check.design	<i>Check if the design is valid</i>
--------------	-------------------------------------

---

**Description**

This function check the validity of the experimental design

**Usage**

```
## S3 method for class 'design'  
check(sTab)
```

**Arguments**

sTab            The data.frame which correspond to the pData function of MSnbase

**Value**

A boolean

**Author(s)**

Thomas Burger, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
check.design(Biobase::pData(Exp1_R25_pept)[,1:3])
```

---

compareNormalizationD *Builds a plot from a dataframe*

---

**Description**

Plot to compare the quantitative proteomics data before and after normalization

**Usage**

```
compareNormalizationD(qDataBefore, qDataAfter, condsForLegend = NULL,
  indData2Show = NULL, palette = NULL)
```

**Arguments**

qDataBefore	A dataframe that contains quantitative data before normalization.
qDataAfter	A dataframe that contains quantitative data after normalization.
condsForLegend	A vector of the conditions (one condition 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 data.frame qDataBefore.
palette	xxx

**Value**

A plot

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qDataBefore <- Biobase::exprs(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
objAfter <- wrapper.normalized(Exp1_R25_pept,"QuantileCentering","within conditions")
compareNormalizationD(qDataBefore, Biobase::exprs(objAfter), conds)
```



---

`compareNormalizationD_HC`

*Builds a plot from a dataframe. Same as `compareNormalizationD` but uses the library `highcharter`*

---

### Description

Plot to compare the quantitative proteomics data before and after normalization using the library `highcharter`

### Usage

```
compareNormalizationD_HC(qDataBefore, qDataAfter, condsForLegend = NULL,
  indData2Show = NULL, palette = NULL)
```

### Arguments

<code>qDataBefore</code>	A dataframe that contains quantitative data before normalization.
<code>qDataAfter</code>	A dataframe that contains quantitative data after normalization.
<code>condsForLegend</code>	A vector of the conditions (one condition per sample).
<code>indData2Show</code>	A vector of the indices of the columns to show in the plot. The indices are those of indices of the columns in the data.frame <code>qDataBefore</code> .
<code>palette</code>	xxx

### Value

A plot

### Author(s)

Samuel Wiczorek

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
qDataBefore <- Biobase::exprs(obj)
conds <- Biobase::pData(obj)[,"Condition"]
objAfter <- wrapper.normalized(obj,"QuantileCentering","within conditions")
compareNormalizationD_HC(qDataBefore, Biobase::exprs(objAfter), conds)
```

---

```
compute.t.tests      xxxxx
```

---

## Description

This function is xxxxxx

## Usage

```
## S3 method for class 't.tests'
compute(qData, sTab, contrast = "OnevsOne",
        type = "Student")
```

## Arguments

qData	A matrix of quantitative data, without any missing values.
sTab	xxxx
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).
type	xxxxx

## Value

A list of two items : logFC and P\_Value; both are dataframe. The first one contains the logFC values of all the comparisons (one column for one comparison), the second one contains the pvalue of all the comparisons (one column for one comparison). The names of the columns for those two dataframes are identical and correspond to the description of the comparison.

## Author(s)

Florence Combes, Samuel Wiczorek

## Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
sTab <- Biobase::pData(obj)
qData <- Biobase::exprs(obj)
ttest <- compute.t.tests(qData,sTab , "OnevsOne")
```

---

corrMatrixD	<i>Displays a correlation matrix of the quantitative data of the exprs() table.</i>
-------------	---

---

**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.
gradientRate	The rate parameter to control the exponential law for the gradient of colors

**Value**

A colored correlation matrix

**Author(s)**

Florence Combes, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
samplesData <- Biobase::pData(Exp1_R25_pept)
corrMatrixD(qData, samplesData)
```

---

corrMatrixD_HC	<i>Displays a correlation matrix of the quantitative data of the exprs() table.</i>
----------------	---

---

**Description**

Correlation matrix based on a MSnSet object. Same as the function [corrMatrixD](#) but uses the package `highcharter`

**Usage**

```
corrMatrixD_HC(object, samplesData = NULL, rate = 0.5)
```

**Arguments**

object	The result of the cor function.
samplesData	A dataframe in which lines correspond to samples and columns to the meta-data for those samples.
rate	The rate parameter to control the exponential law for the gradient of colors

**Value**

A colored correlation matrix

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
samplesData <- Biobase::pData(Exp1_R25_pept)
res <- cor(qData,use = 'pairwise.complete.obs')
corrMatrixD_HC(res, samplesData)
```

---

CountPep

*Compute the number of peptides used to aggregate proteins*

---

**Description**

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

**Usage**

```
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**

```
library(DAPARdata)
data(Exp1_R25_pept)
protID <- "Protein_group_IDs"
M <- BuildAdjacencyMatrix(Exp1_R25_pept[1:1000], 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 meta-data.

**Usage**

```
createMSnset(file, metadata = NULL, indExpData, indFData,
  indiceID = NULL, indexForOriginOfValue = NULL, logData = FALSE,
  replaceZeros = FALSE, pep_prot_data = NULL, proteinId = NULL,
  versions = NULL)
```

**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)
indexForOriginOfValue	xxxxxxxxxxx
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
proteinId	xxxx
versions	A list of the following items: Prostar_Version, DAPAR_Version peptides or proteins.

**Value**

An instance of class MSnSet.

**Author(s)**

Florence Combes, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
require(Matrix)
exprsFile <- system.file("extdata", "Exp1_R25_pept.txt", package="DAPARdata")
metadataFile <- system.file("extdata", "samples_Exp1_R25.txt", package="DAPARdata")
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, indexForOriginOfValue = NULL, pep_prot_data
```

---

CVDistD

*Distribution of CV of entities*

---

**Description**

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

**Usage**

```
CVDistD(qData, conds = NULL, palette = NULL)
```

**Arguments**

<code>qData</code>	A dataframe that contains quantitative data.
<code>conds</code>	A vector of the conditions (one condition per sample).
<code>palette</code>	xxx

**Value**

A density plot

**Author(s)**

Florence Combes, Samuel Wiczorek

**See Also**

[densityPlotD](#).

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
CVDistD(Biobase::exprs(Exp1_R25_pept), conds)
```

---

CVDistD_HC	<i>Distribution of CV of entities</i>
------------	---------------------------------------

---

**Description**

Builds a densityplot of the CV of entities in the `exprs()` table of a object. The CV is calculated for each condition present in the dataset (see the slot 'Condition' in the `pData()` table) Same as the function `CVDistD` but uses the package `highcharter`

**Usage**

```
CVDistD_HC(qData, conds = NULL, palette = NULL)
```

**Arguments**

<code>qData</code>	A dataframe that contains quantitative data.
<code>conds</code>	A vector of the conditions (one condition per sample).
<code>palette</code>	xxx

**Value**

A density plot

**Author(s)**

Samuel Wieczorek

**See Also**

[densityPlotD](#).

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
CVDistD_HC(Biobase::exprs(Exp1_R25_pept), conds)
```

---

`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 = "")
```

**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.

**Value**

An instance of class MSnSet that have been filtered.

**Author(s)**

Florence Combes, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
deleteLinesFromIndices(Exp1_R25_pept, c(1:10))
```

---

densityPlotD                    *Builds a densityplot from a dataframe*

---

**Description**

Densityplot of quantitative proteomics data over samples.

**Usage**

```
densityPlotD(obj, legend = NULL, palette = NULL)
```

**Arguments**

obj                    xxx  
legend                 A vector of the conditions (one condition per sample).  
palette                xxx

**Value**

A density plot

**Author(s)**

Florence Combes, Samuel Wiczorek

**See Also**

[boxPlotD](#), [CVDistD](#)



**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
densityPlotD(Exp1_R25_pept, conds)
```

---

densityPlotD_HC	<i>Builds a densityplot from a dataframe</i>
-----------------	--

---

**Description**

Densityplot of quantitative proteomics data over samples. Same as the function [densityPlotD](#) but uses the package `highcharter`

**Usage**

```
densityPlotD_HC(obj, legend = NULL, palette = NULL)
```

**Arguments**

obj	xxx
legend	A vector of the conditions (one condition per sample).
palette	xxx

**Value**

A density plot

**Author(s)**

Samuel Wieczorek

**See Also**

[boxPlotD](#), [CVDistD](#)

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
densityPlotD_HC(Exp1_R25_pept)
```

---

diffAnaComputeFDR	<i>Computes the FDR corresponding to the p-values of the differential analysis using</i>
-------------------	--

---

### 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{stats}`.

### Usage

```
diffAnaComputeFDR(logFC, pval, threshold_PVal = 0, threshold_LogFC = 0,
  pi0Method = 1)
```

### Arguments

<code>logFC</code>	The result (logFC values) of the differential analysis processed by <a href="#">limmaCompleteTest</a>
<code>pval</code>	The result (p-values) of the differential analysis processed by <a href="#">limmaCompleteTest</a>
<code>threshold_PVal</code>	The threshold on p-value to distinguish between differential and non-differential data
<code>threshold_LogFC</code>	The threshold on log(Fold Change) to distinguish between differential and non-differential data
<code>pi0Method</code>	The parameter <code>pi0.method</code> of the method <code>adjust.p</code> in the package <code>cp4p</code>

### Value

The computed FDR value (floating number)

### Author(s)

Samuel Wieczorek

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
limma <- limmaCompleteTest(qData, sTab)
diffAnaComputeFDR(limma$logFC[,1], limma$P_Value[,1])
```

---

`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**

```
diffAnaGetSignificant(obj)
```

**Arguments**

`obj` An object of class MSnSet.

**Value**

A MSnSet

**Author(s)**

Alexia Dorffer

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
allComp <- limmaCompleteTest(qData,sTab)
data <- list(logFC=allComp$logFC[1], P_Value = allComp$P_Value[1])
obj <- diffAnaSave(obj, allComp, data)
signif <- diffAnaGetSignificant(obj)
```

---

`diffAnaSave` *Returns a MSnSet object with the results of the differential analysis performed with [limma](#) package.*

---

**Description**

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

**Usage**

```
diffAnaSave(obj, allComp, data = NULL, th_pval = 0, th_logFC = 0)
```

**Arguments**

obj	An object of class MSnSet.
allComp	A list of two items which is the result of the function wrapper.limmaCompleteTest or xxxx
data	The result of the differential analysis processed by <a href="#">limmaCompleteTest</a>
th_pval	xxx
th_logFC	xxx

**Value**

A MSnSet

**Author(s)**

Alexia Dorffer, Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
allComp <- limmaCompleteTest(qData,sTab)
data <- list(logFC=allComp$logFC[1], P_Value = allComp$P_Value[1])
diffAnaSave(obj, allComp, data)
```

---

diffAnaVolcanoplot      *Volcanoplot of the differential analysis*

---

**Description**

Plots a volcano plot after the differential analysis. Typically, the log of Fold Change is represented on the X-axis and the log<sub>10</sub> 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, colors = 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.

colors                xxx

**Value**

A volcanoplot

**Author(s)**

Florence Combes, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
limma <- limmaCompleteTest(qData,sTab)
diffAnaVolcanoplot(limma$logFC[,1], limma$P_Value[,1])
```

---

diffAnaVolcanoplot\_rCharts

*Volcanoplot of the differential analysis*

---

**Description**

Plots an interactive 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. With the use of the package Highcharter, a customizable tooltip appears when the user put the mouse's pointer over a point of the scatter plot.

**Usage**

```
diffAnaVolcanoplot_rCharts(df, threshold_pVal = 1e-60,
  threshold_logFC = 0, conditions = NULL, clickFunction = NULL,
  palette = NULL, swap = FALSE)
```

**Arguments**

df                    A dataframe which contains the following slots : x : a vector of the log(fold change) values of the differential analysis, y : a vector of the p-value values returned by the differential analysis. index : a vector of the rownames of the data. This dataframe must has been built with the option stringsAsFactors set to FALSE. There may be additional slots which will be used to show informations

in the tooltip. The name of these slots must begin with the prefix "tooltip\_". It will be automatically removed in the plot.

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.
clickFunction	A string that contains a JavaScript function used to show info from slots in df. The variable this.index refers to the slot named index and allows to retrieve the right row to show in the tooltip.
palette	xxx
swap	A boolean that indicates if the conditions have been swapped

### Value

An interactive volcano plot

### Author(s)

Samuel Wieczorek

### Examples

```
library(highcharter)
library(tidyverse)
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
data <- limmaCompleteTest(qData,sTab)
df <- data.frame(x=data$logFC, y = -log10(data$P_Value), index = as.character(rownames(obj)))
colnames(df) <- c("x", "y", "index")
tooltipSlot <- c("Sequence", "Score")
df <- cbind(df,Biobase::fData(obj)[tooltipSlot])
colnames(df) <- gsub(".", "_", colnames(df), fixed=TRUE)
if (ncol(df) > 3){
  colnames(df)[4:ncol(df)] <-
    paste("tooltip_", colnames(df)[4:ncol(df)], sep="")
}
hc_clickFunction <- JS("function(event) {Shiny.onInputChange('eventPointClicked', [this.index]+'_'+ [this.se
cond <- c("25fmol", "10fmol")
diffAnaVolcanoplot_rCharts(df, 2.5, 1, cond,hc_clickFunction)
```

---

display.CC.visNet	<i>Display a CC</i>
-------------------	---------------------

---

**Description**

Display a CC

**Usage**

```
display.CC.visNet(g, layout = layout_nicely, obj = NULL,  
  prot.tooltip = NULL, pept.tooltip = NULL)
```

**Arguments**

g	A cc (a list)
layout	xxxxx
obj	xxx
prot.tooltip	xxx
pept.tooltip	xxx

**Value**

A plot

**Author(s)**

Thomas Burger, Samuel Wiczorek

**Examples**

```
require(DAPARdata)  
data(Exp1_R25_pept)  
X <- BuildAdjacencyMatrix(Exp1_R25_pept, "Protein_group_IDs", FALSE)  
ll <- get.pep.prot.cc(X)  
g <- buildGraph(ll[[1]], X)  
display.CC.visNet(g)
```

---

enrich_GO	<i>Calculates GO enrichment classes for a given list of proteins/genes ID. It results an enrichResult instance.</i>
-----------	---

---

**Description**

This function is a wrapper to the function `enrichGO` from the package `clusterProfiler`. Given a vector of genes/proteins, it returns an `enrichResult` instance.

**Usage**

```
enrich_GO(data, idFrom, orgdb, ont, readable = FALSE, pval, universe)
```

**Arguments**

data	A vector of ID (among ENSEMBL, ENTREZID, GENENAME, REFSEQ, UNIGENE, UNIPROT -can be different according to organisms)
idFrom	character indicating the input ID format (among ENSEMBL, ENTREZID, GENENAME, REFSEQ, UNIGENE, UNIPROT)
orgdb	annotation Bioconductor package to use (character format)
ont	One of "MF", "BP", and "CC" subontologies
readable	TRUE or FALSE (default FALSE)
pval	The qvalue cutoff (same parameter as in the function <code>enrichGO</code> of the package <code>clusterProfiler</code> )
universe	a list of ID to be considered as the background for enrichment calculation

**Value**

A groupGOResult instance.

**Author(s)**

Florence Combes

**Examples**

```
require(DAPARdata)
data(Exp1_R25_prot)
univ<-univ_AnnotDbPkg("org.Sc.sgd.db") #univ is the background
ego<-enrich_GO(data=fData(Exp1_R25_prot)$Protein.IDs, idFrom="UNIPROT",
  orgdb="org.Sc.sgd.db",ont="MF", pval=0.05, universe = univ)
```

---

finalizeAggregation     *Finalizes the aggregation process*

---

**Description**

Method to finalize the aggregation process

**Usage**

```
finalizeAggregation(obj.pep, pepData, protData, X, lib.loc = NULL)
```

**Arguments**

obj.pep	A peptide object of class MSnset
pepData	xxxx
protData	xxxxx
X	An adjacency matrix in which lines and columns correspond respectively to peptides and proteins.
lib.loc	A list of two items (lib.loc\$Prostar.loc and lib.loc\$DAPAR.loc) to provide the location of the installed packages



**Value**

A protein object of class MSnset

**Author(s)**

Samuel Wieczorek

---

findMECBlock	<i>Finds the LAPALA into a MSnSet object</i>
--------------	--

---

**Description**

This method finds the LAPALA in a dataset.

**Usage**

```
findMECBlock(obj)
```

**Arguments**

obj                    An object of class MSnSet.

**Value**

A data.frame that contains the indexes of LAPALA

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
lapala <- findMECBlock(obj)
```

---

formatLimmaResult	<i>xxx</i>
-------------------	------------

---

**Description**

This function is xxx

**Usage**

```
formatLimmaResult(fit, conds, contrast)
```

**Arguments**

```
fit          xxxx
conds       xxxx
contrast    xxxx
```

**Value**

A list of two dataframes : logFC and P\_Value. The first one contains the logFC values of all the comparisons (one column for one comparison), the second one contains the pvalue of all the comparisons (one column for one comparison). The names of the columns for those two dataframes are identical and correspond to the description of the comparison.

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
limma <- limmaCompleteTest(qData,sTab)
```

---

fudge2LRT

*Heuristic to choose the value of the hyperparameter (fudge factor) used to regularize the variance estimator in the likelihood ratio statistic*

---

**Description**

fudge2LRT: heuristic to choose the value of the hyperparameter (fudge factor) used to regularize the variance estimator in the likelihood ratio statistic (as implemented in samLRT). We follow the heuristic described in [1] and adapt the code of the fudge2 function in the siggene R package. [1] Tusher, Tibshirani and Chu, Significance analysis of microarrays applied to the ionizing radiation response, PNAS 2001 98: 5116-5121, (Apr 24).

**Usage**

```
fudge2LRT(lmm.res.h0, lmm.res.h1, cc, n, p, s, alpha = seq(0, 1, 0.05),
  include.zero = TRUE)
```

**Arguments**

lmm.res.h0 a vector of object containing the estimates (used to compute the statistic) under H0 for each connected component. If the fast version of the estimator was used (as implemented in this package), lmm.res.h0 is a vector containing averages of squared residuals. If a fixed effect model was used, it is a vector of lm objects and if a mixed effect model was used it is a vector or lmer object.

lmm.res.h1	similar to lmm.res.h0, a vector of object containing the estimates (used to compute the statistic) under H1 for each protein.
cc	a list containing the indices of peptides and proteins belonging to each connected component.
n	the number of samples used in the test
p	the number of proteins in the experiment
s	a vector containing the maximum likelihood estimate of the variance for the chosen model. When using the fast version of the estimator implemented in this package, this is the same thing as the input lmm.res.h1. For other models (e.g. mixed models) it can be obtained from samLRT.
alpha	A vector of proportions used to build candidate values for the regularizer. We use quantiles of s with these proportions. Default to seq(0, 1, 0.05)
include.zero	logical value indicating if 0 should be included in the list of candidates. Default to TRUE.

**Value**

(same as the fudge2 function of siggene): s.zero: the value of the fudge factor s0. alpha.hat: the optimal quantile of the 's' values. If s0=0, 'alpha.hat' will not be returned. vec.cv: the vector of the coefficients of variations. Following Tusher et al. (2001), the optimal 'alpha' quantile is given by the quantile that leads to the smallest CV of the modified test statistics. msg: a character string summarizing the most important information about the fudge factor.

**Author(s)**

Thomas Burger, Laurent Jacob

---

get.pep.prot.cc      *Build the list of connex composant of the adjacency matrix*

---

**Description**

Method to build the list of connex composant of the adjacency matrix

**Usage**

```
get.pep.prot.cc(X)
```

**Arguments**

X                      An adjacency matrix

**Value**

A list of CC

**Author(s)**

Thomas Burger, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
X <- BuildAdjacencyMatrix(Exp1_R25_pept[1:1000], "Protein_group_IDs", FALSE)
ll <- get.pep.prot.cc(X)
```

---

GetDetailedNbPeptides *Computes the detailed number of peptides for each protein*

---

**Description**

Method to compute the detailed number of quantified peptides for each protein

**Usage**

```
GetDetailedNbPeptides(X)
```

**Arguments**

X                    An adjacency matrix

**Value**

A data.frame

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj.pep <- Exp1_R25_pept[1:1000]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
GetDetailedNbPeptides(X)
```

---

GetDetailedNbPeptidesUsed  
*Computes the detailed number of peptides used for aggregating each protein*

---

**Description**

Method to compute the detailed number of quantified peptides used for aggregating each protein

**Usage**

```
GetDetailedNbPeptidesUsed(X, pepData)
```

**Arguments**

X                    An adjacency matrix  
pepData            A data.frame of quantitative data

**Value**

A list of two items

**Author(s)**

```
Samuel Wieczorek require(DAPARdata) data(Exp1_R25_pept) obj.pep <- Exp1_R25_pept[1:1000]
protID <- "Protein_group_IDs" X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE) require(DAPARdata)
data(Exp1_R25_pept) obj.pep <- Exp1_R25_pept[1:1000] protID <- "Protein_group_IDs" X <-
BuildAdjacencyMatrix(obj.pep, protID, FALSE) GetDetailedNbPeptidesUsed(X, obj.pep)
```

---

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**

```
getIndicesConditions(conds, cond1, cond2)
```

**Arguments**

conds                A vector of strings containing the column "Condition" of the pData().  
cond1                A vector of Conditions (a slot in the pData() table) for the condition 1.  
cond2                A vector of Conditions (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**

```
require(DAPARdata)
data(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
getIndicesConditions(conds, "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

```
require(DAPARdata)
data(Exp1_R25_pept)
getIndicesOfLinesToRemove(Exp1_R25_pept, "Potential_contaminant", prefix="+")
```

---

getListNbValuesInLines

*Returns the possible number of values in lines in the data*

---

### Description

Returns the possible number of values in lines in a matrix.

### Usage

```
getListNbValuesInLines(obj, type = "wholeMatrix")
```

### Arguments

obj	An object of class MSnSet
type	xxxxxxx

**Value**

An integer

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
getListNbValuesInLines(Exp1_R25_pept)
```

---

GetNbPeptidesUsed	<i>Computes the number of peptides used for aggregating each protein</i>
-------------------	--

---

**Description**

Method to compute the number of quantified peptides used for aggregating each protein

**Usage**

```
GetNbPeptidesUsed(X, pepData)
```

**Arguments**

X	An adjacency matrix
pepData	A data.frame of quantitative data

**Value**

A data.frame

**Author(s)**

Samuel Wieczorek

---

getNumberOf	<i>Number of lines with prefix</i>
-------------	------------------------------------

---

**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**

```
require(DAPARdata)
data(Exp1_R25_pept)
getNumberOf(Exp1_R25_pept, "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

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
getNumberOfEmptyLines(qData)
```



---

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

**Author(s)**

Florence Combes, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
getPourcentageOfMV(Exp1_R25_pept)
```

---

getProcessingInfo      *Returns the contents of the slot processing of an object of class MSnSet*

---

**Description**

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

**Usage**

```
getProcessingInfo(obj)
```

**Arguments**

obj                      An object (peptides) of class MSnSet.

**Value**

The slot processing of obj@processingData

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
getProcessingInfo(Exp1_R25_pept)
```

---

getProteinsStats	<i>Computes the number of proteins that are only defined by specific peptides, shared peptides or a mixture of two.</i>
------------------	---

---

**Description**

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

**Usage**

```
getProteinsStats(matShared)
```

**Arguments**

matShared      The adjacency matrix with both specific and shared peptides.

**Value**

A list

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
protID <- "Protein_group_IDs"
obj <- Exp1_R25_pept[1:1000]
MShared <- BuildAdjacencyMatrix(obj, protID, FALSE)
getProteinsStats(MShared)
```

---

getQuantile4Imp	<i>Quantile imputation value definition</i>
-----------------	---

---

**Description**

This method returns the q-th quantile of each column of an expression set, up to a scaling factor

**Usage**

```
getQuantile4Imp(qData, qval = 0.025, factor = 1)
```

**Arguments**

<code>qData</code>	An expression set containing quantitative values of various replicates
<code>qval</code>	The quantile used to define the imputation value
<code>factor</code>	A scaling factor to multiply the imputation value with

**Value**

A list of two vectors, respectively containing the imputation values and the rescaled imputation values

**Author(s)**

Thomas Burger

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
getQuantile4Imp(qData)
```

---

`getTextForAggregation` *Build the text information for the Aggregation process*

---

**Description**

Builds the text information for the Aggregation process

**Usage**

```
getTextForAggregation(l.params)
```

**Arguments**

<code>l.params</code>	A list of parameters related to the process of the dataset
-----------------------	--

**Value**

A string

**Author(s)**

Samuel Wiczorek

**Examples**

```
params <- list()
getTextForAggregation(params)
```

---

getTextForAnaDiff      *Build the text information for the Aggregation process*

---

**Description**

Build the text information for the differential Analysis process

**Usage**

```
getTextForAnaDiff(l.params)
```

**Arguments**

l.params      A list of parameters related to the process of the dataset

**Value**

A string

**Author(s)**

Samuel Wieczorek

**Examples**

```
getTextForAnaDiff(list(design="OnevsOne",method="Limma"))
```

---

getTextForFiltering      *Build the text information for the filtering process*

---

**Description**

Build the text information for the filtering process

**Usage**

```
getTextForFiltering(l.params)
```

**Arguments**

l.params      A list of parameters related to the process of the dataset

**Value**

A string

**Author(s)**

Samuel Wieczorek

**Examples**

```
getTextForFiltering(list(mvFilterType="wholeMatrix",mvThNA=3))
```

---

`getTextForGOAnalysis` *Build the text information for the Aggregation process*

---

**Description**

Build the text information for the Aggregation process

**Usage**

```
getTextForGOAnalysis(l.params)
```

**Arguments**

`l.params`            A list of parameters related to the process of the dataset

**Value**

A string

**Author(s)**

Samuel Wieczorek

**Examples**

```
getTextForGOAnalysis(list())
```

---

`getTextForHypothesisTest`  
*Build the text information for the hypothesis test process*

---

**Description**

Builds the text information for the hypothesis test process

**Usage**

```
getTextForHypothesisTest(l.params)
```

**Arguments**

`l.params`            A list of parameters related to the process of the dataset

**Value**

A string

**Author(s)**

Samuel Wieczorek

**Examples**

```
params <- list(design='OnevsOne', method='limma')
getTextForHypothesisTest(params)
```

---

```
getTextForNewDataset
```

*Build the text information for a new dataset*

---

**Description**

Build the text information for a new dataset

**Usage**

```
getTextForNewDataset(l.params)
```

**Arguments**

`l.params` A list of parameters related to the process of the dataset

**Value**

A string

**Author(s)**

Samuel Wieczorek

**Examples**

```
getTextForNewDataset(list(filename="foo.MSnet"))
```

---

```
getTextForNormalization
```

*Build the text information for the Normalization process*

---

**Description**

Build the text information for the Normalization process

**Usage**

```
getTextForNormalization(l.params)
```

**Arguments**

`l.params` A list of parameters related to the process of the dataset

**Value**

A string

**Author(s)**

Samuel Wieczorek

**Examples**

```
getTextForNormalization(list(method="SumByColumns"))
```

---

```
getTextForpeptideImputation
```

*Build the text information for the peptide Imputation process*

---

**Description**

Build the text information for the peptide Imputation process

**Usage**

```
getTextForpeptideImputation(l.params)
```

**Arguments**

l.params            A list of parameters related to the process of the dataset

**Value**

A string

**Author(s)**

Samuel Wieczorek

**Examples**

```
params <- list()  
getTextForpeptideImputation(params)
```

---

```
getTextForproteinImputation
```

*Build the text information for the protein Imputation process*

---

**Description**

Build the text information for the Protein Imputation process

**Usage**

```
getTextForproteinImputation(l.params)
```

**Arguments**

l.params            A list of parameters related to the process of the dataset

**Value**

A string

**Author(s)**

Samuel Wiczorek

**Examples**

```
params <- list()
getTextForproteinImputation(params)
```

---

Get_AllComparisons	<i>Returns list that contains a list of the statistical tests performed with DAPAR and recorded in an object of class MSnSet.</i>
--------------------	---

---

**Description**

This method returns a list of the statistical tests performed with DAPAR and recorded in an object of class MSnSet.

**Usage**

```
Get_AllComparisons(obj)
```

**Arguments**

obj                    An object of class MSnSet.

**Value**

A list of two slots: logFC and P\_Value

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
allComp <- limmaCompleteTest(qData, sTab)
data <- list(logFC=allComp$logFC[1], P_Value = allComp$P_Value[1])
obj <- diffAnaSave(obj, allComp, data)
ll <- Get_AllComparisons(obj)
```



---

GOAnalysisSave	<i>Returns an MSnSet object with the results of the GO analysis performed with the functions enrichGO and/or groupGO of the <a href="#">clusterProfiler</a> package.</i>
----------------	--

---

**Description**

This method returns an MSnSet object with the results of the Gene Ontology analysis.

**Usage**

```
GOAnalysisSave(obj, ggo_res = NULL, ego_res = NULL, organism, ontology,
  levels, pvalueCutoff, typeUniverse)
```

**Arguments**

obj	An object of the class MSnSet
ggo_res	The object returned by the function group_GO of the package DAPAR or the function groupGO of the package <a href="#">clusterProfiler</a>
ego_res	The object returned by the function enrich_GO of the package DAPAR or the function enrichGO of the package <a href="#">clusterProfiler</a>
organism	The parameter OrgDb of the functions <a href="#">bitr</a> , <a href="#">groupGO</a> and <a href="#">enrichGO</a>
ontology	One of "MF", "BP", and "CC" subontologies
levels	A vector of the different GO grouping levels to save
pvalueCutoff	The qvalue cutoff (same parameter as in the function enrichGO of the package <a href="#">clusterProfiler</a> )
typeUniverse	The type of background to be used. Values are 'Entire Organism', 'Entire dataset' or 'Custom'. In the latter case, a file should be uploaded by the user

**Value**

An object of the class MSnSet

**Author(s)**

Samuel Wieczorek

---

GraphPepProt	<i>Function to create a histogram that shows the repartition of peptides w.r.t. the proteins</i>
--------------	--

---

**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**

```
require(DAPARdata)
data(Exp1_R25_pept)
mat <- BuildAdjacencyMatrix(Exp1_R25_pept[1:1000], "Protein_group_IDs")
GraphPepProt(mat)
```

---

group_GO	<i>Calculates the GO profile of a vector of genes/proteins at a given level of the Gene Ontology</i>
----------	--

---

**Description**

This function is a wrapper to the function groupGO from the package [clusterProfiler](#). Given a vector of genes/proteins, it returns the GO profile at a specific level. It returns a groupGOResult instance.

**Usage**

```
group_GO(data, idFrom, orgdb, ont, level, readable = FALSE)
```

**Arguments**

data	A vector of ID (among ENSEMBL, ENTREZID, GENENAME, REFSEQ, UNIGENE, UNIPROT -can be different according to organisms)
idFrom	character indicating the input ID format (among ENSEMBL, ENTREZID, GENENAME, REFSEQ, UNIGENE, UNIPROT)
orgdb	annotation Bioconductor package to use (character format)
ont	on which ontology to perform the analysis (MF, BP or CC)
level	level of the ontology to perform the analysis
readable	TRUE or FALSE (default FALSE)

**Value**

GO profile at a specific level

**Author(s)**

Florence Combes

## Examples

```
require(DAPARdata)
data(Exp1_R25_prot)
ggo<-group_G0(data=fData(Exp1_R25_prot)$Protein.IDs, idFrom="UNIPROT",
orgdb="org.Sc.sgd.db", ont="MF", level=2)
```

---

hc\_logFC\_DensityPlot *Density plots of logFC values*

---

## Description

This function show the density plots of Fold Change (the same as calculated by limma) for a list of the comparisons of conditions in a differnetial analysis.

## Usage

```
hc_logFC_DensityPlot(df_logFC, threshold_LogFC = 0, palette = NULL)
```

## Arguments

df_logFC	A dataframe that contains the logFC values
threshold_LogFC	The threshold on log(Fold Change) to distinguish between differential and non-differential data
palette	xxx

## Value

A highcharts density plot

## Author(s)

Samuel Wieczorek

## Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
res <- limmaCompleteTest(qData,sTab)
hc_logFC_DensityPlot(res$logFC, threshold_LogFC=1)
```

---

`hc_mvTypePlot2`*Distribution of Observed values with respect to intensity values*

---

### Description

This method shows density plots which represents the repartition of Partial Observed Values for each replicate in the dataset. The colors correspond to the different conditions (slot Condition 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 observed values for this entity and the considered condition.

### Usage

```
hc_mvTypePlot2(qData, conds, palette = NULL, typeofMV = NULL,  
              title = NULL)
```

### Arguments

<code>qData</code>	A dataframe that contains quantitative data.
<code>conds</code>	A vector of the conditions (one condition per sample).
<code>palette</code>	The different colors for conditions
<code>typeofMV</code>	xxx
<code>title</code>	The title of the plot

### Value

Density plots

### Author(s)

Samuel Wieczorek

### Examples

```
require(DAPARdata)  
data(Exp1_R25_pept)  
qData <- Biobase::exprs(Exp1_R25_pept)  
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]  
hc_mvTypePlot2(qData, conds, title="POV distribution")
```

---

heatmap.DAPAR	<i>This function is inspired from the function <a href="#">heatmap.2</a> that displays quantitative data in the <code>exprs()</code> table of an object of class <code>MSnSet</code>. For more information, please refer to the help of the <code>heatmap.2</code> function.</i>
---------------	--

---

## Description

Heatmap inspired by the `heatmap.2` function.

## Usage

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

## Arguments

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

## Value

A heatmap

## Author(s)

Samuel Wieczorek

## Examples

```
require(DAPARdata)  
data(Exp1_R25_pept)  
obj <- mvFilter(Exp1_R25_pept, "wholeMatrix", 6)  
qData <- Biobase::exprs(obj)  
heatmap.DAPAR(qData)
```

---

heatmapD	<i>This function is a wrapper to <a href="#">heatmap.2</a> that displays quantitative data in the <code>exprs()</code> table of an object of class MSnSet</i>
----------	---

---

**Description**

Heatmap of the quantitative proteomic data of a MSnSet object

**Usage**

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

**Arguments**

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

**Value**

A heatmap

**Author(s)**

Florence Combes, Samuel Wiczorek

**Examples**

```
## Not run:
require(DAPARdata)
data(Exp1_R25_pept)
obj <- mvFilter(Exp1_R25_pept[1:1000], "wholeMatrix", 6)
qData <- Biobase::exprs(obj)
heatmapD(qData)

## End(Not run)
```

---

histPValue_HC	<i>Plots a histogram of p-values</i>
---------------	--------------------------------------

---

**Description**

This function plots a histogram of p-values

**Usage**

```
histPValue_HC(pval_ll, bins = 80, pi0 = 1)
```

**Arguments**

pval\_ll        xxx  
bins            xxx  
pi0            xxx

**Value**

A plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
allComp <- limmaCompleteTest(qData,sTab)
histPValue_HC(allComp$P_Value[1])
```

---

impute.detQuant        *Deterministic imputation*

---

**Description**

This method replaces each missing value by a given value

**Usage**

```
impute.detQuant(qData, values)
```

**Arguments**

qData            An expression set containing quantitative or missing values  
values           A vector with as many elements as the number of columns of qData

**Value**

An imputed dataset

**Author(s)**

Thomas Burger

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
values <- getQuantile4Imp(qData)$shiftedImpVal
impute.detQuant(qData, values)
```

---

impute.pa2

*Missing values imputation from a MSnSet object*


---

**Description**

This method is a variation to the function `impute.pa` from the package `imp4p`.

**Usage**

```
impute.pa2(tab, conditions, q.min = 0, q.norm = 3, eps = 0,
  distribution = "unif")
```

**Arguments**

<code>tab</code>	An object of class <code>MSnSet</code> .
<code>conditions</code>	A vector of conditions in the dataset
<code>q.min</code>	A quantile value of the observed values allowing defining the maximal value which can be generated. This maximal value is defined by the quantile <code>q.min</code> of the observed values distribution minus <code>eps</code> . Default is 0 (the maximal value is the minimum of observed values minus <code>eps</code> ).
<code>q.norm</code>	A quantile value of a normal distribution allowing defining the minimal value which can be generated. Default is 3 (the minimal value is the maximal value minus $qn * \text{median}(\text{sd}(\text{observed values}))$ where <code>sd</code> is the standard deviation of a row in a condition).
<code>eps</code>	A value allowing defining the maximal value which can be generated. This maximal value is defined by the quantile <code>q.min</code> of the observed values distribution minus <code>eps</code> . Default is 0.
<code>distribution</code>	The type of distribution used. Values are <code>unif</code> or <code>beta</code> .

**Value**

The object `obj` which has been imputed

**Author(s)**

Thomas Burger, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.impute.pa2(Exp1_R25_pept[1:1000], distribution="beta")
```



---

```
inner.aggregate.iter  xxxx
```

---

**Description**

Method to xxxxx

**Usage**

```
inner.aggregate.iter(pepData, X, init.method = "Sum", method = "Mean",
  n = NULL)
```

**Arguments**

pepData	xxxxx
X	xxxx
init.method	xxx
method	xxx
n	xxxx

**Value**

xxxxx

**Author(s)**

Samuel Wieczorek require(DAPARdata) data(Exp1\_R25\_pept) protID <- "Protein\_group\_IDs" obj.pep  
 <- Exp1\_R25\_pept[1:1000] X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE) DAPAR::inner.aggregate.iter(exprs(obj.pep), X)

---

```
inner.aggregate.topn  xxxx
```

---

**Description**

Method to xxxxx

**Usage**

```
inner.aggregate.topn(pepData, X, method = "Mean", n = 10)
```

**Arguments**

pepData	A data.frame of quantitative data
X	An adjacency matrix
method	xxxxx
n	xxxxx

**Value**

xxxxx

**Author(s)**

Samuel Wieczorek

---

`inner.mean``xxxx`

---

**Description**

Method to xxxxx

**Usage**`inner.mean(pepData, X)`**Arguments**`pepData` A data.frame of quantitative data`X` An adjacency matrix**Value**

xxxxx

**Author(s)**

Samuel Wieczorek

---

`inner.sum``xxxx`

---

**Description**

Method to xxxxx

**Usage**`inner.sum(pepData, X)`**Arguments**`pepData` A data.frame of quantitative data`X` An adjacency matrix**Value**

A matrix

**Author(s)**

Samuel Wieczorek

---

`is.MV`*Similar to the function `is.na` but focused on the equality with the missing values in the dataset (type 'POV' and 'MEC')*

---

**Description**

Similar to the function `is.na` but focused on the equality with the missing values in the dataset (type 'POV' and 'MEC')

**Usage**`is.MV(data)`**Arguments**`data`            A `data.frame`**Value**

A boolean dataframe

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
data <- Biobase::fData(obj)[,obj@experimentData@other$OriginOfValues]
is.MV(data)
```

---

`is.OfType`*Similar to the function `is.na` but focused on the equality with the parameter 'type'.*

---

**Description**

Similar to the function `is.na` but focused on the equality with the parameter 'type'.

**Usage**`is.OfType(data, type)`

**Arguments**

data	A data.frame
type	The value to search in the dataframe

**Value**

A boolean dataframe

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
data <- Biobase::fData(obj)[,obj@experimentData@other$OriginOfValues]
is.OfType(data, "MEC")
```

---

LH0

xxxxxx

---

**Description**

This function is xxxxxxxx

**Usage**

```
LH0(X, y1, y2)
```

**Arguments**

X	an n.pep*n.prot indicator matrix.
y1	n.pep*n.samples matrice giving the observed counts for
y2	n.pep*n.samples matrice giving the observed counts for

**Value**

xxxxxxxxxxx..

**Author(s)**

Thomas Burger, Laurent Jacob

---

LH0.lm	xxxxxx
--------	--------

---

**Description**

This function is xxxxxxxx

**Usage**

LH0.lm(X, y1, y2)

**Arguments**

X	an n.pep*n.prot indicator matrix.
y1	n.pep*n.samples matrice giving the observed counts for each peptide in each sample from the condition 1
y2	n.pep*n.samples matrice giving the observed counts for each peptide in each sample from the condition 2

**Value**

xxxxxxxxxxx..

**Author(s)**

Thomas Burger, Laurent Jacob

---

LH1	xxxxxx
-----	--------

---

**Description**

This function is xxxxxxxx

**Usage**

LH1(X, y1, y2, j)

**Arguments**

X	an n.pep*n.prot indicator matrix.
y1	n.pep*n.samples matrice giving the observed counts for
y2	n.pep*n.samples matrice giving the observed counts for
j	the index of the protein being tested, ie which has different

**Value**

xxxxxxxxxxx..

**Author(s)**

Thomas Burger, Laurent Jacob

---

LH1.lm                      xxxxxx

---

### Description

This function is xxxxxxxx

### Usage

```
LH1.lm(X, y1, y2, j)
```

### Arguments

X	an n.pep*n.prot indicator matrix.
y1	n.pep*n.samples matrix giving the observed counts for
y2	n.pep*n.samples matrix giving the observed counts for
j	the index of the protein being tested, ie which has different

### Value

xxxxxxxxxxxx..

### Author(s)

Thomas Burger, Laurent Jacob

---

limmaCompleteTest            *Computes a hierarchical differential analysis*

---

### Description

This function is a limmaCompleteTest

### Usage

```
limmaCompleteTest(qData, sTab, comp.type = "OnevsOne")
```

### Arguments

qData	A matrix of quantitative data, without any missing values.
sTab	A dataframe of experimental design (pData()).
comp.type	A string that corresponds to the type of comparison. Values are: 'OnevsOne' and 'OnevsAll'; default is 'OnevsOne'.

### Value

A list of two dataframes : logFC and P\_Value. The first one contains the logFC values of all the comparisons (one column for one comparison), the second one contains the pvalue of all the comparisons (one column for one comparison). The names of the columns for those two dataframes are identical and correspond to the description of the comparison.

**Author(s)**

Thomas Burger, Quentin Giai-Gianetto, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
limma <- limmaCompleteTest(qData,sTab)
```

---

listSheets

*This function returns the list of the sheets names in a Excel file.*

---

**Description**

This function lists all the sheets of an Excel file.

**Usage**

```
listSheets(file)
```

**Arguments**

file            The name of the Excel file.

**Value**

A vector

**Author(s)**

Samuel Wiczorek

---

make.contrast

*Builds the contrast matrix*

---

**Description**

This function builds the contrast matrix

**Usage**

```
make.contrast(design, condition, contrast = 1)
```

**Arguments**

design	The data.frame which correspond to the pData function of MSnbase
condition	xxxxx
contrast	An integer that 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**

A constrat matrix

**Author(s)**

Thomas Burger, Quentin Giai-Gianetto, Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
design <- make.design(Biobase::pData(Exp1_R25_pept))
conds <- Biobase::pData(Exp1_R25_pept)$Condition
make.contrast(design, conds)
```

---

make.design	<i>Builds the design matrix</i>
-------------	---------------------------------

---

**Description**

This function builds the design matrix

**Usage**

```
make.design(sTab)
```

**Arguments**

sTab	The data.frame which correspond to the pData function of MSnbase
------	--

**Value**

A design matrix

**Author(s)**

Thomas Burger, Quentin Giai-Gianetto, Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
make.design(Biobase::pData(Exp1_R25_pept))
```



---

make.design.1	<i>Builds the design matrix for designs of level 1</i>
---------------	--

---

**Description**

This function builds the design matrix for design of level 1

**Usage**

```
make.design.1(sTab)
```

**Arguments**

sTab                    The data.frame which correspond to the pData function of MSnbase

**Value**

A design matrix

**Author(s)**

Thomas Burger, Quentin Giai-Gianetto, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
make.design.1(Biobase::pData(Exp1_R25_pept))
```

---

make.design.2	<i>Builds the design matrix for designs of level 2</i>
---------------	--

---

**Description**

This function builds the design matrix for design of level 2

**Usage**

```
make.design.2(sTab)
```

**Arguments**

sTab                    The data.frame which correspond to the pData function of MSnbase

**Value**

A design matrix

**Author(s)**

Thomas Burger, Quentin Giai-Gianetto, Samuel Wiczorek

## Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
make.design.2(Biobase::pData(Exp1_R25_pept))
```

---

make.design.3	<i>Builds the design matrix for designs of level 3</i>
---------------	--

---

## Description

This function builds the design matrix for design of level 3

## Usage

```
make.design.3(sTab)
```

## Arguments

sTab                    The data.frame which correspond to the pData function of MSnbase

## Value

A design matrix

## Author(s)

Thomas Burger, Quentin Giai-Gianetto, Samuel Wieczorek

## Examples

```
## Not run:
require(DAPARdata)
data(Exp1_R25_pept)
make.design.3(Biobase::pData(Exp1_R25_pept))

## End(Not run)
```

---

mvFilter	<i>Filter lines in the matrix of intensities w.r.t. some criteria</i>
----------	---

---

## 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 Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
mvFilter(Exp1_R25_pept, "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**

```
mvFilterFromIndices(obj, keepThat = NULL, processText = "")
```

**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 Wiczorek

## Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
mvFilterFromIndices(Exp1_R25_pept, 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 = NULL)
```

## Arguments

<code>obj</code>	An object of class <code>MSnSet</code> containing quantitative data.
<code>type</code>	Method used to choose the lines to delete. Values are : "None", "EmptyLines", "wholeMatrix", "allCond", "atLeastOneCond"
<code>th</code>	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 Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
mvFilterGetIndices(Exp1_R25_pept, "wholeMatrix", 2)
```

---

mvHisto

*Histogram of missing values*

---

**Description**

This method plots a histogram of missing values.

**Usage**

```
mvHisto(qData, samplesData, conds, indLegend = "auto",
        showValues = FALSE, palette = NULL)
```

**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.
conds	A vector of the conditions (one condition per sample).
indLegend	The indices of the column name's in pData() tab
showValues	A logical that indicates wether numeric values should be drawn above the bars.
palette	xxx

**Value**

A histogram

**Author(s)**

Florence Combes, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
samplesData <- Biobase::pData(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
mvHisto(qData, samplesData, conds, indLegend="auto", showValues=TRUE)
```

---

mvHisto_HC	<i>Histogram of missing values</i>
------------	------------------------------------

---

### Description

This method plots a histogram of missing values. Same as the function mvHisto but uses the package highcharter

### Usage

```
mvHisto_HC(qData, samplesData, conds, indLegend = "auto",  
           showValues = FALSE, palette = NULL)
```

### 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.
conds	A vector of the conditions (one condition per sample).
indLegend	The indices of the column name's in pData() tab
showValues	A logical that indicates wether numeric values should be drawn above the bars.
palette	xxx

### Value

A histogram

### Author(s)

Florence Combes, Samuel Wiczorek

### Examples

```
require(DAPARdata)  
data(Exp1_R25_pept)  
qData <- Biobase::exprs(Exp1_R25_pept)  
samplesData <- Biobase::pData(Exp1_R25_pept)  
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]  
mvHisto_HC(qData, samplesData, conds, indLegend="auto", showValues=TRUE)
```

---

mvImage	<i>Heatmap of missing values</i>
---------	----------------------------------

---

### 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

```
mvImage(qData, conds)
```

### Arguments

qData	A dataframe that contains quantitative data.
conds	A vector of the conditions (one condition per sample).

### Value

A heatmap

### Author(s)

Samuel Wieczorek, Thomas Burger

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
mvImage(qData, conds)
```

---

mvPerLinesHisto	<i>Bar plot of missing values per lines</i>
-----------------	---

---

### Description

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

### Usage

```
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.

**Value**

A bar plot

**Author(s)**

Florence Combes, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
samplesData <- Biobase::pData(Exp1_R25_pept)
mvPerLinesHisto(qData, samplesData)
```

---

mvPerLinesHistoPerCondition

*Bar plot of missing values per lines and per condition*

---

**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, palette = NULL)
```

**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.
palette	xxx

**Value**

A bar plot



**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
samplesData <- Biobase::pData(Exp1_R25_pept)
mvPerLinesHistoPerCondition(qData, samplesData)
```

---

mvPerLinesHistoPerCondition\_HC

*Bar plot of missing values per lines and per condition*

---

**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. Same as the function [mvPerLinesHistoPerCondition](#) but uses the package `highcharter`.

**Usage**

```
mvPerLinesHistoPerCondition_HC(qData, samplesData, indLegend = "auto",
  showValues = FALSE, palette = NULL)
```

**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 <code>pData()</code> tab
showValues	A logical that indicates wether numeric values should be drawn above the bars.
palette	xxx

**Value**

A bar plot

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
qData <- Biobase::exprs(Exp1_R25_pept)
samplesData <- Biobase::pData(Exp1_R25_pept)
mvPerLinesHistoPerCondition_HC(qData, samplesData)
```

---

mvPerLinesHisto\_HC      *Bar plot of missing values per lines using highcharter*

---

### Description

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

### Usage

```
mvPerLinesHisto_HC(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.

### Value

A bar plot

### Author(s)

Florence Combes, Samuel Wiczorek

### Examples

```
require(DAPARdata)  
data(Exp1_R25_pept)  
qData <- Biobase::exprs(Exp1_R25_pept)  
samplesData <- Biobase::pData(Exp1_R25_pept)  
mvPerLinesHisto_HC(qData, samplesData)
```

---

my\_hc\_chart      *Customised resetZoomButton of highcharts plots*

---

### Description

Customise the resetZoomButton of highcharts plots.

### Usage

```
my_hc_chart(hc, chartType, zoomType = "None")
```

**Arguments**

hc	A highcharter object
chartType	The type of the plot
zoomType	The type of the zoom (one of "x", "y", "xy", "None")

**Value**

A highchart plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
library("highcharter")
hc <- highchart()
hc_chart(hc,type = "line")
hc_add_series(hc,data = c(29, 71, 40))
my_hc_ExportMenu(hc,filename='foo')
```

---

my\_hc\_ExportMenu

*Customised contextual menu of highcharts plots*

---

**Description**

Customise the contextual menu of highcharts plots.

**Usage**

```
my_hc_ExportMenu(hc, filename)
```

**Arguments**

hc	A highcharter object
filename	The filename under which the plot has to be saved

**Value**

A contextual menu for highcharts plots

**Author(s)**

Samuel Wieczorek

**Examples**

```
library("highcharter")
hc <- highchart()
hc_chart(hc,type = "line")
hc_add_series(hc,data = c(29, 71, 40))
my_hc_ExportMenu(hc,filename='foo')
```

---

nonzero	<i>Retrieve the indices of non-zero elements in sparse matrices</i>
---------	---

---

**Description**

This function retrieves the indices of non-zero elements in sparse matrices of class dgCMatrix from package Matrix. This function is largely inspired from the package RINGO

**Usage**

```
nonzero(x)
```

**Arguments**

x                    A sparse matrix of class dgCMatrix

**Value**

A two-column matrix

**Author(s)**

Samuel Wieczorek

**Examples**

```
library(Matrix)
mat <- Matrix(c(0,0,0,0,0,1,0,0,1,1,0,0,0,1),nrow=5, byrow=TRUE, sparse=TRUE)
res <- nonzero(mat)
```

---

NumericalFiltering	<i>Removes lines in the dataset based on numerical conditions.</i>
--------------------	--

---

**Description**

This function removes lines in the dataset based on numerical conditions.

**Usage**

```
NumericalFiltering(obj, name = NULL, value = NULL, operator = NULL)
```

**Arguments**

obj                    An object of class MSnSet.  
name                    The name of the column that correspond to the line to filter  
value                    A number  
operator                A string

**Value**

An list of 2 items : obj : an object of class MSnSet in which the lines have been deleted deleted : an object of class MSnSet which contains the deleted lines

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
NumericalFiltering(Exp1_R25_pept, 'A_Count', '6', '==')
```

---

NumericalgetIndicesOfLinesToRemove

*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**

```
NumericalgetIndicesOfLinesToRemove(obj, name = NULL, value = NULL,
  operator = NULL)
```

**Arguments**

obj	An object of class MSnSet.
name	The name of the column that correspond to the data to filter
value	xxxx
operator	A xxxx

**Value**

A vector of integers.

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
NumericalgetIndicesOfLinesToRemove(Exp1_R25_pept, "A_Count", value="6", operator='==')
```

pepa.test

*PEptide based Protein differential Abundance test***Description**

This function is PEptide based Protein differential Abundance test

**Usage**

```
pepa.test(X, y, n1, n2, global = FALSE, use.lm = FALSE)
```

**Arguments**

X	Binary q x p design matrix for q peptides and p proteins. $X_{(ij)}$ =1 if peptide i belongs to protein j, 0 otherwise.
y	q x n matrix representing the log intensities of q peptides among n MS samples.
n1	number of samples under condition 1. It is assumed that the first n1 columns of y correspond to observations under condition 1.
n2	number of samples under condition 2.
global	if TRUE, the test statistic for each protein uses all residues, including the ones for peptides in different connected components. Can be much faster as it does not require to compute connected components. However the p-values are not well calibrated in this case, as it amounts to adding a ridge to the test statistic. Calibrating the p-value would require knowing the amplitude of the ridge, which in turns would require computing the connected components.
use.lm	if TRUE (and if global=FALSE), use lm() rather than the result in Proposition 1 to compute the test statistic

**Value**

A list of the following elements: llr: log likelihood ratio statistic (maximum likelihood version). llr.map: log likelihood ratio statistic (maximum a posteriori version). llr.pv: p-value for llr. llr.map.pv: p-value for llr.map. mse.h0: Mean squared error under H0 mse.h1: Mean squared error under H1 s: selected regularization hyperparameter for llr.map. wchi2: weight used to make llr.map chi2-distributed under H0.

**Author(s)**

Thomas Burger, Laurent Jacob

---

plotJitter	<i>Jitter plot of CC</i>
------------	--------------------------

---

**Description**

Jitter plot of CC

**Usage**

```
plotJitter(list.of.cc)
```

**Arguments**

list.of.cc      List of cc such as returned by the function get.pep.prot.cc

**Value**

A plot

**Author(s)**

Thomas Burger

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
X <- BuildAdjacencyMatrix(Exp1_R25_pept[1:1000], "Protein_group_IDs", TRUE)
ll <- get.pep.prot.cc(X)
plotJitter(ll)
```

---

plotJitter_rCharts	<i>Display a a jitter plot for CC</i>
--------------------	---------------------------------------

---

**Description**

Display a jitter plot for CC

**Usage**

```
plotJitter_rCharts(df, clickFunction = NULL)
```

**Arguments**

df                      xxxx  
clickFunction      xxxx

**Value**

A plot

**Author(s)**

Thomas Burger, Samuel Wieczorek

---

plotPCA\_Eigen      *Plots the eigen values of PCA*

---

**Description**

Plots the eigen values of PCA

**Usage**

```
plotPCA_Eigen(res.pca)
```

**Arguments**

```
res.pca            xxx
```

**Value**

A histogram

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
res.pca <- wrapper.pca(Exp1_R25_pept, ncp=6)
plotPCA_Eigen(res.pca)
```

---

plotPCA\_Eigen\_hc      *Plots the eigen values of PCA with the highcharts library*

---

**Description**

Plots the eigen values of PCA with the highcharts library

**Usage**

```
plotPCA_Eigen_hc(res.pca)
```

**Arguments**

```
res.pca            xxx
```

**Value**

A histogram



**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
res.pca <- wrapper.pca(Exp1_R25_pept, ncp=6)
plotPCA_Eigen_hc(res.pca)
```

---

plotPCA\_Ind

*Plots individuals of PCA*

---

**Description**

Plots the individuals of PCA

**Usage**

```
plotPCA_Ind(res.pca, chosen.axes = c(1, 2))
```

**Arguments**

res.pca	xxx
chosen.axes	The dimensions to plot

**Value**

A plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
res.pca <- wrapper.pca(Exp1_R25_pept)
plotPCA_Ind(res.pca)
```

---

plotPCA\_Var                      *Plots variables of PCA*

---

**Description**

Plots the variables of PCA

**Usage**

```
plotPCA_Var(res.pca, chosen.axes = c(1, 2))
```

**Arguments**

res.pca	xxx
chosen.axes	The dimensions to plot

**Value**

A plot

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
res.pca <- wrapper.pca(Exp1_R25_pept)
plotPCA_Var(res.pca)
```

---

proportionConRev\_HC                      *Barplot of proportion of contaminants and reverse*

---

**Description**

Plots a barplot of proportion of contaminants and reverse. Same as the function `proportionConRev` but uses the package `highcharter`

**Usage**

```
proportionConRev_HC(nBoth = 0, nCont = 0, nRev = 0, lDataset = 0)
```

**Arguments**

nBoth	The number of both contaminants and reverse identified in the dataset.
nCont	The number of contaminants identified in the dataset.
nRev	The number of reverse entities identified in the dataset.
lDataset	The total length (number of rows) of the dataset

**Value**

A barplot

**Author(s)**

Samuel Wieczorek

**Examples**

```
proportionConRev_HC(10, 20, 100)
```

---

rbindMSnset	<i>Similar to the function rbind but applies on two subsets of the same MSnSet object.</i>
-------------	--

---

**Description**

Similar to the function rbind but applies on two subsets of the same MSnSet object.

**Usage**

```
rbindMSnset(df1 = NULL, df2)
```

**Arguments**

df1	An object (or subset of) of class MSnSet. May be NULL
df2	A subset of the same object as df1

**Value**

An instance of class MSnSet.

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R2_pept)
df1 <- Exp1_R2_pept[1:100]
df2 <- Exp1_R2_pept[200:250]
rbindMSnset(df1, df2)
```

---

readExcel	<i>This function reads a sheet of an Excel file and put the data into a data.frame.</i>
-----------	---

---

**Description**

This function reads a sheet of an Excel file and put the data into a data.frame.

**Usage**

```
readExcel(file, extension, sheet)
```

**Arguments**

file	The name of the Excel file.
extension	The extension of the file
sheet	The name of the sheet

**Value**

A data.frame

**Author(s)**

Samuel Wiczorek

---

reIntroduceMEC	<i>Put back LAPALA into a MSnSet object</i>
----------------	---

---

**Description**

This method is used to put back the LAPALA that have been identified previously

**Usage**

```
reIntroduceMEC(obj, MECIndex)
```

**Arguments**

obj	An object of class MSnSet.
MECIndex	A data.frame that contains index of MEC (see findMECBlock) .

**Value**

The object obj where LAPALA have been reintroduced

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
lapala <- findMECBlock(obj)
obj <- wrapper.impute.detQuant(obj)
obj <- reIntroduceMEC(obj, lapala)
```

---

removeLines	<i>Removes lines in the dataset based on a prefix string.</i>
-------------	---

---

**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**

```
require(DAPARdata)
data(Exp1_R25_pept)
removeLines(Exp1_R25_pept, "Potential_contaminant")
removeLines(Exp1_R25_pept, "Reverse")
```

---

samLRT	xxxxxx
--------	--------

---

### Description

This function computes a regularized version of the likelihood ratio statistic. The regularization adds a user-input fudge factor *s1* to the variance estimator. This is straightforward when using a fixed effect model (cases 'numeric' and 'lm') but requires some more care when using a mixed model.

### Usage

```
samLRT(lmm.res.h0, lmm.res.h1, cc, n, p, s1)
```

### Arguments

<code>lmm.res.h0</code>	a vector of object containing the estimates (used to compute the statistic) under H0 for each connected component. If the fast version of the estimator was used (as implemented in this package), <code>lmm.res.h0</code> is a vector containing averages of squared residuals. If a fixed effect model was used, it is a vector of <code>lm</code> objects and if a mixed effect model was used it is a vector or <code>lmer</code> object.
<code>lmm.res.h1</code>	similar to <code>lmm.res.h0</code> , a vector of object containing the estimates (used to compute the statistic) under H1 for each protein.
<code>cc</code>	a list containing the indices of peptides and proteins belonging to each connected component.
<code>n</code>	the number of samples used in the test
<code>p</code>	the number of proteins in the experiment
<code>s1</code>	the fudge factor to be added to the variance estimate

### Value

`llr.sam`: a vector of numeric containing the regularized log likelihood ratio statistic for each protein.  
`s`: a vector containing the maximum likelihood estimate of the variance for the chosen model. When using the fast version of the estimator implemented in this package, this is the same thing as the input `lmm.res.h1`.  
`lh1.sam`: a vector of numeric containing the regularized log likelihood under H1 for each protein.  
`lh0.sam`: a vector of numeric containing the regularized log likelihood under H0 for each connected component.  
`sample.sizes`: a vector of numeric containing the sample size (number of biological samples times number of peptides) for each protein. This number is the same for all proteins within each connected component.

### Author(s)

Thomas Burger, Laurent Jacob

---

saveParameters	<i>Saves the parameters of a tool in the pipeline of Prostar</i>
----------------	--

---

**Description**

Saves the parameters of a tool in the pipeline of Prostar

**Usage**

```
saveParameters(obj, name.dataset = NULL, name = NULL,  
  l.params = NULL)
```

**Arguments**

obj	An object of class MSnSet
name.dataset	The name of the dataset
name	The name of the tool. Available values are: "Norm, Imputation, anaDiff, GO-Analysis,Aggregation"
l.params	A list that contains the parameters

**Value**

An instance of class MSnSet.

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)  
data(Exp1_R25_pept)  
l.params=list(method="Global quantile alignment", type="overall")  
saveParameters(Exp1_R25_pept, "Filtered.peptide", "Imputation",l.params)
```

---

```
scatterplotEnrichGO_HC
```

*A dotplot that shows the result of a GO enrichment, using the package  
highcharter*

---

**Description**

A scatter plot of GO enrichment analysis

**Usage**

```
scatterplotEnrichGO_HC(ego, maxRes = 10, title = NULL)
```

**Arguments**

ego	The result of the GO enrichment, provides either by the function enrichGO in DAPAR or the function enrichGO of the package <a href="#">clusterProfiler</a>
maxRes	The maximum number of categories to display in the plot
title	The title of the plot

**Value**

A dotplot

**Author(s)**

Samuel Wieczorek

---

setMEC	<i>Sets the MEC tag in the OriginOfValues</i>
--------	---

---

**Description**

Sets the MEC tag in the OriginOfValues

**Usage**

```
setMEC(obj)
```

**Arguments**

obj	An object of class MSnSet
-----	---------------------------

**Value**

An instance of class MSnSet.

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
setMEC(Exp1_R25_pept)
```



---

splitAdjacencyMat	<i>splits an adjacency matrix into specific and shared</i>
-------------------	--

---

**Description**

Method to split an adjacency matrix into specific and shared

**Usage**

```
splitAdjacencyMat(X)
```

**Arguments**

X	An adjacency matrix
---	---------------------

**Value**

A list of two adjacency matrices

**Author(s)**

Samuel Wieczorek

---

StringBasedFiltering	<i>Removes lines in the dataset based on a prefix strings (contaminants, reverse or both).</i>
----------------------	--

---

**Description**

This function removes lines in the dataset based on prefix strings (contaminants, reverse or both).

**Usage**

```
StringBasedFiltering(obj, idCont2Delete = NULL, prefix_Cont = NULL,  
idRev2Delete = NULL, prefix_Rev = NULL)
```

**Arguments**

obj	An object of class MSnSet.
idCont2Delete	The name of the column that correspond to the contaminants to filter
prefix_Cont	A character string that is the prefix for the contaminants to find in the data
idRev2Delete	The name of the column that correspond to the reverse data to filter
prefix_Rev	A character string that is the prefix for the reverse to find in the data

**Value**

An list of 4 items : obj : an object of class MSnSet in which the lines have been deleted deleted.both : an object of class MSnSet which contains the deleted lines corresponding to both contaminants and reverse, deleted.contaminants : n object of class MSnSet which contains the deleted lines corresponding to contaminants, deleted.reverse : an object of class MSnSet which contains the deleted lines corresponding to reverse,

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
StringBasedFiltering(Exp1_R25_pept, 'Potential_contaminant', '+', 'Reverse', '+')
```

---

StringBasedFiltering2 *Removes lines in the dataset based on a prefix strings.*

---

**Description**

This function removes lines in the dataset based on prefix strings.

**Usage**

```
StringBasedFiltering2(obj, cname = NULL, tag = NULL)
```

**Arguments**

obj	An object of class MSnSet.
cname	The name of the column that correspond to the line to filter
tag	A character string that is the prefix for the contaminants to find in the data

**Value**

An list of 4 items : obj : an object of class MSnSet in which the lines have been deleted deleted : an object of class MSnSet which contains the deleted lines

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
StringBasedFiltering2(Exp1_R25_pept, 'Potential_contaminant', '+')
```

---

test.design	<i>Check if xxxxxx</i>
-------------	------------------------

---

**Description**

This function check xxxxx

**Usage**

```
test.design(tab)
```

**Arguments**

tab                    A data.frame which correspond to xxxxxx

**Value**

A list of two items

**Author(s)**

Thomas Burger, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
test.design(Biobase::pData(Exp1_R25_pept)[,1:3])
```

---

translatedRandomBeta	<i>Generator of simulated values</i>
----------------------	--------------------------------------

---

**Description**

Generator of simulated values

**Usage**

```
translatedRandomBeta(n, min, max, param1 = 3, param2 = 1)
```

**Arguments**

n                    An integer which is the number of simulation (same as in rbeta)  
min                   An integer that corresponds to the lower bound of the interval  
max                   An integer that corresponds to the upper bound of the interval  
param1                An integer that is the first parameter of rbeta function.  
param2                An integer that is second parameter of rbeta function.

**Value**

A vector of n simulated values

**Author(s)**

Thomas Burger

**Examples**

```
translatedRandomBeta(1000, 5, 10, 1, 1)
```

---

univ_AnnotDbPkg	<i>Returns the totality of ENTREZ ID (gene id) of an OrgDb annotation package. Careful : org.Pf.plasmo.db : no ENTREZID but ORF</i>
-----------------	---

---

**Description**

Function to compute the "universe" argument for the enrich\_G0 function, in case this latter should be the entire organism. Returns all the ID of the OrgDb annotation package for the corresponding organism.

**Usage**

```
univ_AnnotDbPkg(orgdb)
```

**Arguments**

orgdb                    a Bioconductor OrgDb annotation package

**Value**

A vector of ENTREZ ID

**Author(s)**

Florence Combes

---

violinPlotD	<i>Builds a violinplot from a dataframe</i>
-------------	---

---

**Description**

ViolinPlot for quantitative proteomics data

**Usage**

```
violinPlotD(obj, legend = NULL, palette = NULL)
```

**Arguments**

obj	xxx
legend	A vector of the conditions (one condition per sample).
palette	xxx

**Value**

A violinplot

**Author(s)**

Samuel Wieczorek

**See Also**

[densityPlotD](#)

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
library(vioplot)
legend <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
violinPlotD(Exp1_R25_pept, legend=legend)
```

---

```
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, condsForLegend = NULL,
  indData2Show = NULL, ...)
```

**Arguments**

objBefore	A dataframe that contains quantitative data before normalization.
objAfter	A dataframe that contains quantitative data after normalization.
condsForLegend	A vector of the conditions (one condition 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 data.frame qDataBefore.
...	arguments for palette

**Value**

A plot

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
objAfter <- wrapper.normalized(Exp1_R25_pept, "QuantileCentering", "within conditions")
wrapper.compareNormalizationD(Exp1_R25_pept, objAfter, conds)
```

---

```
wrapper.compareNormalizationD_HC
```

*Builds a plot from a dataframe*

---

**Description**

Wrapper to the function that plot to compare the quantitative proteomics data before and after normalization. Same as the function [wrapper.compareNormalizationD](#) but uses the package `highcharter`

**Usage**

```
wrapper.compareNormalizationD_HC(objBefore, objAfter,
  condsForLegend = NULL, indData2Show = NULL, ...)
```

**Arguments**

<code>objBefore</code>	A dataframe that contains quantitative data before normalization.
<code>objAfter</code>	A dataframe that contains quantitative data after normalization.
<code>condsForLegend</code>	A vector of the conditions (one condition per sample).
<code>indData2Show</code>	A vector of the indices of the columns to show in the plot. The indices are those of indices of the columns in the data.frame <code>qDataBefore</code> .
<code>...</code>	arguments for palette

**Value**

A plot

**Author(s)**

Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)[,"Condition"]
objAfter <- wrapper.normalized(Exp1_R25_pept, "QuantileCentering",
  "within conditions")
wrapper.compareNormalizationD_HC(Exp1_R25_pept, objAfter, conds)
```

---

`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**

```
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**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.corrMatrixD(Exp1_R25_pept)
```

---

`wrapper.corrMatrixD_HC` *Displays a correlation matrix of the quantitative data of the exprs() table*

---

**Description**

Builds a correlation matrix based on a MSnSet object. Same as the function `wrapper.corrMatrixD` but uses the package `highcharter`

**Usage**

```
wrapper.corrMatrixD_HC(obj, rate = 0.5)
```

**Arguments**

`obj` An object of class MSnSet.  
`rate` A float that defines the gradient of colors.

**Value**

A colored correlation matrix

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.corrMatrixD_HC(Exp1_R25_pept)
```

---

wrapper.CVDistD

*Distribution of CV of entities*

---

**Description**

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

**Usage**

```
wrapper.CVDistD(obj, ...)
```

**Arguments**

<code>obj</code>	An object of class <code>MSnSet</code> .
<code>...</code>	arguments for palette

**Value**

A density plot

**Author(s)**

Alexia Dorffer

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.CVDistD(Exp1_R25_pept)
```



---

wrapper.CVDistD\_HC      *Distribution of CV of entities*

---

### Description

Builds a densityplot of the CV of entities in the `exprs()` table. of an object `MSnSet`. The variance is calculated for each condition present in the dataset (see the slot 'Condition' in the `pData()` table). Same as the function `wrapper.CVDistD` but uses the package `highcharter`

### Usage

```
wrapper.CVDistD_HC(obj, ...)
```

### Arguments

<code>obj</code>	An object of class <code>MSnSet</code>
<code>...</code>	arguments for palette.

### Value

A density plot

### Author(s)

Samuel Wieczorek

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.CVDistD_HC(Exp1_R25_pept)
```

---

wrapper.dapar.impute.mi

*Missing values imputation using the LSImpute algorithm.*

---

### Description

This method is a wrapper to the function `impute.mi` of the package `imp4p` adapted to an object of class `MSnSet`.

### Usage

```
wrapper.dapar.impute.mi(obj, nb.iter = 3, nknn = 15, selec = 600,
  siz = 500, weight = 1, ind.comp = 1, progress.bar = TRUE,
  x.step.mod = 300, x.step.pi = 300, nb.rei = 100, method = 4,
  gridsize = 300, q = 0.95, q.min = 0, q.norm = 3, eps = 0,
  methodi = "slsa", lapala = TRUE, distribution = "unif")
```

**Arguments**

obj	An object of class MSnSet.
nb.iter	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
nknn	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
selec	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
siz	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
weight	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
ind.comp	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
progress.bar	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
x.step.mod	Same as the function <code>estim.mix</code> in the package <code>imp4p</code>
x.step.pi	Same as the function <code>estim.mix</code> in the package <code>imp4p</code>
nb.rei	Same as the function <code>estim.mix</code> in the package <code>imp4p</code>
method	Same as the function <code>estim.mix</code> in the package <code>imp4p</code>
gridsize	Same as the function <code>estim.mix</code> in the package <code>imp4p</code>
q	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
q.min	Same as the function <code>impute.pa</code> in the package <code>imp4p</code>
q.norm	Same as the function <code>impute.pa</code> in the package <code>imp4p</code>
eps	Same as the function <code>impute.pa</code> in the package <code>imp4p</code>
methodi	Same as the function <code>mi.mix</code> in the package <code>imp4p</code>
lapala	xxxxxxxxxxx
distribution	The type of distribution used. Values are <code>unif</code> (default) or <code>beta</code> .

**Value**

The `exprs(obj)` matrix with imputed values instead of missing values.

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
dat <- mvFilter(Exp1_R25_pept[1:1000], type="allCond", th = 1)
dat <- wrapper.dapar.impute.mi(dat, nb.iter=1)
```

---

`wrapper.hc_mvTypePlot2`

*Distribution of observed values with respect to intensity values from a MSnSet object*

---

### Description

This method is a wrapper for the function [hc\\_mvTypePlot2](#) adapted to objects of class MSnSet).

### Usage

```
wrapper.hc_mvTypePlot2(obj, ...)
```

### Arguments

`obj` An object of class MSnSet.  
`...` See [hc\\_mvTypePlot2](#)

### Value

A scatter plot

### Author(s)

Florence Combes, Samuel Wiczorek

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.hc_mvTypePlot2(Exp1_R25_pept)
```

---

`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 = "complete",
  dendro = FALSE)
```

**Arguments**

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

**Value**

A heatmap

**Author(s)**

Alexia Dorffer

**Examples**

```
## Not run:
require(DAPARdata)
data(Exp1_R25_pept)
obj <- mvFilter(Exp1_R25_pept[1:1000], "wholeMatrix", 6)
wrapper.heatmapD(obj)

## End(Not run)
```

---

wrapper.impute.detQuant

*Wrapper of the function [impute.detQuant](#) for objects of class MSnSet*

---

**Description**

This method is a wrapper of the function [impute.detQuant](#) for objects of class MSnSet

**Usage**

```
wrapper.impute.detQuant(obj, qval = 0.025, factor = 1)
```

**Arguments**

obj	An instance of class MSnSet
qval	An expression set containing quantitative values of various replicates
factor	A scaling factor to multiply the imputation value with

**Value**

An imputed instance of class MSnSet

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.impute.detQuant(Exp1_R25_pept)
```

---

```
wrapper.impute.fixedValue
```

*Missing values imputation from a MSnSet object*

---

**Description**

This method is a wrapper to objects of class MSnSet and imputes missing values with a fixed value.

**Usage**

```
wrapper.impute.fixedValue(obj, fixVal)
```

**Arguments**

obj	An object of class MSnSet.
fixVal	A float .

**Value**

The object obj which has been imputed

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.impute.fixedValue(Exp1_R25_pept[1:1000], 0.001)
```

---

```
wrapper.impute.KNN
```

*KNN missing values imputation from a MSnSet object*

---

**Description**

This method is a wrapper for objects of class MSnSet and imputes missing values with a fixed value. This function imputes the missing values condition by condition.

**Usage**

```
wrapper.impute.KNN(obj, K)
```

**Arguments**

obj            An object of class MSnSet.  
K              the number of neighbors.

**Value**

The object obj which has been imputed

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.impute.KNN(Exp1_R25_pept[1:1000], 3)
```

---

wrapper.impute.mle      *Imputation of peptides having no values in a biological condition.*

---

**Description**

This method is a wrapper to the function `impute.mle` of the package `imp4p` adapted to an object of class `MSnSet`.

**Usage**

```
wrapper.impute.mle(obj)
```

**Arguments**

obj            An object of class MSnSet.

**Value**

The `exprs(obj)` matrix with imputed values instead of missing values.

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
dat <- mvFilter(Exp1_R25_pept[1:1000,], type="allCond", th = 1)
dat <- wrapper.impute.mle(dat)
```

---

wrapper.impute.pa	<i>Imputation of peptides having no values in a biological condition.</i>
-------------------	---

---

**Description**

This method is a wrapper to the function `impute.pa` of the package `imp4p` adapted to an object of class `MSnSet`.

**Usage**

```
wrapper.impute.pa(obj, q.min = 0.025)
```

**Arguments**

<code>obj</code>	An object of class <code>MSnSet</code> .
<code>q.min</code>	Same as the function <code>impute.pa</code> in the package <code>imp4p</code>

**Value**

The `exprs(obj)` matrix with imputed values instead of missing values.

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
dat <- mvFilter(Exp1_R25_pept[1:1000], type="allCond", th = 1)
dat <- wrapper.impute.pa(dat)
```

---

wrapper.impute.pa2	<i>Missing values imputation from a MSnSet object</i>
--------------------	---

---

**Description**

This method is a wrapper to the function `impute.pa` from the package `imp4p` adapted to objects of class `MSnSet`.

**Usage**

```
wrapper.impute.pa2(obj, q.min = 0, q.norm = 3, eps = 0,
  distribution = "unif")
```

**Arguments**

obj	An object of class MSnSet.
q.min	A quantile value of the observed values allowing defining the maximal value which can be generated. This maximal value is defined by the quantile q.min of the observed values distribution minus eps. Default is 0 (the maximal value is the minimum of observed values minus eps).
q.norm	A quantile value of a normal distribution allowing defining the minimal value which can be generated. Default is 3 (the minimal value is the maximal value minus $qn * \text{median}(sd(\text{observed values}))$ where sd is the standard deviation of a row in a condition).
eps	A value allowing defining the maximal value which can be generated. This maximal value is defined by the quantile q.min of the observed values distribution minus eps. Default is 0.
distribution	The type of distribution used. Values are unif (default) or beta.

**Value**

The object obj which has been imputed

**Author(s)**

Thomas Burger, Samuel Wiczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.impute.pa2(Exp1_R25_pept[1:1000], distribution="beta")
```

---

wrapper.impute.slsa     *Imputation of peptides having no values in a biological condition.*

---

**Description**

This method is a wrapper to the function impute.slsa of the package imp4p adapted to an object of class MSnSet.

**Usage**

```
wrapper.impute.slsa(obj)
```

**Arguments**

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

**Value**

The exprs(obj) matrix with imputed values instead of missing values.



**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
dat <- mvFilter(Exp1_R25_pept[1:1000], type="allCond", th = 1)
dat <- wrapper.impute.slsa(dat)
```

---

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 wether numeric values should be drawn above the bars.

**Value**

A histogram

**Author(s)**

Alexia Dorffer

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.mvHisto(Exp1_R25_pept, showValues=TRUE)
```

---

wrapper.mvHisto\_HC      *Histogram of missing values from a MSnSet object*

---

### Description

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

### Usage

```
wrapper.mvHisto_HC(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 wether numeric values should be drawn above the bars.
...	xxx

### Value

A histogram

### Author(s)

Alexia Dorffer

### Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.mvHisto_HC(Exp1_R25_pept, 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 vizualize 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**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', 1)
obj <- mvFilterFromIndices(obj, keepThat)
wrapper.mvImage(obj)
```

---

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)
```

**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**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.mvPerLinesHisto(Exp1_R25_pept)
```

---

```
wrapper.mvPerLinesHistoPerCondition
```

*Bar plot of missing values per lines and per conditions from an object MSnSet*

---

### 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

```
require(DAPARdata)  
data(Exp1_R25_pept)  
wrapper.mvPerLinesHistoPerCondition(Exp1_R25_pept)
```

---

```
wrapper.mvPerLinesHistoPerCondition_HC
```

*Bar plot of missing values per lines and per conditions from an object MSnSet*

---

### Description

This method is a wrapper to plots (using highcharts) 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_HC(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.
...	xxx

**Value**

A bar plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.mvPerLinesHistoPerCondition_HC(Exp1_R25_pept)
```

---

```
wrapper.mvPerLinesHisto_HC
```

*Histogram of missing values per lines from an object using highcharacter 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_HC(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 histogram

**Author(s)**

Alexia Dorffer

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.mvPerLinesHisto(Exp1_R25_pept)
```

---

 wrapper.normalized      *Normalisation*


---

## Description

Provides several methods to normalize quantitative data from a MSnSet object. They are organized in six main families : GlobalQuantileAlignment, sumByColumns, QuantileCentering, MeanCentering, LOESS, vsn For the first family, there is no type. For the five other families, two type categories are available : "Overall" which means that the value for each protein (ie line in the expression data tab) is computed over all the samples ; "within conditions" which means that the value for each protein (ie line in the exprs() data tab) is computed condition by condition.

## Usage

```
wrapper.normalized(obj, method, type = NULL, scaling = FALSE,
  quantile = 0.15, span = 0.7)
```

## Arguments

obj	An object of class MSnSet.
method	One of the following : "GlobalQuantileAlignment" (for normalizations of important magnitude), "SumByColumns", "QuantileCentering", "Mean Centering", "LOESS" and "vsn".
type	For the method "Global Alignment", the parameters are: "sum by columns": operates on the original scale (not the log2 one) and propose to normalize each abundance by the total abundance of the sample (so as to focus on the analyte proportions among each sample). "Alignment on all quantiles": proposes to align the quantiles of all the replicates; practically it amounts to replace abundances by order statistics. For the two other methods, the parameters are "overall" (shift all the sample distributions at once) or "within conditions" (shift the sample distributions within each condition at a time).
scaling	A boolean that indicates if the variance of the data have to be forced to unit (variance reduction) or not.
quantile	A float that corresponds to the quantile used to align the data.
span	parameter for LOESS method

## Value

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

## Author(s)

Samuel Wiczorek, Thomas Burger, Helene Borges

## Examples

```
require(DAPARdata)
data(Exp1_R25_pept)
wrapper.normalized(Exp1_R25_pept[1:1000], "QuantileCentering", "within conditions")
```

---

wrapper.pca	<i>Compute the PCA</i>
-------------	------------------------

---

**Description**

Compute the PCA

**Usage**

```
wrapper.pca(obj, var.scaling = TRUE, ncp = NULL)
```

**Arguments**

obj	xxx
var.scaling	The dimensions to plot
ncp	xxxx

**Value**

A xxxxxx

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- mvFilter(Exp1_R25_pept, "wholeMatrix", 6)
res.pca <- wrapper.pca(obj)
```

---

wrapper.t_test_Complete	xxxxx
-------------------------	-------

---

**Description**

This function is a wrapper xxxxx

**Usage**

```
wrapper.t_test_Complete(obj, ...)
```

**Arguments**

obj	An object of class MSnSet with no missing values
...	See compute.t.tests

**Value**

xxxxxxx

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
tttest <- wrapper.t_test_Complete(obj, 1)
```

---

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 (one condition per sample).

**Value**

A plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R25_pept)
obj <- Exp1_R25_pept[1:1000]
keepThat <- mvFilterGetIndices(obj, 'wholeMatrix', ncol(obj))
obj <- mvFilterFromIndices(obj, keepThat)
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
limma <- limmaCompleteTest(qData, sTab)
wrapperCalibrationPlot(limma$P_Value[,1])
```



---

writeMSnsetToCSV	<i>Exports a MSnset dataset into a zip archive containing three zipped CSV files.</i>
------------------	---

---

**Description**

This function exports a MSnset dataset into three csv files compressed in a zip file

**Usage**

```
writeMSnsetToCSV(obj, fname)
```

**Arguments**

obj	An object of class MSnSet.
fname	The name of the archive file.

**Value**

A compressed file

**Author(s)**

Samuel Wieczorek

**Examples**

```
require(DAPARdata)
data(Exp1_R2_pept)
obj <- Exp1_R2_pept[1:1000]
writeMSnsetToCSV(obj, "foo")
```

---

writeMSnsetToExcel	<i>This function exports a MSnSet object to a Excel file.</i>
--------------------	---

---

**Description**

This function exports a MSnSet data object to a Excel file. Each of the three data.frames in the MSnSet object (ie experimental data, phenoData and metaData are respectively integrated into separate sheets in the Excel file). The colored cells in the experimental data correspond to the original missing values which have been imputed.

**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**

```
Sys.setenv("R_ZIPCMD"= Sys.which("zip"))
require(DAPARdata)
data(Exp1_R2_pept)
obj <- Exp1_R2_pept[1:1000]
writeMSnsetToExcel(obj, "foo")
```

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