

# Package ‘DAPAR’

May 17, 2024

**Type** Package

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

**Description** The package DAPAR is a Bioconductor distributed R package which provides all the necessary functions to analyze quantitative data from label-free proteomics experiments.

Contrarily to most other similar R packages, it is endowed with rich and user-friendly graphical interfaces, so that no programming skill is required (see ‘Prostar’ package).

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**License** Artistic-2.0

**VignetteBuilder** knitr

**Depends** R (>= 4.3.0)

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---

aggregateIter	xxxx
---------------	------

---

**Description**

xxxx

**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**

```
data(Exp1_R25_pept, package="DAPARdata")
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(10)], protID, FALSE)
ll.agg <- aggregateIter(Exp1_R25_pept[seq_len(10)], X = X)
```

---

```
aggregateIterParallel xxxx
```

---

**Description**

xxxx

**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**

```

xxxxx

```

**Author(s)**

Samuel Wieczorek

**Examples**

```

## Not run:
data(Exp1_R25_pept, package="DAPARdata")
protID <- "Protein_group_IDs"
obj.pep <- Exp1_R25_pept[seq_len(10)]
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
obj.agg <- aggregateIterParallel(obj.pep, X)

## End(Not run)

```

---

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**

```
data(Exp1_R25_pept, package="DAPARdata")
obj.pep <- Exp1_R25_pept[seq_len(10)]
obj.pep.imp <- wrapper.impute.detQuant(obj.pep, na.type = c("Missing POV", "Missing MEC"))
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep.imp, protID, FALSE)
ll.agg <- aggregateMean(obj.pep.imp, X)
```

---

AggregateMetacell      *Symbolic product of matrices*

---

**Description**

Execute a product two matrices: the first is an adjacency one while the second if a simple dataframe

**Usage**

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

**Arguments**

X	An adjacency matrix between peptides and proteins
obj.pep	A dataframe of the cell metadata for peptides

**Value**

XXXX

**Author(s)**

Samuel Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj.pep <- Exp1_R25_pept[seq_len(10)]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
agg.meta <- AggregateMetacell(X, obj.pep)
```

---

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**

```
data(Exp1_R25_pept, package="DAPARdata")
obj.pep <- Exp1_R25_pept[seq_len(20)]
obj.pep.imp <- wrapper.impute.detQuant(obj.pep, na.type = c("Missing POV", "Missing MEC"))
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
ll.agg <- aggregateSum(obj.pep.imp, 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 Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj.pep <- Exp1_R25_pept[seq_len(10)]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
ll.agg <- aggregateTopn(obj.pep, X, n = 3)
```

---

applyAnovasOnProteins *iteratively applies OWAnova() on the features of an MSnSet object*

---

**Description**

iteratively applies OWAnova() on the features of an MSnSet object

**Usage**

```
applyAnovasOnProteins(obj)
```

**Arguments**

obj                    an MSnSet object '

**Value**

a list of linear models

**Author(s)**

Thomas Burger

**Examples**

```
data(Exp1_R25_prot, package='DAPARdata')
exdata <- Exp1_R25_prot[1:5,]
applyAnovasOnProteins(exdata)
```

---

averageIntensities	<i>Average protein/peptide abundances for each condition studied</i>
--------------------	--

---

**Description**

Calculate the average of the abundances for each protein in each condition for an ExpressionSet or MSnSet. Needs to have the array expression data ordered in the same way as the phenotype data (columns of the array data in the same order than the condition column in the phenotype data).

**Usage**

```
averageIntensities(ESet_obj)
```

**Arguments**

ESet\_obj          ExpressionSet object containing all the data

**Value**

a dataframe in wide format providing (in the case of 3 or more conditions) the means of intensities for each protein/peptide in each condition. If there are less than 3 conditions, an error message is returned.

**Author(s)**

Helene Borges

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(1000)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
averageIntensities(obj$new)
```

---

barplotEnrichGO_HC	<i>A barplot that shows the result of a GO enrichment, using the package highcharter</i>
--------------------	--

---

## 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 Wieczorek

## Examples

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(10)]
if (!requireNamespace("org.Sc.sgd.db", quietly = TRUE)) {
  stop("Please install org.Sc.sgd.db:
       BiocManager::install('org.Sc.sgd.db')")
}
library(org.Sc.sgd.db)
univ <- univ_AnnotDbPkg("org.Sc.sgd.db")
ego <- enrich_GO(
  data = Biobase::fData(obj)$Protein.IDs, idFrom = "UNIPROT",
  orgdb = "org.Sc.sgd.db", ont = "MF", pval = 0.05, universe = univ
)
barplotEnrichGO_HC(ego)
```

---

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

---

### Description

A barplot which shows the result of a GO classification, using the package highcharter

### Usage

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

### Arguments

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

### Value

A barplot

### Author(s)

Samuel Wieczorek

### Examples

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(10)]
if (!requireNamespace("org.Sc.sgd.db", quietly = TRUE)) {
  stop("Please install org.Sc.sgd.db:
       BiocManager::install('org.Sc.sgd.db')")
}
library(org.Sc.sgd.db)
univ <- univ_AnnotDbPkg("org.Sc.sgd.db")
ggo <- group_GO(
  data = Biobase::fData(obj)$Protein.IDs, idFrom = "UNIPROT",
  orgdb = "org.Sc.sgd.db", ont = "MF", level = 2
)
barplotGroupGO_HC(ggo)
```

---

`boxPlotD_HC`*Builds a boxplot from a dataframe using the package highcharter*

---

**Description**

Builds a boxplot from a dataframe using the package highcharter

**Usage**

```
boxPlotD_HC(  
  obj,  
  conds,  
  keyId = NULL,  
  legend = NULL,  
  pal = NULL,  
  subset.view = NULL  
)
```

**Arguments**

<code>obj</code>	Numeric matrix
<code>conds</code>	xxx
<code>keyId</code>	xxxx
<code>legend</code>	A vector of the conditions (one condition per sample).
<code>pal</code>	A basis palette for the boxes which length must be equal to the number of unique conditions in the dataset.
<code>subset.view</code>	A vector of index indicating which rows to highlight

**Value**

A boxplot

**Author(s)**

Samuel Wieczorek, Anais Courtier, Enora Fremy

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")  
obj <- Exp1_R25_prot  
conds <- legend <- Biobase::pData(obj)$Condition  
key <- "Protein_IDs"  
pal <- ExtendPalette(length(unique(conds)))  
boxPlotD_HC(obj, conds, key, legend, pal, seq_len(10))
```

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**

```
data(Exp1_R25_pept, package="DAPARdata")
protId <- "Protein_group_IDs"
BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(10)], protId, 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 aggregate the peptides data.
columnName	The name of the column in Biobase::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**

```
data(Exp1_R25_pept, package="DAPARdata")
protID <- "Protein_group_IDs"
obj.pep <- Exp1_R25_pept[seq_len(10)]
M <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
data <- Biobase::fData(obj.pep)
protData <- aggregateMean(obj.pep, M)
name <- "Protein_group_IDs"
proteinNames <- rownames(Biobase::fData(protData$obj.prot))
new.col <- BuildColumnToProteinDataset(data, M, name, proteinNames)
```

---

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 Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
X <- BuildAdjacencyMatrix(obj, "Protein_group_IDs", FALSE)
ll <- get.pep.prot.cc(X)
g <- buildGraph(ll[[1]], X)
```

---

BuildMetaCell

*Builds cells metadata*

---

**Description**

This function the cells metadata info base on the origin of identification for entities. There are actually two different type of origin which are managed by DAPAR: - "Maxquant-like" info which is represented by strings/tags, - Proline-like where the info which is used is an integer

**Usage**

```
BuildMetaCell(from, level, qdata = NULL, conds = NULL, df = NULL)
```

**Arguments**

from	A string which is the name of the software from which the data are. Available values are 'maxquant', 'proline' and 'DIA-NN'
level	xxx
qdata	An object of class MSnSet
conds	xxx
df	A list of integer xxxxxxxx

**Value**

xxxxx

**Author(s)**

Samuel Wiczorek

## Examples

```
file <- system.file("extdata", "Exp1_R25_pept.txt", package = "DAPARdata")
data <- read.table(file, header = TRUE, sep = "\t", stringsAsFactors = FALSE)
metadataFile <- system.file("extdata", "samples_Exp1_R25.txt",
  package = "DAPARdata")
metadata <- read.table(metadataFile,
  header = TRUE, sep = "\t", as.is = TRUE,
  stringsAsFactors = FALSE)
conds <- metadata$Condition
qdata <- data[, seq.int(from = 56, to = 61)]
df <- data[, seq.int(from = 43, to = 48)]
df <- BuildMetaCell(
  from = "maxquant", level = "peptide", qdata = qdata,
  conds = conds, df = df)
df <- BuildMetaCell(
  from = "proline", level = "peptide", qdata = qdata,
  conds = conds, df = df)
```

---

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

---

## Description

Check if the design is valid

## Usage

```
check.conditions(conds)
```

## Arguments

conds            A vector

## Value

A list

## Author(s)

Samuel Wieczorek

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")
check.conditions(Biobase::pData(Exp1_R25_pept)$Condition)
```

---

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

---

**Description**

Check if the design is valid

**Usage**

```
check.design(sTab)
```

**Arguments**

sTab                    The data.frame which correspond to the 'pData()' function of package 'MSnbase'.

**Value**

A boolean

**Author(s)**

Thomas Burger, Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
check.design(Biobase::pData(Exp1_R25_pept)[, seq_len(3)])
```

---

checkClusterability	.xxx
---------------------	------

---

**Description**

The first step is to standardize the data (with the Mfuzz package). Then the function checks that these data are clusterizable or not (use of [diptest::dip.test()] to determine whether the distribution is unimodal or multimodal). Finally, it determines the "optimal" k by the Gap statistic approach.

**Usage**

```
checkClusterability(standards, b = 500)
```

**Arguments**

standards            a matrix or dataframe containing only the standardized mean intensities returned by the function [standardiseMeanIntensities()]

b                     Parameter B of the function [gap\_cluster()]

**Value**

a list of 2 elements: \* `dip_test`: the result of the clusterability of the data \* `gap_cluster`: the gap statistic obtained with the function [`cluster::clusGap()`].

**Author(s)**

Helene Borges

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
averaged_means <- averageIntensities(obj$new)
only_means <- dplyr::select_if(averaged_means, is.numeric)
only_features <- dplyr::select_if(averaged_means, is.character)
means <- purrr::map(purrr::array_branch(as.matrix(only_means), 1), mean)
centered <- only_means - unlist(means)
centered_means <- dplyr::bind_cols(
  feature = dplyr::as_tibble(only_features),
  dplyr::as_tibble(centered))
checkClust <- checkClusterability(centered_means, b = 100)
```

---

Check\_Dataset\_Validity

xxx

---

**Description**

xxx

**Usage**

```
Check_Dataset_Validity(obj)
```

**Arguments**

`obj`                    `xxx`

---

Check\_NbValues\_In\_Columns  
xxx

---

**Description**

xxx

**Usage**

Check\_NbValues\_In\_Columns(qdata)

**Arguments**

qdata            xxx

---

Children            *Names of all children of a node*

---

**Description**

xxx

**Usage**

Children(level, parent = NULL)

**Arguments**

level            xxx  
parent           xxx

**Examples**

```
Children('protein', 'Missing')
Children('protein', 'Missing POV')
Children('protein', c('Missing POV', 'Missing MEC'))
Children('protein', c('Missing', 'Missing POV', 'Missing MEC'))
```

---

classic1wayAnova	<i>Function to perform a One-way Anova statistical test on a MsnBase dataset</i>
------------------	--

---

**Description**

Function to perform a One-way Anova statistical test on a MsnBase dataset

**Usage**

```
classic1wayAnova(current_line, conditions)
```

**Arguments**

current_line	The line currently treated from the quantitative data to perform the ANOVA
conditions	The conditions represent the different classes of the studied factor

**Value**

A named vector containing all the different values of the aov model

**Author(s)**

Hélène Borges

**Examples**

```
## Not run: examples/ex_classic1wayAnova.R
```

---

compareNormalizationD_HC	<i>Builds a plot from a dataframe. Same as compareNormalizationD but uses the library highcharter</i>
--------------------------	---

---

**Description**

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

**Usage**

```
compareNormalizationD_HC(
  qDataBefore,
  qDataAfter,
  keyId = NULL,
  conds = NULL,
  pal = NULL,
  subset.view = NULL,
  n = 1,
  type = "scatter"
)
```

**Arguments**

qDataBefore	A dataframe that contains quantitative data before normalization.
qDataAfter	A dataframe that contains quantitative data after normalization.
keyId	xxx
conds	A vector of the conditions (one condition per sample).
pal	xxx
subset.view	xxx
n	An integer that is equal to the maximum number of displayed points. This number must be less or equal to the size of the dataset. If it is less than it, it is a random selection
type	scatter or line

**Value**

A plot

**Author(s)**

Samuel Wiczorek

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot
qDataBefore <- Biobase::exprs(obj)
conds <- Biobase::pData(obj)[, "Condition"]
id <- Biobase::fData(obj)[, 'Protein_IDs']
pal <- ExtendPalette(2)
objAfter <- wrapper.normalizeD(obj,
  method = "QuantileCentering",
  conds = conds, type = "within conditions"
)

n <- 1
compareNormalizationD_HC(
```



```
qDataBefore = qDataBefore,  
qDataAfter = Biobase::exprs(objAfter),  
keyId = id,  
pal = pal,  
n = n,  
subset.view = seq_len(n),  
conds = conds)
```

---

compute.selection.table

*Applies an FDR threshold on a table of adjusted p-values and summarizes the results*

---

### Description

Applies an FDR threshold on a table of adjusted p-values and summarizes the results

### Usage

```
compute.selection.table(x, fdr.threshold)
```

### Arguments

x                    a table of adjusted p-values  
fdr.threshold      an FDR threshold

### Value

a summary of the number of significantly differentially abundant proteins, overall and per contrast

### Author(s)

Thomas Burger

### Examples

```
data(Exp1_R25_prot, package='DAPARdata')  
exdata <- Exp1_R25_prot[1:5,]  
adjpvaltab <- globalAdjPval(testAnovaModels(applyAnovasOnProteins(exdata), "TukeyHSD"))$P_Value)  
selstab <- compute.selection.table(adjpvaltab, 0.2)  
selstab
```

---

compute_t_tests	xxxxxx
-----------------	--------

---

**Description**

xxxxxx

**Usage**

```
compute_t_tests(obj, contrast = "OnevsOne", type = "Student")
```

**Arguments**

obj	A matrix of quantitative data, without any missing values.
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**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(1000)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
ttest <- compute_t_tests(obj$new)
```

---

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

---

### Description

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

### Usage

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

### 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
showValues	xxx

### Value

A colored correlation matrix

### Author(s)

Samuel Wieczorek

### Examples

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

---

CountPep	<i>Compute the number of peptides used to aggregate proteins</i>
----------	--

---

**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**

```
data(Exp1_R25_pept, package="DAPARdata")
protID <- "Protein_group_IDs"
M <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(10)], protID, FALSE)
CountPep(M)
```

---

createMSnset	<i>Creates an object of class MSnSet from text file</i>
--------------	---

---

**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,
  colnameForID = NULL,
  indexForMetacell = NULL,
  logData = FALSE,
  replaceZeros = FALSE,
  pep_prot_data = NULL,
  proteinId = NULL,
  software = 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 Biobase::fData() table of the MSnSet object.
colnameForID	The name of the column containing the ID of entities (peptides or proteins)
indexForMetacell	xxxxxxxxxxxx
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
software	xxx

**Value**

An instance of class MSnSet.

**Author(s)**

Florence Combes, Samuel Wieczorek

**Examples**

```
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 <- seq.int(from=56, to=61)
colnameForID <- "id"
obj <- createMSnset(exprsFile, metadata, indExpData, colnameForID,
  indexForMetacell = seq.int(from=43, to=48), pep_prot_data = "peptide",
  software = "maxquant"
)

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 <- seq.int(from = 56, to = 61)
colnameForID <- "AutoID"
obj <- createMSnset(exprsFile, metadata, indExpData, colnameForID,
  indexForMetacell = seq.int(from = 43, to = 48),
  pep_prot_data = "peptide", software = "maxquant"
)

```

---

createMSnset2

*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

```

createMSnset2(
  file,
  metadata = NULL,
  qdataNames,
  colnameForID = NULL,
  metacellNames = NULL,
  logData = FALSE,
  replaceZeros = FALSE,
  pep_prot_data = NULL,
  proteinId = NULL,
  software = NULL
)

```

**Arguments**

file	The name of a tab-separated file that contains the data.
metadata	A dataframe describing the samples (in lines).
qdataNames	A vector of string where each element is the name of a column in designTable that have to be integrated in the Biobase::fData() table of the MSnSet object.
colnameForID	The name of the column containing the ID of entities (peptides or proteins)
metacellNames	xxxxxxxxxxxx
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
software	xxx

**Value**

An instance of class MSnSet.

**Author(s)**

Florence Combes, Samuel Wieczorek

**Examples**

```
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 <- seq.int(from=56, to=61)
colnameForID <- "id"
obj <- createMSnset(exprsFile, metadata, indExpData, colnameForID,
  indexForMetacell = seq.int(from=43, to=48), pep_prot_data = "peptide",
  software = "maxquant"
)
```

```
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 <- seq.int(from = 56, to = 61)
```

```
colnameForID <- "AutoID"
obj <- createMSnset(exprsFile, metadata, indExpData, colnameForID,
  indexForMetacell = seq.int(from = 43, to = 48),
  pep_prot_data = "peptide", software = "maxquant"
)
```

---

CVDistD\_HC

*Distribution of CV of entities*

---

### Description

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

### Usage

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

### Arguments

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

### Value

A density plot

### Author(s)

Samuel Wieczorek

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")
conds <- Biobase::pData(Exp1_R25_pept)[, "Condition"]
CVDistD_HC(Biobase::exprs(Exp1_R25_pept), conds)
pal <- ExtendPalette(2, "Dark2")
CVDistD_HC(Biobase::exprs(Exp1_R25_pept), conds, pal)
```



---

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

---

**Description**

Customised resetZoomButton of highcharts plots

**Usage**

```
dapar_hc_chart(hc, chartType, zoomType = "None", width = 0, height = 0)
```

**Arguments**

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

**Value**

A highchart plot

**Author(s)**

Samuel Wiczorek

**Examples**

```
library("highcharter")
hc <- highchart()
hc <- dapar_hc_chart(hc, chartType = "line", zoomType = "x")
hc_add_series(hc, data = c(29, 71, 40))
```

---

dapar\_hc\_ExportMenu      *Customised contextual menu of highcharts plots*

---

**Description**

Customised contextual menu of highcharts plots

**Usage**

```
dapar_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))  
dapar_hc_ExportMenu(hc, filename = "foo")
```

---

deleteLinesFromIndices

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

---

**Description**

Delete the lines in the matrix of intensities and the metadata table given 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 Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- deleteLinesFromIndices(Exp1_R25_pept[seq_len(100)], c(seq_len(10)))
```

---

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

---

**Description**

Densityplot of quantitative proteomics data over samples.

**Usage**

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

**Arguments**

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

**Value**

A density plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
densityPlotD_HC(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)$Condition
pal <- ExtendPalette(2, "Dark2")
densityPlotD_HC(Exp1_R25_pept, pal = pal)
```

---

`diffAnaComputeAdjustedPValues`*Computes the adjusted p-values*

---

## 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

```
diffAnaComputeAdjustedPValues(pval, pi0Method = 1)
```

## Arguments

<code>pval</code>	The result (p-values) of the differential analysis processed by <a href="#">limmaCompleteTest</a>
<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 adjusted p-values

## Author(s)

Samuel Wieczorek

## Examples

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(1000)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
qData <- Biobase::exprs(obj$new)
sTab <- Biobase::pData(obj$new)
limma <- limmaCompleteTest(qData, sTab)
df <- data.frame(id = rownames(limma$logFC), logFC = limma$logFC[, 1], pval = limma$P_Value[, 1])

diffAnaComputeAdjustedPValues(pval = limma$P_Value[, 1])
```

---

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(adj.pvals)
```

**Arguments**

adj.pvals      xxxx

**Value**

The computed FDR value (floating number)

**Author(s)**

Samuel Wieczorek

**Examples**

```
NULL
```

---

diffAnaGetSignificant	<i>Returns a MSnSet object with only proteins significant after differential analysis.</i>
-----------------------	--

---

**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**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
qData <- Biobase::exprs(obj$new)
sTab <- Biobase::pData(obj$new)
allComp <- limmaCompleteTest(qData, sTab)
data <- list(logFC = allComp$logFC[1], P_Value = allComp$P_Value[1])
obj$new <- diffAnaSave(obj$new, allComp, data)
signif <- diffAnaGetSignificant(obj$new)
```

---

diffAnaSave	<i>Returns a MSnSet object with the results of the differential analysis performed with limma package.</i>
-------------	--

---

**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 Wiczorek

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
qData <- Biobase::exprs(obj$new)
sTab <- Biobase::pData(obj$new)
allComp <- limmaCompleteTest(qData, sTab)
data <- list(logFC = allComp$logFC[1], P_Value = allComp$P_Value[1])
diffAnaSave(obj$new, 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 Wieczorek

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
qData <- Biobase::exprs(obj$new)
sTab <- Biobase::pData(obj$new)
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,
  pal = NULL
)
```



**Arguments**

<code>df</code>	A dataframe which contains the following slots : <code>x</code> : a vector of the log(fold change) values of the differential analysis, <code>y</code> : a vector of the p-value values returned by the differential analysis. <code>index</code> : a vector of the rownames of the data. This dataframe must have been built with the option <code>stringsAsFactors</code> set to <code>FALSE</code> . 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 <code>"tooltip_"</code> . It will be automatically removed in the plot.
<code>threshold_pVal</code>	A floating number which represents the p-value that separates differential and non-differential data.
<code>threshold_logFC</code>	A floating number which represents the log of the Fold Change that separates differential and non-differential data.
<code>conditions</code>	A list of the names of condition 1 and 2 used for the differential analysis.
<code>clickFunction</code>	A string that contains a JavaScript function used to show info from slots in <code>df</code> . The variable <code>this.index</code> refers to the slot named <code>index</code> and allows to retrieve the right row to show in the tooltip.
<code>pal</code>	<code>xxx</code>

**Value**

An interactive volcanoplot

**Author(s)**

Samuel Wiczorek

**Examples**

```
library(highcharter)
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")$new
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
data <- limmaCompleteTest(qData, sTab)
df <- data.frame(
  x = data$logFC, y = -log10(data$P_Value),
  index = as.character(rownames(obj))
)
colnames(df) <- c("x", "y", "index")
tooltipSlot <- c("Fasta_headers", "Sequence_length")
df <- cbind(df, Biobase::fData(obj)[, tooltipSlot])
colnames(df) <- gsub(".", "_", colnames(df), fixed = TRUE)
if (ncol(df) > 3) {
  colnames(df)[seq.int(from = 4, to = ncol(df))] <-
```

```
      paste("tooltip_", colnames(df)[seq.int(from = 4, to = ncol(df))],
            sep = "")
    }
    hc_clickFunction <- JS("function(event) {
    Shiny.onInputChange('eventPointClicked',
    [this.index]+'_'+ [this.series.name]);}")
    cond <- c("25fmol", "10fmol")
    diffAnaVolcanoplot_rCharts(df, 2.5, 1, cond, hc_clickFunction)
```

---

display.CC.visNet      *Display a CC*

---

## 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**

```

data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
X <- BuildAdjacencyMatrix(obj, "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**

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

**Value**

A `groupGOResult` instance.

**Author(s)**

Florence Combes

**Examples**

```

data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(10)]
if (!requireNamespace("org.Sc.sgd.db", quietly = TRUE)) {
  stop("Please install org.Sc.sgd.db:
       BiocManager::install('org.Sc.sgd.db')")
}
library(org.Sc.sgd.db)
univ <- univ_AnnotDbPkg("org.Sc.sgd.db") # univ is the background
ego <- enrich_GO(
  data = Biobase::fData(obj)$Protein.IDs, idFrom = "UNIPROT",
  orgdb = "org.Sc.sgd.db", ont = "MF", pval = 0.05, universe = univ
)

```

---

ExtendPalette

*Extends a base-palette of the package RColorBrewer to n colors.*


---

**Description**

The colors in the returned palette are always in the same order

**Usage**

```
ExtendPalette(n = NULL, base = "Set1")
```

**Arguments**

n	The number of desired colors in the palette
base	The name of the palette of the package RColorBrewer from which the extended palette is built. Default value is 'Set1'.

**Value**

A vector composed of n color code.

**Author(s)**

Samuel Wieczorek

**Examples**

```

ExtendPalette(12)
nPalette <- 10
par(mfrow = c(nPalette, 1))
par(mar = c(0.5, 4.5, 0.5, 0.5))
for (i in seq_len(nPalette)) {
  pal <- ExtendPalette(n = i, base = "Dark2")
  barplot(seq_len(length(pal)), col = pal)
}

```

```
    print(pal)
}
```

---

finalizeAggregation     *Finalizes the aggregation process*

---

### Description

Method to finalize the aggregation process

### Usage

```
finalizeAggregation(obj.pep, pepData, protData, protMetacell, X)
```

### Arguments

obj.pep	A peptide object of class MSnset
pepData	xxxx
protData	xxxxx
protMetacell	xxx
X	An adjacency matrix in which lines and columns correspond respectively to peptides and proteins.

### Value

A protein object of class MSnset

### Author(s)

Samuel Wieczorek

### Examples

```
NULL
```

---

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

---

**Description**

Finds the LAPALA into a MSnSet object

**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**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
lapala <- findMECBlock(obj)
```

---

formatHSDResults	.xxx
------------------	------

---

**Description**

.xxx

**Usage**

```
formatHSDResults(post_hoc_models_summaries)
```

**Arguments**

post\_hoc\_models\_summaries  
xxx

**Value**

xxx

**Author(s)**

Thomas Burger

**Examples**

NULL

---

formatLimmaResult	xxx
-------------------	-----

---

**Description**

xxxx

**Usage**

```
formatLimmaResult(fit, conds, contrast, design.level)
```

**Arguments**

fit	xxxx
conds	xxxx
contrast	xxxx
design.level	xxx

**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

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
qData <- Biobase::exprs(obj$new)
sTab <- Biobase::pData(obj$new)
limma <- limmaCompleteTest(qData, sTab)
```

---

formatPHResults	<i>Extract logFC and raw pvalues from multiple post-hoc models summaries</i>
-----------------	--

---

## Description

Extract logFC and raw pvalues from multiple post-hoc models summaries

## Usage

```
formatPHResults(post_hoc_models_summaries)
```

## Arguments

post\_hoc\_models\_summaries  
a list of summaries of post-hoc models.

## Value

a list of 2 dataframes containing the logFC values and pvalues for each comparison.

## Author(s)

Hélène Borges

## Examples

```
## Not run: examples/ex_formatPHResults.R
```



---

formatPHTResults	.xxx
------------------	------

---

**Description**

xxx

**Usage**

formatPHTResults(post\_hoc\_models\_summaries)

**Arguments**post\_hoc\_models\_summaries  
xxx**Value**

xxx

**Author(s)**

Thomas Burger

**Examples**

NULL

---

fudge2LRT	<i>Heuristic to choose the value of the hyperparameter (fudge factor) used to regularize the variance estimator in the likelihood ratio statistic</i>
-----------	---

---

**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**

<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 lm objects and if a mixed effect model was used it is a vector or lmer 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>s</code>	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 <code>lmm.res.h1</code> . For other models (e.g. mixed models) it can be obtained from <code>samLRT</code> .
<code>alpha</code>	A vector of proportions used to build candidate values for the regularizer. We use quantiles of <code>s</code> with these proportions. Default to <code>seq(0, 1, 0.05)</code>
<code>include.zero</code>	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

### Examples

NULL

---

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

---

### Description

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

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
X <- BuildAdjacencyMatrix(obj, "Protein_group_IDs", FALSE)
ll <- get.pep.prot.cc(X)
```

---

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

---

### Description

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

### Usage

```
GetCC(obj)
```

**Arguments**

obj                    An object (peptides) of class MSnSet.

**Value**

A list of connected components

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
Xshared <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(100)],
"Protein_group_IDs", FALSE)
Xunique <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(100)],
"Protein_group_IDs", TRUE)
l1.X <- list(matWithSharedPeptides = Xshared,
matWithUniquePeptides = Xunique)
Exp1_R25_pept <- SetMatAdj(Exp1_R25_pept, l1.X)
l11 <- get.pep.prot.cc(GetMatAdj(Exp1_R25_pept)$matWithSharedPeptides)
l12 <- get.pep.prot.cc(
GetMatAdj(Exp1_R25_pept)$matWithUniquePeptides)
cc <- list(allPep = l11, onlyUniquePep = l12)
Exp1_R25_pept <- SetCC(Exp1_R25_pept, cc)
l1.cc <- GetCC(Exp1_R25_pept)
```

---

GetColorsForConditions

*Builds a complete color palette for the conditions given in argument*

---

**Description**

xxxx

**Usage**

```
GetColorsForConditions(conds, pal = NULL)
```

**Arguments**

conds                The extended vector of samples conditions

pal                   A vector of HEX color code that form the basis palette from which to build the complete color vector for the conditions.

**Value**

A vector composed of HEX color code for the conditions

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
conditions <- Biobase::pData(Exp1_R25_pept)$Condition
GetColorsForConditions(conditions, ExtendPalette(2))
```

---

<code>getDesignLevel</code>	<code>xxx</code>
-----------------------------	------------------

---

**Description**

xxx

**Usage**

```
getDesignLevel(sTab)
```

**Arguments**

sTab            xxx

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
sTab <- Biobase::pData(Exp1_R25_pept)
getDesignLevel(sTab)
```

---

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**

```
data(Exp1_R25_pept, package="DAPARdata")
obj.pep <- Exp1_R25_pept[seq_len(10)]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
n <- 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, qdata.pep)
```

**Arguments**

X                    An adjacency matrix  
qdata.pep           A data.frame of quantitative data

**Value**

A list of two items

**Author(s)**

```
Samuel Wiczorek library(MSNbase) data(Exp1_R25_pept, package="DAPARdata") protID <- "Protein_group_IDs" X <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(10)], protID, FALSE) ll.n <- GetDetailedNbPeptidesUsed(X, Biobase::exprs(Exp1_R25_pept[seq_len(10)]))
```

**Examples**

```
NULL
```

---

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 Biobase::pData().  
cond1                A vector of Conditions (a slot in the Biobase::pData() table) for the condition 1.  
cond2                A vector of Conditions (a slot in the Biobase::pData() table) for the condition 2.

**Value**

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

**Author(s)**

Florence Combes, Samuel Wiczorek

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")
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

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

## Usage

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

## Arguments

obj	An object of class MSnSet.
idLine2Delete	The name of the column that correspond to the data to filter
prefix	A character string that is the prefix to find in the data

## Value

A vector of integers.

## Author(s)

Samuel Wieczorek

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")
ind <- getIndicesOfLinesToRemove(Exp1_R25_pept[seq_len(100)],
  "Potential_contaminant",
  prefix = "+"
)
```



---

GetIndices\_BasedOnConditions

*Search lines which respects request on one or more conditions.*

---

### Description

This function looks for the lines that respect the request in either all conditions or at least one condition.

### Usage

```
GetIndices_BasedOnConditions(metacell.mask, type, conds, percent, op, th)
```

### Arguments

metacell.mask	xxx
type	Available values are: * 'AllCond' (the query is valid in all the conditions), * 'AtLeatOneCond' (the query is valid in at least one condition).
conds	xxx
percent	xxx
op	String for operator to use. List of operators is available with SymFilteringOperators().
th	The threshold to apply

### Value

xxx

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
level <- GetTypeofData(obj)
pattern <- 'Missing'
metacell.mask <- match.metacell(metadata=GetMetacell(obj),
pattern=pattern, level=level)
type <- 'AllCond'
conds <- Biobase::pData(obj)$Condition
op <- '>='
th <- 0.5
percent <- TRUE
ind <- GetIndices_BasedOnConditions(metacell.mask, type, conds,
percent, op, th)
```

---

GetIndices\_MetacellFiltering

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

---

## Description

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

## Usage

```
GetIndices_MetacellFiltering(  
  obj,  
  level,  
  pattern = NULL,  
  type = NULL,  
  percent,  
  op,  
  th  
)
```

## Arguments

obj	An object of class MSnSet containing quantitative data.
level	A vector of integers which are the indices of lines to delete.
pattern	A string to be included in the MSnSet object for log.
type	xxx
percent	xxx
op	xxx
th	xxx

## Value

An instance of class MSnSet that have been filtered.

## Author(s)

Samuel Wieczorek

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")  
obj <- Exp1_R25_pept[seq_len(10)]  
level <- GetTypeofData(obj)  
pattern <- c("Missing", "Missing POV")  
type <- "AtLeastOneCond"
```

```
percent <- FALSE
op <- ">="
th <- 1
indices <- GetIndices_MetacellFiltering(obj, level, pattern, type, percent, op, th)

pattern <- "Quantified"
type <- "AtLeastOneCond"
percent <- FALSE
op <- ">="
th <- 4
indices2.1 <- GetIndices_MetacellFiltering(obj, level, pattern, type, percent, op, th)

pattern <- "Quant. by direct id"
type <- "AtLeastOneCond"
percent <- FALSE
op <- ">="
th <- 3
indices2.2 <- GetIndices_MetacellFiltering(obj, level, pattern, type, percent, op, th)
```

---

GetIndices\_WholeLine *Search lines which respects query on all their elements.*

---

## Description

This function looks for the lines where each element respect the query.

## Usage

```
GetIndices_WholeLine(metacell.mask)
```

## Arguments

```
metacell.mask xxx
```

## Value

```
xxx
```

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq.int(from=20, to=30)]
level <- 'peptide'
pattern <- "Missing POV"
metacell.mask <- match.metacell(metadata = GetMetacell(obj),
pattern = pattern, level = level)
ind <- GetIndices_WholeLine(metacell.mask)
```

---

GetIndices\_WholeMatrix

*Search lines which respects request on one or more conditions.*

---

### Description

This function looks for the lines that respect the request in either all conditions or at least one condition.

### Usage

```
GetIndices_WholeMatrix(metacell.mask, op = "==", percent = FALSE, th = 0)
```

### Arguments

metacell.mask	xxx
op	String for operator to use. List of operators is available with <code>SymFilteringOperators()</code> .
percent	A boolean to indicate whether the threshold represent an absolute value (percent = FALSE) or a percentage (percent=TRUE).
th	A floating number which is in the interval [0, 1]

### Value

xxx

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
level <- 'peptide'
pattern <- "Missing"
metacell.mask <- match.metacell(metadata = GetMetacell(obj),
pattern = pattern, level = level)
percent <- FALSE
th <- 3
op <- ">="
ind <- GetIndices_WholeMatrix(metacell.mask, op, percent, th)
```

---

GetKeyId	.xxx
----------	------

---

**Description**

xxxx

**Usage**

GetKeyId(obj)

**Arguments**

obj	xxx
-----	-----

**Value**

xxx

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
GetKeyId(Exp1_R25_pept)
```

---

getListNbValuesInLines

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

---

**Description**

Returns the possible number of values in lines in the data

**Usage**

getListNbValuesInLines(obj, type)

**Arguments**

obj	An object of class MSnSet
type	xxxxxxx

**Value**

An integer

**Author(s)**

Samuel Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
getListNbValuesInLines(Exp1_R25_pept, "WholeMatrix")
```

---

GetMatAdj

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

---

**Description**

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

**Usage**

```
GetMatAdj(obj)
```

**Arguments**

obj                    An object (peptides) of class MSnSet.

**Value**

The slot processing of obj@processingData

**Author(s)**

Samuel Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
Xshared <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(100)],
"Protein_group_IDs", FALSE)
Xunique <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(100)],
"Protein_group_IDs", TRUE)
ll.X <- list(matWithSharedPeptides = Xshared,
matWithUniquePeptides = Xunique)
Exp1_R25_pept <- SetMatAdj(Exp1_R25_pept, ll.X)
ll.X <- GetMatAdj(Exp1_R25_pept)
```

---

GetMetacell	.xxx
-------------	------

---

**Description**

xxxx

**Usage**

GetMetacell(obj)

**Arguments**

obj	xxxx
-----	------

**Value**

xxx

**Examples**

NULL

---

GetMetacellTags	<i>List of metacell tags</i>
-----------------	------------------------------

---

**Description**

This function gives the list of metacell tags available in DAPAR.

- onlyPresent: In this case, the function gives the tags found in a dataset. In addition, and w.r.t to the hierarchy of tags, if all leaves of a node are present, then the tag corresponding to this node is added.

**Usage**

GetMetacellTags(level = NULL, obj = NULL, onlyPresent = FALSE, all = FALSE)

**Arguments**

level	xxx
obj	An object of class MSnSet
onlyPresent	A boolean that indicates if one wants a list with only the tags present in the dataset.
all	A boolean that indicates if one wants the whole list

**Value**

A vector of tags..

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept
GetMetace11Tags(level="peptide")
GetMetace11Tags(level="peptide", obj, onlyPresent=TRUE)
```

---

GetNbPeptidesUsed      *Computes the number of peptides used for aggregating each protein*

---

**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

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
protID <- "Protein_group_IDs"
obj.pep <- Exp1_R25_pept[seq_len(10)]
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
pepData <- Biobase::exprs(obj.pep)
GetNbPeptidesUsed(X, pepData)
```



---

GetNbTags	<i>Number of each metacell tags</i>
-----------	-------------------------------------

---

**Description**

Number of each metacell tags

**Usage**

```
GetNbTags(obj)
```

**Arguments**

obj	A instance of the class 'MSnset'
-----	----------------------------------

**Examples**

```
NULL
```

---

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 Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
getNumberOf(Exp1_R25_pept[seq_len(100)], "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 Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
qData <- Biobase::exprs(Exp1_R25_pept)
getNumberOfEmptyLines(qData)
```

---

getPourcentageOfMV    *Percentage of missing values*

---

**Description**

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

**Usage**

```
getPourcentageOfMV(obj)
```

**Arguments**

obj                    An object of class MSnSet.

**Value**

A floating number

**Author(s)**

Florence Combes, Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
getPourcentageOfMV(Exp1_R25_pept[seq_len(100), ])
```

---

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

---

**Description**

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

**Usage**

```
getProcessingInfo(obj)
```

**Arguments**

obj                    An object (peptides) of class MSnSet.

**Value**

The slot processing of obj@processingData

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
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**

```
data(Exp1_R25_pept, package="DAPARdata")
protID <- "Protein_group_IDs"
obj <- Exp1_R25_pept[seq_len(20)]
MShared <- BuildAdjacencyMatrix(obj, protID, FALSE)
getProteinsStats(matShared = 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**

qdata	An expression set containing quantitative values of various replicates
qval	The quantile used to define the imputation value
factor	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**

```
data(Exp1_R25_prot, package="DAPARdata")
qdata <- Biobase::exprs(Exp1_R25_prot)
quant <- getQuantile4Imp(qdata)
```

---

GetSoftAvailables      *The set of softwares available*

---

**Description**

The set of softwares available

**Usage**

```
GetSoftAvailables()
```

**Examples**

```
GetSoftAvailables()
```

---

getTextForAggregation *Build the text information for the Aggregation process*

---

**Description**

\* includeSharedPeptides, \* operator, \* considerPeptides, \* proteinId, \* topN

**Usage**

```
getTextForAggregation(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()
getTextForAggregation(params)
```

---

getTextForAnaDiff        *Build the text information for the Aggregation process*

---

**Description**

\* Condition1 \* Condition2 \* Comparison \* filterType \* filter\_th\_NA \* calibMethod \* numValCal-  
ibMethod \* th\_pval \* FDR \* NbSelected

**Usage**

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

**Arguments**

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

**Value**

A string

**Author(s)**

Samuel Wiczorek

**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 Wiczorek

**Examples**

```
getTextForFiltering(list(filename = "foo.msnset"))
```

---

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**

\* design, \* method, \* ttest\_options, \* th\_logFC, \* AllPairwiseCompNames = list( \* logFC, \* P\_Value)

**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.msnset"))
```

---

`getTextForNormalization`*Build the text information for the Normalization process*

---

**Description**

The items of the parameter list for the normalisation is: \* method, \* type, \* varReduction, \* quantile,

**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**

\* pepLevel\_algorithm, \* pepLevel\_basicAlgorithm, \* pepLevel\_detQuantile, \* pepLevel\_detQuant\_factor,  
\* pepLevel\_imp4p\_nbiter, \* pepLevel\_imp4p\_withLapala, \* pepLevel\_imp4p\_qmin, \* pepLevel\_imp4pLAPALA\_distrib

**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**

\* POV\_algorithm, \* POV\_detQuant\_quantile, \* POV\_detQuant\_factor, \* POV\_KNN\_n, \* MEC\_algorithm,  
\* MEC\_detQuant\_quantile, \* MEC\_detQuant\_factor, \* MEC\_fixedValue

**Usage**

```
getTextForproteinImputation(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()  
getTextForproteinImputation(params)
```

---

GetTypeofData	.xxx
---------------	------

---

**Description**

xxxx

**Usage**

GetTypeofData(obj)

**Arguments**

obj	xxx
-----	-----

**Value**

xxx

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
GetTypeofData(Exp1_R25_pept)
```

---

GetUniqueTags	.xxx
---------------	------

---

**Description**

xxx

**Usage**

GetUniqueTags(obj)

**Arguments**

obj	xxx
-----	-----

---

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

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(1000)]
level <- GetTypeofData(obj)
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
qData <- Biobase::exprs(obj$new)
sTab <- Biobase::pData(obj$new)
allComp <- limmaCompleteTest(qData, sTab)
data <- list(logFC = allComp$logFC[1], P_Value = allComp$P_Value[1])
obj$new <- diffAnaSave(obj$new, allComp, data)
ll <- Get_AllComparisons(obj$new)
```

---

globalAdjPval	<i>Computes the adjusted p-values on all the stacked contrasts using CP4P</i>
---------------	---

---

### Description

Computes the adjusted p-values on all the stacked contrasts using CP4P

### Usage

```
globalAdjPval(x, pval.threshold = 1.05, method = 1, display = T)
```

### Arguments

x	a proteins x contrasts dataframe of (raw) p-values
pval.threshold	all the p-values above the threshold are not considered. Default is 1.05 (which is equivalent to have no threshold). Applying a threshold nearby 1 can be instrumental to improve the uniformity under the null, notably in case of upstream multiple contrast correction (for experienced users only)
method	method a method to estimate $\pi_0$ , see CP4P
display	if T, a calibration plot is displayed using CP4P

### Value

a proteins x contrasts table of adjusted p-values

### Author(s)

Thomas Burger

### Examples

```
data(Exp1_R25_prot, package='DAPARdata')
exdata <- Exp1_R25_prot[1:5,]
globalAdjPval(testAnovaModels(applyAnovasOnProteins(exdata), "TukeyHSD"))$P_Value)
```

---

GlobalQuantileAlignment

*Normalisation GlobalQuantileAlignement*

---

### Description

Normalisation GlobalQuantileAlignement

### Usage

```
GlobalQuantileAlignment(qData)
```

### Arguments

qData            xxxx

### Value

A normalized numeric matrix

### Author(s)

Samuel Wiczorek, Thomas Burger, Helene Borges, Anais Courtier, Enora Fremy

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")
qData <- Biobase::exprs(Exp1_R25_pept)
normalized <- GlobalQuantileAlignment(qData)
```

---

GOAnalysisSave

*Returns an MSnSet object with the results of the GO analysis performed with the functions enrichGO and/or groupGO of the 'cluster-Profiler' package.*

---

### 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 'clusterProfiler'
ego_res	The object returned by the function enrich_GO of the package DAPAR or the function enrichGO of the package 'clusterProfiler'
organism	The parameter OrgDb of the functions bitr, groupGO and enrichGO
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 'clusterProfiler')
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

**Examples**

```
NULL
```



---

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**

```
data(Exp1_R25_pept, package="DAPARdata")
mat <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(10)], "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**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(10)]
if (!requireNamespace("org.Sc.sgd.db", quietly = TRUE)) {
  stop("Please install org.Sc.sgd.db:
       BiocManager::install('org.Sc.sgd.db')")
}
library(org.Sc.sgd.db)
ggo <- group_GO(
  data = Biobase::fData(obj)$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 differential analysis.

**Usage**

```
hc_logFC_DensityPlot(df_logFC, threshold_LogFC = 0, pal = 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
pal	xxx

**Value**

A highcharts density plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
qData <- Biobase::exprs(obj$new)
sTab <- Biobase::pData(obj$new)
res <- limmaCompleteTest(qData, sTab, comp.type = "OnevsAll")
pal <- ExtendPalette(2, "Dark2")
hc_logFC_DensityPlot(res$logFC, threshold_LogFC = 1, pal = pal)
```

---

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(obj, pal = NULL, pattern, typeofMV = NULL, title = NULL)
```

**Arguments**

obj	xxx
pal	The different colors for conditions
pattern	xxx
typeofMV	xxx
title	The title of the plot

**Value**

Density plots

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
conds <- Biobase::pData(obj)$Condition
pal <- ExtendPalette(length(unique(conds)), "Dark2")
hc_mvTypePlot2(obj, pattern = "Missing MEC", title = "POV distribution", pal = pal)
```

---

heatmapD

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

---

**Description**

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

**Usage**

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

**Arguments**

qData	A dataframe that contains quantitative data.
conds	A vector containing the conditions
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, Enor Fremy

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10), ]
level <- 'peptide'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeLine(metacell.mask)
qData <- Biobase::exprs(obj)
conds <- Biobase::pData(obj)[["Condition"]]
heatmapD(qData, conds)
```

---

heatmapForMissingValues

.xxx

---

**Description**

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

**Usage**

```
heatmapForMissingValues(
  x,
  col = NULL,
  srtCol = NULL,
  labCol = NULL,
  labRow = NULL,
```

```
key = TRUE,  
key.title = NULL,  
main = NULL,  
ylab = NULL  
)
```

### Arguments

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

### Value

A heatmap

### Author(s)

Samuel Wieczorek

### Examples

```
data(Exp1_R25_prot, package="DAPARdata")  
obj <- Exp1_R25_prot[seq_len(100)]  
level <- 'protein'  
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)  
indices <- GetIndices_WholeLine(metacell.mask)  
obj <- MetaCellFiltering(obj, indices, cmd = "delete")  
qData <- Biobase::exprs(obj$new)  
heatmapForMissingValues(qData)
```

---

histPValue\_HC

*Plots a histogram of p-values*

---

### Description

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**

```
data(Exp1_R25_prot, package="DAPARdata")  
obj <- Exp1_R25_prot[seq_len(100)]  
level <- 'protein'  
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)  
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)  
obj <- MetaCellFiltering(obj, indices, cmd = "delete")  
qData <- Biobase::exprs(obj$new)  
sTab <- Biobase::pData(obj$new)  
allComp <- limmaCompleteTest(qData, sTab)  
histPValue_HC(allComp$P_Value[1])
```

---

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**

tab	An object of class MSnSet.
conditions	A vector of conditions in the dataset
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 $qn * \text{median}(\text{sd}(\text{observed values}))$ 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 or beta.

**Value**

The object obj which has been imputed

**Author(s)**

Thomas Burger, Samuel Wiczorek

**Examples**

```
utils::data(Exp1_R25_pept, package = "DAPARdata")
obj.imp <- wrapper.impute.pa2(Exp1_R25_pept[seq_len(100)],
distribution = "beta")
```

---

```
inner.aggregate.iter  .xxx
```

---

**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

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj[seq_len(10)], protID, FALSE)
qdata.agg <- inner.aggregate.iter(Biobase::exprs(obj[seq_len(10)]), X)
```

---

`inner.aggregate.topn`    `xxxx`

---

**Description**

xxxx

**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 Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj, protID, FALSE)
inner.aggregate.topn(Biobase::exprs(obj), X)
```

---

inner.mean	xxxx
------------	------

---

**Description**

xxxx

**Usage**

```
inner.mean(pepData, X)
```

**Arguments**

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

**Value**

xxxxx

**Author(s)**

Samuel Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj, protID, FALSE)
inner.mean(Biobase::exprs(obj), X)
```

---

inner.sum	xxx
-----------	-----

---

**Description**

xxx

**Usage**

```
inner.sum(pepData, X)
```

**Arguments**

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

**Value**

A matrix

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj, protID, FALSE)
inner.sum(Biobase::exprs(obj), X)
```

---

is.subset	xxx
-----------	-----

---

**Description**

xxx

**Usage**

```
is.subset(set1, set2)
```

**Arguments**

set1	xxx
set2	xxx

**Value**

xxx

**Examples**

```
is.subset('a', letters)
is.subset(c('a', 'c', 't'), letters)
is.subset(c('a', 3, 't'), letters)
is.subset(3, letters)
```

---

LH0

xxxxxx

**Description**

xxxxxx

**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**

xxxxxxxxxx..

**Author(s)**

Thomas Burger, Laurent Jacob

**Examples**

NULL

---

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

---

**Description**

xxxxxx

**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

**Examples**

NULL

---

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

---

**Description**

xxxxxx

**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**

xxxxxxxxxx..

**Author(s)**

Thomas Burger, Laurent Jacob

**Examples**

NULL

---

LH1.lm	xxxxxx
--------	--------

---

**Description**

xxxxxx

**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**

xxxxxxxxxx..

**Author(s)**

Thomas Burger, Laurent Jacob

**Examples**

NULL

---

limmaCompleteTest	<i>Computes a hierarchical differential analysis</i>
-------------------	--

---

## Description

Computes a hierarchical differential analysis

## Usage

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

## Arguments

qData	A matrix of quantitative data, without any missing values.
sTab	A dataframe of experimental design (Biobase::pData()).
comp.type	A string that corresponds to the type of comparison. Values are: 'anova1way', '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)

Hélène Borges, Thomas Burger, Quentin Gai-Gianetto, Samuel Wiczorek

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept
qData <- Biobase::exprs(obj)
sTab <- Biobase::pData(obj)
limma <- limmaCompleteTest(qData, sTab, comp.type = "anova1way")
```

---

listSheets	<i>This function returns the list of the sheets names in a Excel file.</i>
------------	--

---

**Description**

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

**Usage**

```
listSheets(file)
```

**Arguments**

file	The name of the Excel file.
------	-----------------------------

**Value**

A vector

**Author(s)**

Samuel Wieczorek

**Examples**

```
NULL
```

---

LOESS	<i>Normalisation LOESS</i>
-------	----------------------------

---

**Description**

Normalisation LOESS

**Usage**

```
LOESS(qData, conds, type = "overall", span = 0.7)
```

**Arguments**

qData	A numeric matrix.
conds	xxx
type	"overall" (shift all the sample distributions at once) or "within conditions" (shift the sample distributions within each condition at a time).
span	xxx



**Value**

A normalized numeric matrix

**Author(s)**

Thomas Burger, Helene Borges, Anais Courtier, Enora Fremy

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
qData <- Biobase::exprs(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)$Condition
normalized <- LOESS(qData, conds, type = "overall")
```

---

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

---

**Description**

Builds the contrast matrix

**Usage**

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

**Arguments**

design	The data.frame which correspond to the 'pData()' function of package '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).
design.level	xxx

**Value**

A constrat matrix

**Author(s)**

Thomas Burger, Quentin Gaii-Gianetto, Samuel Wiczorek

## Examples

```
data(Exp1_R25_pept, package='DAPARdata')
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

Builds the design matrix

## Usage

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

## Arguments

sTab            The data.frame which correspond to the 'pData()' function of package 'MSnbase'.

## Value

A design matrix

## Author(s)

Thomas Burger, Quentin Giai-Gianetto, Samuel Wiczorek

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")
make.design(Biobase::pData(Exp1_R25_pept))
```

---

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

---

**Description**

Builds the design matrix for designs of level 1

**Usage**

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

**Arguments**

sTab                   The data.frame which correspond to the 'pData()' function of package 'MSnbase'.

**Value**

A design matrix

**Author(s)**

Thomas Burger, Quentin Giai-Gianetto, Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
make.design.1(Biobase::pData(Exp1_R25_pept))
```

---

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

---

**Description**

Builds the design matrix for designs of level 2

**Usage**

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

**Arguments**

sTab                   The data.frame which correspond to the 'pData()' function of package 'MSnbase'.

**Value**

A design matrix

**Author(s)**

Thomas Burger, Quentin Giai-Gianetto, Samuel Wiczorek

**Examples**

```
data(Exp1_R25_pept, package='DAPARdata')
make.design.2(Biobase::pData(Exp1_R25_pept))
```

---

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

---

**Description**

Builds the design matrix for designs of level 3

**Usage**

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

**Arguments**

sTab            The data.frame which correspond to the 'pData()' function of package 'MSnbase'.

**Value**

A design matrix

**Author(s)**

Thomas Burger, Quentin Giai-Gianetto, Samuel Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
sTab <- cbind(Biobase::pData(Exp1_R25_pept), Tech.Rep = 1:6)
make.design.3(sTab)
```

---

match.metacell	<i>Similar to the function is.na but focused on the equality with the paramter 'type'.</i>
----------------	--

---

### Description

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

### Usage

```
match.metacell(metadata, pattern = NULL, level)
```

### Arguments

metadata	A data.frame
pattern	The value to search in the dataframe
level	xxx

### Value

A boolean dataframe

### Author(s)

Samuel Wieczorek

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10), ]
metadata <- GetMetacell(obj)
m <- match.metacell(metadata, pattern = "Missing", level = "peptide")
m <- match.metacell(metadata, pattern = NULL, level = "peptide")
m <- match.metacell(metadata, pattern = c('Missing', 'Missing POV'), level = "peptide")
```

---

MeanCentering	<i>Normalisation MeanCentering</i>
---------------	------------------------------------

---

### Description

Normalisation MeanCentering

**Usage**

```
MeanCentering(
  qData,
  conds,
  type = "overall",
  subset.norm = NULL,
  scaling = FALSE
)
```

**Arguments**

qData	xxx
conds	xxx
type	"overall" (shift all the sample distributions at once) or "within conditions" (shift the sample distributions within each condition at a time).
subset.norm	A vector of index indicating rows to be used for normalization
scaling	A boolean that indicates if the variance of the data have to be forced to unit (variance reduction) or not.

**Value**

A normalized numeric matrix

**Author(s)**

Samuel Wieczorek, Thomas Burger, Helene Borges, Anais Courtier, Enora Fremy

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
qData <- Biobase::exprs(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)$Condition
normalized <- MeanCentering(qData, conds, type = "overall")
```

---

metacell.def

*Metadata vocabulary for entities*


---

**Description**

This function gives the vocabulary used for the metadata of each entity in each condition.

Peptide-level vocabulary

├─ 'Any' │ │ │ │ 1.0 'Quantified' │ │ │ │ │ 1.1 "Quant. by direct id" (color 4, white) │ │ │ │ │ 1.2 "Quant. by recovery" (color 3, lightgrey) │ │ │ │ │ 2.0 "Missing" (no color) │ │ │ │ │ 2.1 "Missing POV" (color 1) │ │ │ │ │ 2.2 'Missing MEC' (color 2) │ │ │ │ │ 3.0 'Imputed' │ │ │ │ │ 3.1 'Imputed POV' (color 1) │ │ │ │ │ 3.2 'Imputed MEC' (color 2)

Protein-level vocabulary: |− 'Any' | | | |− 1.0 'Quantified' | | | | | |− 1.1 "Quant. by direct id" (color 4, white) | | | | | |− 1.2 "Quant. by recovery" (color 3, lightgrey) | | | |− 2.0 "Missing" | | | | | |− 2.1 "Missing POV" (color 1) | | | | | |− 2.2 'Missing MEC' (color 2) | | | |− 3.0 'Imputed' | | | | | |− 3.1 'Imputed POV' (color 1) | | | | | |− 3.2 'Imputed MEC' (color 2) | | | |− 4.0 'Combined tags' (color 3bis, lightgrey)

## Usage

```
metacell.def(level)
```

## Arguments

level	A string designing the type of entity/pipeline. Available values are: 'peptide', 'protein'
-------	--

## Value

```
xxx
```

## Author(s)

Thomas Burger, Samuel Wieczorek

## Examples

```
metacell.def('protein')
metacell.def('peptide')
```

---

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

---

## Description

#' Filters the lines of Biobase::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.

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.

## Usage

```
MetaCellFiltering(obj, indices, cmd, processText = "")
```

**Arguments**

obj                    An object of class MSnSet containing quantitative data.  
 indices                A vector of integers which are the indices of lines to keep.  
 cmd                    xxxx. Available values are: 'delete', 'keep'.  
 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 Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
level <- 'peptide'

#'
#' Delete lines which are entirely filled with any missing values ('Missing MEC' and 'Missing POV')
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeLine(metacell.mask)
obj.filter <- MetaCellFiltering(obj, indices, "delete")

obj <- obj[1:10]

pattern <- "Quantified"
type <- "AtLeastOneCond"
percent <- FALSE
op <- ">="
th <- 3
indices <- GetIndices_MetacellFiltering(obj, level, pattern, type, percent, op, th)
obj <- MetaCellFiltering(obj, indices, "keep")$new
#fData(obj)[, obj@experimentData@other$names_metacell]

pattern <- "Quant. by direct id"
type <- "AtLeastOneCond"
percent <- FALSE
op <- ">="
th <- 3
indices <- GetIndices_MetacellFiltering(obj, level, pattern, type, percent, op, th)
obj <- MetaCellFiltering(obj, indices, "keep")$new
#fData(obj)[, obj@experimentData@other$names_metacell]
names.1 <- rownames(obj)

obj <- Exp1_R25_pept[seq_len(100)]
pattern <- "Quant. by direct id"
```



```
type <- "AtLeastOneCond"
percent <- FALSE
op <- ">="
th <- 3
indices <- GetIndices_MetacellFiltering(obj, level, pattern, type, percent, op, th)
obj <- MetaCellFiltering(obj, indices, "keep")$new
#fData(obj)[, obj@experimentData@other$names_metacell]

pattern <- "Quantified"
type <- "AtLeastOneCond"
percent <- FALSE
op <- ">="
th <- 3
indices <- GetIndices_MetacellFiltering(obj, level, pattern, type, percent, op, th)
obj <- MetaCellFiltering(obj, indices, "keep")$new
#fData(obj)[, obj@experimentData@other$names_metacell]
names.2 <- rownames(obj)
```

---

MetacellFilteringScope

*Lists the metacell scopes for filtering*

---

### **Description**

Lists the metacell scopes for filtering

### **Usage**

```
MetacellFilteringScope()
```

### **Value**

xxx

### **Examples**

```
MetacellFilteringScope()
```

---

metacellHisto\_HC      *Histogram of missing values*

---

### Description

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

### Usage

```
metacellHisto_HC(  
  obj,  
  pattern = NULL,  
  indLegend = "auto",  
  showValues = FALSE,  
  pal = NULL  
)
```

### Arguments

<code>obj</code>	xxx
<code>pattern</code>	xxx
<code>indLegend</code>	The indices of the column name's in <code>Biobase::pData()</code> tab
<code>showValues</code>	A logical that indicates wether numeric values should be drawn above the bars.
<code>pal</code>	xxx

### Value

A histogram

### Author(s)

Florence Combes, Samuel Wieczorek

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")  
obj <- Exp1_R25_pept  
pattern <- "Missing POV"  
pal <- ExtendPalette(2, "Dark2")  
metacellHisto_HC(obj, pattern, showValues = TRUE, pal = pal)
```

---

`metacellPerLinesHistoPerCondition_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.

**Usage**

```
metacellPerLinesHistoPerCondition_HC(  
  obj,  
  pattern = NULL,  
  indLegend = "auto",  
  showValues = FALSE,  
  pal = NULL  
)
```

**Arguments**

<code>obj</code>	xxx
<code>pattern</code>	xxx
<code>indLegend</code>	The indice of the column name's in <code>Biobase::pData()</code> tab
<code>showValues</code>	A logical that indicates wether numeric values should be drawn above the bars.
<code>pal</code>	xxx

**Value**

A bar plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")  
obj <- Exp1_R25_pept  
pal <- ExtendPalette(length(unique(Biobase::pData(obj)$Condition)), "Dark2")  
metacellPerLinesHistoPerCondition_HC(obj, c("Missing POV", "Missing MEC"), pal = pal)  
metacellPerLinesHistoPerCondition_HC(obj, "Quantified")
```

---

metacellPerLinesHisto\_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

```
metacellPerLinesHisto_HC(  
  obj,  
  pattern = NULL,  
  detailed = FALSE,  
  indLegend = "auto",  
  showValues = FALSE  
)
```

### Arguments

obj	xxx.
pattern	xxx
detailed	'value' or 'percent'
indLegend	The indice of the column name's in Biobase::pData() tab
showValues	A logical that indicates whether numeric values should be drawn above the bars.

### Value

A bar plot

### Author(s)

Florence Combes, Samuel Wiczorek

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")  
obj <- Exp1_R25_pept  
  
obj <- obj[1:10]  
  
metacellPerLinesHisto_HC(obj, pattern = "Missing POV")  
  
metacellPerLinesHisto_HC(obj)  
metacellPerLinesHisto_HC(obj, pattern = "Quantified")  
metacellPerLinesHisto_HC(obj, pattern = "Quant. by direct id")
```

```
metacellPerLinesHisto_HC(obj, pattern = "Quant. by recovery")
metacellPerLinesHisto_HC(obj, pattern = c("Quantified", "Quant. by direct id", "Quant. by recovery"))
```

---

Metacell_DIA_NN	<i>Sets the metacell dataframe for datasets which are from Dia-NN software</i>
-----------------	--

---

## Description

Actually, this function uses the generic function to generate metacell info

## Usage

```
Metacell_DIA_NN(qdata, conds, df, level = NULL)
```

## Arguments

qdata	An object of class MSnSet
conds	xxx
df	A list of integer xxxxxxx
level	xxx

## Value

xxxxx

## Author(s)

Samuel Wiczorek

## Examples

```
file <- system.file("extdata", "Exp1_R25_pept.txt", package = "DAPARdata")
data <- read.table(file, header = TRUE, sep = "\t", stringsAsFactors = FALSE)
metadataFile <- system.file("extdata", "samples_Exp1_R25.txt",
  package = "DAPARdata"
)
metadata <- read.table(metadataFile,
  header = TRUE, sep = "\t", as.is = TRUE,
  stringsAsFactors = FALSE
)
conds <- metadata$Condition
qdata <- data[seq_len(100), seq.int(from = 56, to = 61)]
df <- data[seq_len(100), seq.int(from = 43, to = 48)]
df <- Metacell_DIA_NN(qdata, conds, df, level = "peptide")
```

---

Metacell_generic	<i>Sets the metacell dataframe for dataset without information about the origin of identification</i>
------------------	---

---

### Description

In the quantitative columns, a missing value is identified by no value rather than a value equal to 0. Conversion rules QuantiTag NA or 0 NA The only information detected with this function are about missing values ( MEC and POV).

### Usage

```
Metacell_generic(qdata, conds, level)
```

### Arguments

qdata	An object of class MSnSet
conds	xxx
level	xxx

### Value

xxxxx

### Author(s)

Samuel Wieczorek

### Examples

```
file <- system.file("extdata", "Exp1_R25_pept.txt", package = "DAPARdata")
data <- read.table(file, header = TRUE, sep = "\t", stringsAsFactors = FALSE)
metadataFile <- system.file("extdata", "samples_Exp1_R25.txt",
  package = "DAPARdata"
)
metadata <- read.table(metadataFile,
  header = TRUE, sep = "\t", as.is = TRUE,
  stringsAsFactors = FALSE
)
conds <- metadata$Condition
qdata <- data[seq_len(100), seq.int(from = 56, to = 61)]
df <- data[seq_len(100), seq.int(from = 43, to = 48)]
df <- Metacell_generic(qdata, conds, level = "peptide")
```

---

Metacell\_maxquant      *Sets the metacell dataframe*

---

### Description

Initial conversion rules for maxquant |-----|-----|-----| | Quanti | Identification  
 | Tag | |-----|-----|-----| | == 0 | whatever | 2.0 | | > 0 | 'By MS/MS' | 1.1 | | > 0 |  
 'By matching' | 1.2 | | > 0 | unknown col | 1.0 | |-----|-----|-----|

### Usage

```
Metacell_maxquant(qdata, conds, df, level = NULL)
```

### Arguments

qdata	An object of class MSnSet
conds	xxx
df	A list of integer xxxxxxxx
level	xxx

### Value

xxxxx

### Author(s)

Samuel Wiczorek

### Examples

```
file <- system.file("extdata", "Exp1_R25_pept.txt", package = "DAPARdata")
data <- read.table(file, header = TRUE, sep = "\t", stringsAsFactors = FALSE)
metadataFile <- system.file("extdata", "samples_Exp1_R25.txt",
  package = "DAPARdata"
)
metadata <- read.table(metadataFile,
  header = TRUE, sep = "\t", as.is = TRUE,
  stringsAsFactors = FALSE
)
conds <- metadata$Condition
qdata <- data[seq_len(10), seq.int(from = 56, to = 61)]
df <- data[seq_len(10), seq.int(from = 43, to = 48)]
df2 <- Metacell_maxquant(qdata, conds, df, level = "peptide")
```

---

Metacell_proline	<i>Sets the metacell dataframe for datasets which are from Proline software</i>
------------------	---

---

### Description

In the quantitative columns, a missing value is identified by no value rather than a value equal to 0.

In these datasets, the metacell info is computed from the 'PSM count' columns.

Conversion rules Initial conversion rules for proline |-----|-----|----| | Quanti | PSM  
count | Tag | |-----|-----|----| | == 0 | N.A. | whatever | 2.0 | | > 0 | > 0 | 1.1 | | > 0 | ==  
0 | 1.2 | | > 0 | unknown col | 1.0 | |-----|-----|----|

### Usage

```
Metacell_proline(qdata, conds, df, level = NULL)
```

### Arguments

qdata	An object of class MSnSet
conds	xxx
df	A list of integer xxxxxxxx
level	xxx

### Value

xxxxx

### Author(s)

Samuel Wieczorek

### Examples

```
file <- system.file("extdata", "Exp1_R25_pept.txt", package = "DAPARdata")
data <- read.table(file, header = TRUE, sep = "\t", stringsAsFactors = FALSE)
metadataFile <- system.file("extdata", "samples_Exp1_R25.txt", package = "DAPARdata")
metadata <- read.table(metadataFile, header = TRUE, sep = "\t", as.is = TRUE, stringsAsFactors = FALSE)
conds <- metadata$Condition
qdata <- data[seq_len(100), seq.int(from = 56, to = 61)]
df <- data[seq_len(100), seq.int(from = 43, to = 48)]
df <- Metacell_proline(qdata, conds, df, level = "peptide")
```



metacombine

*Combine peptide metadata to build protein metadata***Description**

Aggregation rules for the cells metadata of peptides. Please refer to the metacell vocabulary in 'metacell.def()'

# Basic aggregation (RULE 1) Aggregation of a mix of missing values (2.X) with quantitative and/or imputed values (1.X, 3.X) |----- Not possible (tag : 'STOP') |-----

Aggregation of different types of missing values (among 2.1, 2.2) |----- \* (RULE 2) Aggregation of 2.1 peptides between each other gives a missing value (2.0) \* (RULE 3) Aggregation of 2.2 peptides between each other gives a missing value (2.0) \* (RULE 4) Aggregation of a mix of 2.1 and 2.2 gives a missing value (2.0) |-----

Aggregation of a mix of quantitative and/or imputed values (among 1.x and 3.X) |----- \* (RULE 5) if the type of all the peptides to aggregate is either 1.0, 1.1 or 1.2, then the final metadata is set to the corresponding tag \* (RULE 5bis) if the type of all the peptides to aggregate is either 3.0, 3.1 or 3.2, then the final metadata is set to the corresponding tag \* (RULE 6) if the set of metacell to aggregate is a mix of 1.x, then the final metadata is set to 1.0 \* (RULE 7) if the set of metacell to aggregate is a mix of 3.x, then the final metadata is set to 3.0 \* (RULE 8) if the set of metacell to aggregate is a mix of 3.X and 1.X, then the final metadata is set to 4.0

# Post processing Update metacell with POV/MEC status for the categories 2.0 and 3.0 TODO

**Usage**

```
metacombine(met, level)
```

**Arguments**

```
met          xxx
level       xxx
```

**Value**

```
xxx
```

**Examples**

```
ll <- metacell.def("peptide")$node
for (i in seq_len(length(ll))) {
  test <- lapply(
    combn(ll, i, simplify = FALSE),
    function(x) tag <- metacombine(x, "peptide")
  )
}

metacombine(c('Quant. by direct id', 'Missing POV'), 'peptide')
```

---

`mvImage`*Heatmap of missing values*

---

**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**

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

---

`my_hc_chart`*Customised resetZoomButton of highcharts plots*

---

**Description**

Customised 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	<i>Customised contextual menu of highcharts plots</i>
------------------	---

---

**Description**

Customised 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

*Retrieve the indices of non-zero elements in sparse matrices*

---

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

---

`normalizeMethods.dapar`*List normalization methods with tracking option*

---

**Description**

List normalization methods with tracking option

**Usage**

```
normalizeMethods.dapar(withTracking = FALSE)
```

**Arguments**

```
withTracking    xxx
```

**Value**

```
xxx
```

**Examples**

```
normalizeMethods.dapar()
```

---

`NumericalFiltering`     *Removes lines in the dataset based on numerical conditions.*

---

**Description**

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

**Usage**

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

**Arguments**

<code>obj</code>	An object of class MSnSet.
<code>name</code>	The name of the column that correspond to the line to filter
<code>value</code>	A number
<code>operator</code>	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 Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
NumericalFiltering(Exp1_R25_pept[seq_len(100)], "A_Count", "6", "==")
```

---

NumericalgetIndicesOfLinesToRemove

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

---

**Description**

This function returns the indices 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 Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
NumericalgetIndicesOfLinesToRemove(Exp1_R25_pept[seq_len(100)], "A_Count",
value = "6", operator = "==")
```

---

OWAnova

*Applies aov() on a vector of protein abundances using the design derived from the sample names (simple aov wrapper)*

---

**Description**

Applies aov() on a vector of protein abundances using the design derived from the sample names (simple aov wrapper)

**Usage**

```
OWAnova(current_protein, conditions)
```

**Arguments**

current\_protein      a real vector

conditions          the list of groups the protein belongs to

**Value**

see aov()

**Author(s)**

Thomas Burger

**Examples**

```
protein_abundance <- rep(rnorm(3, mean= 18, sd=2), each=3) + rnorm(9)
groups <- c(rep("group1",3),rep("group2",3),rep("group3",3))
OWAnova(protein_abundance,groups)
```

---

Parent	<i>Parent name of a node</i>
--------	------------------------------

---

**Description**

xxx

**Usage**

Parent(level, node = NULL)

**Arguments**

level xxx

node xxx

#' @examples Parent('protein', 'Missing') Parent('protein', 'Missing POV')  
 Parent('protein', c('Missing POV', 'Missing MEC')) Parent('protein', c('Missing',  
 'Missing POV', 'Missing MEC'))

---

pepa.test	<i>PEptide based Protein differential Abundance test</i>
-----------	--

---

**Description**

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

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
protID <- "Protein_group_IDs"
obj <- Exp1_R25_pept[seq_len(20)]
X <- BuildAdjacencyMatrix(obj, protID, FALSE)
```

---

pkgs.require

*Loads packages*

---

**Description**

Checks if a package is available to load it

**Usage**

```
pkgs.require(ll.deps)
```

**Arguments**

ll.deps            A 'character()' vector which contains packages names

**Author(s)**

Samuel Wieczorek

**Examples**

```
pkgs.require('DAPAR')
```

plotJitter                    *Jitter plot of CC*

---

**Description**

Jitter plot of CC

**Usage**

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

**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**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
X <- BuildAdjacencyMatrix(obj, "Protein_group_IDs", TRUE)
ll <- get.pep.prot.cc(X)
plotJitter(ll)
```

---

plotJitter\_rCharts        *Display a a jitter plot for CC*

---

**Description**

Display a a jitter plot for CC

**Usage**

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

**Arguments**

df                    xxxx  
clickFunction        xxxx

**Value**

A plot

**Author(s)**

Thomas Burger, Samuel Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
X <- BuildAdjacencyMatrix(obj, "Protein_group_IDs", TRUE)
ll <- get.pep.prot.cc(X)[1:4]
n.prot <- unlist(lapply(ll, function(x) {length(x$proteins)}))
n.pept <- unlist(lapply(ll, function(x) {length(x$peptides)}))
df <- tibble::tibble(
  x = jitter(n.pept),
  y = jitter(n.prot),
  index = seq_len(length(ll))
)
plotJitter_rCharts(df)
```

---

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 Wiczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
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 Wiczorek

**Examples**

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

---

plotPCA_Ind	<i>Plots individuals of PCA</i>
-------------	---------------------------------

---

**Description**

Plots 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**

```
data(Exp1_R25_pept, package="DAPARdata")
res.pca <- wrapper.pca(Exp1_R25_pept)
plotPCA_Ind(res.pca)
```

---

plotPCA_Var	<i>Plots variables of PCA</i>
-------------	-------------------------------

---

**Description**

Plots 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 Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
res.pca <- wrapper.pca(Exp1_R25_pept)
plotPCA_Var(res.pca)
```

---

postHocTest

*Post-hoc tests for classic 1-way ANOVA*

---

**Description**

This function allows to compute a post-hoc test after a 1-way ANOVA analysis. It expects as input an object obtained with the function `classic1wayAnova`. The second parameter allows to choose between 2 different post-hoc tests: the Tukey Honest Significant Differences (specified as "TukeyHSD") and the Dunnett test (specified as "Dunnett").

**Usage**

```
postHocTest(aov_fits, post_hoc_test = "TukeyHSD")
```

**Arguments**

`aov_fits` a list containing aov fitted model objects

`post_hoc_test` a character string indicating which post-hoc test to use. Possible values are "TukeyHSD" or "Dunnett". See details for what to choose according to your experimental design.

**Details**

This is a function allowing to realise post-hoc tests for a set of proteins/peptides for which a classic 1-way anova has been performed with the function `classic1wayAnova`. Two types of tests are currently available: The Tukey HSD's test and the Dunnett's test. Default is Tukey's test. The Tukey HSD's test compares all possible pairs of means, and is based on a studentized range distribution. Here is used the `TukeyHSD()` function, which can be applied to balanced designs (same number of samples in each group), but also to midly unbalanced designs. The Dunnett's test compares a single control group to all other groups. Make sure the factor levels are properly ordered.

**Value**

a list of 2 dataframes: first one called "LogFC" contains all pairwise comparisons logFC values (one column for one comparison) for each analysed feature; The second one named "P\_Value" contains the corresponding pvalues.

**Author(s)**

Hélène Borges

**Examples**

```
## Not run: examples/ex_postHocTest.R
```

---

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 Wiczorek

**Examples**

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

---

QuantileCentering      *Normalisation QuantileCentering*

---

### Description

Normalisation QuantileCentering

### Usage

```
QuantileCentering(  
  qData,  
  conds = NULL,  
  type = "overall",  
  subset.norm = NULL,  
  quantile = 0.15  
)
```

### Arguments

qData	xxx
conds	xxx
type	"overall" (shift all the sample distributions at once) or "within conditions" (shift the sample distributions within each condition at a time).
subset.norm	A vector of index indicating rows to be used for normalization
quantile	A float that corresponds to the quantile used to align the data.

### Value

A normalized numeric matrix

### Author(s)

Samuel Wieczorek, Thomas Burger, Helene Borges, Anais Courtier, Enora Fremy

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")  
obj <- Exp1_R25_pept  
conds <- Biobase::pData(Exp1_R25_pept)$Condition  
normalized <- QuantileCentering(Biobase::exprs(obj), conds,  
  type = "within conditions", subset.norm = seq_len(10)  
)
```



---

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**

```
data(Exp1_R25_pept, package="DAPARdata")
df1 <- Exp1_R25_pept[seq_len(100)]
df2 <- Exp1_R25_pept[seq.int(from = 200, to = 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, sheet = NULL)
```

**Arguments**

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

**Value**

A data.frame

**Author(s)**

Samuel Wieczorek

**Examples**

NULL

---

reIntroduceMEC            *Put back LAPALA into a MSnSet object*

---

**Description**

Put back LAPALA into a MSnSet object

**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 Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")  
obj <- Exp1_R25_pept[seq_len(100)]  
lapala <- findMECBlock(obj)  
obj <- wrapper.impute.detQuant(obj, na.type = c("Missing POV", "Missing MEC"))  
obj <- reIntroduceMEC(obj, lapala)
```

---

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

---

**Description**

Removes lines in the dataset based on a prefix string.

**Usage**

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

**Arguments**

obj	An object of class MSnSet.
idLine2Delete	The name of the column that correspond to the data to filter
prefix	A character string that is the prefix to find in the data

**Value**

An object of class MSnSet.

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
removeLines(Exp1_R25_pept[seq_len(100)], "Potential_contaminant")
removeLines(Exp1_R25_pept[seq_len(100)], "Reverse")
```

---

samLRT	<i>xxxxxx</i>
--------	---------------

---

**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**

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
s1	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

**Examples**

NULL

---

saveParameters

*Saves the parameters of a tool in the pipeline of Prostar*

---

**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**

```
data(Exp1_R25_pept, package="DAPARdata")
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 'clusterProfiler'
maxRes	The maximum number of categories to display in the plot
title	The title of the plot

**Value**

A dotplot

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot
if (!requireNamespace("org.Sc.sgd.db", quietly = TRUE)) {
  stop("Please install org.Sc.sgd.db:
       BiocManager::install('org.Sc.sgd.db')")
}
library(org.Sc.sgd.db)
univ <- univ_AnnotDbPkg("org.Sc.sgd.db")
ego <- enrich_GO(
  data = Biobase::fData(obj)$Protein.IDs, idFrom = "UNIPROT",
  orgdb = "org.Sc.sgd.db", ont = "MF", pval = 0.05, universe = univ
)
scatterplotEnrichGO_HC(ego)
```

---

search.metacell.tags *Search pattern in metacell vocabulary*

---

**Description**

Gives all the tags of the metadata vocabulary containing the pattern (parent and all its children).

**Usage**

```
search.metacell.tags(pattern, level, depth = "1")
```

**Arguments**

pattern	The string to search.
level	The available levels are : names()
depth	xxx

**Value**

xxx

**Author(s)**

Samuel Wieczorek

**Examples**

```
search.metacell.tags("Missing POV", "peptide")
search.metacell.tags("Quantified", "peptide", depth = "0")
```

---

separateAdjPval	<i>Computes the adjusted p-values separately on contrast using CP4P</i>
-----------------	---

---

**Description**

Computes the adjusted p-values separately on contrast using CP4P

**Usage**

```
separateAdjPval(x, pval.threshold = 1.05, method = 1)
```

**Arguments**

x	a proteins x contrasts dataframe of (raw) p-values
pval.threshold	all the p-values above the threshold are not considered. Default is 1.05 (which is equivalent to have no threshold). Applying a threshold nearby 1 can be instrumental to improve the uniformity under the null, notably in case of upstream multiple contrast correction (for experienced users only)
method	a method to estimate pi_0, see CP4P

**Value**

a proteins x contrasts table of adjusted p-values

**Author(s)**

Thomas Burger

**Examples**

```
data(Exp1_R25_prot, package='DAPARdata')
exdata <- Exp1_R25_prot[1:5,]
separateAdjPval(testAnovaModels(applyAnovasOnProteins(exdata), "TukeyHSD"))$P_Value)
```

---

SetCC	<i>Returns the connected components</i>
-------	---

---

**Description**

Returns the connected components

**Usage**

```
SetCC(obj, cc)
```

**Arguments**

obj            An object (peptides) of class MSnSet.  
 cc            The connected components list

**Value**

xxx

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package='DAPARdata')
Xshared <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(100)],
  "Protein_group_IDs", FALSE)
Xunique <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(100)],
  "Protein_group_IDs", TRUE)
ll.X <- list(matWithSharedPeptides = Xshared,
  matWithUniquePeptides = Xunique)
Exp1_R25_pept <- SetMatAdj(Exp1_R25_pept, ll.X)
l11 <- get.pep.prot.cc(GetMatAdj(Exp1_R25_pept)$matWithSharedPeptides)
l12 <- get.pep.prot.cc(
  GetMatAdj(Exp1_R25_pept)$matWithUniquePeptides)
cc <- list(allPep = l11, onlyUniquePep = l12)
Exp1_R25_pept <- SetCC(Exp1_R25_pept, cc)
```

---

SetMatAdj

*Record the adjacency matrices in a slot of the dataset of class MSnSet*

---

**Description**

Record the adjacency matrices in a slot of the dataset of class MSnSet

**Usage**

```
SetMatAdj(obj, X)
```

**Arguments**

obj            An object (peptides) of class MSnSet.  
 X            A list of two adjacency matrices

**Value**

NA



**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
Xshared <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(100)],
  "Protein_group_IDs", FALSE)
Xunique <- BuildAdjacencyMatrix(Exp1_R25_pept[seq_len(100)],
  "Protein_group_IDs", TRUE)
ll.X <- list(matWithSharedPeptides = Xshared,
  matWithUniquePeptides = Xunique)
Exp1_R25_pept <- SetMatAdj(Exp1_R25_pept, ll.X)
```

---

Set\_POV\_MEC\_tags      *Sets the MEC tag in the metacell*

---

**Description**

This function is based on the metacell dataframe to look for either missing values (used to update an initial dataset) or imputed values (used when post processing protein metacell after aggregation)

**Usage**

```
Set_POV_MEC_tags(conds, df, level)
```

**Arguments**

conds	xxx
df	An object of class MSnSet
level	Type of entity/pipeline

**Value**

An instance of class MSnSet.

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
cols.for.ident <- c("metacell_Intensity_C_R1", "metacell_Intensity_C_R2",
"metacell_Intensity_C_R3", "metacell_Intensity_D_R1",
"metacell_Intensity_D_R2", "metacell_Intensity_D_R3")
conds <- Biobase::pData(obj)$Condition
df <- Biobase::fData(obj)[, cols.for.ident]
df <- Set_POV_MEC_tags(conds, df, level = "peptide")
```

---

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

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj.pep <- Exp1_R25_pept[seq_len(10)]
protID <- "Protein_group_IDs"
X <- BuildAdjacencyMatrix(obj.pep, protID, FALSE)
ll <- splitAdjacencyMat(X)
```

---

StringBasedFiltering *Removes lines in the dataset based on a prefix strings (contaminants, reverse or both).*

---

### Description

Removes lines in the dataset based on a 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 Wieczorek

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")  
StringBasedFiltering(  
  Exp1_R25_pept[seq_len(100)], "Potential_contaminant", "+", "Reverse", "+")
```

---

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

---

**Description**

Removes lines in the dataset based on a 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 Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj.filter <- StringBasedFiltering2(Exp1_R25_pept[seq_len(100)],
  "Potential_contaminant", "+")
```

---

SumByColumns

*Normalisation SumByColumns*

---

**Description**

Normalisation SumByColumns

**Usage**

```
SumByColumns(qData, conds = NULL, type = NULL, subset.norm = NULL)
```

**Arguments**

qData	xxxx
conds	xxx
type	Available values are "overall" (shift all the sample distributions at once) or "within conditions" (shift the sample distributions within each condition at a time).
subset.norm	A vector of index indicating rows to be used for normalization

**Value**

A normalized numeric matrix

**Author(s)**

Samuel Wiczorek, Thomas Burger, Helene Borges, Anais Courtier, Enora Fremy

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
qData <- Biobase::exprs(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)$Condition
normalized <- SumByColumns(qData, conds,
  type = "within conditions",
  subset.norm = seq_len(10)
)
```

---

SymFilteringOperators xxx

---

**Description**

xxx

**Usage**

```
SymFilteringOperators()
```

**Value**

A 'character()'

**Examples**

```
SymFilteringOperators()
```

test.design                      *Check if xxxxxx*

---

**Description**

Check if xxxxxx

**Usage**

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

**Arguments**

tab                      A data.frame which correspond to xxxxxx

**Value**

A list of two items

**Author(s)**

Thomas Burger, Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
test.design(Biobase::pData(Exp1_R25_pept)[, seq_len(3)])
```

---

testAnovaModels                      *Applies a statistical test on each element of a list of linear models*

---

**Description**

Applies a statistical test on each element of a list of linear models

**Usage**

```
testAnovaModels(aov_fits, test = "Omnibus")
```

**Arguments**

`aov_fits` a list of linear models, such as those outputted by `applyAnovasOnProteins`

`test` a character string among "Omnibus", "TukeyHSD", "TukeySinglestep", "TukeyStepwise", "TukeyNoMTC", "DunnettSinglestep", "DunnettStepwise" and "DunnettNoMTC". "Omnibus" tests the all-mean equality, the Tukey tests compares all pairs of means and the Dunnett tests compare all the means to the first one. For multiple tests (Dunnett's or Tukey's) it is possible to correct for multiplicity (either with single-step or step-wise FWER) or not. All the Tukey's and Dunnett's tests use the `multcomp` package expect for "TukeyHSD" which relies on the `stats` package. "TukeyHSD" and "TukeyStepwise" gives similar results.

**Value**

a list of 2 tables (p-values and fold-changes, respectively)

**Author(s)**

Thomas Burger

**Examples**

```
data(Exp1_R25_prot, package='DAPARdata')
exdata <- Exp1_R25_prot[1:5,]
testAnovaModels(applyAnovasOnProteins(exdata))
```

---

thresholdpval4fdr      xxx

---

**Description**

xxx

**Usage**

```
thresholdpval4fdr(x, pval.T, M)
```

**Arguments**

`x`                    xxx

`pval.T`                xxx

`M`                     xxx

**Value**

xxx

**Author(s)**

Thomas Burger

**Examples**

NULL

---

translatedRandomBeta *Generator of simulated values*

---

**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_GO` 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

**Examples**

```
if (!requireNamespace("org.Sc.sgd.db", quietly = TRUE)) {
  stop("Please install org.Sc.sgd.db:
       BiocManager::install('org.Sc.sgd.db')")
}
library(org.Sc.sgd.db)
univ_AnnotDbPkg("org.Sc.sgd.db")
```

---

`UpdateMetacellAfterImputation`

*Update the cells metadata tags after imputation*

---

**Description**

Update the metacell information of missing values that were imputed

**Usage**

```
UpdateMetacellAfterImputation(obj)
```

**Arguments**

obj                   xxx

**Value**

xxx

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
obj.imp.pov <- wrapper.impute.KNN(obj, K = 3)
```

---

violinPlotD

*Builds a violinplot from a dataframe*

---

**Description**

Builds a violinplot from a dataframe

**Usage**

```
violinPlotD(obj, conds, keyId, legend = NULL, pal = NULL, subset.view = NULL)
```

**Arguments**

obj                   xxx  
conds                 xxx  
keyId                 xxx  
legend                A vector of the conditions (one condition per sample).  
pal                   xxx  
subset.view           xxx

**Value**

A violinplot

**Author(s)**

Samuel Wieczorek, Anais Courtier

## Examples

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot
legend <- conds <- Biobase::pData(obj)$Condition
key <- "Protein_IDs"
violinPlotD(obj, conds, key, legend, subset.view = seq_len(10))
```

---

visualizeClusters	<i>Visualize the clusters according to pvalue thresholds</i>
-------------------	--

---

## Description

Visualize the clusters according to pvalue thresholds

## Usage

```
visualizeClusters(  
  dat,  
  clust_model,  
  adjusted_pValues,  
  FDR_th = NULL,  
  ttl = "",  
  subttl = ""  
)
```

## Arguments

dat	the standardize data returned by the function [checkClusterability()]
clust_model	the clustering model obtained with dat.
adjusted_pValues	vector of the adjusted pvalues obtained for each protein with a 1-way ANOVA (for example obtained with the function [wrapperClassic1wayAnova()]).
FDR_th	the thresholds of FDR pvalues for the coloring of the profiles. The default (NULL) creates 4 thresholds: 0.001, 0.005, 0.01, 0.05 For the sake of readability, a maximum of 4 values can be specified.
ttl	title for the plot.
subttl	subtitle for the plot.

## Value

a ggplot object

## Author(s)

Helene Borges

**Examples**

```

library(dplyr)
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(1000)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
expR25_ttest <- compute_t_tests(obj$new)
averaged_means <- averageIntensities(obj$new)
only_means <- dplyr::select_if(averaged_means, is.numeric)
only_features <- dplyr::select_if(averaged_means, is.character)
means <- purrr::map(purrr::array_branch(as.matrix(only_means), 1), mean)
centered <- only_means - unlist(means)
centered_means <- dplyr::bind_cols(
  feature = dplyr::as_tibble(only_features),
  dplyr::as_tibble(centered))
difference <- only_means[, 1] - only_means[, 2]
clusters <- as.data.frame(difference) %>%
dplyr::mutate(cluster = dplyr::if_else(difference > 0, 1, 2))
vizu <- visualizeClusters(
  dat = centered_means,
  clust_model = as.factor(clusters$cluster),
  adjusted_pValues = expR25_ttest$P_Value$`25fmol_vs_10fmol_pval`,
  FDR_th = c(0.001, 0.005, 0.01, 0.05),
  ttl = "Clustering of protein profiles")

```

vsn

*Normalisation vsn***Description**

Normalisation vsn

**Usage**

vsn(qData, conds, type = NULL)

**Arguments**

qData	A numeric matrix.
conds	xxx
type	"overall" (shift all the sample distributions at once) or "within conditions" (shift the sample distributions within each condition at a time).

**Value**

A normalized numeric matrix

**Author(s)**

Thomas Burger, Helene Borges, Anais Courtier, Enora Fremy

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
qData <- Biobase::exprs(Exp1_R25_pept)
conds <- Biobase::pData(Exp1_R25_pept)$Condition
normalized <- vsn(qData, conds, type = "overall")
```

---

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.

**Usage**

```
wrapper.compareNormalizationD_HC(
  objBefore,
  objAfter,
  condsForLegend = 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).  
...             arguments for palette

**Value**

A plot

**Author(s)**

Samuel Wiczorek

### Examples

```
data(Exp1_R25_pept, package='DAPARdata')
obj <- Exp1_R25_pept
conds <- Biobase::pData(obj)[, "Condition"]
objAfter <- wrapper.normalizeD(
  obj = obj, method = "QuantileCentering",
  conds = conds, type = "within conditions"
)
wrapper.compareNormalizationD_HC(obj, objAfter, conds,
  pal = ExtendPalette(2))
```

---

wrapper.corrMatrixD\_HC

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

---

### Description

Builds a correlation matrix based on a MSnSet object.

### Usage

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

### Arguments

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

### Value

A colored correlation matrix

### Author(s)

Samuel Wiczorek

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")
wrapper.corrMatrixD_HC(Exp1_R25_pept)
```

---

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

---

**Description**

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

**Usage**

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

**Arguments**

obj	An object of class MSnSet
...	arguments for palette.

**Value**

A density plot

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")  
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 = FALSE,
  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 `Biobase::exprs(obj)` matrix with imputed values instead of missing values.

**Author(s)**

Samuel Wieczorek

**Examples**

```
utils::data(Exp1_R25_pept, package = "DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
level <- 'peptide'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj.imp.na <- wrapper.dapar.impute.mi(obj, nb.iter = 1, lapala = TRUE)
obj.imp.pov <- wrapper.dapar.impute.mi(obj, nb.iter = 1, lapala = FALSE)
```

---

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A heatmap

**Author(s)**

Alexia Dorffer

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
level <- 'peptide'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeLine(metacell.mask)
wrapper.heatmapD(obj)
```

---

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, na.type)
```

**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
na.type	A string which indicates the type of missing values to impute. Available values are: 'NA' (for both POV and MEC), 'POV', 'MEC'.

**Value**

An imputed instance of class MSnSet

**Author(s)**

Samuel Wieczorek

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
obj.imp.pov <- wrapper.impute.detQuant(obj, na.type = "Missing POV")
obj.imp.mec <- wrapper.impute.detQuant(obj, na.type = "Missing MEC")
```

---

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 = 0, na.type)
```

## Arguments

obj	An object of class MSnSet.
fixVal	A float.
na.type	A string which indicates the type of missing values to impute. Available values are: 'NA' (for both POV and MEC), 'POV', 'MEC'.

## Value

The object obj which has been imputed

## Author(s)

Samuel Wiczorek

## Examples

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10), ]
obj.imp.pov <- wrapper.impute.fixedValue(obj, 0.001, na.type = "Missing POV")
obj.imp.mec <- wrapper.impute.fixedValue(obj, 0.001, na.type = "Missing MEC")
obj.imp.na <- wrapper.impute.fixedValue(obj, 0.001, na.type = c("Missing MEC", "Missing POV"))
```

---

wrapper.impute.KNN      *KNN missing values imputation from a MSnSet object*

---

### Description

Can impute only POV missing values. 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 = NULL, K)
```

### Arguments

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

### Value

The object obj which has been imputed

### Author(s)

Samuel Wiczorek

### Examples

```
data(Exp1_R25_pept, package="DAPARdata")  
obj.imp.pov <- wrapper.impute.KNN(obj = Exp1_R25_pept[seq_len(10)], K = 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. It does not impute MEC missing values.

### Usage

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

### Arguments

obj                      An object of class MSnSet.

**Value**

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

**Author(s)**

Samuel Wieczorek

**Examples**

```
utils::data(Exp1_R25_pept, package = "DAPARdata")
obj <- Exp1_R25_pept[seq_len(10), ]
level <- 'peptide'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj.imp.na <- wrapper.impute.mle(obj)
```

---

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

---

**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 = NULL, 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 `Biobase::exprs(obj)` matrix with imputed values instead of missing values.

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(10)]
obj.imp.pov <- wrapper.impute.pa(obj)
```

---

wrapper.impute.pa2      *Missing values imputation from a MSnSet object*

---

### Description

This method is a wrapper to the function `impute.pa2()` adapted to objects of class `MSnSet`.

### Usage

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

### Arguments

<code>obj</code>	An object of class <code>MSnSet</code> .
<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 <code>qn*median(sd(observed values))</code> 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> (default) or <code>beta</code> .

### Value

The object `obj` which has been imputed

### Author(s)

Thomas Burger, Samuel Wiczorek

### Examples

```
utils::data(Exp1_R25_pept, package = "DAPARdata")
obj.imp.pa2 <- wrapper.impute.pa2(Exp1_R25_pept[seq_len(100)],
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 = NULL)
```

**Arguments**

`obj`                    An object of class `MSnSet`.

**Value**

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

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(100)]
obj.slsa.pov <- wrapper.impute.slsa(obj)
```

---

wrapper.mvImage             *Heatmap of missing values from a MSnSet object*

---

**Description**

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

**Usage**

```
wrapper.mvImage(obj, pattern = "Missing MEC")
```

**Arguments**

obj                    An object of class MSnSet.  
 pattern                xxx

**Value**

A heatmap

**Author(s)**

Alexia Dorffer

**Examples**

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(1000)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
wrapper.mvImage(obj$new)
```

---

wrapper.normalized      *Normalisation*

---

**Description**

Provides several methods to normalize quantitative data from a MSnSet object. They are organized in six main families : GlobalQuantileAlignement, 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 Biobase::exprs() data tab) is computed condition by condition.

**Usage**

```
wrapper.normalized(obj, method, withTracking = FALSE, ...)
```

**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".  
 withTracking        xxx  
 ...                    xxx



**Value**

xxx

**Author(s)**

Samuel Wieczorek, Thomas Burger, Helene Borges

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
conds <- Biobase::pData(Exp1_R25_pept)$Condition
obj <- wrapper.normalized(
  obj = Exp1_R25_pept, method = "QuantileCentering",
  conds = conds, type = "within conditions"
)
```

---

`wrapper.pca`*Compute the PCA*

---

**Description**

Compute the PCA

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

<code>obj</code>	xxx
<code>var.scaling</code>	The dimensions to plot
<code>ncp</code>	xxxx

**Value**

A xxxxxx

**Author(s)**

Samuel Wieczorek

## Examples

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
res.pca <- wrapper.pca(obj$new)
```

---

## 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

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(100)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
qData <- Biobase::exprs(obj$new)
sTab <- Biobase::pData(obj$new)
limma <- limmaCompleteTest(qData, sTab)
wrapperCalibrationPlot(limma$P_Value[, 1])
```

---

`wrapperClassic1wayAnova`*Wrapper for One-way Anova statistical test*

---

**Description**

Wrapper for One-way Anova statistical test

**Usage**

```
wrapperClassic1wayAnova(obj, with_post_hoc = "No", post_hoc_test = "No")
```

**Arguments**

<code>obj</code>	An object of class MSnSet.
<code>with_post_hoc</code>	a character string with 2 possible values: "Yes" and "No" (default) saying if function must perform a Post-Hoc test or not.
<code>post_hoc_test</code>	character string, possible values are "No" (for no test; default value) or "TukeyHSD" or "Dunnett". See details of <code>postHocTest()</code> function to choose the appropriate one.

**Details**

This function allows to perform a 1-way Analysis of Variance. Also computes the post-hoc tests if the `with_post_hoc` parameter is set to yes. There are two possible post-hoc tests: the Tukey Honest Significant Differences (specified as "TukeyHSD") and the Dunnett test (specified as "Dunnett").

**Value**

A list of two dataframes. First one called "logFC" contains all pairwise comparisons logFC values (one column for one comparison) for each analysed feature (Except in the case without post-hoc testing, for which NAs are returned.); The second one named "P\_Value" contains the corresponding p-values.

**Author(s)**

Hélène Borges

**See Also**

[`postHocTest()`]

**Examples**

```
## Not run: examples/ex_wrapperClassic1wayAnova.R
```

---

wrapperRunClustering *clustering pipeline of protein/peptide abundance profiles.*

---

### Description

This function does all of the steps necessary to obtain a clustering model and its graph from average abundances of proteins/peptides. It is possible to carry out either a kmeans model or an affinity propagation model. See details for exact steps.

### Usage

```
wrapperRunClustering(
  obj,
  clustering_method,
  conditions_order = NULL,
  k_clusters = NULL,
  adjusted_pvals,
  ttl = "",
  subttl = "",
  FDR_thresholds = NULL
)
```

### Arguments

obj	ExpressionSet or MSnSet object.
clustering_method	character string. Three possible values are "kmeans", "affinityProp" and "affinityPropReduced". See the details section for more explanation.
conditions_order	vector specifying the order of the Condition factor levels in the phenotype data. Default value is NULL, which means that it is the order of the condition present in the phenotype data of "obj" which is taken to create the profiles.
k_clusters	integer or NULL. Number of clusters to run the kmeans algorithm. If 'clustering_method' is set to "kmeans" and this parameter is set to NULL, then a kmeans model will be realized with an optimal number of clusters 'k' estimated by the Gap statistic method. Ignored for the Affinity propagation model.
adjusted_pvals	vector of adjusted pvalues returned by the [wrapperClassic1wayAnova()]
ttl	the title for the final plot
subttl	the subtitle for the final plot
FDR_thresholds	vector containing the different threshold values to be used to color the profiles according to their adjusted pvalue. The default value (NULL) generates 4 thresholds: [0.001, 0.005, 0.01, 0.05]. Thus, there will be 5 intervals therefore 5 colors: the pvalues <0.001, those between 0.001 and 0.005, those between 0.005 and 0.01, those between 0.01 and 0.05, and those > 0.05. The highest given value will be considered as the threshold of insignificance, the profiles having a pvalue > this threshold value will then be colored in gray.

## Details

The first step consists in averaging the abundances of proteins/peptides according to the different conditions defined in the phenotype data of the expressionSet / MSnSet. Then we standardize the data if there are more than 2 conditions. If the user asks to realize a kmeans model without specifying the desired number of clusters ('clustering\_method = "kmeans"' and 'k\_clusters = NULL'), the function checks data's clusterability and estimates a number of clusters k using the gap statistic method. It is advise however to specify a k for the kmeans, because the gap stat gives the smallest possible k, whereas in biology a small number of clusters can turn out to be uninformative. If you want to run a kmeans but you don't know what number of clusters to give, you can let the pipeline run the first time without specifying 'k\_clusters', in order to view the profiles the first time and choose by the following is a more appropriate value of k. If it is assumed that the data can be structured with a large number of clusters, it is recommended to use the affinity propagation model instead. This method simultaneously considers all the data as exemplary potentials, unlike hard clustering (kmeans) which initializes with a number k of points taken at random. The "affinityProp" model will use a q parameter set to NA, meaning that exemplar preferences are set to the median of non-Inf values in the similarity matrix (set q to 0.5 will be the same). The "affinityPropReduced" model will use a q set to 0, meaning that exemplar preferences are set to the sample quantile with threshold 0 of non-Inf values. This should lead to a smaller number of final clusters.

## Value

a list of 2 elements: "model" is the clustering model, "ggplot" is the ggplot of profiles clustering.

## Author(s)

Helene Borges

## References

- Tibshirani, R., Walther, G. and Hastie, T. (2001). Estimating the number of data clusters via the Gap statistic. *Journal of the Royal Statistical Society* B, 63, 411–423.
- Frey, B. J. and Dueck, D. (2007) Clustering by passing messages between data points. *Science* 315, 972-976. DOI: [10.1126/science.1136800](https://doi.org/10.1126/science.1136800)

## Examples

```
data(Exp1_R25_prot, package="DAPARdata")
obj <- Exp1_R25_prot[seq_len(1000)]
level <- 'protein'
metacell.mask <- match.metacell(GetMetacell(obj), c("Missing POV", "Missing MEC"), level)
indices <- GetIndices_WholeMatrix(metacell.mask, op = ">=", th = 1)
obj <- MetaCellFiltering(obj, indices, cmd = "delete")
expR25_ttest <- compute_t_tests(obj$new)
wrapperRunClustering(
  obj = obj$new,
  adjusted_pvals = expR25_ttest$P_Value$`25fmol_vs_10fmol_pval`
)
```

---

`write.excel`*This function exports a data.frame to a Excel file.*

---

**Description**

This function exports a data.frame to a Excel file.

**Usage**

```
write.excel(df, tags = NULL, colors = NULL, tabname = "foo", filename = NULL)
```

**Arguments**

<code>df</code>	An data.frame
<code>tags</code>	xxx
<code>colors</code>	xxx
<code>tabname</code>	xxx
<code>filename</code>	A character string for the name of the Excel file.

**Value**

A Excel file (.xlsx)

**Author(s)**

Samuel Wieczorek

**Examples**

```
data(Exp1_R25_pept, package="DAPARdata")
df <- Biobase::exprs(Exp1_R25_pept[seq_len(100)])
tags <- GetMetacell(Exp1_R25_pept[seq_len(100)])
colors <- list(
  "Missing POV" = "lightblue",
  "Missing MEC" = "orange",
  "Quant. by recovery" = "lightgrey",
  "Quant. by direct id" = "white",
  "Combined tags" = "red"
)
write.excel(df, tags, colors, filename = "toto")
```

---

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

---

**Description**

Exports a MSnset dataset into a zip archive containing three zipped CSV files.

**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**

```
data(Exp1_R25_pept, package="DAPARdata")
obj <- Exp1_R25_pept[seq_len(10)]
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 Wiczorek

**Examples**

```
Sys.setenv("R_ZIPCMD" = Sys.which("zip"))  
data(Exp1_R25_pept, package="DAPARdata")  
obj <- Exp1_R25_pept[seq_len(10)]  
writeMSnsetToExcel(obj, "foo")
```



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