Package: DAPAR (via r-universe)

November 25, 2026

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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VignetteBuilder knitr

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Suggests testthat, BiocStyle, AnnotationDbi, clusterProfiler, graph, diptest, cluster, vioplot, visNetwork, vsn, igraph, FactoMineR, factoextra, dendextend, parallel, doParallel, Mfuzz, apcluster, forcats, readxl, openxlsx, multcomp, purrr, tibble, knitr, norm, scales, tidyverse, cp4p, imp4p (>= 1.1),lme4, dplyr, limma, preprocessCore, stringr, tidyr, impute, gplots, grDevices, reshape2, graphics, stats, methods, ggplot2, RColorBrewer, Matrix, org.Sc.sgd.db

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

Description

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

Usage

```
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 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)
agg.meta <- AggregateMetacell(X, obj.pep)
```

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

Description

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

Usage

```
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 — *Compute the intensity of proteins as the sum of the intensities of their n best peptides.*

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 *Average protein/peptide abundances for each condition studied*

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 *A barplot that shows the result of a GO enrichment, using the package* plotly

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 enrichGO in the package 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 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 *A barplot which shows the result of a GO classification, using the package* plotly

---

Description

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

Usage

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

Arguments

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

Value

A barplot

Author(s)

Samuel 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* plotly

---

Description

Builds a boxplot from a dataframe using the package plotly

Usage

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

Arguments

obj	Numeric matrix
conds	xxx
keyId	xxxx
legend	A vector of the conditions (one condition per sample).
pal	A basis palette for the boxes which length must be equal to the number of unique conditions in the dataset.
subset.view	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 Wieczorek, 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 agregate 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 Wieczorek

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 xxxxxxx

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.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 *Check if the design is valid*

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 *Check if the design is valid*

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)])
```

Check_Dataset_Validity

xxx

Description

xxx

Usage

```
Check_Dataset_Validity(obj)
```

Arguments

obj	xxx

Value

xxx

Check_NbValues_In_Columns

xxx

Description

xxx

Usage

```
Check_NbValues_In_Columns(qdata)
```

Arguments

qdata	xxx

Value

xxx

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)
```

Children *Names of all chidren of a node*

Description

xxx

Usage

```
Children(level, parent = NULL)
```

Arguments

level	xxx
parent	xxx

Value

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

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

Description

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

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 Wieczorek

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)
seltab <- compute.selection.table(adjpvaltab, 0.2)
seltab
```

---

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 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")
ttest <- compute_t_tests(obj$new)
```

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

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 *Compute the number of peptides used to aggregate proteins*

Description

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

Usage

```
CountPep(M)
```

Arguments

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

Value

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

Author(s)

Alexia Dorffer

Examples

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

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

Description

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

Usage

```
createMSnset(
  file,
  metadata = NULL,
  indExpData,
  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	xxxxxxxxxxx
logData	A boolean value to indicate if the data have to be log-transformed (Default is FALSE)
replaceZeros	A boolean value to indicate if the 0 and NaN values of intensity have to be replaced by NA (Default is FALSE)
pep_prot_data	A string that indicates whether the dataset is about
proteinId	xxxx
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	xxxxxxxxxx
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

qData	A dataframe that contains quantitative data.
conds	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")
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)
```

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 *Builds a densityplot from a dataframe*

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

pval	The result (p-values) of the differential analysis processed by limmaCompleteTest
pi0Method	The parameter pi0.method of the method adjust.p in the package cp4p

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

Description

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

Usage

```
diffAnaComputeFDR(adj.pvals)
```

Arguments

adj.pvals	xxxx

Value

The computed FDR value (floating number)

Author(s)

Samuel Wieczorek

Examples

```
NULL
```

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

Description

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

Usage

```
diffAnaGetSignificant(obj)
```

Arguments

obj	An object of class MSnSet.

Value

A MSnSet

Author(s)

Alexia Dorffer

Examples

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

Description

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

Usage

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

Arguments

obj	An object of class MSnSet.
allComp	A list of two items which is the result of the function wrapper.limmaCompleteTest or xxxx
data	The result of the differential analysis processed by limmaCompleteTest
th_pval	xxx
th_logFC	xxx

Value

A MSnSet

Author(s)

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

Usage

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

Arguments

`df`	A dataframe which contains the following slots : x : a vector of the log(fold change) values of the differential analysis, y : a vector of the p-value values returned by the differential analysis. index : a vector of the rowanmes of the data. This dataframe must has been built with the option stringsAsFactors set to FALSE. There may be additional slots which will be used to show informations in the tooltip. The name of these slots must begin with the prefix "tooltip_". It will be automatically removed in the plot.
`threshold_pVal`	A floating number which represents the p-value that separates differential and non-differential data.

threshold_logFC
: A floating number which represents the log of the Fold Change that separates differential and non-differential data.

conditions
: A list of the names of condition 1 and 2 used for the differential analysis.

pal
: xxx

Value

An interactive volcanoplot

Author(s)

Samuel Wieczorek

Examples

```
library(plotly)
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 = "")
}
cond <- c("25fmol", "10fmol")
diffAnaVolcanoplot_rCharts(df, 2.5, 1, cond)
```

---

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 Wieczorek

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

Calculates GO enrichment classes for a given list of proteins/genes ID. It results an enrichResult instance.

Description

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

Usage

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

Arguments

data	A vector of ID (among ENSEMBL, ENTREZID, GENENAME, REFSEQ, UNIGENE, UNIPROT -can be different according to organisms)
idFrom	character indicating the input ID format (among ENSEMBL, ENTREZID, GENENAME, REFSEQ, UNIGENE, UNIPROT)
orgdb	annotation Bioconductor package to use (character format)
ont	One of "MF", "BP", and "CC" subontologies
readable	TRUE or FALSE (default FALSE)
pval	The qvalue cutoff (same parameter as in the function enrichGO of the package 'clusterProfiler')
universe	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 *Finds the LAPALA into a* MSnSet *object*

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 *xxxx*

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 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)
```

---

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

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

Description

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

Usage

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

Arguments

lmm.res.h0	a vector of object containing the estimates (used to compute the statistic) under H0 for each connected component. If the fast version of the estimator was used (as implemented in this package), lmm.res.h0 is a vector containing averages of squared residuals. If a fixed effect model was used, it is a vector of lm objects and if a mixed effect model was used it is a vector or lmer object.
lmm.res.h1	similar to lmm.res.h0, a vector of object containing the estimates (used to compute the statistic) under H1 for each protein.
cc	a list containing the indices of peptides and proteins belonging to each connected component.
n	the number of samples used in the test
p	the number of proteins in the experiment
s	a vector containing the maximum likelihood estimate of the variance for the chosen model. When using the fast version of the estimator implemented in this package, this is the same thing as the input lmm.res.h1. For other models (e.g. mixed models) it can be obtained from samLRT.
alpha	A vector of proportions used to build candidate values for the regularizer. We use quantiles of s with these proportions. Default to seq(0, 1, 0.05)
include.zero	logical value indicating if 0 should be included in the list of candidates. Default to TRUE.

Value

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

Author(s)

Thomas Burger, Laurent Jacob

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 Wieczorek

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)
```

`Get_AllComparisons` *Returns list that contains a list of the statistical tests performed with DAPAR and recorded in an object of class* `MSnSet`.

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 Wieczorek

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)
```

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)
ll.X <- list(matWithSharedPeptides = Xshared,
matWithUniquePeptides = Xunique)
Exp1_R25_pept <- SetMatAdj(Exp1_R25_pept, ll.X)
ll1 <- get.pep.prot.cc(GetMatAdj(Exp1_R25_pept)$matWithSharedPeptides)
ll2 <- get.pep.prot.cc(
GetMatAdj(Exp1_R25_pept)$matWithUniquePeptides)
cc <- list(allPep = ll1, onlyUniquePep = ll2)
Exp1_R25_pept <- SetCC(Exp1_R25_pept, cc)
ll.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))
```

getDesignLevel *xxx*

Description

xxx

Usage

```
getDesignLevel(sTab)
```

Arguments

sTab	xxx

Value

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 Wieczorek 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
```

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 leat one condition.
conds	xxx
percent	xxx
op	String for operator to use. List of operators is available with SymFilteringOperators().
th	The theshold 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 SymFilteringOperators().
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)
```

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 Wieczorek

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 = "+"
)
```

GetKeyId *xxxx*

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 Wieczorek

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 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)
ll.X <- GetMatAdj(Exp1_R25_pept)
```

GetMetacell *xxxx*

Description

xxxx

Usage

```
GetMetacell(obj)
```

Arguments

obj	xxxx

Value

xxx

Examples

```
NULL
```

GetMetacellTags *List of metacell tags*

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
GetMetacellTags(level="peptide")
GetMetacellTags(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 *Number of each metacell tags*

Description

Number of each metacell tags

Usage

```
GetNbTags(obj)
```

Arguments

obj	A instance of the class 'MSnset'

Value

xxx

Examples

```
NULL
```

---

getNumberOf *Number of lines with prefix*

Description

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

Usage

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

Arguments

obj	An object of class MSnSet.
name	The name of a column.
prefix	A string

Value

An integer

Author(s)

Samuel Wieczorek

Examples

```
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 Wieczorek

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 — *Computes the number of proteins that are only defined by specific peptides, shared peptides or a mixture of two.*

Description

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

Usage

```
getProteinsStats(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 — *Quantile imputation value definition*

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()
```

Value

xxx

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 * numValCalibMethod * 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 Wieczorek

Examples

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

`getTextForFiltering` *Build the text information for the filtering process*

Description

Build the text information for the filtering process

Usage

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

Arguments

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

Value

A string

Author(s)

Samuel Wieczorek

Examples

```
getTextForFiltering(list(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 *xxxx*

Description

xxxx

Usage

```
GetTypeofData(obj)
```

Arguments

obj	xxx

Value

xxx

Examples

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

GetUniqueTags *xxxx*

Description

xxx

Usage

```
GetUniqueTags(obj)
```

Arguments

obj	xxx

Value

xxx

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

Description

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

Usage

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

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 mutliple contrat correction (for experienced users only)
method	method a method to estimate pi_0, see CP4P
display	if T, a calibration plot is diplayed 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 Wieczorek, 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 'clusterProfiler' 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 *Function to create a histogram that shows the repartition of peptides w.r.t. the proteins*

Description

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

Usage

```
GraphPepProt(mat)
```

Arguments

mat	An adjacency matrix.

Value

A histogram

Author(s)

Alexia Dorffer, Samuel Wieczorek

Examples

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

group_GO *Calculates the GO profile of a vector of genes/proteins at a given level of the Gene Ontology*

Description

This function is a wrappper 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 ontolofy 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 plotly 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 help(heatmap.2)
cluster	the clustering algorithm used to build the dendrogram. See help(heatmap.2)
dendro	A boolean to indicate fi the dendrogram has to be displayed

Value

A heatmap

Author(s)

Florence Combes, Samuel Wieczorek, 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 ov p-values*

Description

Plots a histogram ov 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*median(sd(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 Wieczorek

Examples

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

---

inner.aggregate.iter *xxxx*

Description

Method to xxxxx

Usage

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

Arguments

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

Value

xxxxx

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 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.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 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.mean(Biobase::exprs(obj), X)
```

inner.sum *xxxx*

Description

xxxx

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

xxxxxxxxxx..

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` *Computes a hierarchical differential analysis*

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 Giai-Gianetto, Samuel Wieczorek

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

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 *Normalisation LOESS*

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 *Builds the contrast matrix*

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 Giai-Gianetto, Samuel Wieczorek

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` *Builds the design matrix*

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 Wieczorek

Examples

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

make.design.1 *Builds the design matrix for designs of level 1*

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 *Builds the design matrix for designs of level 2*

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 Wieczorek

Examples

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

---

make.design.3 *Builds the design matrix for designs of level 3*

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 Wieczorek

Examples

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

match.metacell *Similar to the function* is.na *but focused on the equality with the paramter 'type'.*

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 *Normalisation MeanCentering*

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')
```

Metacell_DIA_NN *Sets the metacell dataframe for datasets which are from Dia-NN software*

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 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_DIA_NN(qdata, conds, df, level = "peptide")
```

Metacell_generic *Sets the metacell dataframe for dataset without information about the origin of identification*

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 xxxxxxx
`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(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` *Sets the metacell dataframe for datasets which are from Proline software*

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 xxxxxxx
`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")
```

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 `plotly`

Usage

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

Arguments

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

---

metacellPerLinesHisto_HC

Bar plot of missing values per lines using plotly

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 Wieczorek

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"))
```

---

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

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

---

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 agregate 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 agregate 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 agregate is a mix of 1.x, then the final metadata is set to 1.0 * (RULE 7) if the set of metacell to agregate is a mix of 3.x, then the final metadata is set to 3.0 * (RULE 8) if the set of metacell to agregate 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 vizualize 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)
```

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

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

Value

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

Author(s)

Samuel 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 — *Parent name of a node*

Description

xxx

Usage

```
Parent(level, node = NULL)
```

Arguments

level	xxx
node	xxx

Value

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 *PEptide based Protein differential Abundance test*

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

Value

xxx

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)
```

Arguments

df	xxxx

Value

A plot

Author(s)

Thomas Burger, Samuel Wieczorek

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 Wieczorek

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 plotly library*

Description

Plots the eigen values of PCA with the plotly library

Usage

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

Arguments

`res.pca`	xxx

Value

A histogram

Author(s)

Samuel Wieczorek

Examples

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

plotPCA_Ind *Plots individuals of PCA*

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 *Plots variables of PCA*

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 `plotly`

Usage

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

Arguments

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

Value

A barplot

Author(s)

Samuel Wieczorek

Examples

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

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

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

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 *Removes lines in the dataset based on a prefix string.*

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 *xxxxxx*

Description

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

Usage

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

Arguments

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 plotly

---

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 packaage '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 *Computes the adjusted p-values separately on contrast using CP4P*

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 mutliple contrat 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)
```

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(qmeta, conds, level)
```

Arguments

qmeta	An object of class MSnSet
conds	xxx
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(df, conds, level = "peptide")
```

SetCC *Returns the connected components*

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)
ll1 <- get.pep.prot.cc(GetMatAdj(Exp1_R25_pept)$matWithSharedPeptides)
ll2 <- get.pep.prot.cc(
GetMatAdj(Exp1_R25_pept)$matWithUniquePeptides)
cc <- list(allPep = ll1, onlyUniquePep = ll2)
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)
```

---

splitAdjacencyMat *splits an adjacency matrix into specific and shared*

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 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 <- 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 Dunnet tests compare all the means to the first one. For multiple tests (Dunnet'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 Dunnet'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, respecively)

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 *Returns the totality of ENTREZ ID (gene id) of an OrgDb annotation package. Careful : org.Pf.plasmo.db : no ENTREZID but ORF*

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` *Visualize the clusters according to pvalue thresholds*

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 Wieczorek

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 Wieczorek

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 mi.mix in the package imp4p
nknn	Same as the function mi.mix in the package imp4p
selec	Same as the function mi.mix in the package imp4p
siz	Same as the function mi.mix in the package imp4p
weight	Same as the function mi.mix in the package imp4p
ind.comp	Same as the function mi.mix in the package imp4p
progress.bar	Same as the function mi.mix in the package imp4p
x.step.mod	Same as the function estim.mix in the package imp4p
x.step.pi	Same as the function estim.mix in the package imp4p
nb.rei	Same as the function estim.mix in the package imp4p
method	Same as the function estim.mix in the package imp4p
gridsize	Same as the function estim.mix in the package imp4p
q	Same as the function mi.mix in the package imp4p
q.min	Same as the function impute.pa in the package imp4p
q.norm	Same as the function impute.pa in the package imp4p
eps	Same as the function impute.pa in the package imp4p

methodi	Same as the function mi.mix in the package imp4p
lapala	xxxxxxxxxx
distribution	The type of distribution used. Values are unif (default) or beta.

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)
```

---

wrapper.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

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

Arguments

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

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 Wieczorek

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

obj	An object of class MSnSet.
q.min	Same as the function impute.pa() in the package imp4p

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

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

Value

The object `obj` which has been imputed

Author(s)

Thomas Burger, Samuel Wieczorek

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 vizualize 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

`obj`	xxx
`var.scaling`	The dimensions to plot
`ncp`	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

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

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

df	An data.frame
tags	xxx
colors	xxx
tabname	xxx
filename	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` *Exports a MSnset dataset into a zip archive containing three zipped CSV files.*

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` *This function exports a* `MSnSet` *object to a Excel file.*

Description

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

The colored cells in the experimental data correspond to the original missing values which have been imputed.

Usage

```
writeMSnsetToExcel(obj, filename)
```

Arguments

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

Value

A Excel file (.xlsx)

Author(s)

Samuel Wieczorek

Examples

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

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