

Package ‘MetanIP’

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Type Package

Title What the Package Does (Title Case)

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Depends R (>= 3.5)

Description More about what it does (maybe more than one line)
Use four spaces when indenting paragraphs within the Description.

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Imports SummarizedExperiment, biomaRt, ggplot2, hipathia, limma, mdgsa, stats, ggdendro, ReportingTools, hwriter, methods, metafor, reshape, utils

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deReport	<i>Differential expression analysis report</i>
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Description

deReport reports differential expression (DE) for 1 or 3 contrasts

Usage

```
deReport(fit, genenames, tStat, pVal, pAdj, directory, name)
```

Arguments

fit	An MArrayLM object containing the result of the fits.
genenames	List of gene names ordered as the fit results. Typically obtained from fData(expressionset), being this the expressionset used to compute DE results.
tStat	t statistic from fit
pVal	p values from fit
pAdj	Adjusted p values from fit
directory	Directory where the report should be saved
name	Name for the report file

Value

HTML file with the report information

diffExp	<i>Differential expression analysis</i>
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Description

diffExp computes differential expression analysis for a given data-set

Usage

```
diffExp(data, variable, contrasts, batch = FALSE, paired = FALSE,
        trend = FALSE)
```

Arguments

data	Expressionset
variable	vector with the variable of interest for each sample
contrasts	vector of strings with the contrasts to perform.
batch	vector with the batch variable for each sample
paired	vector with the samples paired, or FALSE
trend	boolean TRUE or FALSE, whether to use or not the trend argument at the <code>limma::eBayes</code> function

Value

MArrayLM object from limma package

doGSEA *Gene Set Enrichment Analysis*

Description

doGSEA performs Gene Set Enrichment Analysis from a limma fit object

Usage

```
doGSEA(fit, annot, ontology, propagate = FALSE, minBlockSize = 10,
       maxBlockSize = 500, contrasts = 1)
```

Arguments

fit	MArrayLM limma object
annot	data-frame with ENTREZIDs in the first column and GO IDs in the second
ontology	string indicating whether you want to use biological process ("bp"), cellular component ("cc") or molecular function ("mf"). If GSEA is going to be performed on KEGG pathways, this must be ("path").
propagate	boolean, uses <code>mdgsa::propagateGO()</code> or not
minBlockSize	minimum block size kept by <code>annotFilter</code>
maxBlockSize	maximum block size kept by <code>annotFilter</code>
contrasts	number of contrasts

Value

results from analysis filtered over 0.05 adjusted p-value

doHipathia *Perform Hipathia signal computing*

Description

doHipathia Performs hipathia signal computing

Usage

```
doHipathia(gse, pathways, decompose = FALSE, verbose = FALSE)
```

Arguments

gse	Expressionset object
pathways	pathways hipathia object
decompose	Boolean, whether to compute the values for the decomposed subpathways. By default, effector subpathways are not computed.
verbose	Boolean, whether to show details about the results of the execution of hipathia. By default, details are not shown.

Value

Hipathia results object

doPathways *Pathway/function activation analysis*

Description

doPathways Performs Hipathia pathway/function activation analysis

Usage

```
doPathways(results, pathways, contrast, pathOrFunc = "pathways",
  batch = FALSE, paired = FALSE)
```

Arguments

results	results Hipathia object
pathways	pathways hipathia object
contrast	vector of strings with the contrasts to perform.
pathOrFunc	string denoting which activation analysis is going to be performed. Values accepted are c("pathways", "uniprot", "GO").
batch	boolean, whether there's available data about batch or not
paired	boolean, whether there's available data about paired samples or not.

Value

list with two lists: pathway results matrix and pathways results summary for each contrast

gseaReport	<i>GSEA report</i>
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Description

gseaReport reports GSEA

Usage

```
gseaReport(GOres, GOMap, directory, name)
```

Arguments

GOres	A dataframe with a row for each Gene Set or block. Columns must be at least: N: number of genes annotated to the Gene Set t: t statistic associated to each log Odds Ratio pval: p-values associated to each log Odds Ratio padj: adjusted p-values Rownames must be GOIDs
GOMap	A data frame with a row for each Gene Set or bloc, in the same order as shown in Gores object. Must contain at least the ordered list of GO terms
directory	Directory where the report should be saved
name	Name for the report file

Value

HTML file with the report information

limmaToHipathia	<i>Apply Hipathia structure to limma results</i>
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Description

limmaToHipathia Changes data format from limma fit object to a data frame compatible with hipathia package

Usage

```
limmaToHipathia(fit, contrastNumber, pathways)
```

Arguments

fit MArrayLM limma object
contrastNumber number of the contrast in fit object to convert
pathways pathways hipathia object

Value

data frame with pathways ID as rownames, pathway name, UP/DOWN sign, t statistic, p value and adjusted p value.

medianReps *Median over irregular replicate probes*

Description

Condense a microarray data object so that values for within-array replicate probes are replaced with their median

Usage

```
medianReps(matriz)
```

Arguments

matriz a matrix-like object

Details

medianReps Median over irregular replicate probes

Value

A data object of the same class as x with a row for each unique value of ID.

metaBoxplot	<i>Boxplots for meta-analysis matrices</i>
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Description

metaBoxplot

Usage

```
metaBoxplot(mat, value, ylab, xlab = "Studies")
```

Arguments

mat	matrix with LOR or SD values for all studies. Rownames must be GO IDs and it must have one column by file or study.
value	string specifying whether the matrix includes sd or lor values, c("sd", "lor")
ylab	string specifying the y title, normally "Log Odds Ratio" or "Standard Error"
xlab	string specifying the x title, by default "Studies".

metaGO	<i>GO meta-analysis</i>
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Description

metaGO computes meta-analysis for a given set of GO ids with log odds ratio and standard deviation values. Saves in a given path dataframes containing the results for each method, the summary of all methods, the intersection of significant results and the union of significant results.

Usage

```
metaGO(mat.lor, mat.sd, methods, res.path = getwd(),
       adj.method = "fdr", alpha = 0.05, OR.threshold = 0.5)
```

Arguments

mat.lor	matrix with LOR values for all studies. Rownames must be GO IDs and it must have one column by file or study.
mat.sd	matrix with SD values for all studies. Rownames must be GO IDs and it must have one column by file or study.
methods	vector with one or several of the following meta-analysis methods: c("DL", "HE", "HS", "FE")
res.path	path where the results should be stored. By default, the current working directory.
adj.method	correction method, c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr"). By default, "fdr".
alpha	threshold to detect significant results. By default, 0.05.
OR.threshold	threshold to detect OR. By default, 0.5.

Value

dataframe with results for each method

metaKEGG	<i>KEGG meta-analysis</i>
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Description

metaKEGG computes differential expression analysis for a given data-set. Saves in a given path dataframes containing the results for each method, the summary of all methods, the intersection of significant results and the union of significant results.

Usage

```
metaKEGG(mat.lor, mat.sd, methods, res.path = getwd(),
  adj.method = "fdr", alpha = 0.05, OR.threshold = 0.5)
```

Arguments

mat.lor	matrix with LOR values for all studies. Rownames must be KEGG IDs and it must have one column by file or study.
mat.sd	matrix with SD values for all studies. Rownames must be KEGG IDs and it must have one column by file or study.
methods	vector with one or several of the following meta-analysis methods: c("DL", "HE", "HS", "FE")
res.path	path where the results should be stored. By default, the current working directory.
adj.method	correction method, c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr"). By default, "fdr".
alpha	threshold to detect significant results. By default, 0.05.
OR.threshold	threshold to detect OR. By default, 0.5.

Value

dataframe with results for each method

metaVolcano	<i>Volcano plot for meta-analysis results with metafor</i>
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Description

metaVolcano

Usage

```
metaVolcano(res.mat, alpha = 0.05, upcol = "royalblue",
            noncol = "white", downcol = "firebrick2", xlab = "log2 Odds Ratio",
            ylab = "-log10 FDR", titl = "Volcano plot")
```

Arguments

res.mat	results res.matrix with LOR or SD values for all studies. Rownames must be GO IDs, and a column named threshold must be added, containing a coloring factor for significant up, down and non-significant GO IDs.
alpha	threshold value for p.adjust value
upcol	string specifying the color for the significant up GO IDs
noncol	string specifying the color for the non significant GO IDs
downcol	string specifying the color for the significant down GO IDs
xlab	string specifying the x title, by default "log2 Odds Ratio"
ylab	string specifying the y title, by default "-log10 FDR"
titl	string specifying the plot title, by default "Volcano plot"

modelHetBoxplot	<i>Boxplot to evaluate heterogeneity for all models.</i>
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Description

modelHetBoxplot

Usage

```
modelHetBoxplot(dat, parameter = "QEp", xlab = "Methods",
                ylab = "QEp")
```

Arguments

dat	data.frame whose columns are: cbind(as.factor(methods)), QEp, SE, I2, H2 and tau2, for each of the methods used
parameter	string specifying whether the parameter to plot, c("QEp", "SE", "I2", "H2", "tau2"), by default "QEp"
xlab	string specifying the x title, by default "Methods".
ylab	string specifying the y title, by default "QEp"

plotBoxplot	<i>Boxplot</i>
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Description

plotBoxplot plots a bloxplot from dataframe

Usage

```
plotBoxplot(data, names, values, condition, palette = "default")
```

Arguments

data	data.frame to plot. Requires 1 row for each value in the normalized gene expression data.frame. There should be 3 columns: the colnames of the gene expression data.frame (sample names), the expression values, a factor with a variable. There could be more columns with more variables.
names	sample names or name of the column in data which contains them
values	expression values or name of the column in data which contains them
condition	variable factor or name of the column in data which contains it
palette	color palette. If missing, a color blind palette is used

plotPca	<i>PCA plot</i>
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Description

plotPca plots a PCA dataframe

Usage

```
plotPca(pcaDf, condition, palette = "default", addNames = TRUE,
        PC1 = 1, PC2 = 2, hjust = 0.5, vjust = 0.5)
```

Arguments

pcaDf	data.frame containing PCA
condition	coloring variable
palette	color palette. If missing, a color blind palette is used
addNames	boolean, adds sample names to the plot or not, TRUE by default
PC1	First principal component to plot, 1 by default
PC2	Second principal component to plot, 2 by default
hjust	ggplot2 hjust parameter. Affects the display of labels in case that addNames is set as TRUE
vjust	ggplot2 vjust parameter. Affects the display of labels in case that addNames is set as TRUE

plotTreeClust	<i>Tree Clustering Plot</i>
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Description

Based on a function written by dmontaner at cipf.es

Usage

```
plotTreeClust(cluster, title)
```

Arguments

cluster	cluster model
title	plot title

Details

plotTreeClust plots a tree clustering from a cluster model

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