Package `pcaExplorer`

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Type Package

Title Interactive Visualization of RNA-seq Data Using a Principal Components Approach

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Description This package provides functionality for interactive visualization of RNA-seq datasets based on Principal Components Analysis. The methods provided allow for quick information extraction and effective data exploration. A Shiny application encapsulates the whole analysis.

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LazyData TRUE

Imports DESeq2, SummarizedExperiment, GenomicRanges, IRanges, S4Vectors, genefilter, ggplot2 (>= 2.0.0), heatmaply, plotly, scales, NMF, plyr, topGO, limma, GOstats, GO.db, AnnotationDbi, shiny (>= 0.12.0), shinydashboard, shinyBS, ggrepel, DT, shinyAce, threejs, biomaRt, pheatmap, knitr, rmarkdown, base64enc, tidyr, grDevices, methods

Suggests testthat, BiocStyle, markdown, airway, org.Hs.eg.db, htmltools


BugReports https://github.com/federicomarini/pcaExplorer/issues

biocViews ImmunoOncology, Visualization, RNASeq, DimensionReduction, PrincipalComponent, QualityControl, GUI, ReportWriting, ShinyApps

VignetteBuilder knitr

RoxygenNote 7.2.3

Encoding UTF-8

NeedsCompilation no

git_url https://git.bioconductor.org/packages/pcaExplorer
correlatePCs

Principal components (cor)relation with experimental covariates

Description

Computes the significance of (cor)relations between PCA scores and the sample experimental covariates, using Kruskal-Wallis test for categorial variables and the cor.test based on Spearman's correlation for continuous variables

Usage

correlatePCs(pcaobj, coldata, pcs = 1:4)
** Arguments 

- `pcaobj`: A `prcomp` object
- `coldata`: A `data.frame` object containing the experimental covariates
- `pcs`: A numeric vector, containing the corresponding PC number

** Value 

A `data.frame` object with computed p values for each covariate and for each principal component

** Examples 

```r
library(DESeq2)
dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
rlt <- DESeq2::rlogTransformation(dds)
pcaobj <- prcomp(t(assay(rlt)))
correlatePCs(pcaobj, colData(dds))
```

---

** distro_expr **

*Plot distribution of expression values*

** Description 

Plot distribution of expression values

** Usage 

```
distro_expr(rld, plot_type = "density")
```

** Arguments 

- `rld`: A `DESeqTransform` object.
- `plot_type`: Character, choose one of boxplot, violin or density. Defaults to density

** Value 

A plot with the distribution of the expression values

** Examples 

```r
dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
rlt <- DESeq2::rlogTransformation(dds)
distro_expr(rlt)
```
gene profiler  *Extract and plot the expression profile of genes*

**Description**

Extract and plot the expression profile of genes

**Usage**

```r
gene profiler(se, genelist = NULL, intgroup = "condition", plotZ = FALSE)
```

**Arguments**

- `se` A `DESeqDataSet` object, or a `DESeqTransform` object.
- `genelist` An array of characters, including the names of the genes of interest of which the profile is to be plotted.
- `intgroup` A factor, needs to be in the `colnames` of `colData(se)`.
- `plotZ` Logical, whether to plot the scaled expression values. Defaults to `FALSE`.

**Value**

A plot of the expression profile for the genes

**Examples**

```r
dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
rlt <- DESeq2::rlogTransformation(dds)
gene profiler(rlt, paste0("gene", sample(1:1000, 20)))
gene profiler(rlt, paste0("gene", sample(1:1000, 20)), plotZ = TRUE)
```

---

**genespca**  *Principal components analysis on the genes*

**Description**

Computes and plots the principal components of the genes, eventually displaying the samples as in a typical biplot visualization.
genespca

Usage

genespca(
  x,
  ntop,
  choices = c(1, 2),
  arrowColors = "steelblue",
  groupNames = "group",
  biplot = TRUE,
  scale = 1,
  pc.biplot = TRUE,
  obs.scale = 1 - scale,
  var.scale = scale,
  groups = NULL,
  ellipse = FALSE,
  ellipse.prob = 0.68,
  labels = NULL,
  labels.size = 3,
  alpha = 1,
  var.axes = TRUE,
  circle = FALSE,
  circle.prob = 0.69,
  varname.size = 4,
  varname.adjust = 1.5,
  varname.abbrev = FALSE,
  returnData = FALSE,
  coordEqual = FALSE,
  scaleArrow = 1,
  useRownamesAsLabels = TRUE,
  point_size = 2,
  annotation = NULL
)

Arguments

x                  A DESeqTransform object, with data in assay(x), produced for example by either rlog or varianceStabilizingTransformation
ntop               Number of top genes to use for principal components, selected by highest row variance
choices            Vector of two numeric values, to select on which principal components to plot
arrowColors        Vector of character, either as long as the number of the samples, or one single value
groupNames         Factor containing the groupings for the input data. Is efficiently chosen as the (interaction of more) factors in the colData for the object provided
biplot             Logical, whether to additionally draw the samples labels as in a biplot representation
scale: Covariance biplot (scale = 1), form biplot (scale = 0). When scale = 1, the inner product between the variables approximates the covariance and the distance between the points approximates the Mahalanobis distance.

pc.biplot: Logical, for compatibility with biplot.princomp()

obs.scale: Scale factor to apply to observations

var.scale: Scale factor to apply to variables

groups: Optional factor variable indicating the groups that the observations belong to. If provided, the points will be colored according to groups

ellipse: Logical, draw a normal data ellipse for each group

ellipse.prob: Size of the ellipse in Normal probability

labels: optional Vector of labels for the observations

labels.size: Size of the text used for the labels

alpha: Alpha transparency value for the points (0 = transparent, 1 = opaque)

var.axes: Logical, draw arrows for the variables?

circle: Logical, draw a correlation circle? (only applies when prcomp was called with scale = TRUE and when var.scale = 1)

circle.prob: Size of the correlation circle in Normal probability

varname.size: Size of the text for variable names

varname.adjust: Adjustment factor the placement of the variable names, >= 1 means farther from the arrow

varname.abbrev: Logical, whether or not to abbreviate the variable names

returnData: Logical, if TRUE returns a data.frame for further use, containing the selected principal components for custom plotting

coordEqual: Logical, default FALSE, for allowing brushing. If TRUE, plot using equal scale cartesian coordinates

scaleArrow: Multiplicative factor, usually >=1, only for visualization purposes, to allow for distinguishing where the variables are plotted

useRownamesAsLabels: Logical, if TRUE uses the row names as labels for plotting

point_size: Size of the points to be plotted for the observations (genes)

annotation: A data.frame object, with row.names as gene identifiers (e.g. ENSEMBL ids) and a column, gene_name, containing e.g. HGNC-based gene symbols

Details

The implementation of this function is based on the beautiful ggbiplot package developed by Vince Vu, available at https://github.com/vqv/ggbiplot. The adaptation and additional parameters are tailored to display typical genomics data such as the transformed counts of RNA-seq experiments

Value

An object created by ggplot, which can be assigned and further customized.
Examples

```r
library(DESeq2)
dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
rlt <- rlogTransformation(dds)
groups <- colData(dds)$condition
groups <- factor(groups, levels = unique(groups))
cols <- scales::hue_pal()(2)[groups]
genespca(rlt, ntop=100, arrowColors = cols, groupNames = groups)

groups_multi <- interaction(as.data.frame(colData(rlt)[, c("condition", "tissue")]))
groups_multi <- factor(groups_multi, levels = unique(groups_multi))
cols_multi <- scales::hue_pal()(length(levels(groups_multi)))[factor(groups_multi)]
genespca(rlt, ntop = 100, arrowColors = cols_multi, groupNames = groups_multi)
```

get_annotation

Get an annotation data frame from biomaRt

Description

Get an annotation data frame from biomaRt

Usage

```r
get_annotation(dds, biomart_dataset, idtype)
```

Arguments

- `dds`: A `DESeqDataSet` object
- `biomart_dataset`: A biomaRt dataset to use. To see the list, type `mart = useMart('ensembl')`, followed by `listDatasets(mart)`.
- `idtype`: Character, the ID type of the genes as in the row names of `dds`, to be used for the call to `getBM`

Value

A data frame for ready use in `pcaExplorer`, retrieved from biomaRt.

Examples

```r
library(airway)
data(airway)
airway
dds_airway <- DESeq2::DESeqDataSetFromMatrix(assay(airway),
  colData = colData(airway),
  design = ~dex+cell)

## Not run:
```
get_annotation(design, org.db.package, id.type, key.for.genenames = "SYMBOL")

Arguments

dds: A DESeqDataSet object
org.db.species: Character string, named as the org.XX.eg.db package which should be available in Bioconductor
id.type: Character, the ID type of the genes as in the row names of dds, to be used for the call to mapIds
key.for.genenames: Character, corresponding to the column name for the key in the orgDb package containing the official gene name (often called gene symbol). This parameter defaults to "SYMBOL", but can be adjusted in case the key is not found in the annotation package (e.g. for org.Sc.sgd.db).

Value

A data frame for ready use in pcaExplorer, retrieved from the org db packages

Examples

library(airway)
data(airway)
airway
dds_airway <- DESeq2::DESeqDataSetFromMatrix(assay(airway),
  colData = colData(airway),
  design = ~dex+cell)
anno_df <- get_annotation(design, org.db.package, id.type, key.for.genenames = "SYMBOL")
head(anno_df)
hi_loadings

Description

Extract genes with highest loadings

Usage

```r
hi_loadings(
  pcaobj,
  whichpc = 1,
  topN = 10,
  exprTable = NULL,
  annotation = NULL,
  title = "Top/bottom loadings"
)
```

Arguments

- `pcaobj`: A `prcomp` object
- `whichpc`: An integer number, corresponding to the principal component of interest
- `topN`: Integer, number of genes with top and bottom loadings
- `exprTable`: A matrix object, e.g. the counts of a `DESeqDataSet`. If not NULL, returns the counts matrix for the selected genes
- `annotation`: A data.frame object, with row.names as gene identifiers (e.g. ENSEMBL ids) and a column, `gene_name`, containing e.g. HGNC-based gene symbols
- `title`: The title of the plot

Value

A ggplot2 object, or a matrix, if `exprTable` is not null

Examples

```r
dds <- makeExampleDESeqDataSet_multifac(betaSD = 3, betaSD_tissue = 1)
rlt <- DESeq2::rlogTransformation(dds)
pcaobj <- prcomp(t(SummarizedExperiment::assay(rlt)))
hi_loadings(pcaobj, topN = 20)
hi_loadings(pcaobj, topN = 10, exprTable = dds)
hi_loadings(pcaobj, topN = 10, exprTable = counts(dds))
```
limmaquickpca2go  
*Functional interpretation of the principal components, based on simple overrepresentation analysis*

**Description**

Extracts the genes with the highest loadings for each principal component, and performs functional enrichment analysis on them using the simple and quick routine provided by the `limma` package.

**Usage**

```r
limmaquickpca2go(
  se, pca_ngenes = 10000, inputType = "ENSEMBL", organism = "Mm", loadings_ngenes = 500, background_genes = NULL, scale = FALSE,
  ...
)
```

**Arguments**

- **se**: A `DESeqTransform` object, with data in `assay(se)`, produced for example by either `rlog` or `varianceStabilizingTransformation`.
- **pca_ngenes**: Number of genes to use for the PCA.
- **inputType**: Input format type of the gene identifiers. Defaults to `ENSEMBL`, then will be converted to ENTREZ ids. Can assume values such as `ENTREZID`, `GENENAME` or `SYMBOL`, like it is normally used with the `select` function of `AnnotationDbi`.
- **organism**: Character abbreviation for the species, using `org.XX.eg.db` for annotation.
- **loadings_ngenes**: Number of genes to extract the loadings (in each direction).
- **background_genes**: Which genes to consider as background.
- **scale**: Logical, defaults to `FALSE`, scale values for the PCA.
- **...**: Further parameters to be passed to the goana routine.

**Value**

A nested list object containing for each principal component the terms enriched in each direction. This object is to be thought in combination with the displaying feature of the main `pcaExplorer` function.
Examples

```r
library(airway)
library(DESeq2)
library(limma)
data(airway)
airway
dds_airway <- DESeqDataSet(airway, design = ~ cell + dex)
## Not run:
rld_airway <- rlogTransformation(dds_airway)
goquick_airway <- limmaquickpca2go(rld_airway,
    pca_ngenes = 10000,
    inputType = "ENSEMBL",
    organism = "Hs")
## End(Not run)
```

makeExampleDESeqDataSet_multifac

Make a simulated DESeqDataSet for two or more experimental factors

Description

Constructs a simulated dataset of Negative Binomial data from different conditions. The fold changes between the conditions can be adjusted with the betaSD_condition and the betaSD_tissue arguments.

Usage

```r
makeExampleDESeqDataSet_multifac(
  n = 1000,
  m = 12,
  betaSD_condition = 1,
  betaSD_tissue = 3,
  interceptMean = 4,
  interceptSD = 2,
  dispMeanRel = function(x) 4/x + 0.1,
  sizeFactors = rep(1, m)
)
```

Arguments

- `n`: number of rows (genes)
- `m`: number of columns (samples)
- `betaSD_condition`: the standard deviation for condition betas, i.e. beta ~ N(0, betaSD)
- `betaSD_tissue`: the standard deviation for tissue betas, i.e. beta ~ N(0, betaSD)
Details

This function is designed and inspired following the proposal of `makeExampleDESeqDataSet` from the DESeq2 package. Credits are given to Mike Love for the nice initial implementation.

Value

A `DESeqDataSet` with true dispersion, intercept for two factors (condition and tissue) and beta values in the metadata columns. Note that the true betas are provided on the log2 scale.

Examples

```r
dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
dds
dds2 <- makeExampleDESeqDataSet_multifac(betaSD_condition = 1, betaSD_tissue = 4)
dds2
```

Description

Pairwise scatter and correlation plot of counts

Usage

```r
pair_corr(df, log = FALSE, method = "pearson", use_subset = TRUE)
```

Arguments

- `df`: A data frame, containing the (raw/normalized/transformed) counts
- `log`: Logical, whether to convert the input values to log2 (with addition of a pseudo-count). Defaults to FALSE.
- `method`: Character string, one of `pearson` (default), `kendall`, or `spearman` as in `cor`
- `use_subset`: Logical value. If TRUE, only 1000 values per sample will be used to speed up the plotting operations.

Value

A plot with pairwise scatter plots and correlation coefficients
Examples

```r
library(airway)
data(airway)
airway
dds_airway <- DESeq2::DESeqDataSetFromMatrix(assay(airway),
    colData = colData(airway),
    design = ~dex+cell)
pair_corr(counts(dds_airway)[1:100, ])
# use just a subset for the example
```

---

### pca2go

#### Functional interpretation of the principal components

**Description**

Extracts the genes with the highest loadings for each principal component, and performs functional enrichment analysis on them using routines and algorithms from the `topGO` package.

**Usage**

```r
pca2go(
    se,
    pca_ngenes = 10000,
    annotation = NULL,
    inputType = "geneSymbol",
    organism = "Mm",
    ensToGeneSymbol = FALSE,
    loadings_ngenes = 500,
    background_genes = NULL,
    scale = FALSE,
    return_ranked_gene_loadings = FALSE,
    annopkg = NULL,
    ...
)
```

**Arguments**

- `se` A `DESeqTransform` object, with data in `assay(se)`, produced for example by either `rlog` or `varianceStabilizingTransformation`
- `pca_ngenes` Number of genes to use for the PCA
- `annotation` A `data.frame` object, with row names as gene identifiers (e.g. ENSEMBL ids) and a column, `gene_name`, containing e.g. HGNC-based gene symbols
- `inputType` Input format type of the gene identifiers. Will be used by the routines of `topGO`
- `organism` Character abbreviation for the species, using `org.XX.eg.db` for annotation
- `ensToGeneSymbol` Logical, whether to expect ENSEMBL gene identifiers, to convert to gene symbols with the annotation provided
loadings_ngenes
    Number of genes to extract the loadings (in each direction)
background_genes
    Which genes to consider as background.
scale
    Logical, defaults to FALSE, scale values for the PCA
return_ranked_gene_loadings
    Logical, defaults to FALSE. If TRUE, simply returns a list containing the top
    ranked genes with hi loadings in each PC and in each direction
annopkg
    String containing the name of the organism annotation package. Can be used to
    override the organism parameter, e.g. in case of alternative identifiers used in
    the annotation package (Arabidopsis with TAIR)
...
    Further parameters to be passed to the topGO routine

Value

A nested list object containing for each principal component the terms enriched in each direction.
This object is to be thought in combination with the displaying feature of the main pcaExplorer
function

Examples

library(airway)
library(DESeq2)
data(airway)
airway
dds_airway <- DESeqDataSet(airway, design= ~ cell + dex)
## Not run:
rld_airway <- rlogTransformation(dds_airway)
# constructing the annotation object
anno_df <- data.frame(gene_id = rownames(dds_airway),
    stringsAsFactors = FALSE)
library("AnnotationDbi")
library("org.Hs.eg.db")
anno_df$gene_name <- mapIds(org.Hs.eg.db, 
    keys = anno_df$gene_id,
    column = "SYMBOL",
    keytype = "ENSEMBL",
    multiVals = "first")
rownames(anno_df) <- anno_df$gene_id
bg_ids <- rownames(dds_airway)[rowSums(counts(dds_airway)) > 0]
library(topGO)
pca2go_airway <- pca2go(rld_airway,
    annotation = anno_df, 
    organism = "Hs", 
    ensToGeneSymbol = TRUE,
    background_genes = bg_ids)

## End(Not run)
**Description**

Launch a Shiny App for interactive exploration of a dataset from the perspective of Principal Components Analysis.

**Usage**

```r
pcaExplorer(
  dds = NULL,
  dst = NULL,
  countmatrix = NULL,
  coldata = NULL,
  pca2go = NULL,
  annotation = NULL,
  runLocal = TRUE
)
```

**Arguments**

- `dds` A `DESeqDataSet` object. If not provided, then a `countmatrix` and a `coldata` need to be provided. If none of the above is provided, it is possible to upload the data during the execution of the Shiny App.
- `dst` A `DESeqTransform` object. Can be computed from the `dds` object if left NULL. If none is provided, then a `countmatrix` and a `coldata` need to be provided. If none of the above is provided, it is possible to upload the data during the execution of the Shiny App.
- `countmatrix` A count matrix, with genes as rows and samples as columns. If not provided, it is possible to upload the data during the execution of the Shiny App.
- `coldata` A data.frame containing the info on the covariates of each sample. If not provided, it is possible to upload the data during the execution of the Shiny App.
- `pca2go` An object generated by the `pca2go` function, which contains the information on enriched functional categories in the genes that show the top or bottom loadings in each principal component of interest. If not provided, it is possible to compute live during the execution of the Shiny App.
- `annotation` A data.frame object, with row.names as gene identifiers (e.g. ENSEMBL ids) and a column, `gene_name`, containing e.g. HGNC-based gene symbols.
- `runLocal` A logical indicating whether the app is to be run locally or remotely on a server, which determines how documentation will be accessed.

**Value**

A Shiny App is launched for interactive data exploration.
Examples

```r
library(airway)
data(airway)
airway
dds_airway <- DESeq2::DESeqDataSetFromMatrix(assay(airway),
    colData = colData(airway),
    design = ~dex+cell)

## Not run:
rld_airway <- DESeq2::rlogTransformation(dds_airway)

pcaExplorer(dds_airway, rld_airway)
pcaExplorer(countmatrix = counts(dds_airway), coldata = colData(dds_airway))
pcaExplorer() # and then upload count matrix, covariate matrix (and eventual annotation)
## End(Not run)
```

Description

pcaExplorer provides functionality for interactive visualization of RNA-seq datasets based on Principal Components Analysis. The methods provided allow for quick information extraction and effective data exploration. A Shiny application encapsulates the whole analysis.

Details

pcaExplorer provides functionality for interactive visualization of RNA-seq datasets based on Principal Components Analysis. The methods provided allow for quick information extraction and effective data exploration. A Shiny application encapsulates the whole analysis.

Author(s)

Federico Marini <marinif@uni-mainz.de>, 2016
Maintainer: Federico Marini <marinif@uni-mainz.de>
pcaplot

Sample PCA plot for transformed data

Description

Plots the results of PCA on a 2-dimensional space

Usage

```r
pcaplot(
  x,
  intgroup = "condition",
  ntop = 500,
  returnData = FALSE,
  title = NULL,
  pcX = 1,
  pcY = 2,
  text_labels = TRUE,
  point_size = 3,
  ellipse = TRUE,
  ellipse.prob = 0.95
)
```

Arguments

- `x` A `DESeqTransform` object, with data in `assay(x)`, produced for example by either `rlog` or `varianceStabilizingTransformation`
- `intgroup` Interesting groups: a character vector of names in `colData(x)` to use for grouping
- `ntop` Number of top genes to use for principal components, selected by highest row variance
- `returnData` logical, if TRUE returns a data.frame for further use, containing the selected principal components and intgroup covariates for custom plotting
- `title` The plot title
- `pcX` The principal component to display on the x axis
- `pcY` The principal component to display on the y axis
- `text_labels` Logical, whether to display the labels with the sample identifiers
- `point_size` Integer, the size of the points for the samples
- `ellipse` Logical, whether to display the confidence ellipse for the selected groups
- `ellipse.prob` Numeric, a value in the interval [0;1)

Value

An object created by `ggplot`, which can be assigned and further customized.
Examples

```r
dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
rlt <- DESeq2::rlogTransformation(dds)
pcaplot(rlt, ntop = 200)
```

pcaplot3d

Sample PCA plot for transformed data

Description

Plots the results of PCA on a 3-dimensional space, interactively

Usage

```r
caplot3d(
  x,
  intgroup = "condition",
  ntop = 500,
  returnData = FALSE,
  title = NULL,
  pcX = 1,
  pcY = 2,
  pcZ = 3,
  text_labels = TRUE,
  point_size = 3
)
```

Arguments

- `x`: A `DESeqTransform` object, with data in `assay(x)`, produced for example by either `rlog` or `varianceStabilizingTransformation`
- `intgroup`: Interesting groups: a character vector of names in `colData(x)` to use for grouping
- `ntop`: Number of top genes to use for principal components, selected by highest row variance
- `returnData`: logical, if TRUE returns a data.frame for further use, containing the selected principal components and `intgroup` covariates for custom plotting
- `title`: The plot title
- `pcX`: The principal component to display on the x axis
- `pcY`: The principal component to display on the y axis
- `pcZ`: The principal component to display on the z axis
- `text_labels`: Logical, whether to display the labels with the sample identifiers
- `point_size`: Integer, the size of the points for the samples
Value

A html-based visualization of the 3d PCA plot

Examples

dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
rlt <- DESeq2::rlogTransformation(dds)
pcaplot3d(rlt, ntop = 200)

Description

Produces a scree plot for investigating the proportion of explained variance, or alternatively the cumulative value

Usage

pcascreet(obj, type = c("pev", "cev"), pc_nr = NULL, title = NULL)

Arguments

<table>
<thead>
<tr>
<th>obj</th>
<th>A prcomp object</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>Display absolute proportions or cumulative proportion. Possible values: &quot;pev&quot; or &quot;cev&quot;</td>
</tr>
<tr>
<td>pc_nr</td>
<td>How many principal components to display max</td>
</tr>
<tr>
<td>title</td>
<td>Title of the plot</td>
</tr>
</tbody>
</table>

Value

An object created by ggplot, which can be assigned and further customized.

Examples

dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
rlt <- DESeq2::rlogTransformation(dds)
pcaobj <- prcomp(t(SummarizedExperiment::assay(rlt)))
pcascreet(pcaobj, type = "pev")
pcascreet(pcaobj, type = "cev", title = "Cumulative explained proportion of variance - Test dataset")
plotPCcorrs

Description

Plots the significance of the (cor)relation of each covariate vs a principal component.

Usage

plotPCcorrs(pccorrs, pc = 1, logp = TRUE)

Arguments

- `pccorrs`: A data.frame object generated by `correlatePCs`.
- `pc`: An integer number, corresponding to the principal component of interest.
- `logp`: Logical, defaults to `TRUE`, displays the -log10 of the p-value instead of the p-value itself.

Value

A base plot object.

Examples

```r
library(DESeq2)
dds <- makeExampleDESeqDataSet_multifac(betaSD_condition = 3, betaSD_tissue = 1)
rlt <- rlogTransformation(dds)
pcaobj <- prcomp(t(assay(rlt)))
res <- correlatePCs(pcaobj, colData(dds))
plotPCcorrs(res)
```

topGOtable

Description

A wrapper for extracting functional GO terms enriched in the DE genes, based on topGO.

Examples

```r
topGOtable
```

```r
library(topGO)
results <- topGOtable(exprs(BTC), gseabaseName = TRUE)
```
**topGOtable**

**Usage**

```r
topGOtable(
    DEgenes,
    BGgenes,
    ontology = "BP",
    annot = annFUN.org,
    mapping = "org.Mm.eg.db",
    geneID = "symbol",
    topTablerows = 200,
    fullNamesInRows = TRUE,
    addGeneToTerms = TRUE,
    plotGraph = FALSE,
    plotNodes = 10,
    writeOutput = FALSE,
    outputFile = "",
    topGO_method2 = "elim",
    do_padj = FALSE
)
```

**Arguments**

- **DEgenes**: A vector of (differentially expressed) genes
- **BGgenes**: A vector of background genes, e.g. all (expressed) genes in the assays
- **ontology**: Which Gene Ontology domain to analyze: **BP** (Biological Process), **MF** (Molecular Function), or **CC** (Cellular Component)
- **annot**: Which function to use for annotating genes to GO terms. Defaults to `annFUN.org`
- **mapping**: Which `org.XX.eg.db` to use for annotation - select according to the species
- **geneID**: Which format the genes are provided. Defaults to `symbol`, could also be `entrez` or `ENSEMBL`
- **topTablerows**: How many rows to report before any filtering
- **fullNamesInRows**: Logical, whether to display or not the full names for the GO terms
- **addGeneToTerms**: Logical, whether to add a column with all genes annotated to each GO term
- **plotGraph**: Logical, if TRUE additionally plots a graph on the identified GO terms
- **plotNodes**: Number of nodes to plot
- **writeOutput**: Logical, if TRUE additionally writes out the result to a file
- **outputFile**: Name of the file the result should be written into
- **topGO_method2**: Character, specifying which of the methods implemented by `topGO` should be used, in addition to the classic algorithm. Defaults to `elim`
- **do_padj**: Logical, whether to perform the adjustment on the p-values from the specific `topGO` method, based on the FDR correction. Defaults to FALSE, since the assumption of independent hypotheses is somewhat violated by the intrinsic DAG-structure of the Gene Ontology Terms
Details

Allowed values assumed by the `topGO_method2` parameter are one of the following: `elim`, `weight`, `weight01`, `lea`, `parentchild`. For more details on this, please refer to the original documentation of the `topGO` package itself.

Value

A table containing the computed GO Terms and related enrichment scores.

Examples

```r
library(airway)
library(DESeq2)
data(airway)
airway
dds_airway <- DESeqDataSet(airway, design= ~ cell + dex)
# Example, performing extraction of enriched functional categories in
# detected significantly expressed genes
## Not run:
dds_airway <- DESeq(dds_airway)
res_airway <- results(dds_airway)
library("AnnotationDbi")
library("org.Hs.eg.db")
res_airway$symbol <- mapIds(org.Hs.eg.db,
   keys = row.names(res_airway),
   column = "SYMBOL",
   keytype = "ENSEMBL",
   multiVals = "first")
res_airway$entrez <- mapIds(org.Hs.eg.db,
   keys = row.names(res_airway),
   column = "ENTREZID",
   keytype = "ENSEMBL",
   multiVals = "first")
resOrdered <- as.data.frame(res_airway[order(res_airway$padj),])
de_df <- resOrdered[resOrdered$padj < .05 & !is.na(resOrdered$padj),]
de_symbols <- de_df$symbol
bg_ids <- rownames(dds_airway)[rowSums(counts(dds_airway)) > 0]
bg_symbols <- mapIds(org.Hs.eg.db,
   keys = bg_ids,
   column = "SYMBOL",
   keytype = "ENSEMBL",
   multiVals = "first")
library(topGO)
topgoDE_airway <- topGOtable(de_symbols, bg_symbols,
   ontology = "BP",
   mapping = "org.Hs.eg.db",
   geneID = "symbol")
## End(Not run)
```
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