Package ‘Rvisdiff’

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Type Package
Version 1.0.0
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Title Interactive Graphs for Differential Expression
Description Creates a multi-graph web page which allows the interactive exploration of differential expression results. The graphical web interface presents results as a table which is integrated with five interactive graphs: MA-plot, volcano plot, box plot, lines plot and cluster heatmap. Graphical aspect and information represented in the graphs can be customized by means of user controls. Final graphics can be exported as PNG format.

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Depends R (>= 4.3.0)
Imports edgeR, utils
Suggests knitr, rmarkdown, DESeq2, limma, SummarizedExperiment, airway, BiocStyle, matrixTests, BiocManager

VignetteBuilder knitr

NeedsCompilation no

biocViews Software, Visualization, RNASEq, DataRepresentation, DifferentialExpression

BugReports https://github.com/BioinfoUSAL/Rvisdiff/issues/

URL https://github.com/BioinfoUSAL/Rvisdiff/
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R topics documented:

DEreport

Description

DEreport produce interactive graphs of the given DE results.

Usage

DEreport(DE, counts = NULL, groups = NULL, cutoff = 0.05, normalized = NULL, genes = NULL, pvalue = NULL, padj = NULL, stat = NULL, baseMean = NULL, log2FoldChange = NULL, directory = "DEreport")

Arguments

DE

a data.frame or object resulting from a differential expression method (DESeq2, edgeR or limma).

counts

a matrix of counts.

groups

a vector of groups.

cutoff

a value to match significant results.

normalized

a matrix of normalized counts. counts parameter will be ignored.

genes

name of the column with genes in the DE and counts tables. It will take rownames by default

pvalue

name of the column with p value in the DE data. "pvalue" by default.

padj

name of the column with adjust p value in the DE data. "padj" by default.

stat

name of the column with statistic in the DE data. "stat" by default.

baseMean

name of the column with base mean in the DE data. "baseMean" by default.

log2FoldChange

name of the column with log 2-fold change in the DE data. "log2FoldChange" by default.

directory

a "character" string representing the directory where the graph will be saved.

Value

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.
Author(s)

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See http://bioinfo.usal.es/

Examples

```r
library("airway")
data("airway")
se <- airway
se$dex <- relevel(se$dex, ref="untrt")
countdata <- assay(se)

library("DESeq2")
dds <- DESeqDataSet(se, design = ~ cell + dex)
dds <- DESeq(dds)

library("DESeq2")
dr <- results(dds, independentFiltering = FALSE)

DEreport(dr, countdata, se$dex)
```

Rvisdiff: Interactive Graphs for Differential Expression

Description

Rvisdiff creates a muti-graph web page which allows the interactive exploration of differential expression results. The graphical web interface presents results as a table which is integrated with five interactive graphs: MA-plot, volcano plot, box plot, lines plot and cluster heatmap. Graphical aspect and information represented in the graphs can be customized by means of user controls. Final graphics can be exported as PNG format.

Details

The main function is:

- `DEreport` - produce interactive graphs of the given differential expression results

For detailed information on usage, see the package vignette, by typing `vignette("Rvisdiff")`. The GitHub repository is https://github.com/BioinfoUSAL/Rvisdiff. This is the place to file an issue, report a bug, or provide a pull request.

Author(s)

David Barrios and Carlos Prieto
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