Package ‘Rvisdiff’

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Type Package

Version 1.8.1

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Title Interactive Graphs for Differential Expression

Description Creates a muti-graph web page which allows the interactive exploration of differential analysis tests. 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 (>= 4.5.0)

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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Contents

`DEreport` *Produce interactive DE reports.*

Description

`DEreport` produce interactive graphs of the given DE results.

Usage

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

Arguments

`DE`	a data.frame or object resulting from a differential test 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.
`variables`	name of the column with variables 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

```
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)
dr <- results(dds, independentFiltering = FALSE)

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

`Rvisdiff` *Rvisdiff: Interactive Graphs for Differential Test*

Description

Rvisdiff creates a muti-graph web page which allows the interactive exploration of differential test 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 test 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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