

# Package ‘Rvisdiff’

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**Type** Package

**Version** 1.4.0

**Date** 2024-02-12

**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.

**License** GPL-2 | GPL-3

**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/>

**git\_url** <https://git.bioconductor.org/packages/Rvisdiff>

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**Repository** Bioconductor 3.20

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DEreport	<i>Produce interactive DE reports.</i>
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**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 row-names 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)
```

## Description

Rvisdiff 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.

## 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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