Package ‘gg4way’

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Title 4way Plots of Differential Expression

Version 1.2.0

Description 4way plots enable a comparison of the logFC values from two contrasts of differential gene expression. The gg4way package creates 4way plots using the ggplot2 framework and supports popular Bioconductor objects. The package also provides information about the correlation between contrasts and significant genes of interest.

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URL https://github.com/ben-laufer/gg4way

BugReports https://github.com/ben-laufer/gg4way/issues

biocViews Software, Visualization, DifferentialExpression,
GeneExpression, Transcription, RNASeq, SingleCell, Sequencing

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Description

Creates a 4way plot

Usage

.plot4way(
    DGEtibble = DGEtibble,
    x = x,
    y = y,
    sep = sep,
    logFCcutoff = logFCcutoff,
    lineColor = lineColor,
    colorKey = colorKey,
    corRes = corRes,
    textKey = textKey,
    hjust = hjust,
    vjust = vjust,
    textSize = textSize,
    label = label
)

Arguments

x Character specifying name of DGE results within object for the x-axis
y Character specifying name of DGE results within object for the y-axis
sep Character specifying the separator between conditions for the contrast
logFCcutoff Numeric for the absolute Log2FC cut-off for DEGs, default is 1
lineColor Color of lines
textSize Numeric specifying size of text with gene overlap category totals
label Character vector specifying genes to label (FALSE for none, TRUE for all blue)
.prepareAnnotations  Prepare annotations

Description

Prepare text annotations of sums for plotting

Usage

```r
.prepareAnnotations(
  totalTibble = totalTibble,
  colorKey = colorKey,
  textNudge = textNudge
)
```

Arguments

- `totalTibble` A tibble of summarized counts
- `textNudge` Numeric specifying nudge of text with gene overlap category totals

Value

A tibble

.prepareData  Prepare data

Description

Prepare data for a 4way plot

Usage

```r
.prepareData(
  DGEdata = DGEdata,
  x = x,
  y = y,
  ID = ID,
  symbol = symbol,
  logFC = logFC,
  FDR = FDR,
  logFCcutoff = logFCcutoff,
  FDRcutoff = FDRcutoff
)
```
Arguments

DGEdata The object to plot from:
- limma: A MArrayLM object from eBayes or treat
- edgeR: A list of DGCRLRT objects from glmQLFTest, glmTreat, or glmLRT
- DESeq2: a DESeqData from DESeq or a list of DESeqResults from results
- Other packages: A list of data.frames, see details section for more information

x Character specifying name of DGE results within object for the x-axis

y Character specifying name of DGE results within object for the y-axis

ID Column name for gene ID

symbol Column name for gene symbol description

logFC Column name for logFC values

FDR Column name for FDR values

logFCcutoff Numeric for the absolute Log2FC cut-off for DEGs, default is 1

FDRcutoff Numeric for the FDR cut-off for DEGs, default is 0.05

Value

A tibble

Description

Test the correlation between DGE contrasts

Usage

.testCor(DGEtibble = DGEtibble)

Arguments

DGEtibble A tibble of DGE results

Value

A numeric of the Pearson correlation
.tidyLabel

Tidy axis labels

Description
Process axis labels from contrast names

Usage
.tidyLabel(label = NULL, sep = " vs ", labelType = c("x", "y"))

Arguments
- label: Character vector specifying genes to label (FALSE for none, TRUE for all blue)
- sep: Character specifying the separator between conditions for the contrast

Value
A call

.totalCounts
Summarize counts

Description
Create a summary table counts for DGE contrast overlaps for shared (quadrants) and non-shared (lines) DEGs

Usage
.totalCounts(DGEtibble = DGEtibble, x = x, y = y, logFCcutoff = logFCcutoff)

Arguments
- DGEtibble: A tibble of DGE results
- x: Character specifying name of DGE results within object for the x-axis
- y: Character specifying name of DGE results within object for the y-axis
- logFCcutoff: Numeric for the absolute Log2FC cut-off for DEGs, default is 1

Value
A tibble
### airwayFit

*airwayFit data*

**Description**

Generate example data from the `airway` data package using `eBayes`.

**Usage**

`data(airwayFit)`

**Format**

An object of class `MArrayLM` with 14516 rows and 2 columns.

**Value**

A `MArrayLM`

**Source**

`airway`

---

### extractors

*Helper Functions for gg4way*

**Description**

These helper functions provide data used in the plot:

- `getCor` Get the correlation of the logFC of all genes
- `getShared` Get only the shared genes that pass the thresholds
- `getTotals` Get the totals of overlap categories

**Usage**

`getCor(p1)`

`getShared(p1)`

`getTotals(p1)`
Arguments

`p1` The plot from `gg4way`

Value

Each function returns a different result:

- `getCor` A numeric
- `getShared` A tibble
- `getTotals` A tabyl

Examples

```r
data("airwayFit")
p1 <- airwayFit |> gg4way(x = "N61311 vs N052611", y = "N061011 vs N052611")
## Correlation
getCor(p1)

## Shared
getShared(p1)

## Totals
getTotals(p1)
```

Description

Create a 4way plot to compare the logFC values from two contrasts of differential gene expression.

Usage

```r
## Default S3 method:
gg4way(
  DGEdata,
  x = NULL,
  y = NULL,
  ID = "ID",
  symbol = "symbol",
  logFC = "logFC",
)```
FDR = "adj.P.Val",
sep = " vs ",
FDRcutoff = 0.05,
logFCcutoff = 1,
label = FALSE,
colorVector = c("grey80", "firebrick", "forestgreen", "mediumblue"),
lineColor = "grey60",
textSize = 4,
textNudge = 0.25,
...
)

Arguments

DGEdata The object to plot from:
  • limma: A MArrayLM object from eBayes or treat
  • edgeR: A list of DGELRT objects from glmQLFTest, glmTreat, or glmLRT
  • DESeq2: a DESeqDataSet from DESeq or a list of DESeqResults from results
  • Other packages: A list of data.frames, see details section for more information

x Character specifying name of DGE results within object for the x-axis

y Character specifying name of DGE results within object for the y-axis

ID Column name for gene ID

symbol Column name for gene symbol description

logFC Column name for logFC values

FDR Column name for FDR values

sep Character specifying the separator between conditions for the contrast

FDRcutoff Numeric for the FDR cut-off for DEGs, default is 0.05

logFCcutoff Numeric for the absolute Log2FC cut-off for DEGs, default is 1

label Character vector specifying genes to label (FALSE for none, TRUE for all blue)

colorVector Character vector of colors in the following order: "not significant", "significant in x", "significant in y", "significant in both"

tintColor Color of lines

textSize Numeric specifying size of text with gene overlap category totals

textNudge Numeric specifying nudge of text with gene overlap category totals

Details

When a list of data.frames is provided to the DGEdata argument, they should have the following column names and data:
ID       Character vector with the feature ID (i.e. EnsemblID)
symbol  Optional character vector with gene symbol for labels
LogFC   Numeric with the logFC
FDR     Numeric with the FDR

The correlation coefficient is useful for comparing across multiple plots. It’s important to consider whether there are any common factors when comparing values, since that can result in a larger value.

Value

A `ggplot`

Examples

```r
data("airwayFit")
airwayFit |> gg4way(x = "N61311 vs N052611",
y = "N061011 vs N052611")```
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