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

Encoding UTF-8

Roxygen list(markdown = TRUE)

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Depends R (>= 4.3.0), ggplot2

Imports DESeq2, dplyr, edgeR, ggrepel, glue, janitor, limma, magrittr, methods, purrr, rlang, scales, stats, stringr, tibble, tidyr

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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)
**Value**

A `ggplot`

**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

---

**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 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

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

### .totalCount

**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  

**Description**

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

**Usage**

```r
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**

```r
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

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

## 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"

lineColor
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

... Support for additional arguments used internally by gg4way.MArrayLM, gg4way.list, and gg4way.DESeqDataSet

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

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