Package 'gg4way'

September 19, 2024

Title 4way Plots of Differential Expression

Version 1.3.0

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)

RoxygenNote 7.3.1

Depends R (>= 4.3.0), ggplot2

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Suggests airway, BiocStyle, knitr, org.Hs.eg.db, rmarkdown, testthat

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Contents

.plot4way   *gg4way plot*

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

.prepareAnnotations   *Prepare annotations*

Description

Prepare text annotations of sums for plotting

Usage

```
.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

```
.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 infromation

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](#)

.testCor	*Correlation test*

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](#)

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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

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

## Correlation
getCor(p1)

## Shared
getShared(p1)

## Totals
getTotals(p1)
```

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gg4way   *Create a 4way plot*

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 infromation

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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