# Package ‘gg4way’

April 7, 2025

**Title** 4way Plots of Differential Expression

**Version** 1.5.0

**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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**Author** Benjamin I Laufer [aut, cre],
Brad A Friedman [aut]

**Maintainer** Benjamin I Laufer <`blaufer@gmail.com`>

# Contents

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## `.checkFeatures` *Missing features warning*

### Description

Warn about features not shared between x and y

### Usage

```
.checkFeatures(DGEdata = DGEdata, x = x, y = y, ID = ID)
```

### Arguments

| | |
|---|---|
| `DGEdata` | The object to plot from:<br>• `limma:` A MArrayLM object from eBayes or treat<br>• `edgeR:` A list of DGELRT objects from glmQLFTest, glmTreat, or glmLRT<br>• `DESeq2:` a DESeqDataSet from DESeq or a list of DESeqResults from results<br>• `Other packages:` A list of data.frames, see details section for more information |
| `x` | Character specifying the name of DGE results within the object for the x-axis |
| `y` | Character specifying the name of DGE results within the object for the y-axis |
| `ID` | Column name for gene IDs |

### Value

A character

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`.checkNames` *Missing names check*

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## Description

Check for missing names in the DGEdata object

## Usage

```
.checkNames(
  DGEdata = DGEdata,
  x = x,
  y = y,
  ID = ID,
  symbol = symbol,
  logFC = logFC,
  FDR = FDR
)
```

## Arguments

| | |
|---|---|
| `DGEdata` | The object to plot from:<br>• `limma:` A MArrayLM object from eBayes or treat<br>• `edgeR:` A list of DGELRT objects from glmQLFTest, glmTreat, or glmLRT<br>• `DESeq2:` a DESeqDataSet from DESeq or a list of DESeqResults from results<br>• `Other packages:` A list of data.frames, see details section for more information |
| `x` | Character specifying the name of DGE results within the object for the x-axis |
| `y` | Character specifying the name of DGE results within the object for the y-axis |
| `ID` | Column name for gene IDs |
| `symbol` | Column name for gene symbols, which can be the same as the value for the ID column if not present in the object |
| `logFC` | Column name for logFC values |
| `FDR` | Column name for FDR values |

## Value

A character

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`.plot4way` *gg4way plot*

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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 the name of DGE results within the object for the x-axis |
| `y` | Character specifying the name of DGE results within the object for the y-axis |
| `sep` | Character specifying the separator between conditions for the contrast name provided to the x and y arguments |
| `logFCcutoff` | Numeric for the absolute logFC cut-off for DEGs (default is 1) |
| `lineColor` | Color of lines |
| `textSize` | Numeric specifying size of text with gene overlap category totals, where 0 will remove the text |
| `label` | Character vector specifying the symbols of genes to label (FALSE for none, TRUE for all blue) |

## Value

A ggplot

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## `.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:<br>• `limma:` A MArrayLM object from eBayes or treat<br>• `edgeR:` A list of DGELRT objects from glmQLFTest, glmTreat, or glmLRT<br>• `DESeq2:` a DESeqDataSet from DESeq or a list of DESeqResults from results<br>• `Other packages:` A list of data.frames, see details section for more information |
| `x` | Character specifying the name of DGE results within the object for the x-axis |
| `y` | Character specifying the name of DGE results within the object for the y-axis |
| `ID` | Column name for gene IDs |
| `symbol` | Column name for gene symbols, which can be the same as the value for the ID column if not present in the object |
| `logFC` | Column name for logFC values |
| `FDR` | Column name for FDR values |
| `logFCcutoff` | Numeric for the absolute logFC 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

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## `.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 the symbols of genes to label (FALSE for none, TRUE for all blue) |
| `sep` | Character specifying the separator between conditions for the contrast name provided to the x and y arguments |

### 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 the name of DGE results within the object for the x-axis |
| `y` | Character specifying the name of DGE results within the object for the y-axis |
| `logFCcutoff` | Numeric for the absolute logFC cut-off for DEGs (default is 1) |

### Value

A tibble

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## `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`

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### 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:<br>• `limma:` A MArrayLM object from eBayes or treat<br>• `edgeR:` A list of DGELRT objects from glmQLFTest, glmTreat, or glmLRT<br>• `DESeq2:` a DESeqDataSet from DESeq or a list of DESeqResults from results<br>• `Other packages:` A list of data.frames, see details section for more information |
| `x` | Character specifying the name of DGE results within the object for the x-axis |
| `y` | Character specifying the name of DGE results within the object for the y-axis |
| `ID` | Column name for gene IDs |
| `symbol` | Column name for gene symbols, which can be the same as the value for the ID column if not present in the object |
| `logFC` | Column name for logFC values |
| `FDR` | Column name for FDR values |
| `sep` | Character specifying the separator between conditions for the contrast name provided to the x and y arguments |
| `FDRcutoff` | Numeric for the FDR cut-off for DEGs (default is 0.05) |
| `logFCcutoff` | Numeric for the absolute logFC cut-off for DEGs (default is 1) |
| `label` | Character vector specifying the symbols of 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, where 0 will remove the text |
| `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 named list of data.frames is provided to the `DGEdata` argument, each data.frame can follow the defaults and have the following columns or specify alternate names for the following to the ID, symbol, logFC, and FDR arguments:

| | |
|---|---|
| `ID` | Character vector with the feature ID (i.e. EnsemblID) |
| `symbol` | Optional character vector with gene symbol for labels |
| `logFC` | Numeric with the logFC |
| `adj.P.Val` | Numeric with the FDR |

The correlation coefficient is useful for comparing across multiple plots. However, it is important to consider whether there are any common factors when comparing values, since that can result in a larger value. Some examples are contrasts with covariates that are shared between groups or contrasts with the same control group.

## Value

A ggplot

## Examples

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

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