Package ‘Glimma’

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Type Package

Title Interactive HTML graphics

Version 2.2.0

Description This package generates interactive visualisations for analysis of RNA-sequencing data using output from limma, edgeR or DESeq2 packages in an HTML page. The interactions are built on top of the popular static representations of analysis results in order to provide additional information.

Encoding UTF-8

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Imports htmlwidgets, edgeR, DESeq2, limma, SummarizedExperiment, stats, jsonlite, methods, S4Vectors

Suggests testthat, knitr, rmarkdown, BiocStyle, IRanges, GenomicRanges, pryr

License GPL-3

URL `https://github.com/hasaru-k/GlimmaV2`

BugReports `https://github.com/hasaru-k/GlimmaV2/issues`

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Author Shian Su [aut, cre],
Hasaru Kariyawasam [aut],
Oliver Voogd [aut],

Matthew Ritchie [aut],
Charity Law [aut],
Stuart Lee [ctb],
Isaac Virshup [ctb]

Maintainer Shian Su `<su.s@wehi.edu.au>`

R topics documented:

`arraydata` *Example microarray for the study of Ezh2.*

Description

Example microarray for the study of Ezh2.

Author(s)

Bhupinder Pal, Toula Bouras, Wei Shi, Francois Vaillant, Julie M. Sheridan, Naiyang Fu, Kelsey Breslin, Kun Jiang, Matthew E. Ritchie, Matthew Young, Geoffrey J. Lindeman, Gordon K. Smyth, Jane E. Visvader

References

`http://www.cell.com/cell-reports/abstract/S2211-1247(13)00007-7`

`as.hexcol` *Numeric to hex colour converter*

Description

Convert numbers and R colour strings into corresponding hex codes for colours

Usage

```
as.hexcol(x)
```

Arguments

`x`	the colour value(s) to be converted to hex values.

Value

hex codes for colours

Examples

```
as.hexcol(c(1, 2, 3))
as.hexcol(c("red", "black", "green"))
```

`glimma` *Glimma: interactive graphics from limma*

Description

The Glimma package provides iteractive versions of plots frequently used in the limma package. Currently the MDS and MD plots have been implemented. The functions can be used with both limma, edgeR and DESeq objecs.

Main functions

`glMDSPlot`, `glMDPlot`, `glXYPlot`

`glimmaMA` *Glimma MA Plot*

Description

Generic function for drawing a two-panel interactive MA plot, a special case of the glimmaXY plot. The function invokes the following methods which depend on the class of the first argument:

- `glimmaMA.MArrayLM` for limma analysis
- `glimmaMA.DGEExact` for edgeR analysis, produced from `exactTest`
- `glimmaMA.DGELRT` for edgeR analysis, produced from `glmLRT`
- `glimmaMA.DESeqDataSet` for DESeq2 analysis

Usage

```
glimmaMA(x, ...)
```

Arguments

`x`	the DE object to plot.
`...`	additional arguments affecting the plots produced. See specific methods for detailed arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the y-axis versus average gene expression calculated as log-counts-per-million (logCPM) values. We call our summary plot an MA plot because this type of plot was originally referred to as an MA plot in the `limma` package, with the M-value representing logFC and A-value representing average expression - it has since been renamed to MD plot in the `limma` package. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

Examples

```
methods(glimmaMA) # show methods for glimmaMA
```

`glimmaMA.DESeqDataSet` *Glimma MA Plot*

Description

Draws a two-panel interactive MA plot from an DESeqDataSet object. This is a special case of the `glimmaXY` plot.

Usage

```
## S3 method for class 'DESeqDataSet'
glimmaMA(
  x,
  counts = DESeq2::counts(x),
  groups = extractGroups(colData(x)),
  status = NULL,
  anno = NULL,
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = "MA Plot",
  xlab = "logCPM",
  ylab = "logFC",
  html = NULL,
  width = 920,
  height = 920,
  ...
)
```

Arguments

`x`	DESeqDataSet object from which summary statistics are extracted from to create summary (left) plot.
`counts`	numeric matrix with nrow(x) rows containing gene expression values.
`groups`	vector/factor representing the experimental group for each sample; see `extractGroups` for default value.
`status`	vector of length nrow(x) indicating the status of each gene.
`anno`	dataframe with `nrow(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from `anno` from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of `-1`, 0 and 1.
`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.
`main`	character string for the main title of summary plot.
`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.
`...`	addition unused arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the y-axis versus average gene expression calculated as log-counts-per-million (logCPM) values. We call our summary plot an MA plot because this type of plot was originally referred to as an MA plot in the `limma` package, with the M-value representing logFC and A-value representing average expression - it has since been renamed to MD plot in the `limma` package. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaMA`, `glimmaMA.MArrayLM`, `glimmaMA.DGEExact`, `glimmaMA.DGELRT`

Examples

```
dge <- readRDS(
  system.file("RNAseq123/dge.rds", package = "Glimma"))

dds <- DESeq2::DESeqDataSetFromMatrix(
  countData = dge$counts,
  colData = dge$samples,
  rowData = dge$genes,
  design = ~group
)

dds <- DESeq2::DESeq(dds, quiet=TRUE)
glimmaMA(dds)
```

`glimmaMA.DGEExact` *Glimma MA Plot*

Description

Draws a two-panel interactive MA plot from an DGEExact object. This is a special case of the `glimmaXY` plot.

Usage

```
## S3 method for class 'DGEExact'
glimmaMA(
  x,
  dge = NULL,
  counts = dge$counts,
  groups = dge$samples$group,
  status = edgeR::decideTestsDGE(x),
  anno = x$genes,
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  p.adj.method = "BH",
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = paste(x$comparison[2], "vs", x$comparison[1]),
  xlab = "logCPM",
```

```
  ylab = "logFC",
  html = NULL,
  width = 920,
  height = 920,
  ...
)
```

Arguments

`x`	DGEExact object from which summary statistics are extracted from to create summary (left) plot.
`dge`	`DGEList` object with `nrow(x)` rows from which expression values are extracted from to create expression (right) plot. Gene counts are taken from `dge$counts` and sample groups from `dge$samples$group`.
`counts`	numeric matrix with `nrow(x)` rows containing gene expression values. This can be used to replace raw gene counts from `dge$counts` with transformed counts e.g. logCPM or logRPKM values.
`groups`	vector of length `ncol(dge)` representing categorisation of samples in expression plot.
`status`	vector of length nrow(x) indicating the status of each gene. By default genes in the summary plot are coloured based on its differential expression status using an adjusted p-value cutoff of 0.05 by calling the `edgeR::decideTestsDGE()` function, where the value of -1 marks down-regulated genes, 0 marks genes with no expression difference, and 1 marks up-regulated genes.
`anno`	dataframe with `nrow(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from anno from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of -1, 0 and 1.
`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`p.adj.method`	character string specifying p-value adjustment method.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.
`main`	character string for the main title of summary plot.
`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.
`...`	addition unused arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the y-axis versus average gene expression calculated as log-counts-per-million (logCPM) values. We call our summary plot an MA plot because this type of plot was originally referred to as an MA plot in the `limma` package, with the M-value representing logFC and A-value representing average expression - it has since been renamed to MD plot in the `limma` package. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaMA`, `glimmaMA.MArrayLM`, `glimmaMA.DGELRT`, `glimmaMA.DESeqDataSet`

Examples

```
dge <- readRDS(
  system.file("RNAseq123/dge.rds", package = "Glimma"))
design <- readRDS(
  system.file("RNAseq123/design.rds", package = "Glimma"))
contr.matrix <- readRDS(
  system.file("RNAseq123/contr.matrix.rds", package = "Glimma"))

dge <- edgeR::estimateDisp(dge, design)
gfit <- edgeR::glmFit(dge, design)
glrt <- edgeR::glmLRT(gfit, design, contrast = contr.matrix)

glimmaMA(glrt, dge = dge)
```

`glimmaMA.DGELRT` *Glimma MA Plot*

Description

Draws a two-panel interactive MA plot from an DGELRT object. This is a special case of the `glimmaXY` plot.

Usage

```
## S3 method for class 'DGELRT'
glimmaMA(
  x,
  dge = NULL,
  counts = dge$counts,
  groups = dge$samples$group,
  status = edgeR::decideTestsDGE(x),
  anno = x$genes,
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  p.adj.method = "BH",
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = paste(x$comparison[2], "vs", x$comparison[1]),
  xlab = "logCPM",
  ylab = "logFC",
  html = NULL,
  width = 920,
  height = 920,
  ...
)
```

Arguments

`x`	DGELRT object from which summary statistics are extracted from to create summary (left) plot.
`dge`	`DGEList` object with `nrow(x)` rows from which expression values are extracted from to create expression (right) plot. Gene counts are taken from `dge$counts` and sample groups from `dge$samples$group`.
`counts`	numeric matrix with `nrow(x)` rows containing gene expression values. This can be used to replace raw gene counts from `dge$counts` with transformed counts e.g. logCPM or logRPKM values.
`groups`	vector of length `ncol(dge)` representing categorisation of samples in expression plot.
`status`	vector of length nrow(x) indicating the status of each gene. By default genes in the summary plot are coloured based on its differential expression status using an adjusted p-value cutoff of 0.05 by calling the `edgeR::decideTestsDGE()` function, where the value of -1 marks down-regulated genes, 0 marks genes with no expression difference, and 1 marks up-regulated genes.
`anno`	dataframe with `nrow(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from anno from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of -1, 0 and 1.

`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`p.adj.method`	character string specifying p-value adjustment method.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.
`main`	character string for the main title of summary plot.
`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.
`...`	addition unused arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the y-axis versus average gene expression calculated as log-counts-per-million (logCPM) values. We call our summary plot an MA plot because this type of plot was originally referred to as an MA plot in the `limma` package, with the M-value representing logFC and A-value representing average expression - it has since been renamed to MD plot in the `limma` package. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaMA`, `glimmaMA.MArrayLM`, `glimmaMA.DGEExact`, `glimmaMA.DESeqDataSet`

`glimmaMA.MArrayLM` *Glimma MA Plot*

Description

Draws a two-panel interactive MA plot from an MArrayLM object. This is a special case of the `glimmaXY` plot.

Usage

```
## S3 method for class 'MArrayLM'
glimmaMA(
  x,
  dge = NULL,
  counts = dge$counts,
  groups = dge$samples$group,
  coef = ncol(x$coefficients),
  status = limma::decideTests(x),
  anno = x$genes,
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  p.adj.method = "BH",
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = colnames(x)[coef],
  xlab = "logCPM",
  ylab = "logFC",
  html = NULL,
  width = 920,
  height = 920,
  ...
)
```

Arguments

x	`MArrayLM` object from which summary statistics are extracted from to create summary (left) plot.
dge	`DGEList` object with `nrow(x)` rows from which expression values are extracted from to create expression (right) plot. Gene counts are taken from `dge$counts` and sample groups from `dge$samples$group`.
counts	numeric matrix with `nrow(x)` rows containing gene expression values. This can be used to replace raw gene counts from `dge$counts` with transformed counts e.g. logCPM or logRPKM values.
groups	vector of length `ncol(dge)` representing categorisation of samples in expression plot.
coef	integer indicating the column in `x` from the summary plot is created.

`status`	vector of length `nrow(x)` indicating the status of each gene. By default genes in the summary plot are coloured based on its differential expression status using an adjusted p-value cutoff of 5% by calling the `limma::decideTests` function, where the value of -1 marks down-regulated genes, 0 marks genes with no expression difference, and 1 marks up-regulated genes.
`anno`	dataframe with `nrow(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from `anno` from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of -1, 0 and 1.
`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`p.adj.method`	character string specifying p-value adjustment method.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.
`main`	character string for the main title of summary plot.
`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.
`...`	addition unused arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the y-axis versus average gene expression calculated as log-counts-per-million (logCPM) values. We call our summary plot an MA plot because this type of plot was originally referred to as an MA plot in the `limma` package, with the M-value representing logFC and A-value representing average expression - it has since been renamed to MD plot in the `limma` package. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaMA`, `glimmaMA.DGEExact`, `glimmaMA.DGELRT`, `glimmaMA.DESeqDataSet`

Examples

```
dge <- readRDS(
  system.file("RNAseq123/dge.rds", package = "Glimma"))
design <- readRDS(
  system.file("RNAseq123/design.rds", package = "Glimma"))
contr.matrix <- readRDS(
  system.file("RNAseq123/contr.matrix.rds", package = "Glimma"))

v <- limma::voom(dge, design)
vfit <- limma::lmFit(v, design)
vfit <- limma::contrasts.fit(vfit, contrasts = contr.matrix)
efit <- limma::eBayes(vfit)

glimmaMA(efit, dge = dge)
```

`glimmaMDS` *Glimma MDS Plot*

Description

Generic function for drawing a two-panel interactive MDS plot. The function invokes the following methods which depend on the class of the first argument:

- `glimmaMDS.DGEList` for edgeR analysis
- `glimmaMDS.DESeqDataSet` for DESeq2 analysis
- `glimmaMDS.default` for all other object types

Usage

```
glimmaMDS(x, ...)
```

Arguments

`x`	the matrix containing the gene expressions.
`...`	the additional arguments affecting the plot produced. See specific methods for detailed arguments.

Details

The left plot shows two MDS dimensions, with sample annotations displayed on hover. The right panel contains a bar plot of the eigenvalues of each dimension. The controls beneath the plots can be used to change the dimensions being displayed, and the scale, colour and shape of points. The interactive MDS plot allows users to adjust sample points by scale, colour and shape for multiple vectors associated with sample information. This is carried out most effectively when `x$samples` includes an abundance of sample information, or when a data frame object is supplied to `groups`. If a simple character or factor vector is given to `groups` (with the default of `continous.colour=FALSE`), then sample points will have no scaling options, but can only be adjusted in colour and shape by `groups` and `labels`. Instead, if `groups` is a numeric vector (e.g. library size or expression level of a specific gene), then the plot can be scaled and coloured by the numeric values with `continous.colour=TRUE`.

Value

htmlwidget object or `NULL` if `html` argument is specified.

Examples

```
dge <- readRDS(system.file("RNAseq123/dge.rds", package = "Glimma"))
glimmaMDS(dge)

# using DESeqDataSet
dds <- DESeq2::DESeqDataSetFromMatrix(
 countData = dge$counts,
 colData = dge$samples,
 rowData = dge$genes,
 design = ~group
)
glimmaMDS(dds)

# using matrix object
expr <- edgeR::cpm(dge, log = TRUE)
glimmaMDS(expr)
```

`glimmaMDS.default` *Glimma MDS Plot*

Description

Draws a two-panel interactive MDS plot.

Usage

```
## Default S3 method:
glimmaMDS(
  x,
  groups = as.character(rep(1, ncol(x))),
  labels = as.character(seq_len(ncol(x))),
  continuous.colour = FALSE,
  top = 500,
  gene.selection = c(”pairwise”, ”common”),
  html = NULL,
  width = 900,
  height = 500,
  ...
)
```

Arguments

`x`	the matrix containing the gene expressions.
`groups`	vector or data frame object with associated sample information such as experimental groups. The information is displayed in mouseover tooltips, and appropriate vector(s) can be used to adjust the plot using `scale_by`, `colour_by` and `shape_by` drop-down boxes of the widget.
`labels`	character vector of sample names or labels.
`continuous.colour`	`TRUE` if continuous colour schemes should be used. Defaults to `FALSE` where distinct colour schemes are used.
`top`	integer indiating number of top genes used to calculate pairwise distances.
`gene.selection`	character string specifying how genes are selected from the plot - "pairwise" if most variable genes are to be chosen for each pair of samples, or "common" to select the same genes for all comparisons.
`html`	character string for naming HTML file or exportation of widget. The extension should be included in the file name e.g. "file.hml".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of widget in pixels.
`...`	additional unused arguments.

Details

The left plot shows two MDS dimensions, with sample annotations displayed on hover. The right panel contains a bar plot of the eigenvalues of each dimension. The controls beneath the plots can be used to change the dimensions being displayed, and the scale, colour and shape of points. The interactive MDS plot allows users to adjust sample points by scale, colour and shape for multiple vectors associated with sample information. This is carried out most effectively when `x$samples` includes an abundance of sample information, or when a data frame object is supplied to `groups`. If a simple character or factor vector is given to `groups` (with the default of `continous.colour=FALSE`), then sample points will have no scaling options, but can only be adjusted in colour and shape by `groups` and `labels`. Instead, if `groups` is a numeric vector (e.g. library size or expression level of a specific gene), then the plot can be scaled and coloured by the numeric values with `continous.colour=TRUE`.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaMDS`, `glimmaMDS.DGEList`, `glimmaMDS.DESeqDataSet`

Examples

```
dge <- readRDS(system.file("RNAseq123/dge.rds", package = "Glimma"))
expr <- edgeR::cpm(dge, log = TRUE)
glimmaMDS(expr)
```

`glimmaMDS.DESeqDataSet`

Glimma MDS Plot

Description

Draws a two-panel interactive MDS plot using a DESeqDataset x. Transforms counts using `edgeR::cpm(DESeq2::counts(x` `= TRUE,prior.count = prior.count)`.

Usage

```
## S3 method for class 'DESeqDataSet'
glimmaMDS(
  x,
  groups = as.data.frame(SummarizedExperiment::colData(x)),
  labels = rownames(SummarizedExperiment::colData(x)),
  continuous.colour = FALSE,
  top = 500,
  gene.selection = c("pairwise", "common"),
  prior.count = 2,
  html = NULL,
  width = 900,
  height = 500,
  ...
)
```

Arguments

`x`	`DESeqDataSet` object containing gene counts.
`groups`	vector or data frame object with associated sample information such as experimental groups. The information is displayed in mouseover tooltips, and appropriate vector(s) can be used to adjust the plot using `scale_by`, `colour_by` and `shape_by` drop-down boxes of the widget.
`labels`	character vector of sample names or labels.
`continuous.colour`	`TRUE` if continuous colour schemes should be used. Defaults to `FALSE` where distinct colour schemes are used.
`top`	integer indiating number of top genes used to calculate pairwise distances.
`gene.selection`	character string specifying how genes are selected from the plot - "pairwise" if most variable genes are to be chosen for each pair of samples, or "common" to select the same genes for all comparisons.
`prior.count`	integer indicating the average count to be added to each observation to avoid taking log of zero when raw counts are transformed to log-counts-per-million values.
`html`	character string for naming HTML file or exportation of widget. The extension should be included in the file name e.g. "file.hml".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of widget in pixels.
`...`	additional unused arguments.

Details

The left plot shows two MDS dimensions, with sample annotations displayed on hover. The right panel contains a bar plot of the eigenvalues of each dimension. The controls beneath the plots can be used to change the dimensions being displayed, and the scale, colour and shape of points. The interactive MDS plot allows users to adjust sample points by scale, colour and shape for multiple vectors associated with sample information. This is carried out most effectively when `x$samples` includes an abundance of sample information, or when a data frame object is supplied to `groups`. If a simple character or factor vector is given to `groups` (with the default of `continous.colour=FALSE`), then sample points will have no scaling options, but can only be adjusted in colour and shape by `groups` and `labels`. Instead, if `groups` is a numeric vector (e.g. library size or expression level of a specific gene), then the plot can be scaled and coloured by the numeric values with `continous.colour=TRUE`.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaMDS`, `glimmaMDS.default`, `glimmaMDS.DGEList`

Examples

```
dge <- readRDS(system.file("RNAseq123/dge.rds", package = "Glimma"))
dds <- DESeq2::DESeqDataSetFromMatrix(
 countData = dge$counts,
 colData = dge$samples,
 rowData = dge$genes,
 design = ~group
)
glimmaMDS(dds)
```

`glimmaMDS.DGEList` *Glimma MDS Plot*

Description

Draws a two-panel interactive MDS plot using a DGEList x. Transforms counts using `edgeR::cpm(x,log=TRUE,prior.cour` `= prior.count)`.

Usage

```
## S3 method for class 'DGEList'
glimmaMDS(
  x,
  groups = x$samples,
  labels = rownames(x$samples),
  continuous.colour = FALSE,
  top = 500,
  gene.selection = c("pairwise", "common"),
  prior.count = 2,
  html = NULL,
  width = 900,
  height = 500,
  ...
)
```

Arguments

`x`	`DGEList` object containing gene counts in `x$counts`.
`groups`	vector or data frame object with associated sample information such as experimental groups. The information is displayed in mouseover tooltips, and appropriate vector(s) can be used to adjust the plot using `scale_by`, `colour_by` and `shape_by` drop-down boxes of the widget.
`labels`	character vector of sample names or labels.
`continuous.colour`	`TRUE` if continuous colour schemes should be used. Defaults to `FALSE` where distinct colour schemes are used.

`top`	integer indiating number of top genes used to calculate pairwise distances.
`gene.selection`	character string specifying how genes are selected from the plot - "pairwise" if most variable genes are to be chosen for each pair of samples, or "common" to select the same genes for all comparisons.
`prior.count`	integer indicating the average count to be added to each observation to avoid taking log of zero when raw counts are transformed to log-counts-per-million values.
`html`	character string for naming HTML file or exportation of widget. The extension should be included in the file name e.g. "file.hml".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of widget in pixels.
`...`	additional unused arguments.

Details

The left plot shows two MDS dimensions, with sample annotations displayed on hover. The right panel contains a bar plot of the eigenvalues of each dimension. The controls beneath the plots can be used to change the dimensions being displayed, and the scale, colour and shape of points. The interactive MDS plot allows users to adjust sample points by scale, colour and shape for multiple vectors associated with sample information. This is carried out most effectively when `x$samples` includes an abundance of sample information, or when a data frame object is supplied to `groups`. If a simple character or factor vector is given to `groups` (with the default of `continous.colour=FALSE`), then sample points will have no scaling options, but can only be adjusted in colour and shape by `groups` and `labels`. Instead, if `groups` is a numeric vector (e.g. library size or expression level of a specific gene), then the plot can be scaled and coloured by the numeric values with `continous.colour=TRUE`.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaMDS`, `glimmaMDS.default`, `glimmaMDS.DESeqDataSet`

Examples

```
dge <- readRDS(system.file("RNAseq123/dge.rds", package = "Glimma"))
glimmaMDS(dge)
```

`glimmaVolcano` *Glimma Volcano Plot*

Description

Generic function for drawing a two-panel interactive volcano plot, a special case of the glimmaXY plot. The function invokes the following methods which depend on the class of the first argument:

- `glimmaVolcano.MArrayLM` for limma analysis
- `glimmaVolcano.DGEExact` for edgeR analysis, produced from `exactTest`
- `glimmaVolcano.DGELRT` for edgeR analysis, produced from `glmLRT`
- `glimmaVolcano.DESeqDataSet` for DESeq2 analysis

Usage

```
glimmaVolcano(x, ...)
```

Arguments

`x`	the DE object to plot.
`...`	additional arguments affecting the plots produced. See specific methods for detailed arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the x-axis versus `-log10(pvalue)`. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

Examples

```
dge <- readRDS(
  system.file("RNAseq123/dge.rds", package = "Glimma"))
design <- readRDS(
  system.file("RNAseq123/design.rds", package = "Glimma"))
contr.matrix <- readRDS(
  system.file("RNAseq123/contr.matrix.rds", package = "Glimma"))
```

```
v <- limma::voom(dge, design)
vfit <- limma::lmFit(v, design)
vfit <- limma::contrasts.fit(vfit, contrasts = contr.matrix)
efit <- limma::eBayes(vfit)

glimmaVolcano(efit, dge = dge)
```

`glimmaVolcano.DESeqDataSet` *Glimma Volcano Plot*

Description

Draws a two-panel interactive volcano plot from an DESeqDataSet object. This is a special case of the `glimmaXY` plot.

Usage

```
## S3 method for class 'DESeqDataSet'
glimmaVolcano(
  x,
  counts = DESeq2::counts(x),
  groups = extractGroups(colData(x)),
  status = NULL,
  anno = NULL,
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = "Volcano Plot",
  xlab = "logFC",
  ylab = "negLog10PValue",
  html = NULL,
  width = 920,
  height = 920,
  ...
)
```

Arguments

`x`	DESeqDataSet object from which summary statistics are extracted from to create summary (left) plot.
`counts`	numeric matrix with nrow(x) rows containing gene expression values.
`groups`	vector/factor representing the experimental group for each sample; see `extractGroups` for default value.

`status`	vector of length nrow(x) indicating the status of each gene.
`anno`	dataframe with `nrow(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from `anno` from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of -1, 0 and 1.
`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.
`main`	character string for the main title of summary plot.
`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.
`...`	addition unused arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the x-axis versus `-log10(pvalue)`. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaVolcano`, `glimmaVolcano.MArrayLM`, `glimmaVolcano.DGEExact`, `glimmaVolcano.DGELRT`

Examples

```
dge <- readRDS(
  system.file("RNAseq123/dge.rds", package = "Glimma"))

dds <- DESeq2::DESeqDataSetFromMatrix(
  countData = dge$counts,
  colData = dge$samples,
  rowData = dge$genes,
  design = ~group
)

dds <- DESeq2::DESeq(dds, quiet=TRUE)
glimmaVolcano(dds)
```

`glimmaVolcano.DGEExact` *Glimma Volcano Plot*

Description

Draws a two-panel interactive volcano plot from an DGEExact object. This is a special case of the `glimmaXY` plot.

Usage

```
## S3 method for class 'DGEExact'
glimmaVolcano(
  x,
  dge = NULL,
  counts = dge$counts,
  groups = dge$samples$group,
  status = edgeR::decideTestsDGE(x),
  anno = x$genes,
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  p.adj.method = "BH",
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = paste(x$comparison[2], "vs", x$comparison[1]),
  xlab = "logFC",
  ylab = "negLog10PValue",
  html = NULL,
  width = 920,
  height = 920,
  ...
)
```

Arguments

`x`	DGEExact object from which summary statistics are extracted from to create summary (left) plot.
`dge`	`DGEList` object with `nrow(x)` rows from which expression values are extracted from to create expression (right) plot. Gene counts are taken from `dge$counts` and sample groups from `dge$samples$group`.
`counts`	numeric matrix with `nrow(x)` rows containing gene expression values. This can be used to replace raw gene counts from `dge$counts` with transformed counts e.g. logCPM or logRPKM values.
`groups`	vector of length `ncol(dge)` representing categorisation of samples in expression plot.
`status`	vector of length nrow(x) indicating the status of each gene. By default genes in the summary plot are coloured based on its differential expression status using an adjusted p-value cutoff of 0.05 by calling the `edgeR::decideTestsDGE()` function, where the value of -1 marks down-regulated genes, 0 marks genes with no expression difference, and 1 marks up-regulated genes.
`anno`	dataframe with `nrow(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from `anno` from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of -1, 0 and 1.
`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`p.adj.method`	character string specifying p-value adjustment method.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.
`main`	character string for the main title of summary plot.
`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.
`...`	addition unused arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the x-axis versus `-log10(pvalue)`. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaVolcano`, `glimmaVolcano.MArrayLM`, `glimmaVolcano.DGELRT`, `glimmaVolcano.DESeqDataSet`

Examples

```
dge <- readRDS(
  system.file("RNAseq123/dge.rds", package = "Glimma"))
design <- readRDS(
  system.file("RNAseq123/design.rds", package = "Glimma"))
contr.matrix <- readRDS(
  system.file("RNAseq123/contr.matrix.rds", package = "Glimma"))

dge <- edgeR::estimateDisp(dge, design)
gfit <- edgeR::glmFit(dge, design)
glrt <- edgeR::glmLRT(gfit, design, contrast = contr.matrix)

glimmaVolcano(glrt, dge = dge)
```

`glimmaVolcano.DGELRT` *Glimma Volcano Plot*

Description

Draws a two-panel interactive volcano plot from an DGELRT object. This is a special case of the `glimmaXY` plot.

Usage

```
## S3 method for class 'DGELRT'
glimmaVolcano(
  x,
  dge = NULL,
  counts = dge$counts,
  groups = dge$samples$group,
  status = edgeR::decideTestsDGE(x),
  anno = x$genes,
```

```
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  p.adj.method = "BH",
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = paste(x$comparison[2], "vs", x$comparison[1]),
  xlab = "logFC",
  ylab = "negLog10PValue",
  html = NULL,
  width = 920,
  height = 920,
  ...
)
```

Arguments

`x`	DGELRT object from which summary statistics are extracted from to create summary (left) plot.
`dge`	`DGEList` object with `nrow(x)` rows from which expression values are extracted from to create expression (right) plot. Gene counts are taken from `dge$counts` and sample groups from `dge$samples$group`.
`counts`	numeric matrix with `nrow(x)` rows containing gene expression values. This can be used to replace raw gene counts from `dge$counts` with transformed counts e.g. logCPM or logRPKM values.
`groups`	vector of length `ncol(dge)` representing categorisation of samples in expression plot.
`status`	vector of length nrow(x) indicating the status of each gene. By default genes in the summary plot are coloured based on its differential expression status using an adjusted p-value cutoff of 0.05 by calling the `edgeR::decideTestsDGE()` function, where the value of -1 marks down-regulated genes, 0 marks genes with no expression difference, and 1 marks up-regulated genes.
`anno`	dataframe with `nrow(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from `anno` from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of -1, 0 and 1.
`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`p.adj.method`	character string specifying p-value adjustment method.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.
`main`	character string for the main title of summary plot.

`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.
`...`	addition unused arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the x-axis versus `-log10(pvalue)`. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaVolcano`, `glimmaVolcano.MArrayLM`, `glimmaVolcano.DGEExact`, `glimmaVolcano.DESeqDataSet`

`glimmaVolcano.MArrayLM` *Glimma Volcano Plot*

Description

Draws a two-panel interactive volcano plot from an MArrayLM object. This is a special case of the `glimmaXY` plot.

Usage

```
## S3 method for class 'MArrayLM'
glimmaVolcano(
  x,
  dge = NULL,
  counts = dge$counts,
  groups = dge$samples$group,
  coef = ncol(x$coefficients),
```

```
  status = limma::decideTests(x),
  anno = x$genes,
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  p.adj.method = "BH",
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = colnames(x)[coef],
  xlab = "logFC",
  ylab = "negLog10PValue",
  html = NULL,
  width = 920,
  height = 920,
  ...
)
```

Arguments

`x`	`MArrayLM` object from which summary statistics are extracted from to create summary (left) plot.
`dge`	`DGEList` object with `nrow(x)` rows from which expression values are extracted from to create expression (right) plot. Gene counts are taken from `dge$counts` and sample groups from `dge$samples$group`.
`counts`	numeric matrix with `nrow(x)` rows containing gene expression values. This can be used to replace raw gene counts from `dge$counts` with transformed counts e.g. logCPM or logRPKM values.
`groups`	vector of length `ncol(dge)` representing categorisation of samples in expression plot.
`coef`	integer indicating the column in `x` from the summary plot is created.
`status`	vector of length `nrow(x)` indicating the status of each gene. By default genes in the summary plot are coloured based on its differential expression status using an adjusted p-value cutoff of 5% by calling the `limma::decideTests` function, where the value of -1 marks down-regulated genes, 0 marks genes with no expression difference, and 1 marks up-regulated genes.
`anno`	dataframe with `nrow(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from `anno` from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of -1, 0 and 1.
`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`p.adj.method`	character string specifying p-value adjustment method.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.

`main`	character string for the main title of summary plot.
`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.
`...`	addition unused arguments.

Details

The summary plot on the left represents gene-wise log-fold-change (logFC) on the x-axis versus `-log10(pvalue)`. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

See Also

`glimmaVolcano`, `glimmaVolcano.DGEExact`, `glimmaVolcano.DGELRT`, `glimmaVolcano.DESeqDataSet`

`glimmaXY` *Glimma XY Plot*

Description

Draws a two-panel interactive XY scatter plot.

Usage

```
glimmaXY(
  x,
  y,
  xlab = "x",
  ylab = "y",
  counts = NULL,
  groups = NULL,
  status = rep(0, length(x)),
```

```
  anno = NULL,
  display.columns = NULL,
  status.cols = c("dodgerblue", "silver", "firebrick"),
  sample.cols = NULL,
  transform.counts = c("logcpm", "cpm", "rpkm", "none"),
  main = "XY Plot",
  html = NULL,
  width = 920,
  height = 920
)
```

Arguments

`x`	numeric vector of values to plot on the x-axis of the summary plot.
`y`	numeric vector of values to plot on the y-axis of the summary plot.
`xlab`	character string for the x-axis label of summary plot.
`ylab`	character string for the y-axis label of summary plot.
`counts`	numeric matrix with `length(x)` rows containing gene expression values. This can be used to replace raw gene counts from dge$counts with transformed counts e.g. logCPM or logRPKM values.
`groups`	vector of length `ncol(counts)` representing categorisation of samples in expression plot.
`status`	vector of length `length(x)` indicating the status of each gene. A value of -1 marks a down-regulated gene, 0 marks a gene with no expression difference, and 1 marks an up-regulated gene.
`anno`	dataframe with `length(x)` rows containing gene annotations.
`display.columns`	character vector containing names of columns from `anno` from which to display in mouseover tooltips and table.
`status.cols`	vector of length 3 containing valid CSS strings for colours associated with `status` in the order of -1, 0 and 1.
`sample.cols`	character vector of length `ncol(counts)` containing valid CSS strings for colours associated with each sample to be displayed on the expression plot. If left unspecified, samples will be coloured according to `groups`.
`transform.counts`	the type of transform used on the counts log-cpm by default. `edgeR::cpm(counts,log=TRUE)`; defaults to FALSE.
`main`	character string for the main title of summary plot.
`html`	character string for naming HTML file for exportation of widget. The extension should be included in the file name e.g. "file.html".
`width`	numeric value indicating width of widget in pixels.
`height`	numeric value indicating width of height in pixels.

Details

The summary plot on the left displays the `x` and `y` values specified. The expression plot on the right displays sample expression values for a single gene. Interactions with the htmlwidget include clicking on genes (points) in the summary plot to bring up associated sample expression values in the expression plot, as well as the summary statistics in the table below. Alternatively, users can interact with the table by clicking on genes (rows) to highlight genes in the summary plot, as well as bring up associated sample expression values in the expression plot. Briefly, other interactive features include a search box for the table, buttons to save plots and data (summary statistics and expression values), additional pop-up information when hovering on points in plots, and rescaling of the y-axis in the expression plot.

Value

htmlwidget object or `NULL` if `html` argument is specified.

Examples

```
dge <- readRDS(
  system.file("RNAseq123/dge.rds", package = "Glimma"))
design <- readRDS(
  system.file("RNAseq123/design.rds", package = "Glimma"))
contr.matrix <- readRDS(
  system.file("RNAseq123/contr.matrix.rds", package = "Glimma"))

v <- limma::voom(dge, design)
vfit <- limma::lmFit(v, design)
vfit <- limma::contrasts.fit(vfit, contrasts = contr.matrix)
efit <- limma::eBayes(vfit)

glimmaXY(efit$Amean, efit$coefficients)
```

`glMDPlot` *Glimma MD Plot*

Description

Draw an interactive MD plot

Usage

```
glMDPlot(x, ...)
```

Arguments

`x`	the DE object to plot.
`...`	additional arguments affecting the plots produced. See specific methods for detailed arguments.

Value

Draws a two-panel interactive MD plot in an html page. The left plot shows the log-fold-change vs average expression. The right plot shows the expression levels of a particular gene of each sample. Hovering over points on left plot will plot expression level for corresponding gene, clicking on points will fix the expression plot to gene. Clicking on rows on the table has the same effect as clicking on the corresponding gene in the plot.

Author(s)

Shian Su

See Also

`glMDPlot.default`, `glMDPlot.DGELRT`, `glMDPlot.DGEExact`, `glMDPlot.MArrayLM`, `glMDPlot.DESeqDataSet`

Examples

```
library(limma)
library(edgeR)

data(lymphomaRNAseq)
x <- lymphomaRNAseq

sel <- rowSums(cpm(x$counts)>0.5)>=3
x <- x[sel,]

genotype <- relevel(x$samples$group, "Smchd1-null")
x <- calcNormFactors(x, method="TMM")
des <- model.matrix(~genotype)

## Apply voom with sample quality weights and fit linear model
v <- voomWithQualityWeights(x, design=des, plot=FALSE)
vfit <- lmFit(v,des)

## Apply treat relative to a fold-change of 1.5
vtfit <- treat(vfit,lfc=log2(1.5))
vfit <- eBayes(vfit)
results <- decideTests(vfit,p.value=0.01)


glMDPlot(vfit, counts=x$counts, anno=x$genes, groups=genotype, samples=1:7,
         status=results[,2], main="MD plot: Wild-type vs Smchd1",
         display.columns=c("Symbols", "GeneID", "GeneName"),
         folder="Smchd1-Lymphoma")
```

`glMDPlot.default` *Glimma MD Plot*

Description

Draw an interactive MD plot from a data.frame

Usage

```
## Default S3 method:
glMDPlot(
  x,
  xval,
  yval,
  counts = NULL,
  anno = NULL,
  groups = NULL,
  samples = NULL,
  status = rep(0, nrow(x)),
  transform = FALSE,
  main = "",
  xlab = xval,
  ylab = yval,
  side.main = "GeneID",
  side.xlab = "Group",
  side.ylab = "Expression",
  side.log = FALSE,
  side.gridstep = ifelse(!transform || side.log, FALSE, 0.5),
  jitter = 30,
  display.columns = side.main,
  cols = c("#00bfff", "#858585", "#ff3030"),
  sample.cols = rep("#1f77b4", ncol(counts)),
  path = getwd(),
  folder = "glimma-plots",
  html = "MD-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the data.frame object containing expression and fold change values.
`xval`	the column to plot on x axis of left plot.
`yval`	the column to plot on y axis of left plot.
`counts`	the matrix of expression values, with samples in columns.
`anno`	the data.frame containing gene annotations.

`groups`	the factor containing experimental groups of the samples.
`samples`	the names of the samples.
`status`	vector giving the control status of data point, of same length as the number of rows of object. If NULL, then all points are plotted in the default colour.
`transform`	TRUE if counts should be log-cpm transformed.
`main`	the title for the left plot.
`xlab`	the label on the x axis for the left plot.
`ylab`	the label on the y axis for the left plot.
`side.main`	the column containing mains for right plot.
`side.xlab`	label for x axis on right plot.
`side.ylab`	label for y axis on right plot.
`side.log`	TRUE to plot expression on the right plot on log scale.
`side.gridstep`	intervals along which to place grid lines on y axis. Currently only available for linear scale.
`jitter`	the amount of jitter to apply to the samples in the expressions plot.
`display.columns`	character vector containing names of columns to display in mouseover tooltips and table.
`cols`	vector of strings denoting colours corresponding to control status -1, 0 and 1. (may be R named colours or Hex values)
`sample.cols`	vector of strings denoting colours for each sample point on the expression plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments to be passed onto the MD plot. (main, xlab, ylab can be set for the left plot)

Value

Draws a two-panel interactive MD plot in an html page. The left plot shows the log-fold-change vs average expression. The right plot shows the expression levels of a particular gene of each sample. Hovering over points on left plot will plot expression level for corresponding gene, clicking on points will fix the expression plot to gene. Clicking on rows on the table has the same effect as clicking on the corresponding gene in the plot.

Author(s)

Shian Su

`glMDPlot.DESeqDataSet` *Glimma MD Plot*

Description

Draw an interactive MD plot from a DESeqDataSet object

Usage

```
## S3 method for class 'DESeqDataSet'
glMDPlot(
  x,
  counts = NULL,
  anno,
  groups,
  samples = NULL,
  status = rep(0, nrow(x)),
  transform = FALSE,
  main = "",
  xlab = "Mean Expression",
  ylab = "log-fold-change",
  side.xlab = "Group",
  side.ylab = "logMean",
  side.log = FALSE,
  side.gridstep = ifelse(!transform || side.log, FALSE, 0.5),
  jitter = 30,
  side.main = "GeneID",
  display.columns = NULL,
  cols = c("#00bfff", "#858585", "#ff3030"),
  sample.cols = rep("#1f77b4", ncol(x)),
  path = getwd(),
  folder = "glimma-plots",
  html = "MD-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the DESeqDataSet object.
`counts`	the matrix of expression values, with samples in columns.
`anno`	the data.frame containing gene annotations.
`groups`	the factor containing experimental groups of the samples.
`samples`	the names of the samples.
`status`	vector giving the control status of data point, of same length as the number of rows of object. If NULL, then all points are plotted in the default colour.

`transform`	TRUE if counts should be log-cpm transformed.
`main`	the title for the left plot.
`xlab`	label for x axis on left plot.
`ylab`	label for y axis on left plot.
`side.xlab`	label for x axis on right plot.
`side.ylab`	label for y axis on right plot.
`side.log`	TRUE to plot expression on the right plot on log scale.
`side.gridstep`	intervals along which to place grid lines on y axis. Currently only available for linear scale.
`jitter`	the amount of jitter to apply to the samples in the expressions plot.
`side.main`	the column containing mains for right plot.
`display.columns`	character vector containing names of columns to display in mouseover tooltips and table.
`cols`	vector of strings denoting colours corresponding to control status -1, 0 and 1. (may be R named colours or Hex values)
`sample.cols`	vector of strings denoting colours for each sample point on the expression plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments to be passed onto the MD plot. (main, xlab, ylab can be set for the left plot)

Value

Draws a two-panel interactive MD plot in an html page. The left plot shows the log-fold-change vs average expression. The right plot shows the expression levels of a particular gene of each sample. Hovering over points on left plot will plot expression level for corresponding gene, clicking on points will fix the expression plot to gene. Clicking on rows on the table has the same effect as clicking on the corresponding gene in the plot.

Author(s)

Shian Su

`glMDPlot.DESeqResults` *Glimma MD Plot*

Description

Draw an interactive MD plot from a DESeqResults object

Usage

```
## S3 method for class 'DESeqResults'
glMDPlot(
  x,
  counts = NULL,
  anno,
  groups,
  samples = NULL,
  status = rep(0, nrow(x)),
  transform = FALSE,
  main = "",
  xlab = "Mean Expression",
  ylab = "log-fold-change",
  side.xlab = "Group",
  side.ylab = "Expression",
  side.log = FALSE,
  side.gridstep = ifelse(!transform || side.log, FALSE, 0.5),
  jitter = 30,
  side.main = "GeneID",
  display.columns = NULL,
  cols = c("#00bfff", "#858585", "#ff3030"),
  sample.cols = rep("#1f77b4", ncol(counts)),
  path = getwd(),
  folder = "glimma-plots",
  html = "MD-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the DESeqResults object.
`counts`	the matrix of expression values, with samples in columns.
`anno`	the data.frame containing gene annotations.
`groups`	the factor containing experimental groups of the samples.
`samples`	the names of the samples.
`status`	vector giving the control status of data point, of same length as the number of rows of object. If NULL, then all points are plotted in the default colour.

`transform`	TRUE if counts should be log-cpm transformed.
`main`	the title for the left plot.
`xlab`	label for x axis on left plot.
`ylab`	label for y axis on left plot.
`side.xlab`	label for x axis on right plot.
`side.ylab`	label for y axis on right plot.
`side.log`	TRUE to plot expression on the right plot on log scale.
`side.gridstep`	intervals along which to place grid lines on y axis. Currently only available for linear scale.
`jitter`	the amount of jitter to apply to the samples in the expressions plot.
`side.main`	the column containing mains for right plot.
`display.columns`	character vector containing names of columns to display in mouseover tooltips and table.
`cols`	vector of strings denoting colours corresponding to control status -1, 0 and 1. (may be R named colours or Hex values)
`sample.cols`	vector of strings denoting colours for each sample point on the expression plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments to be passed onto the MD plot. (main, xlab, ylab can be set for the left plot)

Value

Draws a two-panel interactive MD plot in an html page. The left plot shows the log-fold-change vs average expression. The right plot shows the expression levels of a particular gene of each sample. Hovering over points on left plot will plot expression level for corresponding gene, clicking on points will fix the expression plot to gene. Clicking on rows on the table has the same effect as clicking on the corresponding gene in the plot.

Author(s)

Shian Su

`glMDPlot.DGEExact` *Glimma MD Plot*

Description

Draw an interactive MD plot from a DGELRT objet

Usage

```
## S3 method for class 'DGEExact'
glMDPlot(
  x,
  counts = NULL,
  anno = NULL,
  groups = NULL,
  samples = NULL,
  status = rep(0, nrow(x)),
  transform = FALSE,
  main = "",
  xlab = "Average log CPM",
  ylab = "log-fold-change",
  side.xlab = "Group",
  side.ylab = "Expression",
  side.log = FALSE,
  side.gridstep = ifelse(!transform || side.log, FALSE, 0.5),
  p.adj.method = "BH",
  jitter = 30,
  side.main = "GeneID",
  display.columns = NULL,
  cols = c("#00bfff", "#858585", "#ff3030"),
  sample.cols = rep("#1f77b4", ncol(counts)),
  path = getwd(),
  folder = "glimma-plots",
  html = "MD-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the DGEExact object.
`counts`	the matrix of expression values, with samples in columns.
`anno`	the data.frame containing gene annotations.
`groups`	the factor containing experimental groups of the samples.
`samples`	the names of the samples.

`status`	vector giving the control status of data point, of same length as the number of rows of object. If NULL, then all points are plotted in the default colour.
`transform`	TRUE if counts should be log-cpm transformed.
`main`	the title for the left plot.
`xlab`	label for x axis on left plot.
`ylab`	label for y axis on left plot.
`side.xlab`	label for x axis on right plot.
`side.ylab`	label for y axis on right plot.
`side.log`	TRUE to plot expression on the right plot on log scale.
`side.gridstep`	intervals along which to place grid lines on y axis. Currently only available for linear scale.
`p.adj.method`	character vector indicating multiple testing correction method. See `p.adjust` for available methods. (defaults to "BH")
`jitter`	the amount of jitter to apply to the samples in the expressions plot.
`side.main`	the column containing mains for right plot.
`display.columns`	character vector containing names of columns to display in mouseover tooltips and table.
`cols`	vector of strings denoting colours corresponding to control status -1, 0 and 1. (may be R named colours or Hex values)
`sample.cols`	vector of strings denoting colours for each sample point on the expression plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments to be passed onto the MD plot. (main, xlab, ylab can be set for the left plot)

Value

Draws a two-panel interactive MD plot in an html page. The left plot shows the log-fold-change vs average expression. The right plot shows the expression levels of a particular gene of each sample. Hovering over points on left plot will plot expression level for corresponding gene, clicking on points will fix the expression plot to gene. Clicking on rows on the table has the same effect as clicking on the corresponding gene in the plot.

Author(s)

Shian Su

`glMDPlot.DGELRT` *Glimma MD Plot*

Description

Draw an interactive MD plot from a DGELRT object

Usage

```
## S3 method for class 'DGELRT'
glMDPlot(
  x,
  counts = NULL,
  anno = NULL,
  groups = NULL,
  samples = NULL,
  status = rep(0, nrow(x)),
  transform = FALSE,
  main = "",
  xlab = "Average log CPM",
  ylab = "log-fold-change",
  side.xlab = "Group",
  side.ylab = "Expression",
  side.log = FALSE,
  side.gridstep = ifelse(!transform || side.log, FALSE, 0.5),
  p.adj.method = "BH",
  jitter = 30,
  side.main = "GeneID",
  display.columns = NULL,
  cols = c("#00bfff", "#858585", "#ff3030"),
  sample.cols = rep("#1f77b4", ncol(counts)),
  path = getwd(),
  folder = "glimma-plots",
  html = "MD-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the DGELRT object.
`counts`	the matrix of expression values, with samples in columns.
`anno`	the data.frame containing gene annotations.
`groups`	the factor containing experimental groups of the samples.
`samples`	the names of the samples.

`status`	vector giving the control status of data point, of same length as the number of rows of object. If NULL, then all points are plotted in the default colour.
`transform`	TRUE if counts should be log-cpm transformed.
`main`	the title for the left plot.
`xlab`	label for x axis on left plot.
`ylab`	label for y axis on left plot.
`side.xlab`	label for x axis on right plot.
`side.ylab`	label for y axis on right plot.
`side.log`	TRUE to plot expression on the right plot on log scale.
`side.gridstep`	intervals along which to place grid lines on y axis. Currently only available for linear scale.
`p.adj.method`	character vector indicating multiple testing correction method. See `p.adjust` for available methods. (defaults to "BH")
`jitter`	the amount of jitter to apply to the samples in the expressions plot.
`side.main`	the column containing mains for right plot.
`display.columns`	character vector containing names of columns to display in mouseover tooltips and table.
`cols`	vector of strings denoting colours corresponding to control status -1, 0 and 1. (may be R named colours or Hex values)
`sample.cols`	vector of strings denoting colours for each sample point on the expression plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments to be passed onto the MD plot. (main, xlab, ylab can be set for the left plot)

Value

Draws a two-panel interactive MD plot in an html page. The left plot shows the log-fold-change vs average expression. The right plot shows the expression levels of a particular gene of each sample. Hovering over points on left plot will plot expression level for corresponding gene, clicking on points will fix the expression plot to gene. Clicking on rows on the table has the same effect as clicking on the corresponding gene in the plot.

Author(s)

Shian Su

`glMDPlot.MArrayLM` *Glimma MD Plot*

Description

Draw an interactive MD plot from a MArrayLM object

Usage

```
## S3 method for class 'MArrayLM'
glMDPlot(
  x,
  counts = NULL,
  anno = NULL,
  groups = NULL,
  samples = NULL,
  status = rep(0, nrow(x)),
  transform = FALSE,
  main = "",
  xlab = "Average log CPM",
  ylab = "log-fold-change",
  side.main = "GeneID",
  side.xlab = "Group",
  side.ylab = "Expression",
  side.log = FALSE,
  side.gridstep = ifelse(!transform || side.log, FALSE, 0.5),
  coef = ncol(x$coefficients),
  p.adj.method = "BH",
  jitter = 30,
  display.columns = NULL,
  cols = c("#00bfff", "#858585", "#ff3030"),
  sample.cols = rep("#1f77b4", ncol(counts)),
  path = getwd(),
  folder = "glimma-plots",
  html = "MD-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the MArrayLM object.
`counts`	the matrix of expression values, with samples in columns.
`anno`	the data.frame containing gene annotations.
`groups`	the factor containing experimental groups of the samples.
`samples`	the names of the samples.

`status`	vector giving the control status of data point, of same length as the number of rows of object. If NULL, then all points are plotted in the default colour.
`transform`	TRUE if counts should be log-cpm transformed.
`main`	the title for the left plot.
`xlab`	label for x axis on left plot.
`ylab`	label for y axis on left plot.
`side.main`	the column containing mains for right plot.
`side.xlab`	label for x axis on right plot.
`side.ylab`	label for y axis on right plot.
`side.log`	TRUE to plot expression on the right plot on log scale.
`side.gridstep`	intervals along which to place grid lines on y axis. Currently only available for linear scale.
`coef`	integer or character index vector indicating which column of object to plot.
`p.adj.method`	character vector indicating multiple testing correction method. See `p.adjust` for available methods. (defaults to "BH")
`jitter`	the amount of jitter to apply to the samples in the expressions plot.
`display.columns`	character vector containing names of columns to display in mouseover tooltips and table.
`cols`	vector of strings denoting colours corresponding to control status -1, 0 and 1. (may be R named colours or Hex values)
`sample.cols`	vector of strings denoting colours for each sample point on the expression plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments to be passed onto the MD plot. (main, xlab, ylab can be set for the left plot)

Value

Draws a two-panel interactive MD plot in an html page. The left plot shows the log-fold-change vs average expression. The right plot shows the expression levels of a particular gene of each sample. Hovering over points on left plot will plot expression level for corresponding gene, clicking on points will fix the expression plot to gene. Clicking on rows on the table has the same effect as clicking on the corresponding gene in the plot.

Author(s)

Shian Su

Examples

```
library(limma)
library(edgeR)

data(lymphomaRNAseq)
x <- lymphomaRNAseq

sel <- rowSums(cpm(x$counts)>0.5)>=3
x <- x[sel,]

genotype <- relevel(x$samples$group, "Smchd1-null")
x <- calcNormFactors(x, method="TMM")
des <- model.matrix(~genotype)

## Apply voom with sample quality weights and fit linear model
v <- voomWithQualityWeights(x, design=des, plot=FALSE)
vfit <- lmFit(v,des)

## Apply treat relative to a fold-change of 1.5
vtfit <- treat(vfit,lfc=log2(1.5))
vfit <- eBayes(vfit)
results <- decideTests(vfit,p.value=0.01)


glMDPlot(vfit, counts=x$counts, anno=x$genes, groups=genotype, samples=1:7,
         status=results[,2], main="MD plot: Wild-type vs Smchd1",
         display.columns=c("Symbols", "GeneID", "GeneName"),
         folder="Smchd1-Lymphoma")
```

`glMDRmd` *glMDPlot Rmarkdown link and instructions*

Description

When run inside of a text-block of Rmarkdown document using ‘r ...‘ this produces a link and instructions about the usage of the interactive plots.

Usage

```
glMDRmd(html = "MD-Plot")
```

Arguments

`html`	name of the HTML page containing plots from glMDPlot.

Value

None

See Also

`glMDPlot`

Examples

```
glMDRmd()
```

`glMDSPlot` *Glimma MDS Plot*

Description

Draw an interactive MD plot from a DGEList object with distances calculated from most variable genes.

Usage

```
glMDSPlot(x, ...)
```

Arguments

`x`	the matrix containing the gene expressions.
`...`	additional arguments.

Value

Draws a two-panel interactive MDS plot in an html page. The left panel contains the plot between two MDS dimensions, with annotations displayed on hover. The right panel contains a bar plot of the eigenvalues of each dimension, clicking on any of the bars will plot the corresponding dimension against the next dimension.

Author(s)

Shian Su, Gordon Smyth

See Also

`glMDSPlot.default`, `glMDSPlot.DGEList`

Examples

```
data(lymphomaRNAseq)
genotype <- relevel(lymphomaRNAseq$samples$group, "Smchd1-null")

glMDSPlot(lymphomaRNAseq, labels=1:7, groups=genotype)
```

`glMDSPlot.default` *Glimma MDS Plot*

Description

Draw an interactive MD plot from a DGEList object with distances calculated from most variable genes.

Usage

```
## Default S3 method:
glMDSPlot(
  x,
  top = 500,
  labels = seq_cols(x),
  groups = rep(1, ncol(x)),
  gene.selection = c("pairwise", "common"),
  main = "MDS Plot",
  path = getwd(),
  folder = "glimma-plots",
  html = "MDS-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the matrix containing the gene expressions.
`top`	the number of top most variable genes to use.
`labels`	the labels for each sample.
`groups`	the experimental group to which samples belong.
`gene.selection`	"pairwise" if most variable genes are to be chosen for each pair of samples or "common" to select the same genes for all comparisons.
`main`	the title of the plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments.

Value

Draws a two-panel interactive MDS plot in an html page. The left panel contains the plot between two MDS dimensions, with annotations displayed on hover. The right panel contains a bar plot of the eigenvalues of each dimension, clicking on any of the bars will plot the corresponding dimension against the next dimension.

Author(s)

Shian Su, Gordon Smyth

`glMDSPlot.DESeqDataSet` *Glimma MDS Plot*

Description

Draw an interactive MD plot from a DGEList object with distances calculated from most variable genes.

Usage

```
## S3 method for class 'DESeqDataSet'
glMDSPlot(
  x,
  top = 500,
  labels = NULL,
  groups = NULL,
  gene.selection = c("pairwise", "common"),
  prior.count = 0.25,
  main = "MDS Plot",
  path = getwd(),
  folder = "glimma-plots",
  html = "MDS-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the DESeqDataSet containing the gene expressions.
`top`	the number of top most variable genes to use.
`labels`	the labels for each sample.
`groups`	the experimental group to which samples belong.
`gene.selection`	"pairwise" if most variable genes are to be chosen for each pair of samples or "common" to select the same genes for all comparisons.

`prior.count`	average count to be added to each observation to avoid taking log of zero. Used only if log=TRUE.
`main`	the title of the plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments.

Value

Draws a two-panel interactive MDS plot in an html page. The left panel contains the plot between two MDS dimensions, with annotations displayed on hover. The right panel contains a bar plot of the eigenvalues of each dimension, clicking on any of the bars will plot the corresponding dimension against the next dimension.

Author(s)

Shian Su, Gordon Smyth

`glMDSPlot.DGEList` *Glimma MDS Plot*

Description

Draw an interactive MD plot from a DGEList object with distances calculated from most variable genes.

Usage

```
## S3 method for class 'DGEList'
glMDSPlot(
  x,
  top = 500,
  labels = NULL,
  groups = rep(1, ncol(x)),
  gene.selection = c("pairwise", "common"),
  prior.count = 2,
  main = "MDS Plot",
  path = getwd(),
  folder = "glimma-plots",
  html = "MDS-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	the DGEList containing the gene expressions.
`top`	the number of top most variable genes to use.
`labels`	the labels for each sample.
`groups`	the experimental group to which samples belong.
`gene.selection`	"pairwise" if most variable genes are to be chosen for each pair of samples or "common" to select the same genes for all comparisons.
`prior.count`	average count to be added to each observation to avoid taking log of zero. Used only if log=TRUE.
`main`	the title of the plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.
`launch`	TRUE to launch plot after call.
`...`	additional arguments.

Value

Draws a two-panel interactive MDS plot in an html page. The left panel contains the plot between two MDS dimensions, with annotations displayed on hover. The right panel contains a bar plot of the eigenvalues of each dimension, clicking on any of the bars will plot the corresponding dimension against the next dimension.

Author(s)

Shian Su, Gordon Smyth

`glXYPlot` *Glimma XY Plot*

Description

Draw an interactive XY plot with multiple panels

Usage

```
glXYPlot(
  x,
  y,
  counts = NULL,
  groups = NULL,
  samples = NULL,
  status = rep(0, nrow(data)),
```

```
  anno = NULL,
  display.columns = NULL,
  xlab = "x",
  ylab = "y",
  side.main = "GeneID",
  side.xlab = "Group",
  side.ylab = "Expression",
  sample.cols = rep("#1f77b4", length(groups)),
  cols = c("#00bfff", "#858585", "#ff3030"),
  jitter = 30,
  path = getwd(),
  folder = "glimma-plots",
  html = "XY-Plot",
  launch = TRUE,
  ...
)
```

Arguments

`x`	a numeric vector of values to plot on the x-axis of the summary plot.
`y`	a numeric vector of values to plot on the y-axis of the summary plot.
`counts`	the matrix containing all counts, the column order should correspond to the order of the x and y vectors.
`groups`	the factor containing experimental groups of the samples.
`samples`	the names of the samples.
`status`	vector giving the control status of data point, of same length as the number of rows of object. If NULL, then all points are plotted in the default colour
`anno`	the data.frame containing gene annotations.
`display.columns`	character vector containing names of columns to display in mouseover tooltips and table.
`xlab`	the label on the x axis for the left plot.
`ylab`	the label on the y axis for the left plot.
`side.main`	the column containing mains for right plot.
`side.xlab`	the label on the x axis for the right plot.
`side.ylab`	the label on the y axis for the right plot.
`sample.cols`	vector of strings denoting colours for each sample point on the expression plot.
`cols`	vector of strings denoting colours corresponding to control status -1, 0 and 1. (may be R named colours or Hex values)
`jitter`	the amount of jitter to apply to the samples in the expressions plot.
`path`	the path in which the folder will be created.
`folder`	the name of the fold to save html file to.
`html`	the name of the html file to save plots to.

`launch`	TRUE to launch plot after call.
`...`	additional arguments to be passed onto the MD plot. (main, etc. can be set for the left plot)

Value

Draws a two-panel interactive XY scatter plot in an html page. The left plot shows the x and y values specified. The right plot shows the expression levels of a particular gene in each sample. Hovering over points on left plot will plot expression level for the corresponding gene, clicking on points will fix the expression plot to that gene. Clicking on rows on the table has the same effect as clicking on the corresponding gene in the plot. This function generates a display that is similar in style to glMDPlot, except that it provides more flexibility in what the user can provide.

Author(s)

Charity Law and Shian Su

Examples

```
data(iris)

glXYPlot(iris$Sepal.Width, iris$Sepal.Length,
         xlab="Sepal.Width", ylab="Sepal.Length", side.main="PlantID")
```

`is.hex` *Hexcode colours*

Description

Check if string(s) are valid hex colour representation

Usage

```
is.hex(x)
```

Arguments

`x`	the colour value(s) to check.

Value

Logical vector indicating if strings(s) are valid hex representations

---

`lymphomaRNAseq` *Mouse based RNAseq data for study of smchd1 gene.*

Description

Mouse based RNAseq data for study of smchd1 gene.

Author(s)

Ruijie Liu, Kelan Chen, Natasha Jansz, Marnie E. Blewitt, Matthew E. Ritchie

References

http://www.sciencedirect.com/science/article/pii/S2213596015301306

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