Package 'vidger'

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Title Create rapid visualizations of RNAseq data in R

Version 1.0.0

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Description The aim of vidger is to rapidly generate information-rich visualizations
for the interpretation of differential gene expression results from three
widely-used tools: Cuffdiff, DESeq2, and edgeR.

Depends R (>= 3.5)

Imports Biobase, DESeq2, edgeR, knitr, rmarkdown, GGally, ggplot2,
scales, stats, SummarizedExperiment, tidyr, utils

Suggests testthat, BiocStyle

Encoding UTF-8

LazyData true

VignetteBuilder knitr

RoxygenNote 6.0.1

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biocViews Visualization, RNASeq, DifferentialExpression,
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R topics documented:

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df.cuff   *A 'cuffdiff' example dataset*

Description

A 'cuffdiff' example dataset

Usage

```
data(df.cuff)
```

---

df.deseq   *A 'DESeq2' example dataset*

Description

A 'DESeq2' example dataset

Usage

```
data(df.deseq)
```

---

df.edger   *A 'edgeR' example dataset*

Description

A 'edgeR' example dataset

Usage

```
data(df.edger)
```

---

vsBoxPlot   *Box plot for log10(FPKM or CPM) distributions*

Description

This function allows you to extract necessary results-based data from analytical objects to create a box plot comparing log10(FPKM or CPM) distributions for experimental treatments.

Usage

```
vsBoxPlot(data, d.factor = NULL, type = c("cuffdiff", "deseq", "edger"),
  title = TRUE, legend = TRUE, grid = TRUE)
```

Arguments

data	output generated from calling the main routines of either 'cuffdiff', 'DESeq2', or 'edgeR' analyses. For 'cuffdiff', this will be a '*_exp.diff' file. For 'DESeq2', this will be a generated object of class 'DESeqDataSet'. For 'edgeR', this will be a generated object of class 'DGEList'.
d.factor	a specified factor; for use with 'DESeq2' objects only. This input equates to the first parameter for the contrast argument when invoking the 'results()' function in 'DESeq2'. Defaults to 'NULL'
type	an analysis classifier to tell the function how to process the data. Must be either 'cuffdiff', 'deseq', or 'edger'. 'cuffdiff' must be used with 'cuffdiff' data; 'deseq' must be used for 'DESeq2' output; 'edgeR' must be used with 'edgeR' data. See the 'data' parameter for further details.
title	display the main title of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no title will display in plot.
legend	display legend of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no legend will display in plot.
grid	display major and minor axis lines. Logical; defaults to 'TRUE'. If set to 'FALSE', no axis lines will display in plot.

Value

An object created by ggplot

Author(s)

Brandon Monier, <brandon.monier@sdstate.edu>

Examples

```
# Cuffdiff example
data("df.cuff")
vsBoxPlot(
 data = df.cuff, d.factor = NULL, type = 'cuffdiff', title = TRUE,
 legend = TRUE, grid = TRUE
)

# DESeq2 example
```

```
data("df.deseq")
require(DESeq2)
vsBoxPlot(
 data = df.deseq, d.factor = 'condition', type = 'deseq',
 title = TRUE, legend = TRUE, grid = TRUE
)

# edgeR example
data("df.deseq")
require(edgeR)
vsBoxPlot(
 data = df.edger, d.factor = NULL, type = 'edger', title = TRUE,
 legend = TRUE, grid = TRUE
)
```

vsDEGMatrix	*Differential gene expression matrix*

Description

This function allows you to visualize the number of differentially expressed genes (DEG) at a given #' adjusted P-value for each experimental treatment level. Higher color intensity correlates to a higher number of DEGs.

Usage

```
vsDEGMatrix(data, padj = 0.05, d.factor = NULL, type = c("cuffdiff",
  "deseq", "edger"), title = TRUE, legend = TRUE, grid = TRUE)
```

Arguments

data	output generated from calling the main routines of either 'cuffdiff', 'DESeq2', or 'edgeR' analyses. For 'cuffdiff', this will be a '*_exp.diff' file. For 'DESeq2', this will be a generated object of class 'DESeqDataSet'. For 'edgeR', this will be a generated object of class 'DGEList'.
padj	a user defined adjusted p-value cutoff point. Defaults to '0.05'.
d.factor	a specified factor; for use with 'DESeq2' objects only. This input equates to the first parameter for the contrast argument when invoking the 'results()' function in 'DESeq2'. Defaults to 'NULL'
type	an analysis classifier to tell the function how to process the data. Must be either 'cuffdiff', 'deseq', or 'edger'. 'cuffdiff' must be used with 'cuffdiff' data; 'deseq' must be used for 'DESeq2' output; 'edgeR' must be used with 'edgeR' data. See the 'data' parameter for further details.
title	display the main title of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no title will display in plot.
legend	display legend of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no legend will display in plot.
grid	display major and minor axis lines. Logical; defaults to 'TRUE'. If set to 'FALSE', no axis lines will display in plot.

Value

An object created by `ggplot`

Author(s)

Brandon Monier, `<brandon.monier@sdstate.edu>`

Examples

```
# cuffdiff example
data("df.cuff")
vsDEGMatrix(
 df.cuff, padj = 0.05, d.factor = NULL, type = 'cuffdiff',
 title = TRUE, legend = TRUE, grid = TRUE
)

# DESeq2 example
data("df.deseq")
require(DESeq2)
vsDEGMatrix(
 df.deseq, padj = 0.05, d.factor = 'condition', type = 'deseq',
 title = TRUE, legend = TRUE, grid = TRUE
)

# edgeR example
data("df.edger")
require(edgeR)
vsDEGMatrix(
 df.edger, padj = 0.05, d.factor = NULL, type = 'edger',
 title = TRUE, legend = TRUE, grid = TRUE
)
```

---

vsFourWay	*Four-Way plot for comparison of log fold changes in a multiple factor RNA seq experiment from different analytical objects*

Description

This function allows you to extract necessary results-based data from a DESeq object class to create a .four-way plot to compare log fold changes in various treatments using ggplot2 aesthetics.

Usage

```
vsFourWay(x, y, control, data, d.factor = NULL, type = c("cuffdiff",
  "deseq", "edger"), padj = 0.05, x.lim = NULL, y.lim = NULL,
  lfc = NULL, legend = TRUE, title = TRUE, grid = TRUE,
  data.return = FALSE)
```

Arguments

x	treatment 'x' for comparison (log2(x/control)). This will be a factor level in your data.
y	treatment 'y' for comparison (log2(y/control)). This will be a factor level in your data.
control	'control' treatment for comparisons of the x and y axes. This will be a factor level in your data.
data	output generated from calling the main routines of either 'cuffdiff', 'DESeq2', or 'edgeR' analyses. For 'cuffdiff', this will be a '*_exp.diff' file. For 'DESeq2', this will be a generated object of class 'DESeqDataSet'. For 'edgeR', this will be a generated object of class 'DGEList'.
d.factor	a specified factor; for use with 'DESeq2' objects only. This input equates to the first parameter for the contrast argument when invoking the 'results()' function in 'DESeq2'. Defaults to 'NULL'.
type	an analysis classifier to tell the function how to process the data. Must be either 'cuffdiff', 'deseq', or 'edger'. 'cuffdiff' must be used with 'cuffdiff' data; 'deseq' must be used for 'DESeq2' output; 'edgeR' must be used with 'edgeR' data. See the 'data' parameter for further details.
padj	a user defined adjusted p-value cutoff point. Defaults to '0.05'.
x.lim	set manual limits (boundaries) to the x axis. Defaults to 'NULL'.
y.lim	set manual limits (boundaries) to the y axis. Defaults to 'NULL'.
lfc	log fold change level for setting conditonals. If no user input is added ('NULL'), value defaults to '1'.
legend	display legend of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no legend will display in plot.
title	display the main title of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no title will display in plot.
grid	display major and minor axis lines. Logical; defaults to 'TRUE'. If set to 'FALSE', no axis lines will display in plot.
data.return	returns data output of plot Logical; defaults to 'FALSE'. If set to 'TRUE', a data frame will also be called. Assign to object for reproduction and saving of data frame. See final example for further details.

Details

This function allows the user to extract various elements from a different analytical object class which in turn, creates a temporary data frame to plot the necessary ggplot aesthetics. In order for this function to work, RNA seq experiments must have multiple factors (i.e. two treatments and a control) and levels including treatments and controls. By having the recommended criteria, this function will extract the necessary data dependent on the analysis performed. Data points with 'extreme' values that exceed the default viewing frame of the plot will change character classes (i.e. points of interest a substantially large log fold change).

Value

An object created by `ggplot`

Author(s)

Brandon Monier, <brandon.monier@sdstate.edu>

Examples

```
# Cuffdiff example
data("df.cuff")
vsFourWay(
 x = 'hESC', y = 'iPS', control = 'Fibroblasts', data = df.cuff,
 d.factor = NULL, type = 'cuffdiff', padj = 0.05, x.lim = NULL,
 y.lim = NULL, lfc = 2, title = TRUE, grid = TRUE,
 data.return = FALSE
)

# DESeq2 example
data("df.deseq")
vsFourWay(
 x = 'treated_paired.end', y = 'untreated_paired.end',
 control = 'untreated_single.read', data = df.deseq,
 d.factor = 'condition', type = 'deseq', padj = 0.05,
 x.lim = NULL, y.lim = NULL, lfc = 2, title = TRUE, grid = TRUE,
 data.return = FALSE
)

# edgeR example
data("df.edger")
require(edgeR)
vsFourWay(
 x = 'WM', y = 'WW', control = 'MM', data = df.edger,
 d.factor = NULL, type = 'edger', padj = 0.05, x.lim = NULL,
 y.lim = NULL, lfc = 2, title = TRUE, grid = TRUE,
 data.return = FALSE
)

# Extract data frame from visualization
data("df.cuff")
tmp <- vsFourWay(
 x = 'WM', y = 'WW', control = 'MM', data = df.edger,
 d.factor = NULL, type = 'edger', padj = 0.05,
 x.lim = NULL, y.lim = NULL, lfc = 2, title = TRUE,
 grid = TRUE, data.return = TRUE
)
df.four <- tmp[[1]]
head(df.four)
```

---

vsMAMatrix   *MA plot matrix from log2 fold changes and -log10(p-values)*

Description

This function allows you to generate MA plots for all possible treatment combinations for a given factor in either a cuffdiff, DESeq2, or edgeR data set.

Usage

```
vsMAMatrix(data, d.factor = NULL, type = c("cuffdiff", "deseq", "edger"),
  padj = 0.05, y.lim = NULL, lfc = NULL, title = TRUE, legend = TRUE,
  grid = TRUE, counts = TRUE, data.return = FALSE)
```

Arguments

data	output generated from calling the main routines of either 'cuffdiff', 'DESeq2', or 'edgeR' analyses. For 'cuffdiff', this will be a '*_exp.diff' file. For 'DESeq2', this will be a generated object of class 'DESeqDataSet'. For 'edgeR', this will be a generated object of class 'DGEList'.
d.factor	a specified factor; for use with 'DESeq2' objects only. This input equates to the first parameter for the contrast argument when invoking the 'results()' function in 'DESeq2'. Defaults to 'NULL'.
type	an analysis classifier to tell the function how to process the data. Must be either 'cuffdiff', 'deseq', or 'edger'. 'cuffdiff' must be used with 'cuffdiff' data; 'deseq' must be used for 'DESeq2' output; 'edgeR' must be used with 'edgeR' data. See the 'data' parameter for further details.
padj	a user defined adjusted p-value cutoff point. Defaults to '0.05'.
y.lim	set manual limits (boundaries) to the y axis. Defaults to 'NULL'.
lfc	log fold change level for setting conditonals. If no user input is added ('NULL'), value defaults to '1'.
title	display the main title of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no title will display in plot.
legend	display legend of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no legend will display in plot.
grid	display major and minor axis lines. Logical; defaults to 'TRUE'. If set to 'FALSE', no axis lines will display in plot.
counts	displays the number of differentially expressed genes for each treatment comparison. Defaults to 'TRUE'.
data.return	returns data output of plot Logical; defaults to 'FALSE'. If set to 'TRUE', a data frame will also be called. Assign to object for reproduction and saving of data frame. See final example for further details.

Value

An object created by ggplot

Author(s)

Brandon Monier, <brandon.monier@sdstate.edu>

Examples

```
# Cuffdiff example
data("df.cuff")
vsMAMatrix(
 data = df.cuff, d.factor = NULL, type = 'cuffdiff',
 padj = 0.05, y.lim = NULL, lfc = 1, title = TRUE,
 grid = TRUE, counts = TRUE, data.return = FALSE
)

# DESeq2 example
data("df.deseq")
require(DESeq2)
vsMAMatrix(
 data = df.deseq, d.factor = 'condition', type = 'deseq',
```

```
 padj = 0.05, y.lim = NULL, lfc = 1, title = TRUE,
 grid = TRUE, counts = TRUE, data.return = FALSE
)

# edgeR example
data("df.edger")
require(edgeR)
vsMAMatrix(
 data = df.edger, d.factor = NULL, type = 'edger',
 padj = 0.05, y.lim = NULL, lfc = 1, title = TRUE,
 grid = TRUE, counts = TRUE, data.return = FALSE
)

# Extract data frame from visualization
data("df.cuff")
tmp <- vsMAMatrix(
 data = df.cuff, d.factor = NULL,
 type = 'cuffdiff', padj = 0.05, y.lim = NULL,
 lfc = 1, title = TRUE, grid = TRUE,
 counts = TRUE, data.return = TRUE
)
df.vmat <- tmp[[1]]
head(df.vmat)
```

---

vsMAPlot   *MA plot from mean expression and log fold changes from different analytical objects*

Description

This function allows you to extract necessary results-based data from different output files to create a MA plot (i.e. a scatter plot) of log2 fold changes versus normalized mean counts while implementing ggplot2 aesthetics.

Usage

```
vsMAPlot(x, y, data, d.factor = NULL, type = c("cuffdiff", "deseq",
  "edger"), padj = 0.05, y.lim = NULL, lfc = NULL, title = TRUE,
  legend = TRUE, grid = TRUE, data.return = FALSE)
```

Arguments

x	treatment 'x' for comparison (log2(x/control)). This will be a factor level in your data.
y	treatment 'y' for comparison (log2(y/control)). This will be a factor level in your data.
data	output generated from calling the main routines of either 'cuffdiff', 'DESeq2', or 'edgeR' analyses. For 'cuffdiff', this will be a '*_exp.diff' file. For 'DESeq2', this will be a generated object of class 'DESeqDataSet'. For 'edgeR', this will be a generated object of class 'DGEList'.
d.factor	a specified factor; for use with 'DESeq2' objects only. This input equates to the first parameter for the contrast argument when invoking the 'results()' function in 'DESeq2'. Defaults to 'NULL'.

type	an analysis classifier to tell the function how to process the data. Must be either 'cuffdiff', 'deseq', or 'edger'. 'cuffdiff' must be used with 'cuffdiff' data; 'deseq' must be used for 'DESeq2' output; 'edgeR' must be used with 'edgeR' data. See the 'data' parameter for further details.
padj	a user defined adjusted p-value cutoff point. Defaults to '0.05'.
y.lim	set manual limits (boundaries) to the y axis. Defaults to 'NULL'.
lfc	log fold change level for setting conditonals. If no user input is added ('NULL'), value defaults to '1'.
title	display the main title of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no title will display in plot.
legend	display legend of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no legend will display in plot.
grid	display major and minor axis lines. Logical; defaults to 'TRUE'. If set to 'FALSE', no axis lines will display in plot.
data.return	returns data output of plot Logical; defaults to 'FALSE'. If set to 'TRUE', a data frame will also be called. Assign to object for reproduction and saving of data frame. See final example for further details.

Value

An object created by `ggplot`

Author(s)

Brandon Monier, <brandon.monier@sdstate.edu>

Examples

```
# Cuffdiff example
data("df.cuff")
vsMAPlot(
 x = 'hESC', y = 'iPS', data = df.cuff, d.factor = NULL,
 type = 'cuffdiff', padj = 0.05, y.lim = NULL, lfc = 1,
 title = TRUE, legend = TRUE, grid = TRUE, data.return = FALSE
)

# DESeq2 example
data("df.deseq")
require(DESeq2)
vsMAPlot(
 x = 'treated_paired.end', y = 'untreated_paired.end',
 data = df.deseq, d.factor = 'condition', type = 'deseq',
 padj = 0.05, y.lim = NULL, lfc = NULL, title = TRUE,
 legend = TRUE, grid = TRUE, data.return = FALSE
)

# edgeR example
data("df.edger")
require(edgeR)
vsMAPlot(
 x = 'WM', y = 'MM', data = df.edger, d.factor = NULL,
 type = 'edger', padj = 0.1, y.lim = NULL, lfc = 1,
 title = FALSE, legend = TRUE, grid = TRUE, data.return = FALSE
```

```
)

# Extract data frame from visualization
data("df.cuff")
tmp <- vsMAPlot(
 x = 'hESC', y = 'iPS', data = df.cuff,
 d.factor = NULL, type = 'cuffdiff', padj = 0.05,
 y.lim = NULL, lfc = 1, title = TRUE, grid = TRUE,
 data.return = TRUE
)
df.ma <- tmp[[1]]
head(df.ma)
```

---

vsScatterMatrix   *Scatter plot matrix of log10(FPKM or CPM) values*

Description

This function will generate a matrix of scatterplots for all possible treatment combinations with additional distribution info.

Usage

```
vsScatterMatrix(data, d.factor = NULL, type = c("cuffdiff", "deseq",
  "edger"), comp = NULL, title = TRUE, grid = TRUE, man.title = NULL)
```

Arguments

data	output generated from calling the main routines of either 'cuffdiff', 'DESeq2', or 'edgeR' analyses. For 'cuffdiff', this will be a '*_exp.diff' file. For 'DESeq2', this will be a generated object of class 'DESeqDataSet'. For 'edgeR', this will be a generated object of class 'DGEList'.
d.factor	a specified factor; for use with 'DESeq2' objects only. This input equates to the first parameter for the contrast argument when invoking the 'results()' function in 'DESeq2'. Defaults to 'NULL'.
type	an analysis classifier to tell the function how to process the data. Must be either 'cuffdiff', 'deseq', or 'edger'. 'cuffdiff' must be used with 'cuffdiff' data; 'deseq' must be used for 'DESeq2' output; 'edgeR' must be used with 'edgeR' data. See the 'data' parameter for further details.
comp	treatments you would like to compare in the form of a vector. If no parameter is specified, all possible treatment comparisons will be made. Defaults to 'NULL'.
title	display the main title of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no title will display in plot.
grid	display major and minor axis lines. Logical; defaults to 'TRUE'. If set to 'FALSE', no axis lines will display in plot.
man.title	a manually specified title at the authors discretion. Defaults to 'NULL'.

Value

An object created by ggplot

Author(s)

Brandon Monier, <brandon.monier@sdstate.edu>

Examples

```
# Cuffdiff example
data("df.cuff")
vsScatterMatrix(
 data = df.cuff, d.factor = NULL, type = 'cuffdiff',
 comp = NULL, title = TRUE, grid = TRUE,
 man.title = 'Example title'
)

# DESeq2 example
data("df.deseq")
require(DESeq2)
vsScatterMatrix(
 data = df.deseq, d.factor = 'condition', type = 'deseq',
 comp = NULL, title = TRUE, grid = FALSE, man.title = NULL
)

# edgeR example
data("df.edger")
require(edgeR)
vsScatterMatrix(
 data = df.edger, d.factor = NULL, type = 'edger',
 comp = c('WM', 'MM'), title = TRUE, grid = TRUE,
 man.title = NULL
)
```

---

vsScatterPlot   *Scatter plot of log10(FPKM or CPM) values*

Description

This function allows you to visualize comparisons of log10 values of either FPKM or CPM measurements of two treatments depending on analytical type.

Usage

```
vsScatterPlot(x, y, data, d.factor = NULL, type = c("cuffdiff", "deseq",
  "edger"), title = TRUE, grid = TRUE)
```

Arguments

x	treatment 'x' for comparison (log2(x/control)). This will be a factor level in your data.
y	treatment 'y' for comparison (log2(y/control)). This will be a factor level in your data.
data	output generated from calling the main routines of either 'cuffdiff', 'DESeq2', or 'edgeR' analyses. For 'cuffdiff', this will be a '*_exp.diff' file. For 'DESeq2', this will be a generated object of class 'DESeqDataSet'. For 'edgeR', this will be a generated object of class 'DGEList'.

d.factor   a specified factor; for use with 'DESeq2' objects only. This input equates to the
             first parameter for the contrast argument when invoking the 'results()' function
             in 'DESeq2'. Defaults to 'NULL'.

type   an analysis classifier to tell the function how to process the data. Must be ei-
             ther 'cuffdiff', 'deseq', or 'edger'. 'cuffdiff' must be used with 'cuffdiff' data;
             'deseq' must be used for 'DESeq2' output; 'edgeR' must be used with 'edgeR'
             data. See the 'data' parameter for further details.

title   display the main title of plot. Logical; defaults to 'TRUE'. If set to 'FALSE',
             no title will display in plot.

grid   display major and minor axis lines. Logical; defaults to 'TRUE'. If set to
             'FALSE', no axis lines will display in plot.

Value

An object created by `ggplot`

Author(s)

Brandon Monier, `<brandon.monier@sdstate.edu>`

Examples

```
# Cuffdiff example
data("df.cuff")
vsScatterPlot(
 x = 'hESC', y = 'iPS', data = df.cuff, d.factor = NULL,
 type = 'cuffdiff', title = TRUE, grid = TRUE
)

# DESeq2 example
data("df.deseq")
require(DESeq2)
vsScatterPlot(
 x = 'treated_paired.end', y = 'untreated_paired.end',
 data = df.deseq, d.factor = 'condition', type = 'deseq',
 title = TRUE, grid = TRUE
)

# edgeR example
data("df.edger")
require(edgeR)
vsScatterPlot(
 x = 'WW', y = 'WM', data = df.edger, d.factor = NULL,
 type = 'edger', title = TRUE, grid = TRUE
)
```

vsVolcano   *Volcano plot from log2 fold changes and -log10(p-values)*

Description

This function allows you to extract necessary results-based data from a DESEq object class to create
a volcano plot (i.e. a scatter plot) of the negative log of the p-value versus the log of the fold change
while implementing ggplot2 aesthetics.

Usage

```
vsVolcano(x, y, data, d.factor = NULL, type = c("cuffdiff", "deseq",
  "edger"), padj = 0.05, x.lim = NULL, lfc = NULL, title = TRUE,
  legend = TRUE, grid = TRUE, data.return = FALSE)
```

Arguments

x
: treatment 'x' for comparison (log2(x/control)). This will be a factor level in your data.

y
: treatment 'y' for comparison (log2(y/control)). This will be a factor level in your data.

data
: output generated from calling the main routines of either 'cuffdiff', 'DESeq2', or 'edgeR' analyses. For 'cuffdiff', this will be a '*_exp.diff' file. For 'DESeq2', this will be a generated object of class 'DESeqDataSet'. For 'edgeR', this will be a generated object of class 'DGEList'.

d.factor
: a specified factor; for use with 'DESeq2' objects only. This input equates to the first parameter for the contrast argument when invoking the 'results()' function in 'DESeq2'. Defaults to 'NULL'.

type
: an analysis classifier to tell the function how to process the data. Must be either 'cuffdiff', 'deseq', or 'edger'. 'cuffdiff' must be used with 'cuffdiff' data; 'deseq' must be used for 'DESeq2' output; 'edgeR' must be used with 'edgeR' data. See the 'data' parameter for further details.

padj
: a user defined adjusted p-value cutoff point. Defaults to '0.05'.

x.lim
: set manual limits (boundaries) to the x axis. Defaults to 'NULL'.

lfc
: log fold change level for setting conditonals. If no user input is added ('NULL'), value defaults to '1'.

title
: display the main title of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no title will display in plot.

legend
: display legend of plot. Logical; defaults to 'TRUE'. If set to 'FALSE', no legend will display in plot.

grid
: display major and minor axis lines. Logical; defaults to 'TRUE'. If set to 'FALSE', no axis lines will display in plot.

data.return
: returns data output of plot Logical; defaults to 'FALSE'. If set to 'TRUE', a data frame will also be called. Assign to object for reproduction and saving of data frame. See final example for further details.

Value

An object created by `ggplot`

Author(s)

Brandon Monier, <brandon.monier@sdstate.edu>

Examples

```
# Cuffdiff example
data("df.cuff")
vsVolcano(
 x = 'hESC', y = 'iPS', data = df.cuff, d.factor = NULL,
```

```
  type = 'cuffdiff', padj = 0.05, x.lim = NULL, lfc = 2,
  title = TRUE, grid = TRUE, data.return = FALSE
)

# DESeq2 example
data("df.deseq")
require(DESeq2)
vsVolcano(
 x = 'treated_paired.end', y = 'untreated_paired.end',
 data = df.deseq, d.factor = 'condition',
 type = 'deseq', padj = 0.05, x.lim = NULL, lfc = NULL,
 title = TRUE, grid = TRUE, data.return = FALSE
)

# edgeR example
data("df.edger")
require(edgeR)
vsVolcano(
 x = 'WM', y = 'MM', data = df.edger, d.factor = NULL,
 type = 'edger', padj = 0.1, x.lim = NULL, lfc = 2,
 title = FALSE, grid = TRUE, data.return = FALSE
)

# Extract data frame from visualization
data("df.cuff")
tmp <- vsVolcano(
 x = 'hESC', y = 'iPS', data = df.cuff,
 d.factor = NULL, type = 'cuffdiff', padj = 0.05,
 x.lim = NULL, lfc = 2, title = TRUE, grid = TRUE,
 data.return = TRUE
)
df.volcano <- tmp[[1]]
head(df.volcano)
```

---

vsVolcanoMatrix   *Volcano plot matrix from log2 fold changes and -log10(p-values)*

Description

This function allows you to extract necessary results-based data from a DESEq object class to create
a volcano plot (i.e. a scatter plot) of the negative log of the p-value versus the log of the fold change
while implementing ggplot2 aesthetics for all possible combinations of treatments.

Usage

```
vsVolcanoMatrix(data, d.factor = NULL, type = c("cuffdiff", "deseq",
  "edger"), padj = 0.05, x.lim = NULL, lfc = NULL, title = TRUE,
  legend = TRUE, grid = TRUE, counts = TRUE, data.return = FALSE)
```

Arguments

data	a cuffdiff, DESeq2, or edgeR object.
d.factor	a specified factor; for use with DESeq2 objects only. Defaults to 'NULL'

type	an analysis classifier to tell the function how to process the data. Must be either 'cuffdiff', 'deseq', or 'edgeR'.
padj	a user defined adjusted p-value cutoff point. Defaults to '0.05'.
x.lim	set manual limits to the x axis. Defaults to 'NULL'.
lfc	log fold change level for setting conditonals. If no user input is added ('NULL'), value defaults to '1'.
title	show title of plot. Defaults to 'TRUE'.
legend	shows legend of plot. Defaults to 'TRUE'.
grid	show major and minor axis lines. Defaults to 'TRUE'.
counts	displays the number of differentially expressed genes for each treatment comparison. Defaults to 'TRUE'.
data.return	returns data output of plot if set to 'TRUE'. Defaults to 'FASLSE'.

Value

An object created by `ggplot`

Author(s)

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Examples

```
# Cuffdiff example
data("df.cuff")
vsVolcanoMatrix(
 data = df.cuff, d.factor = NULL, type = 'cuffdiff',
 padj = 0.05, x.lim = NULL, lfc = 2, title = TRUE,
 grid = TRUE, counts = TRUE, data.return = FALSE
)

# DESeq2 example
data("df.deseq")
require(DESeq2)
vsVolcanoMatrix(
 data = df.deseq, d.factor = 'condition', type = 'deseq',
 padj = 0.05, x.lim = NULL, lfc = 2, title = TRUE,
 grid = TRUE, counts = TRUE, data.return = FALSE
)

# edgeR example
data("df.edger")
require(edgeR)
vsVolcanoMatrix(
 data = df.edger, d.factor = NULL, type = 'edger',
 padj = 0.05, x.lim = NULL, lfc = 2, title = TRUE,
 grid = TRUE, counts = TRUE, data.return = FALSE
)

# Extract data frame from visualization
data("df.cuff")
tmp <- vsVolcanoMatrix(
 data = df.cuff, d.factor = NULL,
```

```
 type = 'cuffdiff', padj = 0.05, x.lim = NULL,
 lfc = 2, title = TRUE, grid = TRUE,
 counts = TRUE, data.return = TRUE
)
df.vmat <- tmp[[1]]
head(df.vmat)
```

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