

Package ‘ivolcano’

December 2, 2025

Title Interactive Volcano Plot

Version 0.0.4

Description Generate interactive volcano plots for exploring gene expression data. Built with 'ggplot2', the plots are rendered interactive using 'ggiraph', enabling users to hover over points to display detailed information or click to trigger custom actions.

Depends R (>= 4.1.0)

Imports dplyr, ggplot2, ggiraph, ggrepel, knitr, rlang, stats, utils

Suggests fanyi, org.Hs.eg.db, quarto, yulab.utils

VignetteBuilder quarto

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URL <https://github.com/YuLab-SMU/ivolcano>

BugReports <https://github.com/YuLab-SMU/ivolcano/issues>

Encoding UTF-8

RoxygenNote 7.3.3

NeedsCompilation no

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geom_ivolcano_gene	<i>geom_ivolcano_gene</i>
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Description

Add gene labels to ivolcano plot
interactive volcano plot

Usage

```
geom_ivolcano_gene(  
  top_n = 10,  
  label_mode = "separate",  
  fontface = "italic",  
  label_sig_only = TRUE,  
  filter = NULL  
)  
  
ivolcano(  
  data,  
  logFC_col = "logFC",  
  pval_col = "adj.P.Val",  
  gene_col = "gene",  
  title = "Volcano Plot",  
  interactive = TRUE,  
  onclick_fun = NULL,  
  pval_cutoff = 0.05,  
  logFC_cutoff = 1,  
  pval_cutoff2 = NULL,  
  logFC_cutoff2 = NULL,  
  size_by = "none",  
  point_size = list(base = 2, medium = 4, large = 6),  
  threshold_line = list(color = "black", linetype = "dashed", linewidth = 0.5),  
  top_n = 10,  
  label_mode = "separate",  
  fontface = "italic",  
  label_sig_only = TRUE,  
  filter = NULL  
)
```

Arguments

top_n	top N genes to display the labels (gene ID)
label_mode	one of 'all' or 'separate' (default). If label_mode = 'all', top_n genes with minimal p values will be displayed, otherwise, top_n up-regulated and top_n down-regulated genes will be displayed.
fontface	one of 'plain', 'bold', 'italic' (default) and their combination, e.g. 'bold.italic'
label_sig_only	whether filter significant genes before subset 'top_n' genes
filter	custom filter expression to select genes for labeling
data	A data frame that contains minimal information with gene id, logFC and adjusted P values
logFC_col	column name in 'data' that stored the logFC values
pval_col	column name in 'data' that stored the adjusted P values
gene_col	column name in 'data' that stored the gene IDs
title	plot title
interactive	whether plot the graph in interactive mode
onclick_fun	effects when click on the dot (gene), default is NULL
pval_cutoff	cutoff of the adjusted P values
logFC_cutoff	cutoff of the logFC values
pval_cutoff2	second cutoff of the adjusted P values for advanced mode
logFC_cutoff2	second cutoff of the logFC values for advanced mode
size_by	one of "none" (default), "manual" (set by point_size), "negLogP", "absLogFC", or other variable in the input data to scale dot sizes.
point_size	set point size when size_by is "manual", a list with three elements: base, medium, large.
threshold_line	customize threshold line style (e.g., line color, type, and width)

Value

volcano plot

Author(s)

Guangchuang Yu

Examples

```
# example data
f <- system.file("extdata/airway.rds", package = "ivolcano")
df <- readRDS(f)
# plot
ivolcano(df,
  logFC_col = "log2FoldChange",
  pval_col = "padj",
  gene_col = "symbol",
  onclick_fun = onclick_genecards
)
```

geom_ivolcano_line	<i>geom_ivolcano_line</i>
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Description

Add threshold lines to an iVolcano plot

Usage

```
geom_ivolcano_line(linetype = "longdash", color = "grey40", linewidth = 0.5)
```

Arguments

linetype	line type for the threshold lines
color	line color for the threshold lines
linewidth	line width for the threshold lines

Value

A ggplot2 layer object

ivolcano_point	<i>ivolcano_point</i>
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Description

Visualize points in volcano plot

Usage

```
ivolcano_point(
  data,
  logFC_col = "logFC",
  pval_col = "adj.P.Val",
  gene_col = "gene",
  title = "Volcano Plot",
  interactive = TRUE,
  onclick_fun = NULL,
  pval_cutoff = 0.05,
  logFC_cutoff = 1,
  pval_cutoff2 = NULL,
  logFC_cutoff2 = NULL,
  size_by = "none",
  point_size = list(base = 2, medium = 4, large = 6)
)
```

Arguments

data	A data frame that contains minimal information with gene id, logFC and adjusted P values
logFC_col	column name in 'data' that stored the logFC values
pval_col	column name in 'data' that stored the adjusted P values
gene_col	column name in 'data' that stored the gene IDs
title	plot title
interactive	whether plot the graph in interactive mode
onclick_fun	effects when click on the dot (gene), default is NULL
pval_cutoff	cutoff of the adjusted P values
logFC_cutoff	cutoff of the logFC values
pval_cutoff2	second cutoff of the adjusted P values for advanced mode
logFC_cutoff2	second cutoff of the logFC values for advanced mode
size_by	one of "none" (default), "manual" (set by point_size), "negLogP", "absLogFC", or other variable in the input data to scale dot sizes.
point_size	set point size when size_by is "manual", a list with three elements: base, medium, large.

Value

base plot of a volcano plot

onclick_ensembl	<i>onclick_ensembl</i>
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Description

onclick function to popup Ensembl gene webpage

Usage

onclick_ensembl(gene)

Arguments

gene	query gene
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Value

onclick action

Author(s)

Guangchuang Yu

onclick_fanyi	<i>onclick_fanyi</i>
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Description

generate onclick function from `fanyi::gene_summary()` output

Usage

```
onclick_fanyi(gene_summary, cols)
```

Arguments

gene_summary	output from <code>fanyi::gene_summary()</code>
cols	selected columns from 'gene_summary'

Value

onclick function

Author(s)

Guangchuang Yu

onclick_genecards	<i>onclick_genecards</i>
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Description

onclick function to popup genecards webpage

Usage

```
onclick_genecards(gene)
```

Arguments

gene	query gene
------	------------

Value

onclick action

Author(s)

Guangchuang Yu

onlick_hgnc	<i>onlick_hgnc</i>
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Description

onlick function to popup HGNC gene webpage

Usage

```
onlick_hgnc(gene)
```

Arguments

gene	query gene
------	------------

Value

onlick action

Author(s)

Guangchuang Yu

onlick_ncbi	<i>onlick_ncbi</i>
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Description

onlick function to popup NCBI gene webpage

Usage

```
onlick_ncbi(gene)
```

Arguments

gene	query gene
------	------------

Value

onlick action

Author(s)

Guangchuang Yu

onclick_pubmed	<i>onclick_pubmed</i>
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Description

onclick function to popup PubMed webpage

Usage

```
onclick_pubmed(gene)
```

Arguments

gene	query gene
------	------------

Value

onclick action

Author(s)

Guangchuang Yu

onclick_uniprot	<i>onclick_uniprot</i>
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Description

onclick function to popup UniProt webpage

Usage

```
onclick_uniprot(gene)
```

Arguments

gene	query gene
------	------------

Value

onclick action

Author(s)

Guangchuang Yu

scale_color_figureya *scale_color_figureya*

Description

scale_color_figureya

Usage

```
scale_color_figureya(  
  mode = c("classic", "advanced"),  
  na.value = "grey80",  
  guide = "none",  
  ...  
)
```

Arguments

mode	one of "classic" or "advanced"
na.value	color for NA values
guide	guide parameter passed to <code>ggplot2::scale_color_manual</code>
...	additional parameters passed to <code>ggplot2::scale_color_manual</code>

Value

A ggplot2 scale object

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