Package ‘ivolcano’

September 11, 2025

Title Interactive Volcano Plot

Version 0.0.1

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, rlang

Suggests quarto, yulab.utils

VignetteBuilder quarto

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

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Repository CRAN

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Contents

`ivolcano` *ivolcano*

Description

interactive volcano plot

Usage

```
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,
  top_n = 10,
  label_mode = "separate",
  fontface = "italic",
  label_sig_only = TRUE,
  threshold_line = list(color = "black", linetype = "dashed", linewidth = 0.5),
  sig_colors = c(Up = "red", Down = "blue", Not_Significant = "grey70"),
  size_by = "none"
)
```

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
`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
`threshold_line`	customize threshold line style (e.g., line color, type, and width)
`sig_colors`	customize colors for up- and down-regulated, and non-significant genes
`size_by`	one of "none" (default), "negLogP", or "absLogFC" to scale dot sizes.

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",
        top_n = 5,
        onclick_fun=onclick_genecards)
```

`onclick_fanyi` *onclick_fanyi*

Description

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

Usage

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

Arguments

`gene_summary`	output from `fanyi::gene_summary()`
`cols`	selected columns from 'gene_summary'

Value

onclick function

Author(s)

Guangchuang Yu

`onclick_genecards` *onclick_genecards*

Description

onclick function to popup genecards webpage

Usage

```
onclick_genecards(gene)
```

Arguments

`gene`	query gene

Value

onclick action

Author(s)

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