Package ‘ivolcano’

June 5, 2026

Title Interactive Volcano Plot

Version 0.0.6

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, htmltools, htmlwidgets, knitr, methods, patchwork, rlang, stats, utils

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

VignetteBuilder quarto

License Artistic-2.0

URL `https://github.com/YuLab-SMU/ivolcano`

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

Encoding UTF-8

Config/roxygen2/version 8.0.0

NeedsCompilation no

Author Guangchuang Yu [aut, cre, cph] (ORCID: <`https://orcid.org/0000-0002-6485-8781`>)

Maintainer Guangchuang Yu <`guangchuangyu@gmail.com`>

Repository CRAN

Date/Publication 2026-06-05 06:50:02 UTC

Contents

`geom_ivolcano_gene` *geom_ivolcano_gene*

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),
  tooltip_cols = NULL,
  tooltip_labels = NULL,
  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)
`tooltip_cols`	extra column names in 'data' to display in tooltip (e.g., c("biotype", "description")). When NULL (default), only gene ID, logFC, and p-value are shown.
`tooltip_labels`	display labels for the extra columns. If NULL or length differs from tooltip_cols, raw column names are used.

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` *geom_ivolcano_line*

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

`idotplot` *idotplot*

Description

Interactive Dot Plot

Usage

```
idotplot(
  object,
  x = "GeneRatio",
  color = "p.adjust",
  showCategory = 10,
  size = "Count",
  label_format = 30,
  trigger = c("click", "hover"),
  title = "",
  ...
)
```

Arguments

`object`	enrichment result object (e.g. enrichResult) or a data frame
`x`	x-axis variable, one of 'GeneRatio', 'Count', etc.
`color`	variable for color, e.g., 'p.adjust'
`showCategory`	number of categories to show
`size`	variable for size, e.g., 'Count'
`label_format`	a numeric value sets wrap length, alternatively a custom function to format axis labels.
`trigger`	interaction trigger, one of "click" or "hover"
`title`	plot title
`...`	additional parameters passed to fortify

Value

ggplot object with interactive layers

Author(s)

Guangchuang Yu

`ivolcano_point` *ivolcano_point*

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),
  tooltip_cols = NULL,
  tooltip_labels = NULL
)
```

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.
`tooltip_cols`	extra column names in ’data’ to display in tooltip (e.g., c("biotype", "description")). When NULL (default), only gene ID, logFC, and p-value are shown.
`tooltip_labels`	display labels for the extra columns. If NULL or length differs from tooltip_cols, raw column names are used.

Value

base plot of a volcano plot

`onclick_ensembl` *onclick_ensembl*

Description

onclick function to popup Ensembl gene webpage

Usage

```
onclick_ensembl(gene)
```

Arguments

`gene`	query gene

Value

onclick action

Author(s)

Guangchuang Yu

`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)

Guangchuang Yu

`onclick_hgnc` *onclick_hgnc*

Description

onclick function to popup HGNC gene webpage

Usage

```
onclick_hgnc(gene)
```

Arguments

`gene`	query gene

Value

onclick action

Author(s)

Guangchuang Yu

`onclick_ncbi` *onclick_ncbi*

Description

onclick function to popup NCBI gene webpage

Usage

```
onclick_ncbi(gene)
```

Arguments

`gene`	query gene

Value

onclick action

Author(s)

Guangchuang Yu

`onclick_pubmed` *onclick_pubmed*

Description

onclick function to popup PubMed webpage

Usage

```
onclick_pubmed(gene)
```

Arguments

`gene`	query gene

Value

onclick action

Author(s)

Guangchuang Yu

`onclick_uniprot` *onclick_uniprot*

Description

onclick function to popup UniProt webpage

Usage

```
onclick_uniprot(gene)
```

Arguments

`gene`	query gene

Value

onclick action

Author(s)

Guangchuang Yu

`pathway_volcano` *pathway_volcano*

Description

Combine Interactive Pathway Dot Plot and Volcano Plot

Usage

```
pathway_volcano(
  p1,
  p2,
  widths = c(1, 1),
  trigger = c("click", "hover"),
  hover_css = "stroke:red;stroke-width:2px;",
  hover_inv_css = "opacity:0.15;",
  tooltip_css =
   "background:#fff;color:#000;border:1px solid #999;padding:6px;border-radius:4px;",
  non_selected_color = "#BDBDBD",
  non_selected_opacity = 0.25,
  label_follow = TRUE,
  ...
)
```

Arguments

`p1`	interactive dot plot (from idotplot)
`p2`	interactive volcano plot (from ivolcano)
`widths`	relative widths of the two plots, default is c(1, 1)
`trigger`	interaction trigger, one of "click" or "hover"
`hover_css`	css for hovered elements
`hover_inv_css`	css for non-hovered elements
`tooltip_css`	css for tooltip
`non_selected_color`	color for non-selected volcano points
`non_selected_opacity`	opacity for non-selected volcano points
`label_follow`	whether volcano labels follow pathway selection
`...`	additional parameters passed to ggiraph::girafe

Value

a girafe object

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 ggplot2::scale_color_manual
`...`	additional parameters passed to ggplot2::scale_color_manual

Value

A ggplot2 scale object

Index