

Package: ivolcano (via r-universe)

September 28, 2026

Title Interactive Volcano Plot

Version 0.0.7

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

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

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, methods, rlang, stats, utils

Suggests DT, clusterProfiler, enrichplot, fanyi, org.Hs.eg.db, quarto, shiny, 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

Roxygen list(markdown = TRUE)

Config/roxygen2/version 8.1.0

Config/pak/sysreqs

libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev make libpng-dev libuv1-dev

Repository <https://yulab-smu.r-universe.dev>

Date/Publication 2026-09-28 07:29:53 UTC

RemoteUrl <https://github.com/yulab-smu/ivolcano>

RemoteRef HEAD

RemoteSha 5e799189740c2d7b389d4dc23cb6e7b9669663cc

Contents

geom_ivolcano_gene	2
geom_ivolcano_line	4
idotplot	5
ivolcano_point	6
onclick_ensembl	7
onclick_fanyi	8
onclick_genecards	8
onclick_hgnc	9
onclick_ncbi	9
onclick_pubmed	10
onclick_uniprot	10
pathway_app	11
scale_color_figureya	12
Index	13

geom_ivolcano_gene	<i>geom_ivolcano_gene</i>
--------------------	---------------------------

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	<i>geom_ivolcano_line</i>
--------------------	---------------------------

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	<i>idotplot</i>
----------	-----------------

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	<i>ivolcano_point</i>
----------------	-----------------------

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	<i>onclick_ensembl</i>
-----------------	------------------------

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	<i>onclick_fanyi</i>
---------------	----------------------

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>
-------------------	--------------------------

Description

onclick function to popup genecards webpage

Usage

```
onclick_genecards(gene)
```

Arguments

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

Value

onclick action

Author(s)

Guangchuang Yu

onclick_hgnc	<i>onclick_hgnc</i>
--------------	---------------------

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	<i>onclick_ncbi</i>
--------------	---------------------

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	<i>onclick_pubmed</i>
----------------	-----------------------

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>
-----------------	------------------------

Description

onclick function to popup UniProt webpage

Usage

```
onclick_uniprot(gene)
```

Arguments

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

Value

onclick action

Author(s)

Guangchuang Yu

pathway_app

*Launch a pathway-selection Shiny explorer***Description**

The application presents pathway enrichment results in a searchable DT table. Selecting one or more rows reactively highlights the union of their matched genes in a ggplot2/ggiraph volcano plot and lists the selected genes below the plot.

Usage

```
pathway_app(
  enrichment,
  gene_data,
  pathway_col = "Description",
  pathway_gene_col = "geneID",
  pathway_p_col = "p.adjust",
  pathway_ratio_col = "GeneRatio",
  gene_col = "gene",
  gene_effect_col = "logFC",
  gene_p_col = "adj.P.Val",
  show_pathways = NULL,
  gene_id_case = c("asis", "upper", "lower"),
  pval_cutoff = 0.05,
  logFC_cutoff = 1,
  launch = FALSE,
  app_title = "Pathway-gene explorer"
)
```

Arguments

enrichment	enrichment result object or data frame. Objects supported by <code>ggplot2::fortify()</code> (for example, <code>clusterProfiler::enrichResult</code>) are converted automatically.
gene_data	data frame containing one row per gene and its effect size.
pathway_col	column containing pathway descriptions.
pathway_gene_col	column containing pathway member IDs. IDs may be separated by /, ;, , , or .
pathway_p_col	pathway adjusted P-value column. If absent, the table displays NA for FDR.
pathway_ratio_col	optional GeneRatio column.
gene_col	gene identifier column in gene_data.
gene_effect_col	gene effect column, usually logFC.
gene_p_col	gene P-value column, usually adjusted P-value.
show_pathways	optional number of pathways to show. NULL keeps all pathways.

gene_id_case	whether IDs should be matched as-is, upper-cased, or lower-cased.
pval_cutoff	gene P-value cutoff used for volcano classification.
logFC_cutoff	absolute effect cutoff used for volcano classification.
launch	whether to immediately launch the application with <code>shiny::runApp()</code> . The default returns a <code>shiny.appobj</code> for embedding or testing.
app_title	title shown above the application.

Value

A `shiny.appobj` invisibly when `launch = FALSE`; when `launch = TRUE` the function runs the application and returns after it is closed.

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

Index

`geom_ivolcano_gene`, [2](#)
`geom_ivolcano_line`, [4](#)

`idotplot`, [5](#)
`ivolcano (geom_ivolcano_gene)`, [2](#)
`ivolcano_point`, [6](#)

`onclick_ensembl`, [7](#)
`onclick_fanyi`, [8](#)
`onclick_genecards`, [8](#)
`onclick_hgnc`, [9](#)
`onclick_ncbi`, [9](#)
`onclick_pubmed`, [10](#)
`onclick_uniprot`, [10](#)

`pathway_app`, [11](#)

`scale_color_figureya`, [12](#)