

Package: ivolcano (via r-universe)

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

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

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

Encoding UTF-8

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

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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),
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

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

Value

ggplot object with interactive layers

Author(s)

Guangchuang Yu

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),
  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
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Value

onclick action

Author(s)

Guangchuang Yu

<code>onclick_fanyi</code>	<i>onclick_fanyi</i>
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Description

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

Usage

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

Arguments

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

Value

onclick function

Author(s)

Guangchuang Yu

<code>onclick_genecards</code>	<i>onclick_genecards</i>
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Description

onclick function to popup genecards webpage

Usage

```
onclick_genecards(gene)
```

Arguments

<code>gene</code>	query gene
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Value

onclick action

Author(s)

Guangchuang Yu

<code>onclick_hgnc</code>	<i>onclick_hgnc</i>
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Description

onclick function to popup HGNC gene webpage

Usage

`onclick_hgnc(gene)`

Arguments

gene query gene

Value

onclick action

Author(s)

Guangchuang Yu

<code>onclick_ncbi</code>	<i>onclick_ncbi</i>
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Description

onclick function to popup NCBI gene webpage

Usage

`onclick_ncbi(gene)`

Arguments

gene query gene

Value

onclick action

Author(s)

Guangchuang Yu

<code>onclick_pubmed</code>	<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

<code>onclick_uniprot</code>	<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

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 ggraph::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

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

ValueA `ggplot2` scale object

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