

# Package ‘ivolcano’

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**Title** Interactive Volcano Plot

**Version** 0.0.5

**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

**RoxygenNote** 7.3.3

**NeedsCompilation** no

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**Repository** CRAN

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geom\_ivolcano\_gene      *geom\_ivolcano\_gene*

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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
)
```

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`geom_ivolcano_line`      *geom\_ivolcano\_line*

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## Description

Add threshold lines to an iVolcano plot

## Usage

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

## Arguments

<code>linetype</code>	line type for the threshold lines
<code>color</code>	line color for the threshold lines
<code>linewidth</code>	line width for the threshold lines

## Value

A ggplot2 layer object

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`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

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ivolcano\_point

*ivolcano\_point*

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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**

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

**Value**

base plot of a volcano plot

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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

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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

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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

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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

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*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

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*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

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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

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pathway\_volcano      *pathway\_volcano*

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**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 gggraph::girafe

**Value**

a girafe object

**Author(s)**

Guangchuang Yu

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scale\_color\_figureya *scale\_color\_figureya*

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**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

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