Package: ggheatmap (via r-universe)

November 15, 2026

Title Plot Heatmap

Version 2.2.9001

Maintainer Baiwei Luo <2734782653@qq.com>

Description The flexibility and excellence of 'ggplot2' is unquestionable, so many drawing tools basically need 'ggplot2' as the operating object. In order to develop a heatmap drawing system based on ggplot2, we developed this tool, mainly to solve the heatmap puzzle problem and the flexible connection between the heatmap and the 'ggplot2' object. The advantages of this tool are as follows: 1. More flexible label settings; 2. Realize the linkage of heatmap and 'ggplot2' drawing system, which is helpful for operations such as puzzles; 3. Simple and easy to operate; 4. Optimization of clustering tree visualization. Compatibility updates by Renova.

License GPL-3

Encoding UTF-8

LazyData false

RoxygenNote 7.1.1

Depends ggplot2

Imports aplot, factoextra, tibble, ggpubr, tidyr, patchwork

Suggests grDevices, stats, testthat

NeedsCompilation no

Author Baiwei Luo [aut, cre]

Config/pak/sysreqs cmake libfreetype6-dev make libicu-dev libpng-dev libuv1-dev zlib1g-dev

Repository https://renova-r.r-universe.dev

Date/Publication 2026-11-15 20:25:39 UTC

RemoteUrl https://github.com/renova-r/ggheatmap

RemoteRef renova-2.2.9001

RemoteSha 4cdc19db1ab11f32b1bae594773f5e1ba2d1c73e

Contents

ggheatmap 2
ggheatmap_plotlist 4
ggheatmap_test 5
ggheatmap_theme 5

Index **6**

---

ggheatmap *ggplot2 Version of Heatmap*

Description

The flexibility and excellence of 'ggplot2' is unquestionable, so many drawing tools basically need 'ggplot2' as the operating object. In order to develop a heatmap drawing system based on ggplot2, we developed this tool, mainly to solve the heatmap puzzle problem and the flexible connection between the heatmap and the 'ggplot2' object. The advantages of this tool are as follows: 1. More flexible label settings; 2. Realize the linkage of heatmap and 'ggplot2' drawing system, which is helpful for operations such as puzzles; 3. Simple and easy to operate; 4. Optimization of clustering tree visualization.

Usage

```
ggheatmap(data,
  color=colorRampPalette(c( "#0073c2","white","#efc000"))(100),
  legendName="Express",
  scale="none",
  shape=NULL,
  border=NA,
  cluster_rows = F,
  cluster_cols = F,
  dist_method="euclidean",
  hclust_method="complete",
  text_show_rows=waiver(),
  text_show_cols=waiver(),
  text_position_rows="right",
  text_position_cols="bottom",
  annotation_cols=NULL,
  annotation_rows=NULL,
  annotation_color,
  annotation_width=0.03,
  annotation_position_rows="left",
  annotation_position_cols="top",
  show_cluster_cols=T,
  show_cluster_rows=T,
  cluster_num=NULL,
  tree_height_rows=0.1,
```

```
  tree_height_cols=0.1,
  tree_color_rows=NULL,
  tree_color_cols=NULL,
  tree_position_rows="left",
  tree_position_cols="top",
  levels_rows=NULL,
  levels_cols=NULL
)
```

Arguments

data	input data(matrix or data.frame)
color	the color of heatmap
legendName	character,the title of heatmap legend
scale	character,the way of scale data("none", "row" or "column")
border	character, the colour of border
shape	character, the shape of cell("square", "circle" and "triangle").Default is NULL
cluster_rows	whether rows should be clustered(TRUE of FALSE)
cluster_cols	whether column should be clustered(TRUE of FALSE)
dist_method	character,the method parameter of dist function. see dist
hclust_method	character,the method parameter of hclust function, see hclust
text_show_rows	a character you want to show for y-axis
text_show_cols	a character you want to show for x-axis
text_position_rows	character,the position of y-axis label("right" or "left")
text_position_cols	character,the position of x-axis label("bottom" or "top")
annotation_cols	a data.frame for column annotation
annotation_rows	a data.frame for row annotation
annotation_color	a list for annotation color
annotation_width	a numeric for annotation width
annotation_position_rows	character,the position of column annotation("right" or "left")
annotation_position_cols	character,the position of row annotation("bottom" or "top")
show_cluster_cols	whether show column cluster tree(TRUE of FALSE)
show_cluster_rows	whether show row cluster tree(TRUE of FALSE)
cluster_num	a numeric for cut cluster tree

`tree_height_rows`
: row cluster tree height

`tree_height_cols`
: column cluster tree height

`tree_color_rows`
: a character for row cluster tree color

`tree_color_cols`
: a character for column cluster tree color

`tree_position_rows`
: character,the position of row cluster tree("right" or "left")

`tree_position_cols`
: character,the position of column cluster tree("bottom" or "top")

`levels_rows`
: a character for y-axis label levels

`levels_cols`
: a character for x-axis label levels

Value

p

Author(s)

Baiwei Luo

`ggheatmap_plotlist` *Show ggheatmap Plot List*

Description

Display the basic elements of the ggheatmap

Usage

```
ggheatmap_plotlist(ggheatmap)
```

Arguments

`ggheatmap`
: heatmap, the result of ggheatmap

Value

plotlist

ggheatmap_test *Sample data for ggheatmap*

Description

This data is simulated data, not real data, including 12 samples, 50 simulated gene expression data, and 3 annotation data.

ggheatmap_theme *The Theme of ggheatmap*

Description

Set the styles of the drawing elements of each component of the ggheatmap except cluster tree.

Usage

```
ggheatmap_theme(ggheatmap, plotlist, theme)
```

Arguments

ggheatmap	the result of ggheatmap
plotlist	integer,the plotlist in ggheatmap. Use ggheatmap_plotlist
theme	list, the theme of plotlist. More detail can see theme

Value

ggheatmap

Index

∗ **datasets**
ggheatmap_test, 5

dist, *3*

ggheatmap, 2
ggheatmap_plotlist, 4, *5*
ggheatmap_test, 5
ggheatmap_theme, 5

hclust, *3*

theme, *5*