

# Package ‘ggheatmap’

September 10, 2022

**Title** Plot Heatmap

**Version** 2.2

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**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.

**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

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**Repository** CRAN

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## R topics documented:

ggheatmap . . . . .	2
ggheatmap_plotlist . . . . .	4
ggheatmap_test . . . . .	4
ggheatmap_theme . . . . .	5

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 <a href="#">dist</a>
hclust_method	character,the method parameter of hclust function, see <a href="#">hclust</a>
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**

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**Author(s)**

Baiwei Luo

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ggheatmap\_plotlist      *Show ggheatmap Plot List*

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**Description**

Display the basic elements of the ggheatmap

**Usage**

ggheatmap\_plotlist(ggheatmap)

**Arguments**

ggheatmap            heatmap, the result of ggheatmap

**Value**

plotlist

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ggheatmap\_test            *Sample data for ggheatmap*

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**Description**

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

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ggheatmap_theme	<i>The Theme of ggheatmap</i>
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**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 <a href="#">ggheatmap_plotlist</a>
theme	list, the theme of plotlist. More detail can see <a href="#">theme</a>

**Value**

ggheatmap

# Index

## \* datasets

ggheatmap\_test, 4

dist, 3

ggheatmap, 2

ggheatmap\_plotlist, 4, 5

ggheatmap\_test, 4

ggheatmap\_theme, 5

hclust, 3

theme, 5