

Package: ggheatmap (via r-universe)

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Title Plot Heatmap

Version 2.11

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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.

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LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Depends ggplot2

Imports aplot, ggtree, tibble, ggpubr, tidyr, patchwork

Suggests grDevices, stats, testthat

Repository <https://xiaoluo-boy.r-universe.dev>

RemoteUrl <https://github.com/xiaoluo-boy/ggheatmap>

RemoteRef HEAD

RemoteSha 5c373eb99f758c0a4d34ed1b008e59a7245226e4

Contents

ggheatmap	2
ggheatmap_plotlist	6
ggheatmap_theme	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

Examples

```

#Create data
library(ggheatmap)
library(tidyr)
library(aplot)
set.seed(123)
df <- matrix(runif(600,0,10),ncol = 12)
colnames(df) <- paste("sample",1:12,sep = "")
rownames(df) <- sapply(1:50, function(x)paste(sample(LETTERS,3,replace = FALSE),collapse = ""))
head(df)
#example 1
text_rows <- sample(rownames(df),3)
p <- ggheatmap(df,scale = "row",cluster_rows = TRUE,cluster_cols = TRUE,
  text_show_rows = text_rows)%>%
  ggheatmap_theme(1,theme =list(
    theme(axis.text.x = element_text(angle = 90,face = "bold"),
    axis.text.y = element_text(colour = "red",face = "bold"))
  ))

#example 2
ggheatmap(df,cluster_rows = TRUE,cluster_cols = TRUE,
  border = "grey",
  shape = "circle",
  cluster_num = c(5,4),
  tree_color_rows = c("#3B4992FF", "#EE0000FF", "#008B45FF", "#631879FF", "#008280FF"),
  tree_color_cols = c("#0073C2FF", "#EFC000FF", "#868686FF", "#CD534CFF")
)

#sample 3
row_metaData <- data.frame(exprtype=sample(c("Up", "Down"),50,replace = TRUE),
  genetype=sample(c("Metabolism", "Immune", "None"),50,replace = TRUE))
rownames(row_metaData) <- rownames(df)
col_metaData <- data.frame(tissue=sample(c("Normal", "Tumor"),12,replace = TRUE),

```

```

                                risklevel=sample(c("High","Low"),12,replace = TRUE))
rownames(col_metaData) <- colnames(df)
exprcol <- c("#EE0000FF","#008B45FF" )
names(exprcol) <- c("Up","Down")
genecol <- c("#EE7E30","#5D9AD3","#D0DFE6FF")
names(genecol) <- c("Metabolism","Immune","None")
tissuecol <- c("#98D352","#FF7F0E")
names(tissuecol) <- c("Normal","Tumor")
riskcol <- c("#EEA236FF","#46B8DAFF")
names(riskcol) <- c("High","Low")
col <- list(exprtype=exprcol,genetype=genecol,tissue=tissuecol,risklevel=riskcol)

p<- ggheatmap(df,cluster_rows = TRUE,cluster_cols = TRUE,scale = "row",
              cluster_num = c(5,3),
              tree_color_rows = c("#3B4992FF","#EE0000FF","#008B45FF","#631879FF","#008280FF"),
              tree_color_cols = c("#1F77B4FF","#FF7F0EFF","#2CA02CFF"),
              annotation_rows = row_metaData,
              annotation_cols = col_metaData,
              annotation_color = col
            )
p
ggheatmap_theme(p,2:5,theme = list(
  theme(legend.text = element_text(face = "bold")),
  theme(legend.text = element_text(face = "bold")),
  theme(legend.text = element_text(face = "bold")),
  theme(legend.text = element_text(face = "bold"))
))

#sample 4
ggheatmap(df,cluster_rows = TRUE,cluster_cols = TRUE,scale = "row",
          cluster_num = c(5,3),
          tree_color_rows = c("#3B4992FF","#EE0000FF","#008B45FF","#631879FF","#008280FF"),
          tree_color_cols = c("#1F77B4FF","#FF7F0EFF","#2CA02CFF"),
          annotation_rows = row_metaData,
          annotation_cols = col_metaData,
          annotation_color = col,
          annotation_position_rows="right"
        )

#sample 5
dat <- data.frame(marker=sample(c(1,NA),50,replace = TRUE),
                 gene=rownames(df),
                 shape=sample(c("T","F"),50,replace = TRUE))
p1 <- ggplot(dat,aes(x=1,y=gene,size=marker,color=shape,shape=shape))+
  geom_point()+theme_classic()+
  scale_color_manual(values = c("#D2691E","#1E87D2"))+
  theme(line = element_blank(),axis.text = element_blank(),axis.title = element_blank())+
  guides(size = FALSE)

p%>%insert_right(p1,width = 0.1)

```

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_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

`dist`, 3

`ggheatmap`, 2

`ggheatmap_plotlist`, 6, 6

`ggheatmap_theme`, 6

`hclust`, 3

`theme`, 6