Package ‘pairheatmap’

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Title A tool for comparing heatmaps
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Description A tool to compare two heatmaps and discover patterns within and across groups. In the context of biology, group can be defined based on gene ontology.
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pairheatmap-package A tool for comparing heatmaps

Description

A tool to compare two heatmaps and discover patterns within and across groups. In the context of biology, group can be defined based on gene ontology.

Details
The main interface is pairheatmap() function

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Examples
pairheatmap(mtcarsL mtcars)

Description
The main function for comparing heatmaps

Usage
pairheatmap (data1, data2,
scale="none", dendrogram="both",
matDist=0.5, matrixBorderCol = "grey",
colorStyle="s1",
rowGroup=rowGroup,
orderRowGroup=NULL,
rowGroupColor=FALSE,
rowGroupColor.choice,
groupBorder="line",
groupBorder.selectList=list(),
groupBorder.lwd=3,
groupBorder.col="green",
rowNameColor="blue",
colNameColor="blue",
rowNameFontSize=7,
colNameFontSize=7,
rowNameGroupColor=NULL,
clustermethod="complete", clusterMembers=NULL,
clusterRow=TRUE, clusterCol=TRUE, clusterColTogether=FALSE,
legend.pos="middle", legend.percent=0.5, legend.fontSize=7)
Arguments

data1 numeric matrix 1. It is considered as the standard matrix.
data2 numeric matrix 2. Its row order is same as that in data1. Its column order is either same as that in data1 or use separate cluster method.
scale character. It takes four values: "row", "col", "rowsep", "none" (default value). It indicates whether or not the data matrix is scaled in row/column direction. When "rowsep" is selected, the two data matrices are scaled separately in row direction.
dendrogram character. It takes three values: "row", "col", "both" (default value). It indicates whether or not to draw the row/col/both dendrogram.
matDist the separate distance between two data matrices. Default value is 0.5. If its value is 1, the distance between two matrices is exactly one data column.
matrixBorderCol the color of the matrix border. Default value is "grey".
colorStyle the color style for the matrix cell. It takes four values: "s1" (default value), "s2", "s3", "s4". s1 ranges from blue to red; s2 ranges from green to red; s3 uses a default color style from R package, pheatmap; s4 ranges from white to black.
rowGroup Row group variable.
orderRowGroup variable. The default value is "NULL". It is the row levels that should be ordered.
rowGroupColor logical value. It takes two values: "TRUE", "FALSE". It indicates whether or not to draw the row group bar.
rowGroupColor.choice character. It works when rowGroupColor is set as TRUE. The character length must match the unique groups in the rowGroup. If it is not specified, the colorStyle is used as default value.
groupBorder character. It takes two values: "line" (default value), "rect". It controls the shape of the group border.
groupBorder.selectList a list. It controls which group to be selected, which includes four components, "xgroup.start", "xgroup.end", "ygroup.start" and "ygroup.end". The selected groups will utilize the same graphical parameters as groupBorder.
groupBorder.lwd numeric. Default value is 3. It controls the line width of the groupBorder.
groupBorder.col character. Default value is "green". It controls the line color of the groupBorder.
rowNameColor character string. Default value is "blue". It controls the label color of the row name.
colNameColor character string. Default value is "blue". It controls the label color of the column name.
rowNameFontSize numeric scalar. Default value is 7. It controls the font size of the row name.
colNameFontSize numeric scalar. Default value is 7. It controls the font size of the column name.
rowNameGroupColor

character variable. The character length must match the unique groups in the rowGroup. It controls the color of different groups of row names.

clusterMethod

character. It takes the follow values: "ward", "single", "complete" (default value), "average", "mcquitty", "median" or "centroid".

clusterMembers

NULL or a vector. See function "hclust" of the package "stats" for details.

clusterRow

logical. It takes two values: "TRUE" (default value), "FALSE". It indicates whether or not to cluster rows.

clusterCol

logical. It takes two values: "TRUE" (default value), "FALSE". It indicates whether or not to cluster columns.

clusterColTogether

logical. It takes two values: "TRUE", "FALSE" (default value). It indicates whether or not the columns of data matrix 2 follows the same clustering order of that in data matrix 1. If the column number of data matrix 2 is different from that of data matrix 1, only the columns matching those of data matrix 1 are reordered.

legend.pos

character. It takes three values: "top", "middle" (default value), "bottom". It controls the position of the legend.

legend.percent

numeric. It takes value from 0 to 1. Default value is 0.5. If its value is 1, the height of the legend will be equal to the height of the heatmap.

legend.fontsize

numeric. Default value is 7. It controls the font size of the legend labels.

Details

This function compares two heatmaps and discovers links and patterns within and across groups. In the context of biology, group can be defined based on gene ontology or selected gene lists.

Value

Invisibly return the row and column index for two matrices.

Author(s)

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Examples

```r
## simple demo
cvalue <- pairheatmap(mtcars, mtcars)
cvalue
pairheatmap(mtcars, mtcars, scale="row")
pairheatmap(mtcars, mtcars[,1:5], scale="row")
pairheatmap(mtcars, mtcars[,1:5], scale="rowsep")
pairheatmap(mtcars, mtcars[,1:5], scale="col")
## row group bar
pairheatmap(mtcars, mtcars, rowGroup=mtcars$gear,
```

pairheatmap

```r
rowNameFontSize=6,
colNameFontSize=6,
rowNameGroupColor=rev(c("blue", "green", "orange")),
rowNameColor="blue",
)
## group options
pairheatmap(mtcars, mtcars,
rowGroup=mtcars$gear,
orderRowGroup=c(5, 4, 3)
)
## legend
pairheatmap(mtcars, mtcars,
legend.pos="middle", legend.percent=0.6, legend.fontsize=7)
## cluster analysis
pairheatmap(mtcars, mtcars, clusterMethod="ward", clusterRow=FALSE)
pairheatmap(mtcars, cbind(mtcars, mtcars), clusterColTogether=TRUE)
## selected groups
pairheatmap(mtcars, cbind(mtcars, mtcars),
groupBorder.selectList=
list(xgroup.start=c(2, 7), xgroup.end=c(4, 9),
ygroup.start=c(3, 30), ygroup.end=c(10, 32)
))
## more demo
pairheatmap(mtcars, mtcars, legend.percent=1, legend.pos="middle",
groupBorder.selectList=list(xgroup.start=c(2, 7), xgroup.end=c(4, 9), ygroup.start=c(3, 30),
ygroup.end=c(10, 32)))
pairheatmap(mtcars, mtcars, scale="row", colorStyle="s3",
groupBorder.selectList=list(xgroup.start=c(8), xgroup.end=c(11),
ygroup.start=c(11), ygroup.end=c(15)),
legend.pos="top")
pairheatmap(mtcars, mtcars,
colorStyle="s4", rowGroup=mtcars$gear,
rowGroupColor=TRUE,
rowGroupColor.choice = rev(c("blue", "orange", "green")),
groupBorder.selectList=list(xgroup.start=c(8), xgroup.end=c(11), ygroup.start=c(22), ygroup.end=c(25)),
legend.pos="top", legend.percent=0.6, legend.fontsize=5, orderRowGroup=c(5, 4, 3),
clusterRow=TRUE, clusterCol=TRUE, clusterColTogether=TRUE
)
mtcars2 <- mtcars[, rev(1:ncol(mtcars))]
pairheatmap(mtcars, mtcars2,
colorStyle="s1", rowGroup=mtcars$gear,
rowGroupColor=TRUE,
rowGroupColor.choice = rev(c("blue", "orange", "green")),
groupBorder.selectList=list(xgroup.start=c(8), xgroup.end=c(11), ygroup.start=c(22), ygroup.end=c(25)),
legend.pos="top", legend.percent=0.6, legend.fontsize=5, orderRowGroup=c(5, 4, 3),
clusterRow=TRUE, clusterCol=TRUE, clusterColTogether=FALSE
)
pairheatmap(mtcars, mtcars,
dendrogram="row", colorStyle="s1", rowGroup=mtcars$am,
rowGroupColor=TRUE,
groupBorder.selectList=list(xgroup.start=c(8), xgroup.end=c(11), ygroup.start=c(22), ygroup.end=c(25)),
legend.pos="top", legend.percent=0.6, legend.fontsize=5,
orderRowGroup=c(0, 1),
```
pairheatmap

clusterRow=TRUE, clusterCol=TRUE, clusterColTogether=FALSE
)

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