Package ‘heatmap3’

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Type Package

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VignetteBuilder knitr

Description An improved heatmap package. Completely compatible with the original R function 'heatmap', and provides more powerful and convenient features.

License GPL (>= 2)

Imports fastcluster

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Description

The function `colByValue` convert the values in matrix into colors

Usage

`colByValue(x, col, range = NA, breaks = NA, cex.axis = 2, las = 1, ...)`

Arguments

- **x**: matrix with values.
- **col**: a list of colors such as that generated by `rainbow`, `heat.colors`, `topo.colors`, `terrain.colors` or similar functions.
- **range**: the range of x. values out of the range will be changed to the max or min value of the range.
- **breaks**: either a numeric vector of two or more unique cut points or a single number (greater than or equal to 2) giving the number of intervals into which x is to be cut.
- **cex.axis**: The magnification to be used for axis annotation relative to the current setting of cex.
- **las**: numeric in 0,1,2,3; the style of axis labels.
- **...**: additional arguments passed on to `image` function to generate the color bar.

Value

A matrix with colors.

Examples

```r
temp<-rnorm(1000)
col<-colByValue(temp,col=colorRampPalette(c('chartreuse4','white','firebrick'))(1024),range=range(c(-2,2)))
col<-colByValue(temp,col=colorRampPalette(c('chartreuse4','white','firebrick'))(5),breaks=c(-5,-1,-0.1,0.1,1,5),cex.axis=0.8)
```
Description

The function heatmap3 is completely compatible with the original R function heatmap, and provides more new features.

Usage

heatmap3(x, Rowv = NULL, Colv = if (symm) "Rowv" else NULL, 
  distfun = function(x) as.dist(1 - cor(t(x), use = "pa")), distfunC, 
  distfunR, balanceColor = F, ColSideLabs, RowSideLabs, 
  showColDendro = T, showRowDendro = T, 
  col = colorRampPalette(c("navy", "white", "firebrick3"))(1024), 
  legendfun, method = "complete", ColAxisColors = 0, 
  RowAxisColors = 0, hclustfun = hclust, reorderfun = function(d, w) 
  reorder(d, w), add.expr, symm = FALSE, revC = identical(Colv, 
  "Rowv"), scale = c("row", "column", "none"), na.rm = TRUE, 
  ColSideFun, ColSideAnn, ColSideWidth = 0.4, ColSideCut, colorCell, 
  highlightCell, file = "heatmap3.pdf", topN = NA, filterFun = sd, 
  returnDistMatrix = FALSE, margins = c(5, 5), ColSideColors, 
  RowSideColors, cexRow = 0.2 + 1/log10(nrow(x)), cexCol = 0.2 + 
  1/log10(ncol(x)), lasRow = 2, lasCol = 2, labRow = NULL, 
  labCol = NULL, main = NULL, xlab = NULL, ylab = NULL, 
  keepDendro = FALSE, verbose =getOption("verbose"), useRaster = if 
  (ncol(x) * nrow(x) >= 50000) TRUE else FALSE, ...)

Arguments

x numeric matrix of the values to be plotted.

Rowv determines if and how the row dendrogram should be computed and reordered. 
Either a dendrogram or a vector of values used to reorder the row dendrogram or 
NA to suppress any row dendrogram (and reordering) or by default, NULL, see 
‘Details’ below.

Colv determines if and how the column dendrogram should be reordered. Has the 
same options as the Rowv argument above and additionally when x is a square 
matrix, Colv = "Rowv" means that columns should be treated identically 
to the rows (and so if there is to be no row dendrogram there will not be a column 
one either).

distfun function used to compute the distance (dissimilarity) between both rows and 
columns. Defaults to dist.

distfunC function used to compute the distance (dissimilarity) between and columns. Will 
be the same as distfun if not specified.

distfunR function used to compute the distance (dissimilarity) between and rows. Will be 
the same as distfun if not specified.
balanceColor: logical indicating if the colors need to be balanced so that the median color will represent the 0 value. The default value is F.

ColSideLabs: label for ColSideColors

RowSideLabs: label for RowSideColors

showColDendro: logical indicating if the column dendrogram should be plotted (when Colv isn’t NA).

showRowDendro: logical indicating if the row dendrogram should be plotted (when Rowv isn’t NA).

col: specifying the colors, used in image function.

legendfun: function used to generate legend in top left of the figure. If not specified, the color bar will be plotted. The users can use any plot functions to generate their own legend. Or a function showLegend is also provided as an example.

method: the agglomeration method to be used by hclust function. This should be (an unambiguous abbreviation of) one of "ward", "single", "complete", "average", "mcquitty", "median" or "centroid".

ColAxisColors: integer indicating which column of ColSideColors will be used as colors for labels in column axis. The default value is 0, which means all column labels will be in black color.

RowAxisColors: integer indicating which column of RowSideColors will be used as colors for labels in row axis. The default value is 0, which means all row labels will be in black color.

hclustfun: function used to compute the hierarchical clustering when Rowv or Colv are not dendrograms. Defaults to hclust. Should take as argument a result of distfun and return an object to which as.dendrogram can be applied.

reorderfun: function(d, w) of dendrogram and weights for reordering the row and column dendrograms. The default uses reorder.dendrogram.

add.expr: expression that will be evaluated after the call to image. Can be used to add components to the plot.

symm: logical indicating if x should be treated symmetrically; can only be true when x is a square matrix.

revC: logical indicating if the column order should be reversed for plotting, such that e.g., for the symmetric case, the symmetry axis is as usual.

scale: character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. The default is "row" if symm false, and "none" otherwise.

na.rm: logical indicating whether NA’s should be removed.

ColSideFun: function used to generate annotation and labeling figure in column side. The users can use any plot functions to generate their own figure. And a function showAnn is also provided as an example.

ColSideAnn: data frame with continuous and factor variables as annotation information. This parameter will be sorted by column dendrogram and then passed to ColSideFun.

ColSideWidth: numeric the height of column side area, which can be used by ColSideFun function.
ColSideCut numeric the value to be used in cutting column dendrogram. The dendrogram and annotation will be divided into different parts and labeled respectively.

colorCell A data.frame with 3 columns, indicating which cells will be colored by specific colors. The first column is row index, second column is column index, and the third column is color.

highlightCell A data.frame with 3 or 4 columns, indicating which cells will be highlighted by rectangles with specific colors. The first column is row index, second column is column index, the third column is color for rectangle border, and the optional forth column is width for rectangle border.

file pdf file name, only works when topN was used.

topN vector a list of numbers. topN genes will be used to generate the heatmaps.

filterFun function used to filter genes, such as sd, mean, sum. It will be used in a apply function to calculate for each row.

returnDistMatrix logical indicating if the distance matrix will be returned

margins numeric vector of length 2 containing the margins (see par(mar = *)) for column and row names, respectively.

ColSideColors (optional) character vector of length ncol(x) containing the color names for a horizontal side bar that may be used to annotate the columns of x.

RowSideColors (optional) character vector of length nrow(x) containing the color names for a vertical side bar that may be used to annotate the rows of x.

cexRow, cexCol positive numbers, used as cex.axis in for the row or column axis labeling. The defaults currently only use number of rows or columns, respectively.

lasRow, lasCol the style of row or column axis labels.

labRow, labCol character vectors with row and column labels to use; these default to rownames(x) or colnames(x), respectively.

main, xlab, ylab main, x- and y-axis titles; defaults to none.

keep.dendro logical indicating if the dendrogram(s) should be kept as part of the result (when Rowv and/or Colv are not NA).

verbose logical indicating if information should be printed.

useRaster logical; if TRUE a bitmap raster is used to plot the image instead of polygons. The grid must be regular in that case, otherwise an error is raised.

Value The same return value as hclust function.

Examples

```r
# generate data
set.seed(123456789)
rnormData <- matrix(rnorm(1000), 40, 25)
```
showAnn

Description

The function showAnn is an example for generating annotation figure in the result of heatmap3 function. You can use your any plot functions to generate your own annotation figure.

Usage

showAnn(annData)

Arguments

annData a data frame contains the annotation information for samples. It can only contain factor or numeric variables, and each row represent a sample with the same order of the columns in expression matrix.

Examples

annData<-data.frame(mtcars[,c("mpg","am","wt","gear")])
annData[,2]<-as.factor(annData[,2])
annData[,4]<-as.factor(annData[,4])
#Display annotation
## Not run:
The function `showLegend` is an example for generating legend in the figure of heatmap3 function. You can use your any plot functions to generate your own legend.

**Usage**

```
showLegend(legend = c("Group A", "Group B"), lwd = 3, cex = 1.1,
            col = c("red", "blue"), ...
```

**Arguments**

- `legend` (a character or expression vector of length \( \geq 1 \) to appear in the legend. Other objects will be coerced by `as.graphicsAnnot`.
- `lwd` (the line widths for lines appearing in the legend.
- `cex` (character expansion factor relative to current `par("cex")`. Used for text, and provides the default for `pt.cex`.
- `col` (the color of points or lines appearing in the legend.
- `...` (additional arguments passed on to `legend`)

**Examples**

```
RowSideColors<-rep("steelblue2",nrow(mtcars))
RowSideColors[c(4:6,15:17,22:26,29)]<-"lightgoldenrod"
RowSideColors[c(1:3,19:21)]<-"brown1"
heatmap3(mtcars,scale="col",margins=c(2,10),RowSideColors=RowSideColors,legendfun=function()
showLegend(legend=c("European","American","Japanese"),col=c("steelblue2","lightgoldenrod","brown1"),cex=1.5))
```
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