

Package: heatmap4 (via r-universe)

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Title Simple Heatmap Function

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Description A color image of a numerical matrix. A dendrogram can be added to the left side and to the top. This package takes the original heatmap function and reduces the argument complexity.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

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LazyData true

Depends R (>= 3.5.0)

Suggests knitr, rmarkdown, stats, marray, RColorBrewer, psy

VignetteBuilder knitr

Repository <https://rituroy.r-universe.dev>

RemoteUrl <https://github.com/rituroy/heatmap4>

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amplifDat	<i>Gene amplification status</i>
-----------	----------------------------------

Description

A numeric matrix of 0s and 1s of the same dimension as genomDat. ...

Usage

```
amplifDat
```

Format

```
amplifDat:
A matrix with 3469 rows and 39 columns.
```

anno	<i>Gene information</i>
------	-------------------------

Description

A data.frame containing gene information. ...

Usage

```
anno
```

Format

```
anno:
A data.frame with 3469 rows and 2 columns.
```

chrInfo	<i>Chromosomal information</i>
---------	--------------------------------

Description

A data.frame containing information for each chromosome. ...

Usage

```
chrInfo
```

Format

```
chrInfo:  
A data.frame with 24 rows and 3 columns.
```

colorBar	<i>Calibration bar for color images.</i>
----------	--

Description

Produces a color image (color bar)

Usage

```
colorBar(  
  x,  
  horizontal = TRUE,  
  col = grDevices::heat.colors(50),  
  scale = 1:length(x),  
  k = 10,  
  cexAxis = 1,  
  ...  
)
```

Arguments

x	.
horizontal	.
col	.
scale	.
k	.
cexAxis	.
...	additional arguments.

Value

A color vector.

cutCluster	<i>Cluster designation.</i>
------------	-----------------------------

Description

Cuts the tree into desired number of groups.

Usage

```
cutCluster(clustObj, ann, nClust = 2, rev = F)
```

Arguments

clustObj	a hclust object.
ann	a data.frame containing annotation for each observation.
nClust	number of groups desired.
rev	reverse the order of observations.

Value

a data.frame.

generate_heatmap	<i>Generate a Heat Map.</i>
------------------	-----------------------------

Description

A heat map is a false color image (basically `image(t(x))`) with a dendrogram added to the left side and to the top. Typically, reordering of the rows and columns according to some set of values (row or column means) within the restrictions imposed by the dendrogram is carried out. This package takes the original heatmap function and reduces the argument complexity.

Usage

```

generate_heatmap(
  x,
  col_lab = c(FALSE, TRUE),
  row_lab = c(FALSE, TRUE),
  col_lab_vtr = NULL,
  row_lab_vtr = NULL,
  col_anno = c(FALSE, TRUE),
  row_anno = c(FALSE, TRUE),
  col_info = NULL,
  row_info = NULL,
  col_anno_var = NULL,
  row_anno_var = NULL,
  col_var_info = NULL,
  row_var_info = NULL,
  col_dend = c(FALSE, TRUE),
  row_dend = c(FALSE, TRUE),
  col_anno_name = NULL,
  row_anno_name = NULL,
  col_clust = NULL,
  row_clust = NULL,
  plot_info = list(margins = c(0.5, 0.5), cexCol = NULL, cexRow = NULL, cexColSide =
    NULL, cexRowSide = NULL, colorCatCol = NULL, colorCatRow = NULL, colorContCol = NULL,
    colorContRow = NULL),
  file_name = NULL,
  h_title = NULL,
  input_legend = c(FALSE, TRUE),
  legend_title = NULL,
  heatmap_color = c("red", "blue", "grey"),
  zlm = c(-0.5, 0.5),
  ...
)

```

Arguments

x	numeric matrix; values to be plotted in the heatmap.
col_lab	boolean (T, F); to display column labels; default is FALSE.
row_lab	boolean (T, F); to display row labels; default is FALSE.
col_lab_vtr	character vector; with column labels to use; defaults to colnames(x).
row_lab_vtr	character vector; with row labels to use; defaults to rownames(x).
col_anno	boolean (T, F); to display column annotations; defaults to FALSE.
row_anno	boolean (T, F); to display row annotations; defaults to FALSE.
col_info	data frame; data to be used in column annotations; default is NULL.
row_info	data frame; data to be used in row annotations; default is NULL.
col_anno_var	character vector; with specific column annotation variables to see in column annotations; defaults to colnames(col_info).

row_anno_var	character vector; with specific row annotation variables to see in row annotations; defaults to colnames(row_info).
col_var_info	nested list; of column annotation variables that need specific colors and placement; default is NULL.
row_var_info	nested list; of row annotation variables that need specific colors and placement; default is NULL.
col_dend	boolean (T, F); to display column dendrogram; default is FALSE.
row_dend	boolean (T, F); to display row dendrogram; default is FALSE.
col_anno_name	character vector; to name column color bars; default is NULL.
row_anno_name	character vector; to name row color bars; default is NULL.
col_clust	variable of hclust or dendrogram class; to cluster by the column; default NULL when col_dend is FALSE.
row_clust	variable of hclust or dendrogram class; to cluster by the row; default NULL when row_dend is FALSE.
plot_info	list; of 8 variables to control heatmap and annotation column/row label size (in that order); default is list(margins=c(0.5,0.5), "cexCol" = NULL, "cexRow" = NULL, "cexColSide" = NULL, "cexRowSide" = NULL, colorCatCol=NULL, colorCatRow=NULL, colorContCol=NULL, colorContRow=NULL); 'cex': heatmap labels and 'cexSide': annotation labels.
file_name	string; denotes the name of the file, must contain one of the following file types: .pdf, .jpeg, .png, .tiff; default is NULL.
h_title	string; gives the heatmap output a title; default is NULL.
input_legend	boolean (T, F); to display annotations legend; row, column or both will be added if selected; default is FALSE.
legend_title	string; denotes the title of the legend; default is NULL.
heatmap_color	character vector of length 3; colors for high, low and middle values respectively; default is c("red", "blue", "grey").
zlm	numeric vector of length 2; the minimum and maximum x values for which colors should be plotted; default is c(-0.5, 0.5).
...	additional arguments.

Value

A list.

genomDat

Gene expression data

Description

A numeric matrix with gene expression data with rows representing genes and columns representing subjects. ...

Usage

genomDat

Format

genomDat:
A matrix with 3469 rows and 39 columns.

getCluster *Hierarchical cluster analysis based on various distance methods.*

Description

Computes distance matrix and then performs hierarchical clustering.

Usage

getCluster(dat, distMethod, linkMethod, absolute = F)

Arguments

dat a numeric matrix.
distMethod distance function.
linkMethod agglomeration method.
absolute a logical value. TRUE means absolute value of correlation is to be returned.

Value

an object of class "hclust".

getCosineDist *Cosine distance based distance matrix.*

Description

Computes cosine distances and returns them as a distance matrix.

Usage

getCosineDist(x)

Arguments

x a numeric matrix.

Value

an object of class "dist".

getDist	<i>Returns a distance matrix.</i>
---------	-----------------------------------

Description

Computes correlation coefficients and returns them as a distance matrix.

Usage

```
getDist(dat, method = "pearson", absolute = FALSE)
```

Arguments

dat	a numeric matrix passed to function cor.
method	a character string indicating which correlation coefficient is to be computed. One of "pearson" (default), "kendall", or "spearman": can be abbreviated.
absolute	a logical value. TRUE means absolute value of correlation is to be returned.

Value

an object of class "dist".

getKappaDist	<i>Cohen's kappa coefficient based distance matrix.</i>
--------------	---

Description

Computes Cohen's kappa coefficients and returns them as a distance matrix.

Usage

```
getKappaDist(x, type = "Cohen", absolute = FALSE)
```

Arguments

x	a numeric matrix passed to function cor.
type	a character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman": can be abbreviated.
absolute	a logical value. TRUE means absolute value of correlation is to be returned.

Value

an object of class "dist".

`heatmap4`*Heatmap internal function.*

Description

Called by `generate_heatmap` to create heatmap.

Usage

```
heatmap4(  
  x,  
  imp = TRUE,  
  Rowv = NA,  
  Colv = NULL,  
  distfun = stats::dist,  
  hclustfun = stats::hclust,  
  add.expr,  
  symm = FALSE,  
  revC = identical(Colv, "Rowv"),  
  scale = "none",  
  na.rm = TRUE,  
  margins = c(5, 5),  
  ColSideColors,  
  RowSideColors,  
  cexRow = 0.2 + 1/log10(nr),  
  cexCol = 0.2 + 1/log10(nc),  
  fontRow = 1,  
  fontCol = 1,  
  labRow = NULL,  
  labCol = NULL,  
  lineRow = NULL,  
  lineCol = NULL,  
  lineColor = "black",  
  totalR = nr,  
  totalC = nc,  
  ncr = NA,  
  ncc = NA,  
  main = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  verbose = getOption("verbose"),  
  methodR = "ward.D",  
  methodC = "ward.D",  
  zlm = c(-0.5, 0.5),  
  high = "green",  
  low = "red",  
  mid = "black",
```

```

addAmp = NULL,
colAmp = NULL,
cexAmp = 0.25,
addText = NULL,
cexText = 1,
lwdRect = graphics::par("lwd"),
lwidHeatmap = 4,
lheiHeatmap = 4,
lwidRowSide = 0.2,
lheiColSide = 0.2,
cexRowSide = 1,
cexColSide = 1,
densColor = NULL,
sideLabRow = 4,
sideLabCol = 1,
layoutRespect = T,
sideColSide = c("left", "right"),
sideRowSide = c("bottom", "top"),
...
)

```

Arguments

<code>x</code>	numeric matrix of the values to be plotted.
<code>imp</code>	logical impute missing values if TRUE.
<code>Rowv</code>	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.
<code>Colv</code>	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).
<code>distfun</code>	function used to compute the distance (dissimilarity) between both rows and columns. Defaults to dist.
<code>hclustfun</code>	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.
<code>add.expr</code>	expression that will be evaluated after the call to image. Can be used to add components to the plot.
<code>symm</code>	logical indicating if x should be treated symmetrically; can only be true when x is a square matrix.
<code>revC</code>	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 <code>symm</code> false, and "none" otherwise.
na.rm	logical indicating whether NA's should be removed.
margins	numeric vector of length 2 containing the margins (see <code>graphics::par(mar = *)</code>) for column and row names, respectively.
ColSideColors	(optional) character vector of length <code>ncol(x)</code> containing the color names for a horizontal side bar that may be used to annotate the columns of <code>x</code> .
RowSideColors	(optional) character vector of length <code>nrow(x)</code> containing the color names for a vertical side bar that may be used to annotate the rows of <code>x</code> .
cexRow	positive number, used as <code>cex.axis</code> in for the row axis labeling. The default currently only uses number of rows.
cexCol	positive number, used as <code>cex.axis</code> in for the column axis labeling. The default currently only uses number of columns.
fontRow	positive number, used as <code>font.axis</code> in for the row axis labeling. The default is 1.
fontCol	positive number, used as <code>font.axis</code> in for the column axis labeling. The default is 1.
labRow	character vector with row labels to use; defaults to <code>rownames(x)</code> .
labCol	character vector with column labels to use; these defaults to <code>colnames(x)</code> .
lineRow	(optional) positive number vector, used to draw horizontal lines. The default is NULL.
lineCol	(optional) positive number vector, used to draw vertical lines. The default is NULL.
lineColor	(optional) Color of lines drawn with <code>lineRow</code> and <code>lineCol</code> .
totalR	.
totalC	.
ncr	.
ncc	.
main	main title; defaults to none.
xlab	x-axis title; defaults to none.
ylab	y-axis title; defaults to none.
verbose	logical indicating if information should be printed.
methodR	Agglomeration method for clustering rows.
methodC	Agglomeration method for clustering columns.
zlm	the minimum and maximum x values for which colors should be plotted.
high	color for high values.
low	color for low values.
mid	color for middle values.
addAmp	(optional) matrix 0s and 1s of the same size as <code>x</code> to be added to the heatmap
colAmp	(optional) color of <code>addAmp</code>

```

cexAmp      (optional) size of addAmp
addText     (optional) character matrix of the same size as x to be added to the heatmap
cexText     (optional) color of addText
lwdRect     .
lwidHeatmap .
lheiHeatmap .
lwidRowSide .
lheiColSide .
cexRowSide  .
cexColSide  .
densColor   .
sideLabRow  .
sideLabCol  .
layoutRespect .
sideColSide .
sideRowSide .
...         additional arguments passed on to image, e.g., col specifying the colors.

```

Value

A List.

```
heatmapColorBar      Returns a color bar.
```

Description

Produces a color image (color bar) which can be used for the legend to another color image obtained from heatmap4.

Usage

```

heatmapColorBar(
  limit,
  cols = c("green", "red", "black"),
  main = NULL,
  marginHMCSBar = NULL,
  cexAxisHMCSBar = 1,
  ...
)

```

Arguments

limit .
 cols .
 main .
 marginHMBar .
 cexAxisHMBar .
 ... additional arguments.

Value

A color vector.

phen	<i>Phenotypic (patient information) data</i>
------	--

Description

A data.frame containing subject information. ...

Usage

phen

Format

phen:
 A data.frame with 39 rows and 7 columns.

rect.hclust.my	<i>rect.hclust.my.</i>
----------------	------------------------

Description

Draws rectangles around the branches of a dendrogram highlighting the corresponding clusters.
 First the dendrogram is cut at a certain level, then a rectangle is drawn around selected branches.

Usage

```
rect.hclust.my(
  tree,
  k = NULL,
  which = NULL,
  x = NULL,
  h = NULL,
  border = 2,
  cluster = NULL,
  horiz = FALSE,
  lwd = graphics::par("lwd")
)
```

Arguments

tree	an object of the type produced by hclust.
k	Scalar. Cut the dendrogram such that exactly k clusters are produced.
which	A vector selecting the clusters around which a rectangle should be drawn. which selects clusters by number (from left to right in the tree). Default is which = 1:k.
x	A vector selecting the clusters around which a rectangle should be drawn. x selects clusters containing the respective horizontal coordinates.
h	Scalar. Cut the dendrogram by cutting at height h.
border	Vector with border colors for the rectangles.
cluster	Optional vector with cluster memberships as returned by stats::cutree(hclust.obj, k = k), can be specified for efficiency if already computed.
horiz	Horizontal or vertical.
lwd	Line width of the rectangles.

Value

(Invisibly) returns a list where each element contains a vector of data points contained in the respective cluster.

sampleColorLegend *Returns a legend.*

Description

Adds legends to row and column color bars.

Usage

```
sampleColorLegend(  
  tls,  
  col = NULL,  
  lty = NULL,  
  border = NULL,  
  pch = NULL,  
  lwd = NULL,  
  legendTitle = NULL,  
  cex = NULL,  
  density = NULL,  
  ...  
)
```

Arguments

tls	.
col	.
lty	.
border	.
pch	.
lwd	.
legendTitle	.
cex	.
density	.
...	additional arguments.

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