Package 'heatmapFlex'

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Type Package

Title Tools to Generate Flexible Heatmaps

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Description A set of tools supporting more flexible heatmaps. The graphics is grid-like using
the old graphics system. The main function is heatmap.n2(), which is a wrapper around the various functions
constructing individual parts of the heatmap, like sidebars, picket plots, legends etc. The function supports zooming
and splitting, i.e., having (unlimited) small heatmaps underneath each other in one plot deriving from the same data set,
e.g., clustered and ordered by a supervised clustering method.

Depends Biobase, Heatplus, grDevices, stats, graphics

Imports RColorBrewer, utils

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Suggests rmarkdown, knitr

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R topics documented:

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draw_heatmap *Function to draw a heatmap based on prepared "display list" (dl)*

Description

Normally, draw_heatmap is called from within [heatmap.n2](#) (if argument plot is TRUE which is the default) but if that is not desired, e.g., for zooming, it can be called separately.

Usage

```
draw_heatmap(dl, set.oma = TRUE, ...)
```

Arguments

dl (list). The "display list": A list with all parameters needed for plotting the heatmap.

set.oma (logical). Should the outer margins be set to optimized values? Defaults to TRUE.

... (list). Additional parameters passed to [plot](#).

Value

Invisibly returns a list with graphical parameters. But mainly the function is called for its side-effect of generating a plot.

See Also

[par](#)

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heatmap.n2 *Main heatmap function*

Description

This is the main function to be called be end users. It accepts a numeric matrix and draws a heatmap.

Usage

```
heatmap.n2(
  x,
  main = "Heatmap",
  ...,
  na.color = "gray80",
  sidebars = NULL,
  picketdata = NULL,
  r.cex = 1,
  c.cex = 1,
  titleheight = lcm(1.2),
  dendroheight = lcm(3),
  dendrowidth = lcm(3),
  labelheight = lcm(1),
  labelwidth = lcm(1),
  picketheight = 0.4,
  sidebarwidth = lcm(1),
  sidebar.cex = 1,
  colorkeylabels = FALSE,
  legendcorner = "bottomleft",
  plot = TRUE,
  factorpalettefn = "Pastel1",
  add.sig = FALSE,
  pv = NULL,
  order_list = TRUE,
  genes2highl = NULL
)
```

Arguments

x	(numeric). Numeric matrix.
main	(character). Main plot title.
...	Additional arguments passed to `prepare_heatmap_data2`.
na.color	(character). Colour code or name used for missing values. Defaults to `gray80`.
sidebars	(list). List of data frames for each of the four sides of the heatmap ("bottom", "left", "top", "right"). Each column in the data frame represents some statistics or other numerical variable describing the rows or columns of the data matrix.
picketdata	(data.frame or numeric). Usually a data frame with columns consisting of 0 and 1. The columns describe categories that the samples (rows in the picketdata) belong to, such as sex or a health stage. The categories must be binary, so the data frame would for example have two rows, 'female' and 'male', and the rows (=samples) are coded with 1 (=TRUE) and 0 (=FALSE). See [picketPlot](#) for a description of the general purpose of a picket plot.
r.cex	(numeric). Font size for row labels.
c.cex	(numeric). Font size for column labels.

titleheight	(numeric or lcm(numeric)). Relative or absolute height (using [lcm](), see [layout]()) of the plot title.
dendroheight	(numeric or lcm(numeric)). Relative or absolute height (using [lcm](), see [layout]()) of the dendrogram.
dendrowidth	(numeric or lcm(numeric)). Relative or absolute width (using [lcm](), see [layout]()) of the dendrogram.
labelheight	(numeric or lcm(numeric)). Relative or absolute height (using [lcm](), see [layout]()) of the labels.
labelwidth	(numeric or lcm(numeric)). Relative or absolute width (using [lcm](), see [layout]()) of the labels.
picketheight	(numeric or lcm(numeric)). Relative or absolute height (using [lcm](), see [layout]()) of the picket plots.
sidebarwidth	(numeric or lcm(numeric)). Relative or absolute width (using [lcm](), see [layout]()) of the sidebars.
sidebar.cex	(numeric). Font size for sidebar labels.
colorkeylabels	(logical). Should colour key labels be added?
legendcorner	(character). Position of the legend.
plot	(logical). Draw the plot? Defaults to TRUE.
factorpalettefn	
	(character). Name of the colour palette.
add.sig	(logical). Should significance asterixes be drawn?
pv	(numeric). Matrix of the same dimensions as x with P-Values for correlation significance.
order_list	(logical). Should the order of the correlation matrix be reversed? Meaningful if the order of input variables should be preserved because [image]() turns the input matrix.
genes2highl	(character). Vector of gene symbols (or whatever labels are used) to be highlighted. If not NULL will draw a semi-transparent rectangle around the labels and rows or columns in the heatmap labels.

Details

The result can be used for zooming. For simple basic cases, picketvar can be given directly. Factor sidebars are supported, but legends are only shown for the first two. Arguments that will be passed on the prepare_heatmap_data2:

labRow (character). Custom row labels
labCol (character). Custom column labels
Rowv (dendrogram or integer). Custom dendrogram object or integer vector giving the ordering index for rows
Colv (dendrogram or integer). Custom dendrogram object or integer vector giving the ordering index for columns
reorder (logical). Boolean of length 2 for rows and columns. Should rows and/or columns be reordered according to Rowv
distfun (function). Distance function. Defaults to [dist]()
hclustfun (function). Hierarchical clustering function. Defaults to [hclust]()
rowMembers (character). Group vector to split rows by

colMembers (character). Group vector to split columns by

spacer (integer). Length 1 integer used as spacer to separate groups (see rowMembers/colMembers). Defaults to 1

scale (character). One of "row", "column" or "none": By which dimension should data be scaled? Defaults to "none"

trim (numeric). Value to "cut off" data distribution. Values and both ends of the distribution, larger or smaller, respectively,

zlim (numeric). Value to set the ranges for plotting x and y values. Supports both symmetrical (with default NULL) and asy

col (character) Name (acronym) of the colour palette to use. Can be one of "RdBkGn" (c("green", "black", "red")), "BuY

filter (integer or logical.) For filtering rows/columns: TRUE (=1.0) = remove rows/columns with only NAs, 0.5 = remov

Value

In addition to its side-effect of plotting the heatmap (if plot is TRUE, which is the default), the function will invisibly returns the prepared "display list", a list of all parts of the heatmap used by hlayout() to actually draw the final heatmap.

See Also

layout

brewer.pal

colorRampPalette

dist

hclust

picketPlot

Examples

```
# Generate a random 10x10 matrix and plot it using default values
mat <- matrix(rnorm(100), nrow = 10)
heatmap.n2(mat)

# Generate a random 10x10 matrix with two distinct sets, order it using
# default clustering methods, split it into each two groups along both rows
# and columns and adjust colour palette and dendrogram dimensions:
mat <- matrix(c(rnorm(50, mean = 1), rnorm(50, mean = -1)), nrow = 10)
heatmap.n2(mat, col = "BuWtRd", rowMembers=rep(1:2, each=5),
    colMembers=rep(1:2, each=5), labRow=paste0("gene-", 1:10),
    labCol=paste0(c("A", "B"), rep(1:5, 2)), r.cex=0.8,
    dendroheight = lcm(2.2), dendrowidth = lcm(2.4))
```

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heatmapFlex   *Tools to Generate Flexible Heatmaps*

Description

The package has a number of tools supporting more flexible heatmaps. The graphics is grid-like using the old graphics system. The main function is `heatmap.n2`, which is a wrapper around the various functions constructing individual parts of the heatmap, like sidebars, picket plots, legends etc. The function supports zooming and splitting, i.e., having (unlimited) small heatmaps underneath each other in one plot deriving from the same data set, e.g., clustered and ordered by a supervised clustering method.

Details

Package:	heatmapFlex
Type:	Package
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License:	GPL-3
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prepare_heatmap_data2   *Function to prepare data for a heatmap: scaling, dendrograms, ...*

Description

Function to prepare data for a heatmap: scaling, dendrograms, ...

Usage

```
prepare_heatmap_data2(
  x,
  labRow = NA,
  labCol = NA,
  Rowv = NULL,
  Colv = NULL,
  reorder = c(TRUE, TRUE),
  distfun = dist,
  hclustfun = hclust,
  rowMembers = NULL,
  colMembers = NULL,
  spacer = 1,
```

```
    scale = "none",
    trim = NULL,
    zlim = NULL,
    col = NULL,
    filter = c(TRUE, TRUE),
    add.sig = FALSE,
    pv = NULL
)
```

Arguments

`x`	(numeric). Numeric matrix.
`labRow`	(character). Custom row labels.
`labCol`	(character). Custom column labels.
`Rowv`	(dendrogram or integer). Custom dendrogram object or integer vector giving the ordering index for rows.
`Colv`	(dendrogram or integer). Custom dendrogram object or integer vector giving the ordering index for columns
`reorder`	(logical). Boolean of length 2 for rows and columns. Should rows and/or columns be reordered according to Rowv/Colv?
`distfun`	(function). Distance function. Defaults to [dist]().
`hclustfun`	(function). Hierarchical clustering function. Defaults to [hclust]().
`rowMembers`	(character). Group vector to split rows by.
`colMembers`	(character). Group vector to split columns by.
`spacer`	(integer). Length 1 integer used as spacer to separate groups (see rowMembers/colMembers). Defaults to 1.
`scale`	(character). One of "row", "column" or "none": By which dimension should data be scaled? Defaults to "none".
`trim`	(numeric). Value to "cut off" data distribution. Values and both ends of the distribution, larger or smaller, respectively, will be made equal to +/-trim. Defaults to NULL, no trimming.
`zlim`	(numeric). Value to set the ranges for plotting x and y values. Supports both symmetrical (with default NULL) and asymmetrical (NA) automatic zlim. Used for zooming.
`col`	(character) Name (acronym) of the colour palette to use. Can be one of "RdBkGn" (c("green", "black", "red")), "BuYl" (c("blue", "yellow")), "BuWtRd" (c("blue", "white", "red")) or a valid name used by [brewer.pal](). Defaults to NULL which will set "RdBkGn".
`filter`	(integer or logical.) For filtering rows/columns: TRUE (=1.0) = remove rows/columns with only NAs, 0.5 = remove if >= 50 per cent NAs, etc. Defaults to c(TRUE, TRUE).
`add.sig`	(logical). Should significance asterixes be drawn?
`pv`	(numeric). Matrix of the same dimensions as x with P-Values for correlation significance.

Details

This function is used by `heatmap.n2` and should not be called bu the user directly. It is only documented because its arguments are passed by the main function when given there.

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zoom_heatmap   *Function to zoom into an already drawn heatmap*

Description

After the heatmap was drawn in a screen device such as X11, windows and quartz it can be zoomed by using the mouse.

Usage

```
zoom_heatmap(dl, ...)
```

Arguments

dl	(`list`). The "display list": A list with all parameters needed for plotting the heatmap.
`...`	(`list`). Additional parameters passed to [draw_heatmap](and eventually to [plot]().

Value

Invisibly returns a list with graphical parameters but is mainly called for its side-effect of drawing a zoomed plot.

See Also

[locator]

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