

Heatplus

October 25, 2011

RGBColVec

Alternative color schemes

Description

RGBColVec returns a vector of colors that is equally spaced from red through black to green, suitable for heatmaps.

RainbowPastel returns a vector of colors like rainbow, but more pastelly.

Usage

```
RGBColVec(nrgcols = 12)
```

```
RainbowPastel(n, blanche = 200, ...)
```

Arguments

nrgcols, n desired number of colors
blanche the amount of whiteness added; value between 0 and 255
... extra arguments to rainbow

Value

A character vector of length nrgcols or n giving the RGB codes for the colors.

Author(s)

RGBColVec is based on function rcolors.func in package sma by Sandrine Dudoit and Jane Fridlyand.

RGBColVec as documented and RainbowPastel by Alexander Ploner

See Also

[heat.colors](#)

Examples

```

# A Color Wheel
pie(rep(1,12), col=RGBColVec(12))

# A color wheel in the original rainbow
pie(rep(1,6), col=rainbow(6))

# Pastel
pie(rep(1,6), col=RainbowPastel(6))

# Less whiteness
pie(rep(1,6), col=RainbowPastel(6, blanche=127))

# More steps require less whiteness
pie(rep(1,12), col=RainbowPastel(12, blanche=60))

# Test your screen & eyes: any differences?
pie(rep(1,12), col=RainbowPastel(12, blanche=80))

```

cutplot.dendrogram *Plot Subtrees of a Dendrogram in Different Colors*

Description

Plot a dendrogram, cut the tree at a given height, and draw the resulting subtrees in different colors.

Usage

```
cutplot.dendrogram(x, h, cluscol, leaflab = "none", horiz = FALSE, lwd = 3, ...)
```

Arguments

x	a dendrogram.
h	the height at which the dendrogram is cut.
cluscol	the colors used for the subtrees; defaults to rainbow.
leaflab	indicates how leaf labels are to be drawn< defaults to 'perpendicular'.
horiz	logical indicating whether to plot the dendrogram horizontally or vertically.
lwd	the line width used for the color subtrees.
...	arguments to plot.dendrogram.

Details

This routine makes use of the functions `plot.dendrogram` and `plotNode` in package `stats`.

Author(s)

Alexander Ploner <Alexander.Ploner@ki.se>

See Also

[as.dendrogram](#)

Examples

```
data(swiss)
cc = as.dendrogram(hclust(dist(swiss)))
cutplot.dendrogram(cc, h=80)
```

heatmap_2

*Display Data as Heatmap***Description**

This function displays an expression data matrix as a heatmap. It is based on an old version of `heatmap` in the `stats` package, but offers more flexibility (e.g. skipping dendrograms, skipping row/column labelling, adding a legend).

Usage

```
heatmap_2(x, Rowv, Colv, distfun = dist, hclustfun = hclust, add.expr,
          scale = c("row", "column", "none"), na.rm = TRUE,
          do.dendro = c(TRUE, TRUE), legend = 0, legfrac = 8,
          col = heat.colors(12), trim, ...)
```

Arguments

<code>x</code>	the numerical data matrix to be displayed.
<code>Rowv</code>	either a dendrogram or a vector of reordering indexes for the rows.
<code>Colv</code>	either a dendrogram or a vector of reordering indexes for the columns.
<code>distfun</code>	function to compute the distances between rows and columns. Defaults to <code>dist</code> .
<code>hclustfun</code>	function used to cluster rows and columns. Defaults to <code>hclust</code> .
<code>add.expr</code>	Expression to be evaluated after the call to <code>image</code> . See Details.
<code>scale</code>	indicates whether values should be scaled by either by row, column, or not at all. Defaults to <code>row</code> .
<code>na.rm</code>	logical indicating whether to remove NAs.
<code>do.dendro</code>	logical vector of length two, indicating (in this order) whether to draw the row and column dendrograms.
<code>legend</code>	integer between 1 and 4, indicating on which side of the plot the legend should be drawn, as in <code>mtext</code> .
<code>legfrac</code>	fraction of the plot that is taken up by the legend; larger values correspond to smaller legends.
<code>col</code>	the color scheme for <code>image</code> . The default sucks.
<code>trim</code>	Percentage of values to be trimmed. This helps to keep an informative color scale, see Details.
<code>...</code>	extra arguments to <code>image</code> .

Details

With all parameters at their default, this gives the same result as a very old version of `heatmap` that was the base for the modifications. All parameters of the same name have the same function as in `heatmap`, though `add.expr`, which can be used for adding graphical elements after the call to `image`, will probably not produce useful results. Note also that row- and column labels are optional, i.e. if the corresponding `dimname` of `x` is `NULL`, no labels are displayed.

Note that setting `Rowv` or `Colv` to `NA` completely suppresses re-ordering of rows or columns as well as the corresponding dendrogram. Setting both to `NA` works basically like `image` (though you can still add a legend).

Setting `trim` to a number between 0 and 1 uses equidistant classes between the (`trim`)- and (1-`trim`)-quantile, and lumps the values below and above this range into separate open-ended classes. If the data comes from a heavy-tailed distribution, this can save the display from putting too many values into too few classes.

Value

Same as `heatmap` with `keep.dendro=FALSE`: an invisible list giving the reordered indices of the row- and column-elements as `elements$rowInd` and `elements$colInd`.

Author(s)

Original by Andy Liaw, with revisions by Robert Gentleman and Martin Maechler.

Alexander Ploner for this version.

See Also

[heatmap](#), [hclust](#), [heatmap_plus](#)

Examples

```
# create data
mm = matrix(rnorm(1000, m=1), 100,10)
mm = cbind(mm, matrix(rnorm(2000), 100, 20))
mm = cbind(mm, matrix(rnorm(1500, m=-1), 100, 15))
mm2 = matrix(rnorm(450), 30, 15)
mm2 = cbind(mm2, matrix(rnorm(900,m=1.5), 30,30))
mm=rbind(mm, mm2)
colnames(mm) = paste("Sample", 1:45)
rownames(mm) = paste("Gene", 1:130)

# similar to base heatmap
heatmap_2(mm)

# remove column dendrogram
heatmap_2(mm, do.dendro=c(TRUE, FALSE))

# add a legend under the plot
heatmap_2(mm, legend=1)
# make it smaller
heatmap_2(mm, legend=1, legfrac=10)
# ... on the left side
heatmap_2(mm, legend=2, legfrac=10)

# remove the column labels by removing the column names
```

```

colnames(mm)=NULL
heatmap_2(mm, legend=1, legfrac=10)

# truncate the data drastically
heatmap_2(mm, legend=1, legfrac=10, trim=0.1)

```

heatmap_plus *Display an Annotated Heatmap*

Description

This function displays an expression data matrix as a heatmap with a column dendrogram. A given clustering will be shown in color. Additionally, a number of binary and interval scaled covariates can be added to characterize these clusters.

Usage

```

heatmap_plus(x, addvar, covariate = NULL, picket.control = list(), h, clus,
             cluscol, cluslabel = NULL, Rowv, Colv, reorder = c(TRUE, TRUE),
             distfun = dist, hclustfun = hclust, scale = c("row", "column",
             "none"), na.rm = TRUE, do.dendro = TRUE, col = heat.colors(12),
             trim, equalize = FALSE, ...)

```

Arguments

x	the numerical data matrix to be displayed.
addvar	data frame with (mostly binary) covariates.
covariate	integer indicating the one column in addvar that is interval scaled.
picket.control	list of option for drawing the covariates, passed to picketplot.
h	height at which to cut the dendrogram, as in cutree; overrides clus.
clus	an explicit vector of cluster memberships for the columns of x, if no dendrogram is used; ignored if do.dendro=TRUE and h is specified.
cluscol	a vector of colors used to indicate clusters.
cluslabel	labels to designate cluster names.
Rowv	either a dendrogram or a vector of reordering indexes for the rows.
Colv	either a dendrogram or a vector of reordering indexes for the columns.
reorder	logical vector of length two, indicating whether the rows and columns (in this order) should be reordered using order.dendrogram.
distfun	function to compute the distances between rows and columns. Defaults to dist.
hclustfun	function used to cluster rows and columns. Defaults to hclust.
scale	indicates whether values should be scaled by either by row, column, or not at all. Defaults to row.
na.rm	logical indicating whther to remove NAs.
do.dendro	logical indicating whether to draw the column dendrogram.
col	the color scheme for image. The default sucks.

<code>trim</code>	Percentage of values to be trimmed. This helps to keep an informative color scale, see Details.
<code>equalize</code>	logical indicating whther to use the ranks of the data for setting the color scheme; alternative to <code>trim</code> , see Details.
<code>...</code>	extra arguments to <code>image</code> .

Details

This is a heavily modified version of `heatmap_2`, which is a heavily modified version of an old version of `heatmap` in package `stats`, so some of the arguments are described in more detail there. The main distinguishing feature of this routine is the possibility to color a cluster solution, and to add a covariate display.

Covariates are assumed to be binary, coded as 0 and 1 (or `FALSE` and `TRUE` respectively). One of the covariates can be interval scaled, the column index of this variable is supplied via argument `covariate`. The details of the added display are handled by the function `picketplot`.

Setting `trim` to a number between 0 and 1 uses equidistant classes between the (`trim`)- and (1-`trim`)-quantile, and lumps the values below and above this range into separate open-ended classes. If the data comes from a heavy-tailed distribution, this can save the display from putting too many values into to few classes. Alternatively, you can set `equal=TRUE`, which uses an equidistant color scheme for the ranks of the values.

Value

A list with components

<code>rowInd</code>	indices of the rows of the display in terms of the rows of <code>x</code> .
<code>colInd</code>	ditto for the columns of the display.
<code>clus</code>	the cluster indices of the columns of the display.

Author(s)

Original by Andy Liaw, with revisions by Robert Gentleman and Martin Maechler.

Alexander Ploner for the modifications documented here.

See Also

[heatmap_2](#), [heatmap](#), [picketplot](#), [cutplot.dendrogram](#), [RGBColVec](#)

Examples

```
# create data
mm = matrix(rnorm(1000, m=1), 100,10)
mm = cbind(mm, matrix(rnorm(2000), 100, 20))
mm = cbind(mm, matrix(rnorm(1500, m=-1), 100, 15))
mm2 = matrix(rnorm(450), 30, 15)
mm2 = cbind(mm2, matrix(rnorm(900,m=1.5), 30,30))
mm=rbind(mm, mm2)
colnames(mm) = paste("Sample", 1:45)
rownames(mm) = paste("Gene", 1:130)
addvar = data.frame(Var1=rep(c(0,1,0),c(10,20,15)),
                    Var2=rep(c(1,0,0),c(10,20,15)),
                    Var3=rep(c(1,0), c(15,30)),
                    Var4=rep(seq(0,1,length=4), c(10,5,15,15))+rnorm(45, sd=0.5))
```

```

addvar[3,3] = addvar[17,2] = addvar[34,1] =NA
colnames(addvar) = c("Variable X", "Variable Y", "ZZ", "Interval")

# the lame default, without clustering
# Labels do not look too hot that way
heatmap_plus(mm)

# without labels, but with cluster
dimnames(mm)=NULL
heatmap_plus(mm, h=40)

# add some covariates, with nice names
heatmap_plus(mm, addvar=addvar, cov=4)

# covariates and clustering
heatmap_plus(mm, addvar=addvar, cov=4, h=20, col=RGBColVec(64), equal=TRUE)

# Clustering without the dendrogram
cc = cutree(hclust(dist(t(mm))), k=5)
heatmap_plus(mm, addvar=addvar, cov=4, clus=cc, do.dendro=FALSE)

```

picketplot

Barplots for Several Binary Variables

Description

Display one or more binary variables by using black bars for presence/validity of a condition, empty space for absence/invalidity, and an extra color for missing values. Additionally, an index plot for one interval scaled variable can be added, possibly with a smoothing function.

This routine is primarily intended for augmenting heatmaps. It might be useful in other contexts, but misses most frills for using it comfortably.

Usage

```

picketplot(x, covariate = NULL, grp = NULL, grpcol, grplabel = NULL,
           add = FALSE, control = list())

```

Arguments

<code>x</code>	a matrix or data frame containing the data.
<code>covariate</code>	the index of the column in <code>x</code> that contains the interval scaled variable, if any.
<code>grp</code>	cluster indices for the rows of <code>x</code> , used for assigning background color.
<code>grpcol</code>	colors corresponding to the clusters.
<code>grplabel</code>	cluster names.
<code>add</code>	logical indicating whether to start a new plot, or whether to add the plot to the existing one.
<code>control</code>	a list of parameters controlling the appearance of the plot, see Details.

Details

The following named list elements can be set to change the appearance of the plot:

boxw the relative width of a marking box.

boxh the relative height of a marking box.

hbuff the horizontal separation around marking boxes; equals half the horizontal distance between two marking boxes.

vbuff ditto for vertical separation.

span passed on to `loess` used for the smoothing curve.

nacol color for missing values of binary variables.

degree if 0, no smoothing line is drawn; otherwise passed on to `loess` used for the smoothing curve.

cex.label the character size for `grplabel`.

Note

The plot looks like a more or less derelict picket fence, and 'picketplot' sounds somewhat like the 'pocketplot' used in geostatistics.

Author(s)

Alexander Ploner <Alexander.Ploner@ki.se>

See Also

[heatmap_plus](#)

Examples

```
# without covariate
mm = cbind(sample(0:1, 42, rep=TRUE), sample(0:1, 42, rep=TRUE))
mm[sample(42, 5), 1] = NA
picketplot(mm)
```

```
# with clustering
cl = rep(1:3, c(10,22,10))
cn = c("Cluster I", "Cluster II", "Cluster III")
cc = c("lightblue", "lightgreen", "lightpink") # windows palette
picketplot(mm, grp=cl, grplabel=cn, grpcol=cc)
```

```
# add a covariate; setting the colnames makes the variable labels
mm = cbind(mm, rnorm(42) + cl/2)
colnames(mm) = c("State A", "State B", "X")
picketplot(mm, covariate=3, grp=cl, grplabel=cn, grpcol=cc)
```

```
# using extra controls
picketplot(mm, covariate=3, grp=cl, grplabel=cn, grpcol=cc, control=list(nacol="white", de
```

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