visBoxplotAdv

July 22, 2015

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visBoxplotAdv	*Function to visualise a data frame using advanced boxplot*

Description

visBoxplotAdv is supposed to visualise a data frame using advanced boxplot. In addition to boxplot, a scatter plot is also drawn with various methods to avoid co-incident points so that each point is visible (with fine-controling the color and plotting character). Also, these points can be pies or thermometers, which allows an additional proportation data to be visualised as well.

Usage

```
visBoxplotAdv(formula, data, orientation = c("vertical", "horizontal"),
method = c("center", "hex", "square", "swarm"), corral = c("none",
"gutter", "wrap", "random", "omit"), corralWidth, cex = 1, spacing = 1,
breaks = NULL, labels, at = NULL, add = FALSE, log = FALSE,
xlim = NULL, ylim = NULL, xlab = NULL, ylab = NULL,
pch = c("circles", "thermometers", "pies")[1], col =
graphics::par("col"),
bg = NA, pwpch = NULL, pwcol = NULL, pwbg = NULL, pwpie = NULL,
do.plot = TRUE, do.boxplot = TRUE, boxplot.notch = FALSE,
boxplot.border = "#888888C0", boxplot.col = "transparent", ...)
```

Arguments

formula	a formula, such as 'y ~ grp', where 'y' is a numeric vector of data values to be split into groups according to the grouping variable 'grp' (usually a factor)
data	a data.frame (or list) from which the variables in 'formula' should be taken.
orientation	the orientation. It can be one of "vertical" for the vertical orientation, "horizontal" for the horizontal orientation
method	the method for arranging the points. It can be one of "swarm" for arranging points in increasing order (if a point would overlap an existing point, it is shifted sideways (along the group axis) by a minimal amount sufficient to avoid overlap), "center" for first discretizing the values along the data axis (in order to create more efficient packing) and then using a square grid to produce a symmetric swarm, "hex" for first discretization and then arranging points in a hexagonal grid, and "square" for first discretization and then arranging points in a square grid

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corral	the method to adjust points that would be placed outside their own group region. It can be one of "none" for not adjusting runaway points, "gutter" for collecting runaway points along the boundary between groups, "wrap" for wrapping runaway points to produce periodic boundaries, "random" for placing runaway points randomly in the region, and "omit" for omitting runaway points
corralWidth	the width of the "corral" in user coordinates
cex	size of points relative to the default. This must be a single value
spacing	relative spacing between points
breaks	breakpoints (optional). If NULL, breakpoints are chosen automatically
labels	labels for each group. Recycled if necessary. By default, these are inferred from the data
at	numeric vector giving the locations where the swarms should be drawn; defaults to '1:n' where n is the number of groups
add	whether to add to an existing plot
log	whether to use a logarithmic scale on the data axis
xlim	limits for x-axis
ylim	limits for y-axis
xlab	labels for x-aixs
ylab	labels for y-aixs
pch	plotting characters, specified by group and recycled if necessary. In additon to the convertional pch values, it can also be "circles", "thermometers", or "pies". For "pies" (or "thermometers"), users can also specify the proportional values (see below "pwpie") to visualise another information in the pie (or themometer) chart
col	plotting colors, specified by group and recycled if necessary
bg	plotting background, specified by group and recycled if necessary
pwpch	point-wise version of pch
pwcol	point-wise version of col
pwbg	point-wise version of bg
pwpie	point-wise proportion used when drawing pies or themometers
do.plot	whether to draw main plot
do.boxplot	whether to draw boxplot. It only works when the main plot is drawn
boxplot.notch	whether to draw a notch in the boxplot. If the notches of two plots do not overlap this is 'strong evidence' that the two medians differ
boxplot.border	the color for the outlines of the boxplots
boxplot.col	the color for the bodies of the boxplots
...	additional graphic parameters for the plot

Value

A data frame with plotting information. It has the same row names as the input data

Note

See Also

visBoxplotAdv

Examples

```
data(TCGA_mutations)
pd <- Biobase::pData(TCGA_mutations)
# only tumor types "LAML" or "BLCA"
data <- pd[pd$TCGA_tumor_type=="LAML" | pd$TCGA_tumor_type=="BLCA",]
labels <- levels(as.factor(data$TCGA_tumor_type))
# colors for gender
pwcol <- as.numeric((data$Gender))
# pie for relative age
pwpie <- data$Age/(max(data$Age))
out <- visBoxplotAdv(formula=time ~ TCGA_tumor_type, data=data,
pch="pies", pwcol=pwcol, pwpie=pwpie)
legend("topright", legend=levels(data$Gender), box.col="transparent",
pch=19, col=unique(pwcol))
```