Package ‘vioplot’

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Title Violin Plot
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Description A violin plot is a combination of a box plot and a kernel density plot. This package allows extensive customisation of violin plots.
Depends sm, zoo
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Violin Plot

Description

Produce violin plot(s) of the given (grouped) values with enhanced annotation and colour per group. Includes customisation of colours for each aspect of the violin, boxplot, and separate violins. This supports input of data as a list or formula, being backwards compatible with `vioplot` (0.2) and taking input in a formula as used for `boxplot`.

Interpreting the columns (or rows) of a matrix as different groups, draw a boxplot for each.

Usage

```r
## S3 method for class 'matrix'
vioplot(x, use.cols = TRUE, ...)

## S3 method for class 'list'
vioplot(x, ...)

## S3 method for class 'data.frame'
vioplot(x, ...)

## S3 method for class 'matrix'
vioplot(x, use.cols = TRUE, ...)

## S3 method for class 'formula'
vioplot(
  formula,
  data = NULL,
  ..., 
  subset,
  na.action = NULL,
  add = FALSE,
  ann = !add,
  horizontal = FALSE,
  side = "both",
  xlab = mklab(y_var = horizontal),
  ylab = mklab(y_var = !horizontal),
  names = NULL,
  drop = FALSE,
  sep = ".",
  lex.order = FALSE
)
```

## Default S3 method:
vioplot(
```
x,
..., data = NULL,
range = 1.5,
h = NULL,
xlim = NULL,
ylim = NULL,
names = NULL,
horizontal = FALSE,
col = "grey50",
border = par()$fg,
lty = 1,
lwd = 1,
rectCol = par()$fg,
lineCol = par()$fg,
pchMed = 19,
colMed = "white",
colMed2 = "grey 75",
at,
add = FALSE,
wex = 1,
drawRect = TRUE,
areaEqual = FALSE,
axes = TRUE,
frame.plot = axes,
panel.first = NULL,
panel.last = NULL,
asp = NA,
main = "",
sub = "",
xlab = NA,
ylab = NA,
line = NA,
outer = FALSE,
xlog = NA,
ylog = NA,
adj = NA,
ann = NA,
ask = NA,
bg = NA,
bty = NA,
cex = NA,
cex.axis = NA,
cex.lab = NA,
cex.main = NA,
cex.names = NULL,
cex.sub = NA,
cin = NA,
col.axis = NA,
col.lab = NA,
col.main = NA,
col.sub = NA,
cra = NA,
crt = NA,
csi = NA,
cxy = NA,
din = NA,
err = NA,
family = NA,
fg = NA,
fig = NA,
fin = NA,
font = NA,
font.axis = NA,
font.lab = NA,
font.main = NA,
font.sub = NA,
lab = NA,
las = NA,
lend = NA,
lheight = NA,
ljoin = NA,
lmitre = NA,
mai = NA,
mar = NA,
mex = NA,
mfcol = NA,
mfg = NA,
mfrow = NA,
mgp = NA,
mkh = NA,
new = NA,
oma = NA,
ord = NA,
omi = NA,
page = NA,
pch = NA,
pin = NA,
plt = NA,
ps = NA,
pty = NA,
smo = NA,
srt = NA,
tck = NA,
tcl = NA,
usr = NA,
Arguments

x | a numeric matrix.
...
use.cols | logical indicating if columns (by default) or rows (use.cols = FALSE) should be plotted.
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.
subset | an optional vector specifying a subset of observations to be used for plotting.
aา.action | a function which indicates what should happen when the data contain NAs. The default is to ignore missing values in either the response or the group.
add | logical. if FALSE (default) a new plot is created
horizontal | logical. To use horizontal or vertical violins. Note that log scale can only be used on the x-axis for horizontal violins, and on the y-axis otherwise.
side | defaults to "both". Assigning "left" or "right" enables one sided plotting of violins. May be applied as a scalar across all groups.
names | one label, or a vector of labels for the data must match the number of data given
drop, sep, lex.order | defines groups to plot from formula, passed to split.default, see there.
range | a factor to calculate the upper/lower adjacent values
h | the height for the density estimator, if omit as explained in sm.density, h will be set to an optimum
xlim, ylim | numeric vectors of length 2, giving the x and y coordinates ranges.
col | Graphical parameter for fill colour of the violin(s) polygon. NA for no fill colour. If col is a vector, it specifies the colour per violin, and colours are reused if necessary.
border

Graphical parameters for the colour of the violin border passed to lines. NA for no border. If border is a vector, it specifies the colour per violin, and colours are reused if necessary.

lty, lwd

Graphical parameters for the violin passed to lines and polygon

rectCol

Graphical parameters to control fill colour of the box. NA for no fill colour. If col is a vector, it specifies the colour per violin, and colours are reused if necessary.

lineCol

Graphical parameters to control colour of the box outline and whiskers. NA for no border. If lineCol is a vector, it specifies the colour per violin, and colours are reused if necessary.

pchMed

Graphical parameters to control shape of the median point. If pchMed is a vector, it specifies the shape per violin.

colMed, colMed2

Graphical parameters to control colour of the median point. If colMed is a vector, it specifies the colour per violin. colMed specifies the fill colour in all cases unless pchMed is 21:25 in which case colMed is the border colour and colMed2 is the fill colour.

at

position of each violin. Default to 1:n

wex

relative expansion of the violin. If wex is a vector, it specifies the area/width size per violin and sizes are reused if necessary.

drawRect

logical. The box is drawn if TRUE.

areaEqual

logical. Density plots checked for equal area if TRUE. wex must be scalar, relative widths of violins depend on area.

axes, frame.plot, panel.first, panel.last, asp, line, outer, adj, ann, ask, bg, bty, cin, col.axis, col.lab, col.main, ... mkh, new, oma, omd, omi, page, pch, pin, plt, ps, pty, smo, srt, tck, tcl, usr, xaxp, xaxs, xaxt, xpd, yaxp, yaxs, ylbias

Arguments to be passed to methods, such as graphical parameters (see par)).

main, sub, xlab, ylab

graphical parameters passed to plot.

ylog, xlog

A logical value (see log in plot.default). If ylog is TRUE, a logarithmic scale is in use (e.g., after plot(*, log = "y")). For horizontal = TRUE then, if xlog is TRUE, a logarithmic scale is in use (e.g., after plot(*, log = "x")). For a new device, it defaults to FALSE, i.e., linear scale.

cex

A numerical value giving the amount by which plotting text should be magnified relative to the default.

cex.axis

The magnification to be used for y axis annotation relative to the current setting of cex.

cex.lab

The magnification to be used for x and y labels relative to the current setting of cex.

cex.main

The magnification to be used for main titles relative to the current setting of cex.

cex.names

The magnification to be used for x axis annotation relative to the current setting of cex. Takes the value of cex.axis if not given.

cex.sub

The magnification to be used for sub-titles relative to the current setting of cex.

yaxt

A character which specifies the y axis type. Specifying "n" suppresses plotting.
log

Logarithmic scale if log = "y" or TRUE. Invokes ylog = TRUE. If horizontal is
TRUE then invokes xlog = TRUE.

logLab

Increments for labelling y-axis on log-scale, defaults to numbers starting with 1,
2, 5, and 10.

na.rm

logical value indicating whether NA values should be stripped before the com-
putation proceeds. Defaults to TRUE.

plotCentre

defaults to "points", plotting a central point at the median. If "line" is given a
median line is plotted (subject to side) alternatively.

Examples

# box- vs violin-plot
par(mfrow=c(2,1))
mu<-2
si<-.6
bimodal<-c(rnorm(1000,-mu,si),rnorm(1000,mu,si))
uniform<-runif(2000,-4,4)
normal<-rnorm(2000,0,3)
vioplot(bimodal,uniform,normal)
boxplot(bimodal,uniform,normal)

# add to an existing plot
x <- rnorm(100)
y <- rnorm(100)
plot(x, y, xlim=c(-5,5), ylim=c(-5,5))
vioplot(x, col="tomato", horizontal=TRUE, at=-4, add=TRUE,lty=2, rectCol="gray")
vioplot(y, col="cyan", horizontal=FALSE, at=-4, add=TRUE,lty=2)

# formula input
data("iris")
vioplot(Sepal.Length~Species, data = iris, main = "Sepal Length",
col=c("lightgreen", "lightblue", "palevioletred"))
legend("topleft", legend=c("setosa", "versicolor", "virginica"),
fill=c("lightgreen", "lightblue", "palevioletred"), cex = 0.5)
data("diamonds", package = "ggplot2")
palette <- RColorBrewer::brewer.pal(9, "Pastel1")
par(mfrow=c(3, 1))
vioplot(price ~ cut, data = diamonds, las = 1, col = palette)
vioplot(price ~ clarity, data = diamonds, las = 2, col = palette)
vioplot(price ~ color, data = diamonds, las = 2, col = palette)
par(mfrow=c(3, 1))

#generate example data
data_one <- rnorm(100)
data_two <- rnorm(50, 1, 2)

#generate violin plot with similar functionality to vioplot
vioplot(data_one, data_two, col="magenta")
#note vioplox defaults to a greyscale plot
vioplot(data_one, data_two)

#colours can be customised separately, with axis labels, legends, and titles
vioplot(data_one, data_two, col=c("red", "blue"), names=c("data one", "data two"),
main="data violin", xlab="data class", ylab="data read")
legend("topleft", fill=c("red", "blue"), legend=c("data one", "data two"))

#colours can be customised for the violin fill and border separately
vioplot(data_one, data_two, col="grey85", border="purple", names=c("data one", "data two"),
main="data violin", xlab="data class", ylab="data read")

#colours can also be customised for the boxplot rectangle and lines (border and whiskers)
vioplot(data_one, data_two, col="grey85", rectCol="lightblue", lineCol="blue",
border="purple", names=c("data one", "data two"),
main="data violin", xlab="data class", ylab="data read")

#these colours can also be customised separately for each violin
vioplot(data_one, data_two, col=c("skyblue", "plum"), rectCol=c("lightblue", "palevioletred"),
lineCol="blue", border=c("royalblue", "purple"), names=c("data one", "data two"),
main="data violin", xlab="data class", ylab="data read")

#this applies to any number of violins, given that colours are provided for each
vioplot(data_one, data_two, rnorm(200, 3, 0.5), rpois(200, 2.5), rbinom(100, 10, 0.4),
col=c("red", "orange", "green", "blue", "violet"),
rectCol=c("palevioletred", "peachpuff", "lightgreen", "lightblue", "plum"),
lineCol=c("red4", "orangered", "forestgreen", "royalblue", "mediumorchid"),
border=c("red4", "orangered", "forestgreen", "royalblue", "mediumorchid"),
names=c("data one", "data two", "data three", "data four", "data five"),
main="data violin", xlab="data class", ylab="data read")

#The areaEqual parameter scales with width of violins
#Violins will have equal density area (including missing tails) rather than equal maximum width
vioplot(data_one, data_two, areaEqual=TRUE)

vioplot(data_one, data_two, areaEqual=TRUE,
col=c("skyblue", "plum"), rectCol=c("lightblue", "palevioletred"),
lineCol="blue", border=c("royalblue", "purple"), names=c("data one", "data two"),
main="data violin", xlab="data class", ylab="data read")

vioplot(data_one, data_two, rnorm(200, 3, 0.5), rpois(200, 2.5), rbinom(100, 10, 0.4),
areaEqual=TRUE, col=c("red", "orange", "green", "blue", "violet"),
rectCol=c("palevioletred", "peachpuff", "lightgreen", "lightblue", "plum"),
lineCol=c("red4", "orangered", "forestgreen", "royalblue", "mediumorchid"),
border=c("red4", "orangered", "forestgreen", "royalblue", "mediumorchid"),
names=c("data one", "data two", "data three", "data four", "data five"),
main="data violin", xlab="data class", ylab="data read")

---

vioplot.stats

Violin Plot Statistics
vioplot.stats

Description

This function is typically called by another function to gather the statistics necessary for producing box plots, but may be invoked separately. See: boxplot.stats

Usage

```r
## S3 method for class 'stats'
vioplot(x, coef = 1.5, do.conf = TRUE, do.out = TRUE, ...)
```

Arguments

- `x` : a numeric vector for which the violin plot will be constructed (NAs and NaNs are allowed and omitted).
- `coef` : this determines how far the plot ‘whiskers’ extend out from the box. If coef is positive, the whiskers extend to the most extreme data point which is no more than coef times the length of the box away from the box. A value of zero causes the whiskers to extend to the data extremes (and no outliers be returned).
- `do.conf, do.out` : logicals; if FALSE, the conf or out component respectively will be empty in the result.
- `...` : arguments passed to `vioplot`.
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