

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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URL <https://github.com/TomKellyGenetics/vioplot>

BugReports <https://github.com/TomKellyGenetics/vioplot/issues>

RoxygenNote 7.3.2

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add_labels	<i>Annotated Violin Plot</i>
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Description

Annotate violin plots with custom labels

Usage

```
add_labels(variable, categories, cex = par()$cex, col = par()$fg, height = 0.5)
```

Arguments

variable	continuous variable to plot on y-axis (numeric or integer)
categories	discrete variable to break down groups (factor or string).
cex	size of text.
col	colour of text
height	adjust placement of text.

Examples

```
# box- vs violin-plot
par(mfrow=c(2,1))
mu<-2
si<-0.6
bimodal<-c(rnorm(1000,-mu,si),rnorm(1000,mu,si))
uniform<-runif(2000,-4,4)
normal<-rnorm(2000,0,3)

# annotate a violin plot
group <- rep(c("bimodal", "uniform", "normal"),
            sapply(list(bimodal, uniform, normal), length))
table(group)
vioplot(bimodal,uniform,normal)
add_labels(c(bimodal,uniform,normal), group, height = -2.5, cex = 0.8)

# boxplots are also supported
boxplot(bimodal,uniform,normal)
add_labels(c(bimodal,uniform,normal), group, height = -2.5, cex = 0.8)

# formula input
data("iris")
vioplot(Sepal.Length~Species, data = iris, main = "Sepal Length",
        col=c("lightgreen", "lightblue", "palevioletred"))
legend("bottomright", legend=c("setosa", "versicolor", "virginica"),
      fill=c("lightgreen", "lightblue", "palevioletred"), cex = 0.6)
```

```

add_labels(unlist(iris$Sepal.Length), iris$Species, height = 0, cex = 0.8)

# demo with outliers
iris2 <- iris
iris2 <- rbind(iris2, c(7, 0, 0, 0, "setosa"))
iris2 <- rbind(iris2, c(0, 0, 0, 0, "setosa"))
iris2 <- rbind(iris2, c(9, 0, 0, 0, "versicolor"))
iris2 <- rbind(iris2, c(2, 0, 0, 0, "versicolor"))
iris2 <- rbind(iris2, c(10, 0, 0, 0, "virginica"))
iris2 <- rbind(iris2, c(12, 0, 0, 0, "virginica"))
iris2$Species <- factor(iris2$Species)
iris2$Sepal.Length <- as.numeric(iris2$Sepal.Length)

vioplot(Sepal.Length~Species, data = iris2, main = "Sepal Length",
        col=c("lightgreen", "lightblue", "palevioletred"))
add_outliers(unlist(iris2$Sepal.Length), iris2$Species,
            col = "grey50", fill = "red", bars = "grey85")
legend("bottomright", legend=c("setosa", "versicolor", "virginica"),
      fill=c("lightgreen", "lightblue", "palevioletred"), cex = 0.6)
add_labels(unlist(iris2$Sepal.Length), iris2$Species, height = 0, cex = 0.8)

```

add_outliers

Annotated Violin Plot

Description

Annotation to highlight outliers.

Usage

```

add_outliers(variable, categories, cutoff = 3,
            fill = par()$bg, col = par()$fg, bars = par()$fg, lwd = par()$lwd,
            verbose = FALSE)

```

Arguments

variable	continuous variable to plot on y-axis (numeric or integer).
categories	discrete variable to break down groups (factor or string).
cutoff	minimum number (default 3L) of standard deviations to report.
fill	colour of spots. Scalar applied to all columns or a vector for each category.
col	colour of rings or borders. Scalar applied to all columns or a vector for each category.
bars	colour of horizontal bars. Scalar applied to all columns or a vector for each category.
lwd	thickness of border.
verbose	to print logs (defaults to FALSE).

Details

Annotate violin plots with outliers

histoplot

histoplot

Description

Produce histogram plot(s) of the given (grouped) values with enhanced annotation and colour per group. Includes customisation of colours for each aspect of the histogram, boxplot, and separate histograms. This supports input of data as a list or formula, being backwards compatible with [histoplot](#) (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

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

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

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

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

## S3 method for class 'formula'
histoplot(
  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:
histplot(
  x,
  ...,
  data = NULL,
  breaks = "Sturges",
  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,  
omd = 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,
    xaxp = NA,
    xaxs = NA,
    xaxt = NA,
    xpd = NA,
    yaxp = NA,
    yaxs = NA,
    yaxt = NA,
    ylbias = NA,
    log = "",
    logLab = c(1, 2, 5),
    na.action = NULL,
    na.rm = T,
    side = "both"
)

```

Arguments

<code>x</code>	a numeric matrix.
<code>...</code>	Further arguments to histplot .
<code>use.cols</code>	logical indicating if columns (by default) or rows (<code>use.cols = FALSE</code>) should be plotted.
<code>formula</code>	a formula, such as <code>y ~ grp</code> , where <code>y</code> is a numeric vector of data values to be split into groups according to the grouping variable <code>grp</code> (usually a factor).
<code>data</code>	a data.frame (or list) from which the variables in formula should be taken.
<code>subset</code>	an optional vector specifying a subset of observations to be used for plotting.
<code>na.action</code>	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.
<code>add</code>	logical. if <code>FALSE</code> (default) a new plot is created
<code>horizontal</code>	logical. To use horizontal or vertical histograms. Note that log scale can only be used on the x-axis for horizontal histograms, and on the y-axis otherwise.
<code>side</code>	defaults to "both". Assigning "left" or "right" enables one sided plotting of histograms. May be applied as a scalar across all groups.
<code>names</code>	one label, or a vector of labels for the data must match the number of data given
<code>drop, sep, lex.order</code>	defines groups to plot from formula, passed to <code>split.default</code> , see there.
<code>breaks</code>	the breaks for the density estimator, as explained in <code>hist</code>
<code>xlim, ylim</code>	numeric vectors of length 2, giving the x and y coordinates ranges.
<code>col</code>	Graphical parameter for fill colour of the histogram(s) polygon. NA for no fill colour. If <code>col</code> is a vector, it specifies the colour per histogram, and colours are reused if necessary.
<code>border</code>	Graphical parameters for the colour of the histogram border passed to <code>lines</code> . NA for no border. If <code>border</code> is a vector, it specifies the colour per histogram, and colours are reused if necessary.

lty, lwd	Graphical parameters for the histogram 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 histogram, 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 histogram, 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 histogram.
colMed, colMed2	Graphical parameters to control colour of the median point. If colMed is a vector, it specifies the colour per histogram. 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 histogram. Default to 1:n
wex	relative expansion of the histogram. If wex is a vector, it specifies the area/width size per histogram 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 histograms 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, col.sub, cra, crt, csi, cxy, din, err, family, fg, fig, fin, font, font.axis, font.lab, font.main, font.sub, lab, las, lend, lheight, ljoin, lmitre, mai, mar, mex, mfcoll, mfg, mfrow, mgp, 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 <code>plot(*, log = "y")</code>). For horizontal = TRUE then, if xlog is TRUE, a logarithmic scale is in use (e.g., after <code>plot(*, log = "x")</code>). 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 computation proceeds. Defaults to TRUE.

Examples

```
# box- vs histogram-plot
par(mfrow=c(2,1))
mu<-2
si<-0.6
bimodal<-c(rnorm(1000,-mu,si),rnorm(1000,mu,si))
uniform<-runif(2000,-4,4)
normal<-rnorm(2000,0,3)
histoplot(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))
histoplot(x, col="tomato", horizontal=TRUE, at=-4, add=TRUE,lty=2, rectCol="gray")
histoplot(y, col="cyan", horizontal=FALSE, at=-4, add=TRUE,lty=2)

# formula input
data("iris")
histoplot(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))
histoplot(price ~ cut, data = diamonds, las = 1, col = palette)
histoplot(price ~ clarity, data = diamonds, las = 2, col = palette)
histoplot(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 histogram plot with similar functionality to histoplot
histoplot(data_one, data_two, col="magenta")

#note vioplox defaults to a greyscale plot
histoplot(data_one, data_two)

#colours can be customised separately, with axis labels, legends, and titles
```

```

histplot(data_one, data_two, col=c("red","blue"), names=c("data one", "data two"),
  main="data histogram", xlab="data class", ylab="data read")
legend("topleft", fill=c("red","blue"), legend=c("data one", "data two"))

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

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

#these colours can also be customised separately for each histogram
histplot(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 histogram", xlab="data class", ylab="data read")

#this applies to any number of histograms, given that colours are provided for each
histplot(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 histogram", xlab="data class", ylab="data read")

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

histplot(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 histogram", xlab="data class", ylab="data read")

histplot(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 histogram", xlab="data class", ylab="data read")

#To compare multiple groups of histogram densities, it helps to adjust the wex.

dlist1 <- lapply(c(10,20,30,40), function(n) runif(n))
dlist2 <- lapply(c(100,200,300,400), function(n) runif(n))

hscale1 <- sapply(dlist1, function(r){
  max(hist(r, plot=FALSE, breaks=seq(0,1,by=.05))$density)})
histplot(dlist1, side='left', col=grey(.3),
  breaks=seq(0,1,by=.05), add=FALSE, pchMed=NA, drawRect=FALSE, border=NA,

```

```

wex=hscale1/length(hscale1))

hscale2 <- sapply(dlist2, function(r){
  max(hist(r, plot=FALSE, breaks=seq(0,1,by=.05))$density)})
histoplot(dlist2, side='right', col=grey(.7),
  breaks=seq(0,1,by=.05), add=TRUE, pchMed=NA, drawRect=FALSE, border=NA,
  wex=hscale2/length(hscale2))

#Sometimes, it is helpful to see the raw counts instead.

dvec <- length(unlist(c(dlist1, dlist2)))/4

histoplot(dlist1, side='left', col=grey(.3),
  breaks=seq(0,1,by=.05), add=FALSE, pchMed=NA, drawRect=FALSE, border=NA,
  wex=sapply(dlist1, length)/dvec*hscale1/length(hscale1))
histoplot(dlist2, side='right', col=grey(.7),
  breaks=seq(0,1,by=.05), add=TRUE, pchMed=NA, drawRect=FALSE, border=NA,
  wex=sapply(dlist2, length)/dvec*hscale2/length(hscale2))

#It may also benefit some users to pass density and angle arguments to the
# histograms (ultimately rect) and create outer legends

hist(runif(100), density=c(10,20), angle=c(22,90+22) ,col=1)

outer_legend <- function(...) {
  opar <- par(fig=c(0, 1, 0, 1), oma=c(0, 0, 0, 0), mar=c(0, 0, 0, 0), new=TRUE)
  on.exit(par(opar))
  plot(0, 0, type='n', bty='n', xaxt='n', yaxt='n')
  legend(...)
}
outer_legend('topright', pch=15, density=c(10,20), angle=c(22,90+22), col=0, legend=c('Y', 'N'))

```

vioplot

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

```
## 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",
  cex.axis = par()$cex,
  srt.axis = c(0, 90),
  xlab = mklab(y_var = horizontal),
  ylab = mklab(y_var = !horizontal),
  main = "",
  sub = "",
  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 = 1,  
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,  
omd = NA,  
omi = NA,  
page = NA,  
pch = NA,  
pin = NA,  
plt = NA,  
ps = NA,  
pty = NA,  
smo = NA,  
srt = NA,  
srt.axis = c(0, 90),  
tck = NA,  
tcl = NA,  
usr = NA,  
xaxp = NA,  
xaxs = NA,  
xaxt = NA,  
xpd = NA,  
yaxp = NA,  
yaxs = NA,  
yaxt = NA,  
ylbias = NA,  
log = "",  
logLab = c(1, 2, 5),  
na.action = NULL,  
na.rm = T,  
side = "both",
```

```

    plotCentre = "point"
  )

```

Arguments

x	a numeric matrix.
...	Further arguments to <code>vioplot</code> .
use.cols	logical indicating if columns (by default) or rows (<code>use.cols = FALSE</code>) should be plotted.
formula	a formula, such as <code>y ~ grp</code> , where <code>y</code> is a numeric vector of data values to be split into groups according to the grouping variable <code>grp</code> (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.
na.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 <code>FALSE</code> (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.
cex.axis	The magnification to be used for y axis annotation relative to the current setting of <code>cex</code> .
srt.axis	angle for axis labels, scalar applies to both axes or vector with 2 components. <code>[x, y]</code> defaults to <code>c(0, 90)</code> with angles counter-clockwise from vertical.
main, sub, xlab, ylab	graphical parameters passed to plot.
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 <code>split.default</code> , see there.
range	a factor to calculate the upper/lower adjacent values
h	the height for the density estimator, if omit as explained in <code>sm.density</code> , <code>h</code> will be set to an optimum. A vector of length one, two or three, defining the smoothing parameter. A normal kernel function is used and <code>h</code> is its standard deviation. If this parameter is omitted, a normal optimal smoothing parameter is used.
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. <code>NA</code> for no fill colour. If <code>col</code> 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. <code>NA</code> for no border. If <code>border</code> 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, col.sub, cra, crt, csi, cxy, din, err, family, fg, fig, fin, font, font.axis, font.lab, font.main, font.sub, lab, las, lend, lheight, ljoin, lmitre, mai, mar, mex, mfc, mfg, mfrow, mgp, 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).
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.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 computation 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<-0.6
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 vioplot 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

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

```

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

```

Arguments

<code>x</code>	a numeric vector for which the violin plot will be constructed (NAs and NaNs are allowed and omitted).
<code>coef</code>	this determines how far the plot ‘whiskers’ extend out from the box. If <code>coef</code> is positive, the whiskers extend to the most extreme data point which is no more than <code>coef</code> 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).
<code>do.conf</code> , <code>do.out</code>	logicals; if FALSE, the <code>conf</code> or <code>out</code> component respectively will be empty in the result.
<code>...</code>	arguments passed to vioplot .

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