

# Package ‘gplots’

January 27, 2019

**Title** Various R Programming Tools for Plotting Data

**Description** Various R programming tools for plotting data, including:

- calculating and plotting locally smoothed summary function as ('bandplot', 'wapply'),
- enhanced versions of standard plots ('barplot2', 'boxplot2', 'heatmap.2', 'smartlegend'),
- manipulating colors ('col2hex', 'colorpanel', 'redgreen', 'greenred', 'bluered', 'redblue', 'rich.colors'),
- calculating and plotting two-dimensional data summaries ('ci2d', 'hist2d'),
- enhanced regression diagnostic plots ('lplot2', 'residplot'),
- formula-enabled interface to 'stats::lowess' function ('lowess'),
- displaying textual data in plots ('textplot', 'sinkplot'),
- plotting a matrix where each cell contains a dot whose size reflects the relative magnitude of the elements ('balloonplot'),
- plotting ``Venn" diagrams ('venn'),
- displaying Open-Office style plots ('ooplot'),
- plotting multiple data on same region, with separate axes ('overplot'),
- plotting means and confidence intervals ('plotCI', 'plotmeans'),
- spacing points in an x-y plot so they don't overlap ('space').

**Depends** R (>= 3.0)

**Imports** gtools, gdata, stats, caTools, KernSmooth

**Suggests** grid, MASS

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angleAxis

*Add a Axis to a Plot with Rotated Labels*

---

### Description

Add a labeled axis to the current plot with rotated text

### Usage

```
angleAxis(side, labels, at = 1:length(labels), srt = 45, adj, xpd = TRUE, ...)
```

**Arguments**

side	an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
labels	character or expression vector of labels to be placed at the tickpoints.
at	the points at which tick-marks are to be drawn. Non-finite (infinite, NaN or NA) values are omitted.
srt	The string rotation in degrees. Defaults to 45 degrees (clockwise).
adj	Text justification. A value of 0 produces left-justified text, 0.5 centered text and 1 right-justified text. For side=1 and side=2, the default value is adj=1. For side=3 and side=4 the default value is adj=0.
xpd	A logical value or NA. If FALSE, labels are clipped to the plot region, if TRUE, labels are clipped to the figure region, and if NA, labels are clipped to the device region.
...	optional arguments passed to text. Common examples are col, cex.

**Details**

This function augments the feature of the `axis` function by allowing the axis labels to be rotated.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

[axis](#)

**Examples**

```
# create a vector with some values and long labels
values <- sample(1:10)
names(values) <- sapply(letters[1:10],
                        function(x) paste(rep(x, 10), sep="", collapse=""))
)

# barplot labels are too long for the available space, hence some are not plotted
barplot(values)

# to add angled labels, tell barplot not to label the x axis, and store the bar location
at <- barplot(values, xaxt="n")
# then use angleAxis
angleAxis(1, at=at, labels = names(values))

# angle counter-clockwise instead
at <- barplot(values, xaxt="n")
angleAxis(1, at=at, labels = names(values), srt=-45, adj=0)

# put labels at the top
```

```

oldpar <- par()$mar
par(mar=c(1,4,5,2)+0.1)
at <- barplot(values, xaxt="n")
angleAxis(3, at=at, labels = names(values))
par(oldpar)

# put labels on the left
oldpar <- par()$mar
par(mar=c(5,5,3,2)+0.1)
at <- barplot(values, yaxt="n", horiz=TRUE)
angleAxis(2, at=at, labels = names(values))
par(oldpar)

# put labels on the right
oldpar <- par()$mar
par(mar=c(2,5,3,5)+0.1)
at <- barplot(values, yaxt="n", horiz=TRUE)
angleAxis(4, at=at, labels = names(values))
par(oldpar)

# specify colors for bars and labels
at <- barplot(values, xaxt="n", col=1:10)
angleAxis(1, at=at, labels = names(values), col=1:10)

```

---

balloonplot

*Plot a graphical matrix where each cell contains a dot whose size reflects the relative magnitude of the corresponding component.*

---

### Description

Plot a graphical matrix where each cell contains a dot whose size reflects the relative magnitude of the corresponding component.

### Usage

```

balloonplot(x, ...)
## S3 method for class 'table'
balloonplot(x, xlab, ylab, zlab, show.zeros=FALSE, show.margins=TRUE, ...)
## Default S3 method:
balloonplot(x,y,z,
            xlab,
            ylab,
            zlab=deparse(substitute(z)),
            dotsize=2/max(strwidth(19),strheight(19)),
            dotchar=19,
            dotcolor="skyblue",
            text.size=1,
            text.color=par("fg"),
            main,

```

```

label=TRUE,
label.digits=2,
label.size=1,
label.color=par("fg"),
scale.method=c("volume","diameter"),
scale.range=c("absolute","relative"),
colsrt=par("srt"),
rowsrt=par("srt"),
colmar=1,
rowmar=2,
show.zeros=FALSE,
show.margins=TRUE,
cum.margins=TRUE,
sorted=TRUE,
label.lines=TRUE,
fun=function(x)sum(x,na.rm=T),
hide.duplicates=TRUE,
... )

```

### Arguments

x	A table object, or either a vector or a list of several categorical vectors containing grouping variables for the first (x) margin of the plotted matrix.
y	Vector or list of vectors for grouping variables for the second (y) dimension of the plotted matrix.
z	Vector of values for the size of the dots in the plotted matrix.
xlab	Text label for the x dimension. This will be displayed on the x axis and in the plot title.
ylab	Text label for the y dimension. This will be displayed on the y axis and in the plot title.
zlab	Text label for the dot size. This will be included in the plot title.
dotsize	Maximum dot size. You may need to adjust this value for different plot devices and layouts.
dotchar	Plotting symbol or character used for dots. See the help page for the points function for symbol codes.
dotcolor	Scalar or vector specifying the color(s) of the dots in the plot.
text.size, text.color	Character size and color for row and column headers
main	Plot title text.
label	Boolean flag indicating whether the actual value of the elements should be shown on the plot.
label.digits	Number of digits used in formatting value labels.
label.size, label.color	Character size and color for value labels.
scale.method	Method of scaling the sizes of the dot, either "volume" or "diameter". See below.

<code>scale.range</code>	Method for scaling original data to compute circle diameter. <code>scale.range="absolute"</code> scales the data relative to 0 (i.e. maps $[0, \max(z)] \rightarrow [0, 1]$ ), while <code>scale.range="relative"</code> scales the data relative to $\min(z)$ (i.e. maps $[\min(z), \max(z)] \rightarrow [0, 1]$ ).
<code>rowsrt</code> , <code>colsrt</code>	Angle of rotation for row and column labels.
<code>rowmar</code> , <code>colmar</code>	Space allocated for row and column labels. Each unit is the width/height of one cell in the table.
<code>show.zeros</code>	boolean. If FALSE, entries containing zero will be left blank in the plotted matrix. If TRUE, zeros will be displayed.
<code>show.margins</code>	boolean. If TRUE, row and column sums are printed in the bottom and right margins, respectively.
<code>cum.margins</code>	boolean. If TRUE, marginal fractions are graphically presented in grey behind the row/column label area.
<code>sorted</code>	boolean. If TRUE, the rows will be arranged in sorted order by using the levels of the first y factor, then the second y factor, etc. The same process is used for the columns, based on the x factors
<code>label.lines</code>	boolean. If TRUE, borders will be drawn for row and column level headers.
<code>hide.duplicates</code>	boolean. If TRUE, column and row headers will omit duplicates within row/column to reduce clutter. Defaults to TRUE.
<code>fun</code>	function to be used to combine data elements with the same levels of the grouping variables x and y. Defaults to sum
<code>...</code>	Additional arguments passed to <code>balloonplot.default</code> or <code>plot</code> , as appropriate.

### Details

This function plots a visual matrix. In each x,y cell a dot is plotted which reflects the relative size of the corresponding value of z. When `scale.method="volume"` the volume of the dot is proportional to the relative size of z. When `scale.method="diameter"`, the diameter of the dot is proportional to the the relative size of z. The "volume" method is default because the "diameter" method visually exaggerates differences.

### Value

Nothing of interest.

### Note

z is expected to be non-negative. The function will still operate correctly if there are negative values of z, but the corresponding dots will have 0 size and a warning will be generated.

### Author(s)

Gregory R. Warnes <greg@warnes.net>

### References

Function inspired by question posed on R-help by Ramon Alonso-Allende <allende@cnb.uam.es>.

**See Also**[plot.table](#)**Examples**

```

# Create an Example Data Frame Containing Car x Color data
carnames <- c("bmw","renault","mercedes","seat")
carcolors <- c("red","white","silver","green")
datavals <- round(rnorm(16, mean=100, sd=60),1)
data <- data.frame(Car=rep(carnames,4),
                  Color=rep(carcolors, c(4,4,4,4) ),
                  Value=datavals )

# show the data
data

# generate balloon plot with default scaling
balloonplot( data$Car, data$Color, data$Value)

# show margin label rotation & space expansion, using some long labels
levels(data$Car) <- c("BMW: High End, German","Renault: Medium End, French",
                    "Mercedes: High End, German", "Seat: Imaginary, Unknown Producer")

# generate balloon plot with default scaling
balloonplot( data$Car, data$Color, data$Value, colmar=3, colsrt=90)

# Create an example using table
xnames <- sample( letters[1:3], 50, replace=2)
ynames <- sample( 1:5, 50, replace=2)

tab <- table(xnames, ynames)

balloonplot(tab)

# Example of multiple classification variabls using the Titanic data
library(datasets)
data(Titanic)

dframe <- as.data.frame(Titanic) # convert to 1 entry per row format
attach(dframe)
balloonplot(x=Class, y=list(Survived, Age, Sex), z=Freq, sort=TRUE)

# colorize: surviors lightblue, non-survivors: grey
Colors <- Titanic
Colors[,,"Yes"] <- "skyblue"
Colors[,,"No"] <- "grey"
colors <- as.character(as.data.frame(Colors)$Freq)

balloonplot(x=list(Age,Sex),
            y=list(Class=Class,

```

```

Survived=gdata::reorder.factor(Survived,new.order=c(2,1))
),
z=Freq,
zlab="Number of Passengers",
sort=TRUE,
dotcol = colors,
show.zeros=TRUE,
show.margins=TRUE)

```

---

bandplot

*Plot x-y Points with Locally Smoothed Mean and Standard Deviation*


---

## Description

Plot x-y points with curves for locally smoothed mean and standard deviation.

## Usage

```

bandplot(x,...)
## S3 method for class 'formula'
bandplot(x, data, subset, na.action, ...,
         xlab=NULL, ylab=NULL, add = FALSE, sd = c(-2:2),
         sd.col=c("magenta", "blue", "red", "blue", "magenta"),
         sd.lwd=c(2, 2, 3, 2, 2), sd.lty=c(2, 1, 1, 1, 2),
         method = "frac", width = 1/5, n=50)
## Default S3 method:
bandplot(x, y, ..., add = FALSE, sd = c(-2:2),
         sd.col=c("magenta", "blue", "red", "blue", "magenta"),
         sd.lwd=c(2, 2, 3, 2, 2), sd.lty=c(2, 1, 1, 1, 2),
         method = "frac", width = 1/5, n=50)

```

## Arguments

x	either formula providing a single dependent variable (y) and an single independent variable (x) to use as coordinates in the scatter plot or a numeric vector of x locations
y	numeric vector of y locations
data	an optional data.frame, list, or environment containing the variables used in the model (and in subset). If not found in data, the variables are taken from environment(formula), typically the environment from which lm is called.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The factory-fresh default is na.omit. Another possible value is NULL, no action. Value na.exclude can be useful.



...	Additional plotting parameters
xlab, ylab	x and y axis labels
add	Boolean indicating whether the local mean and standard deviation lines should be added to an existing plot. Defaults to FALSE.
sd	Vector of multiples of the standard deviation that should be plotted. 0 gives the mean, -1 gives the mean minus one standard deviation, etc. Defaults to -2:2.
sd.col, sd.lwd, sd.lty	Color, line width, and line type of each plotted line.
method, width, n	Parameters controlling the smoothing. See the help page for <a href="#">wapply</a> for details.

### Details

bandplot was created to look for changes in the mean or variance of scatter plots, particularly plots of regression residuals.

The local mean and standard deviation are calculated by calling 'wapply'. By default, bandplot asks wapply to smooth using intervals that include the nearest 1/5 of the data. See the documentation of that function for details on the algorithm.

### Value

Invisibly returns a list containing the x,y points plotted for each line.

### Author(s)

Gregory R. Warnes <greg@warnes.net>

### See Also

[wapply](#), [lowess](#)

### Examples

```
# fixed mean, changing variance
x <- 1:1000
y <- rnorm(1000, mean=1, sd=1 + x/1000 )
bandplot(x,y)
bandplot(y~x)

# fixed variance, changing mean
x <- 1:1000
y <- rnorm(1000, mean=x/1000, sd=1)
bandplot(x,y)

#
# changing mean and variance
#
x <- abs(rnorm(500))
```

```

y <- rnorm(500, mean=2*x, sd=2+2*x)

# the changing mean and dispersion are hard to see with the points alone:
plot(x,y )

# regression picks up the mean trend, but not the change in variance
reg <- lm(y~x)
summary(reg)
abline(reg=reg, col="blue", lwd=2)

# using bandplot on the original data helps to show the mean and
# variance trend
bandplot(y ~ x)

# using bandplot on the residuals helps to see that regression removes
# the mean trend but leaves the trend in variability
bandplot(predict(reg),resid(reg))

```

---

barplot2

*Enhanced Bar Plots*


---

## Description

An enhancement of the standard `barplot()` function. Creates a bar plot with vertical or horizontal bars. Can plot confidence intervals for each bar, a lined grid behind the bars, change plot area color and logarithmic axes may be used.

## Usage

```

## Default S3 method:
barplot2(height, width = 1, space = NULL,
          names.arg = NULL, legend.text = NULL, beside = FALSE,
          horiz = FALSE, density = NULL, angle = 45,
          col = NULL, pcol = NULL, border = par("fg"),
          main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
          xlim = NULL, ylim = NULL, xpd = TRUE, log = "",
          axes = TRUE, axisnames = TRUE,
          cex.axis = par("cex.axis"), cex.names = par("cex.axis"),
          inside = TRUE, plot = TRUE, axis.lty = 0, offset = 0,
          plot.ci = FALSE, ci.l = NULL, ci.u = NULL,
          ci.color = "black", ci.lty = "solid", ci.lwd = 1, ci.width = 0.5,
          plot.grid = FALSE, grid.inc = NULL,
          grid.lty = "dotted", grid.lwd = 1, grid.col = "black",
          add = FALSE, panel.first = NULL, panel.last = NULL, ...)

```

**Arguments**

height	either a vector or matrix of values describing the bars which make up the plot. If height is a vector, the plot consists of a sequence of rectangular bars with heights given by the values in the vector. If height is a matrix and beside is FALSE then each bar of the plot corresponds to a column of height, with the values in the column giving the heights of stacked “sub-bars” making up the bar. If height is a matrix and beside is TRUE, then the values in each column are juxtaposed rather than stacked.
width	optional vector of bar widths. Re-cycled to length the number of bars drawn. Specifying a single value will no visible effect unless xlim is specified.
space	the amount of space (as a fraction of the average bar width) left before each bar. May be given as a single number or one number per bar. If height is a matrix and beside is TRUE, space may be specified by two numbers, where the first is the space between bars in the same group, and the second the space between the groups. If not given explicitly, it defaults to $c(0, 1)$ if height is a matrix and beside is TRUE, and to 0.2 otherwise.
names.arg	a vector of names to be plotted below each bar or group of bars. If this argument is omitted, then the names are taken from the names attribute of height if this is a vector, or the column names if it is a matrix.
legend.text	a vector of text used to construct a legend for the plot, or a logical indicating whether a legend should be included. This is only useful when height is a matrix. In that case given legend labels should correspond to the rows of height; if legend.text is true, the row names of height will be used as labels if they are non-null.
beside	a logical value. If FALSE, the columns of height are portrayed as stacked bars, and if TRUE the columns are portrayed as juxtaposed bars.
horiz	a logical value. If FALSE, the bars are drawn vertically with the first bar to the left. If TRUE, the bars are drawn horizontally with the first at the bottom.
density	a vector giving the the density of shading lines, in lines per inch, for the bars or bar components. The default value of NULL means that no shading lines are drawn. Non-positive values of density also inhibit the drawing of shading lines.
angle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the bars or bar components.
col	a vector of colors for the bars or bar components. By default, grey is used if height is a vector, and <code>heat.colors(nrow(height))</code> if height is a matrix.
prcol	the color to be used for the plot region.
border	the color to be used for the border of the bars.
main, sub	overall and sub titles for the plot.
xlab	a label for the x axis.
ylab	a label for the y axis.
xlim	limits for the x axis.
ylim	limits for the y axis.
xpd	logical. Should bars be allowed to go outside region?

<code>log</code>	a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic.
<code>axes</code>	logical. If TRUE, a vertical (or horizontal, if <code>horiz</code> is true) axis is drawn.
<code>axisnames</code>	logical. If TRUE, and if there are <code>names.arg</code> (see above), the other axis is drawn (with <code>lty = 0</code> ) and labeled.
<code>cex.axis</code>	expansion factor for numeric axis labels.
<code>cex.names</code>	expansion factor for names.
<code>inside</code>	logical. If TRUE, the lines which divide adjacent (non-stacked!) bars will be drawn. Only applies when <code>space = 0</code> (which it partly is when <code>beside = TRUE</code> ).
<code>plot</code>	logical. If FALSE, nothing is plotted.
<code>axis.lty</code>	the graphics parameter <code>lty</code> applied to the axis and tick marks of the categorical (default horizontal) axis. Note that by default the axis is suppressed.
<code>offset</code>	a vector indicating how much the bars should be shifted relative to the x axis.
<code>plot.ci</code>	logical. If TRUE, confidence intervals are plotted over the bars. Note that if a stacked bar plot is generated, confidence intervals will not be plotted even if <code>plot.ci = TRUE</code>
<code>ci.l, ci.u</code>	The confidence intervals ( <code>ci.l</code> = lower bound, <code>ci.u</code> = upper bound) to be plotted if <code>plot.ci = TRUE</code> . Values must have the same dim structure as <code>height</code> .
<code>ci.color</code>	the color for the confidence interval line segments
<code>ci.lty</code>	the line type for the confidence interval line segments
<code>ci.lwd</code>	the line width for the confidence interval line segments
<code>ci.width</code>	length of lines used for the "t" at the end of confidence interval line segments, as a multiple of <code>width</code> . Defaults to 0.5.
<code>plot.grid</code>	if TRUE a lined grid will be plotted behind the bars
<code>grid.inc</code>	the number of grid increments to be plotted
<code>grid.lty</code>	the line type for the grid
<code>grid.lwd</code>	the line width for the grid
<code>grid.col</code>	the line color for the grid
<code>add</code>	logical, if TRUE add barplot to current plot.
<code>panel.first</code>	An expression to be evaluated after the plot region coordinates have been set up, but prior to the drawing of the bars and other plot region contents. This can be useful to add additional plot region content behind the bars. This will also work if <code>add = TRUE</code>
<code>panel.last</code>	An expression to be evaluated after the bars have been drawn, but prior to the addition of confidence intervals, a legend and the axis annotation
<code>...</code>	further graphical parameters ( <code>par</code> ) are passed to <code>plot.window()</code> , <code>title()</code> and <code>axis</code> .

### Details

This is a generic function, it currently only has a default method. A formula interface may be added eventually.

**Value**

A numeric vector (or matrix, when `beside = TRUE`), say `mp`, giving the coordinates of *all* the bar midpoints drawn, useful for adding to the graph.

If `beside` is true, use `colMeans(mp)` for the midpoints of each *group* of bars, see example.

**Note**

Prior to R 1.6.0, `barplot` behaved as if `axis.lty = 1`, unintentionally. 0 (zero) and NA values in `height` will not be plotted if using logarithmic scales. If there are NA values in `height` and `beside = FALSE`, values after the NA will not be plotted in stacked bars.

**Author(s)**

Original `barplot()` by R-Core. Enhancements by Marc Schwartz <marc\\_schwartz@comcast.net>

**See Also**

[plot\(..., type = "h"\)](#), [dotchart](#), [hist](#).

**Examples**

```
tN <- table(Ni <- rpois(100, lambda = 5))
r <- barplot2(tN, col = 'gray')

#- type = "h" plotting *is* `bar`plot
lines(r, tN, type = 'h', col = 'red', lwd = 2)

barplot2(tN, space = 1.5, axisnames = FALSE,
         sub = "barplot2(..., space = 1.5, axisnames = FALSE)")

data(VADeaths, package = "datasets")
barplot2(VADeaths, plot = FALSE)
barplot2(VADeaths, plot = FALSE, beside = TRUE)

mp <- barplot2(VADeaths) # default
tot <- colMeans(VADeaths)
text(mp, tot + 3, format(tot), xpd = TRUE, col = "blue")
barplot2(VADeaths, beside = TRUE,
        col = c("lightblue", "mistyrose", "lightcyan",
               "lavender", "cornsilk"),
        legend = rownames(VADeaths), ylim = c(0, 100))
title(main = "Death Rates in Virginia", font.main = 4)

# Example with confidence intervals and grid
hh <- t(VADeaths)[, 5:1]
mybarcol <- "gray20"
ci.l <- hh * 0.85
ci.u <- hh * 1.15
mp <- barplot2(hh, beside = TRUE,
              col = c("lightblue", "mistyrose",
                    "lightcyan", "lavender"),
```

```

        legend = colnames(VADeaths), ylim = c(0, 100),
        main = "Death Rates in Virginia", font.main = 4,
        sub = "Faked 95 percent error bars", col.sub = mybarcol,
        cex.names = 1.5, plot.ci = TRUE, ci.l = ci.l, ci.u = ci.u,
        plot.grid = TRUE)
mtext(side = 1, at = colMeans(mp), line = -2,
      text = paste("Mean", formatC(colMeans(hh))), col = "red")
box()

# Example with horizontal bars, grid and logarithmic x axis
barplot2(1:10 , log = "x", plot.grid = TRUE, grid.inc = 10,
        xlim = c(0.5, 20), horiz = TRUE, cex.axis = 0.9,
        prcol = "gray95")
box()

# Bar shading example
barplot2(VADeaths, angle = 15 + 10 * 1:5, density = 20, col = "black",
        legend = rownames(VADeaths))
title(main = list("Death Rates in Virginia", font = 4))

# border :
barplot2(VADeaths, border = "dark blue")

```

---

 boxplot2

---

*Produce a Boxplot Annotated with the Number of Observations*


---

## Description

This function uses `boxplot` to produce a boxplot which is then annotated with the number of observations in each group.

## Usage

```
boxplot2(..., top=FALSE, shrink=1, textcolor=NULL)
```

## Arguments

<code>...</code>	parameters passed to <code>boxplot</code> .
<code>top</code>	logical indicating whether the number of observations should be added to the top or the bottom of the plotting region. Defaults to <code>FALSE</code> .
<code>shrink</code>	value to shrink character size ( <code>cex</code> ) when annotating.
<code>textcolor</code>	text color.

## Note

This function replaces `boxplot.n`, which has been deprecated avoid potential problems with S3 method dispatching.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

[boxplot](#), [text](#)

**Examples**

```
data(state)

# n's at bottom
boxplot2( state.area ~ state.region)

# n's at top
boxplot2( state.area ~ state.region, top=TRUE)

# small red text
boxplot2( state.area ~ state.region, shrink=0.8, textcolor="red")
```

---

ci2d

*Create 2-dimensional empirical confidence regions*

---

**Description**

Create 2-dimensional empirical confidence regions from provided data.

**Usage**

```
ci2d(x, y = NULL,
     nbins=51, method=c("bkde2D", "hist2d"),
     bandwidth, factor=1.0,
     ci.levels=c(0.50, 0.75, 0.90, 0.95, 0.975),
     show=c("filled.contour", "contour", "image", "none"),
     col=topo.colors(length(breaks)-1),
     show.points=FALSE,
     pch=par("pch"),
     points.col="red",
     xlab, ylab,
     ...)
## S3 method for class 'ci2d'
print(x, ...)
```

**Arguments**

<code>x</code>	either a vector containing the x coordinates or a matrix with 2 columns.
<code>y</code>	a vector containing the y coordinates, not required if 'x' is matrix
<code>nbins</code>	number of bins in each dimension. May be a scalar or a 2 element vector. Defaults to 51.
<code>method</code>	One of "bkde2D" (for <code>KernSmooth::bkde2d</code> ) or "hist2d" (for <code>gplots::hist2d</code> ) specifying the name of the method to create the 2-d density summarizing the data. Defaults to "bkde2D".
<code>bandwidth</code>	Bandwidth to use for <code>KernSmooth::bkde2D</code> . See below for default value.
<code>factor</code>	Numeric scaling factor for bandwidth. Useful for exploring effect of changing the bandwidth. Defaults to 1.0.
<code>ci.levels</code>	Confidence level(s) to use for plotting data. Defaults to <code>c(0.5, 0.75, 0.9, 0.95, 0.975)</code>
<code>show</code>	Plot type to be displayed. One of "filled.contour", "contour", "image", or "none". Defaults to "filled.contour".
<code>show.points</code>	Boolean indicating whether original data values should be plotted. Defaults to TRUE.
<code>pch</code>	Point type for plots. See <code>points</code> for details.
<code>points.col</code>	Point color for plotting original data. Defaults to "red".
<code>col</code>	Colors to use for plots.
<code>xlab, ylab</code>	Axis labels
<code>...</code>	Additional arguments passed to <code>KernSmooth::bkde2D</code> or <code>gplots::hist2d</code> .

**Details**

This function utilizes either `KernSmooth::bkde2D` or `gplots::hist2d` to estimate a 2-dimensional density of the data passed as an argument. This density is then used to create and (optionally) display confidence regions.

When `bandwidth` is omitted and `method="bkde2d"`, `KernSmooth::dpik` is applied in x and y dimensions to select the bandwidth.

**Value**

A `ci2d` object consisting of a list containing (at least) the following elements:

<code>nobs</code>	number of original data points
<code>x</code>	x position of each density estimate bin
<code>y</code>	y position of each density estimate bin
<code>density</code>	Matrix containing the probability density of each bin (count in bin/total count)
<code>cumDensity</code>	Matrix where each element contains the cumulative probability density of all elements with the same density (used to create the confidence region plots)
<code>contours</code>	List of contours of each confidence region.
<code>call</code>	Call used to create this object



**Note**

Confidence intervals generated by `ci2d` are *approximate*, and are subject to biases and/or artifacts induced by the binning or kernel smoothing method, bin locations, bin sizes, and kernel bandwidth.

The `conf2d` function in the **r2d2** package may create a more accurate confidence region, and reports the actual proportion of points inside the region.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

[bkde2D](#), [conf2d](#), [dpik](#), [hist2d](#)

**Examples**

```
#####
## Basic usage
#####
data(geyser, package="MASS")

x <- geyser$duration
y <- geyser$waiting

# 2-d confidence intervals based on binned kernel density estimate
ci2d(x,y) # filled contour plot
ci2d(x,y, show.points=TRUE) # show original data

# image plot
ci2d(x,y, show="image")
ci2d(x,y, show="image", show.points=TRUE)

# contour plot
ci2d(x,y, show="contour", col="black")
ci2d(x,y, show="contour", col="black", show.points=TRUE)

#####
## Control Axis scales
#####
x <- rnorm(2000, sd=4)
y <- rnorm(2000, sd=1)

# 2-d confidence intervals based on binned kernel density estimate
ci2d(x,y)

# 2-d confidence intervals based on 2d histogram
ci2d(x,y, method="hist2d", nbins=25)

# Require same scale for each axis, this looks oval
ci2d(x,y, range.x=list(c(-20,20), c(-20,20)))
```

```

ci2d(x,y, method="hist2d", same.scale=TRUE, nbins=25) # hist2d

####
## Control smoothing and binning
####
x <- rnorm(2000, sd=4)
y <- rnorm(2000, mean=x, sd=2)

# Default 2-d confidence intervals based on binned kernel density estimate
ci2d(x,y)

# change the smoother bandwidth
ci2d(x,y,
     bandwidth=c(sd(x)/8, sd(y)/8)
     )

# change the smoother number of bins
ci2d(x,y, nbins=10)
ci2d(x,y)
ci2d(x,y, nbins=100)

# Default 2-d confidence intervals based on 2d histogram
ci2d(x,y, method="hist2d", show.points=TRUE)

# change the number of histogram bins
ci2d(x,y, nbin=10, method="hist2d", show.points=TRUE )
ci2d(x,y, nbin=25, method="hist2d", show.points=TRUE )

####
## Perform plotting manually
####
data(geyser, package="MASS")

# let ci2d handle plotting contours...
ci2d(geyser$duration, geyser$waiting, show="contour", col="black")

# call contour() directly, show the 90 percent CI, and the mean point
est <- ci2d(geyser$duration, geyser$waiting, show="none")
contour(est$x, est$y, est$cumDensity,
        xlab="duration", ylab="waiting",
        levels=0.90, lwd=4, lty=2)
points(mean(geyser$duration), mean(geyser$waiting),
        col="red", pch="X")

####
## Extract confidence region values
###
data(geyser, package="MASS")

## Empirical 90 percent confidence limits
quantile( geyser$duration, c(0.05, 0.95) )
quantile( geyser$waiting, c(0.05, 0.95) )

```

```

## Bivariate 90 percent confidence region
est <- ci2d(geyser$duration, geyser$waiting, show="none")
names(est$contours) ## show available contours

ci.90 <- est$contours[names(est$contours)=="0.9"] # get region(s)
ci.90 <- rbind(ci.90[[1]],NA, ci.90[[2]], NA, ci.90[[3]]) # join them

print(ci.90) # show full contour
range(ci.90$x, na.rm=TRUE) # range for duration
range(ci.90$y, na.rm=TRUE) # range for waiting

####
## Visually compare confidence regions
####
data(geyser, package="MASS")

## Bivariate smoothed 90 percent confidence region
est <- ci2d(geyser$duration, geyser$waiting, show="none")
names(est$contours) ## show available contours

ci.90 <- est$contours[names(est$contours)=="0.9"] # get region(s)
ci.90 <- rbind(ci.90[[1]],NA, ci.90[[2]], NA, ci.90[[3]]) # join them

plot( waiting ~ duration, data=geyser,
      main="Comparison of 90 percent confidence regions" )
polygon( ci.90, col="green", border="green", density=10)

## Univariate Normal-Theory 90 percent confidence region
mean.x <- mean(geyser$duration)
mean.y <- mean(geyser$waiting)
sd.x <- sd(geyser$duration)
sd.y <- sd(geyser$waiting)

t.value <- qt(c(0.05,0.95), df=gdata::nobs(geyser$duration), lower=TRUE)
ci.x <- mean.x + t.value* sd.x
ci.y <- mean.y + t.value* sd.y

plotCI(mean.x, mean.y,
       li=ci.x[1],
       ui=ci.x[2],
       barcol="blue", col="blue",
       err="x",
       pch="X",
       add=TRUE )

plotCI(mean.x, mean.y,
       li=ci.y[1],
       ui=ci.y[2],
       barcol="blue", col="blue",
       err="y",
       pch=NA,
       add=TRUE )

```

```

# rect(ci.x[1], ci.y[1], ci.x[2], ci.y[2], border="blue",
#      density=5,
#      angle=45,
#      col="blue" )

## Empirical univariate 90 percent confidence region
box <- cbind( x=quantile( geysers$duration, c(0.05, 0.95 )),
              y=quantile( geysers$waiting, c(0.05, 0.95 )) )

rect(box[1,1], box[1,2], box[2,1], box[2,2], border="red",
      density=5,
      angle=-45,
      col="red" )

## now a nice legend
legend( "topright", legend=c("      Region type",
                             "Univariate Normal Theory",
                             "Univariate Empirical",
                             "Smoothed Bivariate"),
        lwd=c(NA,1,1,1),
        col=c("black","blue","red","green"),
        lty=c(NA,1,1,1)
      )

####
## Test with a large number of points
####
## Not run:
x <- rnorm(60000, sd=1)
y <- c( rnorm(40000, mean=x, sd=1),
        rnorm(20000, mean=x+4, sd=1) )

hist2d(x,y)
ci <- ci2d(x,y)
ci

## End(Not run)

```

---

col2hex

*Convert color names to hex RGB strings*


---

### Description

Convert color names to hex RGB strings

### Usage

```
col2hex(cname)
```

**Arguments**

cname            Color name(s)

**Value**

Character vector giving the hex color code translation of the provided color names.

**Author(s)**

Gregory R. Warnes

**See Also**

[col2rgb](#), [colors](#), [rgb](#)

**Examples**

```
col2hex(c("red", "yellow", "lightgrey"))
```

---

colorpanel	<i>Generate a smoothly varying set of colors</i>
------------	--

---

**Description**

colorpanel generate a set of colors that varies smoothly. redgreen, greenred, bluered, and redblue generate red-black-green, green-black-red, red-white-blue, and blue-white-red colorbars, respectively. colors

**Usage**

```
colorpanel(n, low, mid, high)
redgreen(n)
greenred(n)
bluered(n)
redblue(n)
```

**Arguments**

n                    Desired number of color elements in the panel.  
low, mid, high    Colors to use for the Lowest, middle, and highest values. mid may be omitted.

**Details**

The values for low, mid, high can be given as color names ('red'), plot color index (2=red), and HTML-style RGB, ("#FF0000"=red).

If mid is supplied, then the returned color panel will consist of  $n - \text{floor}(n/2)$  HTML-style RGB elements which vary smoothly between low and mid, then between mid and high. Note that if n is even, the color mid will occur twice at the center of the sequence.

If mid is omitted, the color panel will vary smoothly between low and high.

**Value**

Vector of HTML-style RGB colors.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

[colors](#)

**Examples**

```
showpanel <- function(col)
{
  image(z=matrix(1:100, ncol=1), col=col, xaxt="n", yaxt="n" )
}

par(mfrow=c(3,3))

# two colors only:
showpanel(colorpanel(8,low="red",high="green"))

# three colors
showpanel(colorpanel(8,"red","black","green"))
# note the duplication of black at the center, using an odd
# number of elements resolves this:
showpanel(colorpanel(9,"red","black","green"))

showpanel(greenred(64))
showpanel(redgreen(64))
showpanel(bluered(64))
showpanel(redblue(64))
```

---

gplots-defunct

*Defunct functions*

---

**Description**

These functions are defunct and have been removed from the gplots package.

**Usage**

```
boxplot.n(..., top=FALSE, shrink=1, textcolor=NULL)
plot.lm2(
  x,
  which = 1:5,
```

```
caption = c("Residuals vs Fitted", "Normal Q-Q plot",
           "Scale-Location plot", "Cook's distance plot"),
panel = panel.smooth,
sub.caption = deparse(x$call),
main = "",
ask,
...,
id.n = 3,
labels.id = names(residuals(x)),
cex.id = 0.75,
band=TRUE,
rug=TRUE,
width=1/10,
max.n=5000
)
smartlegend(x = c("left", "center", "right"),
            y = c("top", "center", "bottom"),
            ...,
            inset = 0.05)
```

### Arguments

ask, band, caption, cex.id, id.n, inset, labels.id, main, max.n, panel, rug, shrink, sub.caption, t  
see man page for the corresponding replacement function

### Details

These functions are no longer available. Please refer to the manual page for the replacement function:

- `boxplot.n` has been replaced by [boxplot2](#)
- `plot.lm2` has been replaced by [lmplot2](#)
- `smartlegend` is no longer needed because relative positioning has been implemented in [legend](#).

### Author(s)

Gregory R. Warnes <greg@warnes.net>

### See Also

[boxplot2](#), [lmplot2](#), [legend](#), [Defunct](#)

---

gplots-deprecated      *Deprecated functions*

---

### Description

These functions have been deprecated and will be removed in future releases of gplots.

### Usage

```
## No deprecated functions at this time ##
```

### Details

These functions have been deprecated. Please refer to the manual page for the replacement function:

- (No deprecated functions at this time)

### Author(s)

Gregory R. Warnes <greg@warnes.net>

### See Also

[Deprecated](#)

---

heatmap.2      *Enhanced Heat Map*

---

### Description

A heat map is a false color image (basically `image(t(x))`) with a dendrogram added to the left side and/or to the top. Typically, reordering of the rows and columns according to some set of values (row or column means) within the restrictions imposed by the dendrogram is carried out.

This heatmap provides a number of extensions to the standard R `heatmap` function.

### Usage

```
heatmap.2 (x,  
  
          # dendrogram control  
          Rowv = TRUE,  
          Colv = if(symm) "Rowv" else TRUE,  
          distfun = dist,  
          hclustfun = hclust,  
          dendrogram = c("both", "row", "column", "none"),  
          reorderfun = function(d, w) reorder(d, w),
```



```
symm = FALSE,  
  
# data scaling  
scale = c("none","row", "column"),  
na.rm=TRUE,  
  
# image plot  
revC = identical(Colv, "Rowv"),  
add.expr,  
  
# mapping data to colors  
breaks,  
symsbreaks=any(x < 0, na.rm=TRUE) || scale!="none",  
  
# colors  
col="heat.colors",  
  
# block separation  
colsep,  
rowsep,  
sepcolor="white",  
sepwidth=c(0.05,0.05),  
  
# cell labeling  
cellnote,  
notecex=1.0,  
notecol="cyan",  
na.color=par("bg"),  
  
# level trace  
trace=c("column","row","both","none"),  
tracecol="cyan",  
hline=median(breaks),  
vline=median(breaks),  
linecol=tracecol,  
  
# Row/Column Labeling  
margins = c(5, 5),  
ColSideColors,  
RowSideColors,  
cexRow = 0.2 + 1/log10(nr),  
cexCol = 0.2 + 1/log10(nc),  
labRow = NULL,  
labCol = NULL,  
srtRow = NULL,  
srtCol = NULL,  
adjRow = c(0,NA),  
adjCol = c(NA,0),
```

```

offsetRow = 0.5,
offsetCol = 0.5,
colRow = NULL,
colCol = NULL,

# color key + density info
key = TRUE,
keysize = 1.5,
density.info=c("histogram","density","none"),
denscol=tracecol,
symkey = any(x < 0, na.rm=TRUE) || symbreaks,
densadj = 0.25,
key.title = NULL,
key.xlab = NULL,
key.ylab = NULL,
key.xtickfun = NULL,
key.ytickfun = NULL,
key.par=list(),

# plot labels
main = NULL,
xlab = NULL,
ylab = NULL,

# plot layout
lmat = NULL,
lhei = NULL,
lwid = NULL,

# extras
extrafun=NULL,
...
)

```

## Arguments

x	numeric matrix of the values to be plotted.
Rowv	determines if and how the <i>row</i> dendrogram should be reordered. By default, it is TRUE, which implies dendrogram is computed and reordered based on row means. If NULL or FALSE, then no dendrogram is computed and no reordering is done. If a <a href="#">dendrogram</a> , then it is used "as-is", ie without any reordering. If a vector of integers, then dendrogram is computed and reordered based on the order of the vector.
Colv	determines if and how the <i>column</i> dendrogram should be reordered. Has the options as the Rowv argument above and <i>additionally</i> when x is a square matrix, Colv="Rowv" means that columns should be treated identically to the rows.

distfun	function used to compute the distance (dissimilarity) between both rows and columns. Defaults to <code>dist</code> .
hclustfun	function used to compute the hierarchical clustering when Rowv or Colv are not dendrograms. Defaults to <code>hclust</code> .
dendrogram	character string indicating whether to draw 'none', 'row', 'column' or 'both' dendrograms. Defaults to 'both'. However, if Rowv (or Colv) is FALSE or NULL and dendrogram is 'both', then a warning is issued and Rowv (or Colv) arguments are honoured.
reorderfun	function(d, w) of dendrogram and weights for reordering the row and column dendrograms. The default uses <code>stats{reorder.dendrogram}</code> .
symm	logical indicating if x should be treated <b>symmetrically</b> ; can only be true when x is a square matrix.
scale	character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. The default is "none".
na.rm	logical indicating whether NA's should be removed.
revC	logical indicating if the column order should be <b>reversed</b> for plotting, such that e.g., for the symmetric case, the symmetry axis is as usual.
add.expr	expression that will be evaluated after the call to <code>image</code> . Can be used to add components to the plot.
breaks	(optional) Either a numeric vector indicating the splitting points for binning x into colors, or a integer number of break points to be used, in which case the break points will be spaced equally between <code>min(x)</code> and <code>max(x)</code> .
symbreaks	Boolean indicating whether breaks should be made symmetric about 0. Defaults to TRUE if the data includes negative values, and to FALSE otherwise.
col	colors used for the image. Defaults to heat colors ( <code>heat.colors</code> ).
colsep, rowsep, sepcolor	(optional) vector of integers indicating which columns or rows should be separated from the preceding columns or rows by a narrow space of color <code>sepcolor</code> .
sepwidth	(optional) Vector of length 2 giving the width ( <code>colsep</code> ) or height ( <code>rowsep</code> ) the separator box drawn by <code>colsep</code> and <code>rowsep</code> as a function of the width ( <code>colsep</code> ) or height ( <code>rowsep</code> ) of a cell. Defaults to <code>c(0.05, 0.05)</code>
cellnote	(optional) matrix of character strings which will be placed within each color cell, e.g. p-value symbols.
notecex	(optional) numeric scaling factor for <code>cellnote</code> items.
notecol	(optional) character string specifying the color for <code>cellnote</code> text. Defaults to "cyan".
na.color	Color to use for missing value (NA). Defaults to the plot background color.
trace	character string indicating whether a solid "trace" line should be drawn across 'row's or down 'column's, 'both' or 'none'. The distance of the line from the center of each color-cell is proportional to the size of the measurement. Defaults to 'column'.
tracecol	character string giving the color for "trace" line. Defaults to "cyan".

<code>hline</code> , <code>vline</code> , <code>linecol</code>	Vector of values within cells where a horizontal or vertical dotted line should be drawn. The color of the line is controlled by <code>linecol</code> . Horizontal lines are only plotted if <code>trace</code> is 'row' or 'both'. Vertical lines are only drawn if <code>trace</code> 'column' or 'both'. <code>hline</code> and <code>vline</code> default to the median of the breaks, <code>linecol</code> defaults to the value of <code>tracecol</code> .
<code>margins</code>	numeric vector of length 2 containing the margins (see <code>par(mar=*)</code> ) for column and row names, respectively.
<code>ColSideColors</code>	(optional) character vector of length <code>ncol(x)</code> containing the color names for a horizontal side bar that may be used to annotate the columns of <code>x</code> .
<code>RowSideColors</code>	(optional) character vector of length <code>nrow(x)</code> containing the color names for a vertical side bar that may be used to annotate the rows of <code>x</code> .
<code>cexRow</code> , <code>cexCol</code>	positive numbers, used as <code>cex.axis</code> in for the row or column axis labeling. The defaults currently only use number of rows or columns, respectively.
<code>labRow</code> , <code>labCol</code>	character vectors with row and column labels to use; these default to <code>rownames(x)</code> or <code>colnames(x)</code> , respectively.
<code>srtRow</code> , <code>srtCol</code>	angle of row/column labels, in degrees from horizontal
<code>adjRow</code> , <code>adjCol</code>	2-element vector giving the (left-right, top-bottom) justification of row/column labels (relative to the text orientation).
<code>offsetRow</code> , <code>offsetCol</code>	Number of character-width spaces to place between row/column labels and the edge of the plotting region.
<code>colRow</code> , <code>colCol</code>	color of row/column labels, either a scalar to set the color of all labels the same, or a vector providing the colors of each label item
<code>key</code>	logical indicating whether a color-key should be shown.
<code>keysize</code>	numeric value indicating the size of the key
<code>density.info</code>	character string indicating whether to superimpose a 'histogram', a 'density' plot, or no plot ('none') on the color-key.
<code>denscol</code>	character string giving the color for the density display specified by <code>density.info</code> , defaults to the same value as <code>tracecol</code> .
<code>symkey</code>	Boolean indicating whether the color key should be made symmetric about 0. Defaults to TRUE if the data includes negative values, and to FALSE otherwise.
<code>densadj</code>	Numeric scaling value for tuning the kernel width when a density plot is drawn on the color key. (See the <code>adjust</code> parameter for the density function for details.) Defaults to 0.25.
<code>key.title</code>	main title of the color key. If set to NA no title will be plotted.
<code>key.xlab</code>	x axis label of the color key. If set to NA no label will be plotted.
<code>key.ylab</code>	y axis label of the color key. If set to NA no label will be plotted.
<code>key.xtickfun</code>	function computing tick location and labels for the xaxis of the color key. Returns a named list containing parameters that can be passed to <code>axis</code> . See examples.
<code>key.ytickfun</code>	function computing tick location and labels for the y axis of the color key. Returns a named list containing parameters that can be passed to <code>axis</code> . See examples.

key.par	graphical parameters for the color key. Named list that can be passed to par.
main, xlab, ylab	main, x- and y-axis titles; defaults to none.
lmat, lhei, lwid	visual layout: position matrix, column height, column width. See below for details
extrafun	A function to be called after all other work. See examples.
...	additional arguments passed on to <a href="#">image</a>

## Details

If either Rowv or Colv are dendrograms they are honored (and not reordered). Otherwise, dendrograms are computed as `dd <- as.dendrogram(hclustfun(distfun(X)))` where `X` is either `x` or `t(x)`.

If either is a vector (of “weights”) then the appropriate dendrogram is reordered according to the supplied values subject to the constraints imposed by the dendrogram, by [reorder](#)(`dd`, `Rowv`), in the row case.

If either is missing, as by default, then the ordering of the corresponding dendrogram is by the mean value of the rows/columns, i.e., in the case of rows, `Rowv <- rowMeans(x, na.rm=na.rm)`.

If either is `NULL`, *no reordering* will be done for the corresponding side.

If `scale="row"` (or `scale="col"`) the rows (columns) are scaled to have mean zero and standard deviation one. There is some empirical evidence from genomic plotting that this is useful.

The default colors range from red to white (`heat.colors`) and are not pretty. Consider using enhancements such as the **RColorBrewer** package, <https://cran.r-project.org/package=RColorBrewer> to select better colors.

By default four components will be displayed in the plot. At the top left is the color key, top right is the column dendrogram, bottom left is the row dendrogram, bottom right is the image plot. When `RowSideColor` or `ColSideColor` are provided, an additional row or column is inserted in the appropriate location. This layout can be overridden by specifying appropriate values for `lmat`, `lwid`, and `lhei`. `lmat` controls the relative position of each element, while `lwid` controls the column width, and `lhei` controls the row height. See the help page for [layout](#) for details on how to use these arguments.

## Value

Invisibly, a list with components

rowInd	row index permutation vector as returned by <a href="#">order.dendrogram</a> .
colInd	column index permutation vector.
call	the matched call
rowMeans, rowSDs	mean and standard deviation of each row: only present if <code>scale="row"</code>
colMeans, colSDs	mean and standard deviation of each column: only present if <code>scale="column"</code>

carpet	reordered and scaled 'x' values used generate the main 'carpet'
rowDendrogram	row dendrogram, if present
colDendrogram	column dendrogram, if present
breaks	values used for color break points
col	colors used
vline	center-line value used for column trace, present only if trace="both" or trace="column"
hline	center-line value used for row trace, present only if trace="both" or trace="row"
colorTable	A three-column data frame providing the lower and upper bound and color for each bin
layout	A named list containing the values used for lmat, lhei, and lwid.

**Note**

The original rows and columns are reordered to match the dendrograms Rowv and Colv (if present).

heatmap.2() uses [layout](#) to arragent the plot elements. Consequentially, it can **not** be used in a multi column/row layout using [layout\(...\)](#), [par\(mfrow=...\)](#) or [par\(mfcol=...\)](#).

**Author(s)**

Andy Liaw, original; R. Gentleman, M. Maechler, W. Huber, G. Warnes, revisions.

**See Also**

[image](#), [hclust](#)

**Examples**

```
data(mtcars)
x <- as.matrix(mtcars)
rc <- rainbow(nrow(x), start=0, end=.3)
cc <- rainbow(ncol(x), start=0, end=.3)

##
## demonstrate the effect of row and column dendrogram options
##
heatmap.2(x)                ## default - dendrogram plotted and reordering done.
heatmap.2(x, dendrogram="none") ## no dendrogram plotted, but reordering done.
heatmap.2(x, dendrogram="row")  ## row dendrogram plotted and row reordering done.
heatmap.2(x, dendrogram="col")  ## col dendrogram plotted and col reordering done.

heatmap.2(x, keysize=2)      ## default - dendrogram plotted and reordering done.

heatmap.2(x, Rowv=FALSE, dendrogram="both") ## generates a warning!
heatmap.2(x, Rowv=NULL, dendrogram="both")  ## generates a warning!
heatmap.2(x, Colv=FALSE, dendrogram="both") ## generates a warning!

## Reorder dendrogram by branch means rather than sums
heatmap.2(x, reorderfun=function(d, w) reorder(d, w, aggro.FUN = mean) )
```

```

## plot a sub-cluster using the same color coding as for the full heatmap
full <- heatmap.2(x)
heatmap.2(x, Colv=full$colDendrogram[[2]], breaks=full$breaks) # column subset
heatmap.2(x, Rowv=full$rowDendrogram[[1]], breaks=full$breaks) # row subset
heatmap.2(x, Colv=full$colDendrogram[[2]],
          Rowv=full$rowDendrogram[[1]], breaks=full$breaks) # both

## Show effect of row and column label rotation
heatmap.2(x, srtCol=NULL)
heatmap.2(x, srtCol=0, adjCol = c(0.5,1) )
heatmap.2(x, srtCol=45, adjCol = c(1,1) )
heatmap.2(x, srtCol=135, adjCol = c(1,0) )
heatmap.2(x, srtCol=180, adjCol = c(0.5,0) )
heatmap.2(x, srtCol=225, adjCol = c(0,0) ) ## not very useful
heatmap.2(x, srtCol=270, adjCol = c(0,0.5) )
heatmap.2(x, srtCol=315, adjCol = c(0,1) )
heatmap.2(x, srtCol=360, adjCol = c(0.5,1) )

heatmap.2(x, srtRow=45, adjRow=c(0, 1) )
heatmap.2(x, srtRow=45, adjRow=c(0, 1), srtCol=45, adjCol=c(1,1) )
heatmap.2(x, srtRow=45, adjRow=c(0, 1), srtCol=270, adjCol=c(0,0.5) )

## Show effect of offsetRow/offsetCol (only works when srtRow/srtCol is
## not also present)
heatmap.2(x, offsetRow=0, offsetCol=0)
heatmap.2(x, offsetRow=1, offsetCol=1)
heatmap.2(x, offsetRow=2, offsetCol=2)
heatmap.2(x, offsetRow=-1, offsetCol=-1)

heatmap.2(x, srtRow=0, srtCol=90, offsetRow=0, offsetCol=0)
heatmap.2(x, srtRow=0, srtCol=90, offsetRow=1, offsetCol=1)
heatmap.2(x, srtRow=0, srtCol=90, offsetRow=2, offsetCol=2)
heatmap.2(x, srtRow=0, srtCol=90, offsetRow=-1, offsetCol=-1)

## Show how to use 'extrafun' to replace the 'key' with a scatterplot
lmat <- rbind( c(5,3,4), c(2,1,4) )
lhei <- c(1.5, 4)
lwid <- c(1.5, 4, 0.75)

myplot <- function() {
  oldpar <- par("mar")
  par(mar=c(5.1, 4.1, 0.5, 0.5))
  plot(mpg ~ hp, data=x)
}

heatmap.2(x, lmat=lmat, lhei=lhei, lwid=lwid, key=FALSE, extrafun=myplot)

## show how to customize the color key
heatmap.2(x,
          key.title=NA, # no title

```

```

key.xlab=NA, # no xlab
key.par=list(mgp=c(1.5, 0.5, 0),
             mar=c(2.5, 2.5, 1, 0)),
key.xtickfun=function() {
  breaks <- parent.frame()$breaks
  return(list(
    at=parent.frame()$scale01(c(breaks[1],
                               breaks[length(breaks)])),
    labels=c(as.character(breaks[1]),
             as.character(breaks[length(breaks)]))
  ))
})

heatmap.2(x,
          breaks=256,
          key.title=NA,
          key.xlab=NA,
          key.par=list(mgp=c(1.5, 0.5, 0),
                      mar=c(1, 2.5, 1, 0)),
          key.xtickfun=function() {
            cex <- par("cex")*par("cex.axis")
            side <- 1
            line <- 0
            col <- par("col.axis")
            font <- par("font.axis")
            mtext("low", side=side, at=0, adj=0,
                 line=line, cex=cex, col=col, font=font)
            mtext("high", side=side, at=1, adj=1,
                 line=line, cex=cex, col=col, font=font)
            return(list(labels=FALSE, tick=FALSE))
          })

##
## Show effect of z-score scaling within columns, blue-red color scale
##
hv <- heatmap.2(x, col=bluered, scale="column", tracecol="#303030")

###
## Look at the return values
###
names(hv)

## Show the mapping of z-score values to color bins
hv$colorTable

## Extract the range associated with white
hv$colorTable[hv$colorTable[, "color"]=="#FFFFFF",]

## Determine the original data values that map to white
whiteBin <- unlist(hv$colorTable[hv$colorTable[, "color"]=="#FFFFFF", 1:2])
rbind(whiteBin[1] * hv$colSDs + hv$colMeans,
      whiteBin[2] * hv$colSDs + hv$colMeans )

```



```

##
## A more decorative heatmap, with z-score scaling along columns
##
hv <- heatmap.2(x, col=cm.colors(255), scale="column",
  RowSideColors=rc, ColSideColors=cc, margin=c(5, 10),
  xlab="specification variables", ylab= "Car Models",
  main="heatmap(<Mtcars data>, ..., scale=\"column\")",
  tracecol="green", density="density")
## Note that the breakpoints are now symmetric about 0

## Color the labels to match RowSideColors and ColSideColors
hv <- heatmap.2(x, col=cm.colors(255), scale="column",
  RowSideColors=rc, ColSideColors=cc, margin=c(5, 10),
  xlab="specification variables", ylab= "Car Models",
  main="heatmap(<Mtcars data>, ..., scale=\"column\")",
  tracecol="green", density="density", colRow=rc, colCol=cc,
  srtCol=45, adjCol=c(0.5,1))

data(attitude)
round(Ca <- cor(attitude), 2)
symnum(Ca) # simple graphic

# with reorder
heatmap.2(Ca,  symm=TRUE, margin=c(6, 6), trace="none" )

# without reorder
heatmap.2(Ca, Rowv=FALSE, symm=TRUE, margin=c(6, 6), trace="none" )

## Place the color key below the image plot
heatmap.2(x, lmat=rbind( c(0, 3), c(2,1), c(0,4) ), lhei=c(1.5, 4, 2 ) )

## Place the color key to the top right of the image plot
heatmap.2(x, lmat=rbind( c(0, 3, 4), c(2,1,0 ) ), lwid=c(1.5, 4, 2 ) )

## For variable clustering, rather use distance based on cor():
data(USJudgeRatings)
symnum( cU <- cor(USJudgeRatings) )

hU <- heatmap.2(cU, Rowv=FALSE, symm=TRUE, col=topo.colors(16),
  distfun=function(c) as.dist(1 - c), trace="none")

## The Correlation matrix with same reordering:
hM <- format(round(cU, 2))
hM

# now with the correlation matrix on the plot itself

heatmap.2(cU, Rowv=FALSE, symm=TRUE, col=rev(heat.colors(16)),
  distfun=function(c) as.dist(1 - c), trace="none",

```

```

        cellnote=hM)

## genechip data examples
## Not run:
library(affy)
data(SpikeIn)
pms <- SpikeIn@pm

# just the data, scaled across rows
heatmap.2(pms, col=rev(heat.colors(16)), main="SpikeIn@pm",
          xlab="Relative Concentration", ylab="Probeset",
          scale="row")

# fold change vs "12.50" sample
data <- pms / pms[, "12.50"]
data <- ifelse(data>1, data, -1/data)
heatmap.2(data, breaks=16, col=redgreen, tracecol="blue",
          main="SpikeIn@pm Fold Changes\nrelative to 12.50 sample",
          xlab="Relative Concentration", ylab="Probeset")

## End(Not run)

```

---

hist2d

---

*Compute and Plot a 2-Dimensional Histogram*


---

## Description

Compute and plot a 2-dimensional histogram.

## Usage

```

hist2d(x,y=NULL, nbins=200, same.scale=FALSE, na.rm=TRUE, show=TRUE,
       col=c("black", heat.colors(12)), FUN=base::length, xlab, ylab,
       ... )
## S3 method for class 'hist2d'
print(x, ...)

```

## Arguments

x	either a vector containing the x coordinates or a matrix with 2 columns.
y	a vector containing the y coordinates, not required if 'x' is matrix
nbins	number of bins in each dimension. May be a scalar or a 2 element vector. Defaults to 200.
same.scale	use the same range for x and y. Defaults to FALSE.
na.rm	Indicates whether missing values should be removed. Defaults to TRUE.
show	Indicates whether the histogram be displayed using image once it has been computed. Defaults to TRUE.

col	Colors for the histogram. Defaults to "black" for bins containing no elements, a set of 16 heat colors for other bins.
FUN	Function used to summarize bin contents. Defaults to <code>base::length</code> . Use, e.g., <code>mean</code> to calculate means for each bin instead of counts.
xlab, ylab	(Optional) x and y axis labels
...	Parameters passed to the image function.

### Details

This function creates a 2-dimensional histogram by cutting the x and y dimensions into `nbins` sections. A 2-dimensional matrix is then constructed which holds the counts of the number of observed (x,y) pairs that fall into each bin. If `show=TRUE`, this matrix is then passed to `image` for display.

### Value

A list containing 5 elements:

counts	Matrix containing the number of points falling into each bin
x.breaks, y.breaks	Lower and upper limits of each bin
x,y	midpoints of each bin

### Author(s)

Gregory R. Warnes <greg@warnes.net>

### See Also

[image](#), [persp](#), [hist](#), [freq2d](#)

### Examples

```
## example data, bivariate normal, no correlation
x <- rnorm(2000, sd=4)
y <- rnorm(2000, sd=1)

## separate scales for each axis, this looks circular
hist2d(x,y)

## same scale for each axis, this looks oval
hist2d(x,y, same.scale=TRUE)

## use different ## bins in each dimension
hist2d(x,y, same.scale=TRUE, nbins=c(100,200) )

## use the hist2d function to create an h2d object
h2d <- hist2d(x,y,show=FALSE, same.scale=TRUE, nbins=c(20,30))

## show object summary
```

```

h2d

## object contents
str(h2d)

## perspective plot
persp( h2d$x, h2d$y, h2d$counts,
       ticktype="detailed", theta=30, phi=30,
       expand=0.5, shade=0.5, col="cyan", ltheta=-30)

## for contour (line) plot ...
contour( h2d$x, h2d$y, h2d$counts, nlevels=4 )

## for a filled contour plot ...
filled.contour( h2d$x, h2d$y, h2d$counts, nlevels=4,
               col=gray((4:0)/4) )

```

---

lplot2

*Plots to assess the goodness of fit for the linear model objects*


---

## Description

Plots to assess the goodness of fit for the linear model objects

## Usage

```

lplot2(
  x,
  which = 1:5,
  caption = c("Residuals vs Fitted", "Normal Q-Q plot",
             "Scale-Location plot", "Cook's distance plot"),
  panel = panel.smooth,
  sub.caption = deparse(x$call),
  main = "",
  ask = interactive() && nb.fig < length(which)
  && .Device != "postscript",
  ...,
  id.n = 3,
  labels.id = names(residuals(x)),
  cex.id = 0.75,
  band=TRUE,
  rug=TRUE,
  width=1/10,
  max.n=5000
)

```

**Arguments**

x	lm object
which	Numerical values between 1 and 5, indicating which plots to be shown. The codes are: <ol style="list-style-type: none"> <li>1 Fitted vs residuals</li> <li>2 Normal Q-Q</li> <li>3 Scale-Location</li> <li>4 Cook's distance</li> <li>5 Residuals vs. predictor</li> </ol>
caption	Caption for each type of plot
panel	function to draw on the existing plot
sub.caption	SubCaption for the plots
main	Main title of the plot
ask	whether interactive graphics
...	parameters passed to lplot2.
id.n	integer value, less than or equal to residuals of lm object
labels.id	Names of the residuals of the lm object
cex.id	Parameter to control the height of text strings
band	logical vector indicating whether bandplot should also be plotted
rug	logical vector indicating whether rug should be added to the existing plot
width	Fraction of the data to use for plot smooths
max.n	Maximum number of points to display in plots

**Note**

This function replaces `plot.lm2`, which has been deprecated to avoid potential problems with S3 method dispatching.

**Author(s)**

Gregory R. Warnes <greg@warnes.net> and Nitin Jain <nitin.jain@pfizer.com>

**See Also**

[plot.lm](#)

**Examples**

```
ctl <- rnorm(100, 4)
trt <- rnorm(100, 4.5)
group <- gl(2,100,200, labels=c("Ctl","Trt"))
weight <- c(ctl, trt)
wt.err <- rnorm(length(weight), mean=weight, sd=1/2)
x <- lm(weight ~ group + wt.err)
```

```

lplot2(x)

lplot2(x, which=1, width=1/3)
lplot2(x, which=1:3, width=1/3)

```

---

lowess

*Scatter Plot Smoothing*


---

### Description

The `lowess` function performs the computations for the *LOWESS* smoother (see the reference below). `lowess` returns an object containing components `x` and `y` which give the coordinates of the smooth. The smooth can then be added to a plot of the original points with the function `lines`.

Alternatively, `plot` can be called directly on the object returned from `lowess` and the `'lowess'` method for `plot` will generate a scatterplot of the original data with a `lowess` line superimposed.

Finally, the `plotLowess` function both calculates the `lowess` smooth and plots the original data with a `lowess` smooth.

### Usage

```

lowess(x, ...)

## Default S3 method:
lowess(x, y=NULL, f=2/3, iter=3L, delta=0.01 *
       diff(range(x)), ...)

## S3 method for class 'formula'
lowess(formula,data=parent.frame(), ..., subset, f=2/3,
       iter=3L, delta=.01*diff(range(mf[-response])))

## S3 method for class 'lowess'
plot(x, y, ..., col.lowess="red", lty.lowess=2)

plotLowess(formula, data=parent.frame(), ..., subset=parent.frame(),
           col.lowess="red", lty.lowess=2 )

```

### Arguments

<code>formula</code>	formula providing a single dependent variable ( <code>y</code> ) and an single independent variable ( <code>x</code> ) to use as coordinates in the scatter plot.
<code>data</code>	a <code>data.frame</code> (or list) from which the variables in <code>'formula'</code> should be taken.
<code>subset</code>	an optional vector specifying a subset of observations to be used in the fitting process.
<code>x, y</code>	vectors giving the coordinates of the points in the scatter plot. Alternatively a single plotting structure can be specified.

<code>f</code>	the smoother span. This gives the proportion of points in the plot which influence the smooth at each value. Larger values give more smoothness.
<code>iter</code>	the number of robustifying iterations which should be performed. Using smaller values of <code>iter</code> will make <code>lowess</code> run faster.
<code>delta</code>	values of <code>x</code> which lie within <code>delta</code> of each other replaced by a single value in the output from <code>lowess</code> .
<code>...</code>	parameters for methods.
<code>col.lowess, lty.lowess</code>	color and line type for plotted line

## References

Cleveland, W. S. (1979) Robust locally weighted regression and smoothing scatterplots. *J. Amer. Statist. Assoc.* **74**, 829–836.

Cleveland, W. S. (1981) LOWESS: A program for smoothing scatterplots by robust locally weighted regression. *The American Statistician*, **35**, 54.

## See Also

[loess](#) (in package `modreg`), a newer formula based version of `lowess` (with different defaults!).

## Examples

```
data(cars)

#
# x,y method
#
plot(cars$speed, cars$dist, main="lowess(cars)")
lines(lowess(cars$speed, cars$dist), col=2)
lines(lowess(cars$speed, cars$dist, f=.2), col=3)
legend(5, 120, c(paste("f=", c("2/3", ".2"))), lty=1, col=2:3)

#
# formula method: plot, then calculate the lowess smoother,
#                   then add smooth to the plot
#
plot(dist ~ speed, data=cars, main="lowess(cars)")
lines(lowess(dist ~ speed, data=cars), col=2, lty=2)
lines(lowess(dist ~ speed, data=cars, f=.2), col=3) # smaller bandwidth
legend(5, 120, c(paste("f=", c("2/3", ".2"))), lty=1, col=2:3)

#
# formula method: calculate lowess() smoother, then call plot()
#                   on the lowess object
#
lw <- lowess(dist ~ speed, data=cars)
plot(lw, main="lowess(cars)" )

#
```

```
# formula method: calculate and plot in a single command
#
plotLowess(dist ~ speed, data=cars, main="lowess(cars)")
```

---

ooplot.default                      *Create an OpenOffice style plot*

---

## Description

An extension of barplot2. Creates bar- and line-plots mimicking the style of OpenOffice plots. This utility can plot the values next to each point or bar as well as confidence intervals.

## Usage

```
ooplot(data, ...)
## Default S3 method:
ooplot(data, width=1, space=NULL, names.arg=NULL,
        legend.text=NULL, horiz=FALSE,
        density=NULL, angle=45, kmg="fpnumkMGTP",
        kmglim=TRUE,
        type=c("xyplot", "linear", "barplot", "stackbar"),
        col=heat.colors(NC), prcol=NULL,
        border=par("fg"), main=NULL, sub=NULL,
        xlab=NULL, ylab=NULL, xlim=NULL, ylim=NULL,
        xpd=TRUE, log="", axes=TRUE,
        axisnames=TRUE, prval=TRUE, lm=FALSE,
        cex.axis=par("cex.axis"),
        cex.names=par("cex.axis"),
        cex.values=par("cex"), inside=TRUE,
        plot=TRUE, axis.lty=0, plot.ci=FALSE,
        ci.l=NULL, ci.u=NULL, ci.color="black",
        ci.lty="solid", ci.lwd=1, plot.grid=FALSE,
        grid.inc=NULL, grid.lty="dotted",
        grid.lwd=1, grid.col="black", add=FALSE,
        by.row=FALSE, ...)
```

## Arguments

data	a matrix of values describing the values that make up the plot. The first column of data is taken as the axis against which all the other values are plotted. The first column of data may not be sparse.
width	optional vector of barwidths. Re-cycled to the number of bars drawn. A single value will have no visible effect.



space	the amount of space left before each bar. May be given as a single number or one number per bar. If type is <code>stackbar</code> , space may be specified by two numbers, where the first is the space between bars in the same group, and the second the space between groups. Defaults to <code>c(0,1)</code> if type is a <code>stackbar</code> , and to 0.2 otherwise.
names.arg	a vector of names to be plotted below each bar or group of bars. If this argument is omitted, then the names are taken from the row names of data.
legend.text	a vector of text used to construct a legend for the plot, or a logical indicating whether a legend should be included; if <code>legend.text</code> is true, the row names of data will be used as labels if they are non-null.
horiz	a logical value. If FALSE, the bars are drawn vertically with the first bar to the left. If TRUE, the bars are drawn horizontally with the first at the bottom.
density	a vector giving the the density of shading lines, in lines per inch, for the bars or bar components. The default value of NULL means that no shading lines are drawn. Non-positive values of <code>density</code> also inhibit the drawing of shading lines.
angle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the bars or bar components.
kmg	the set of SI units to convert, defaults to "fpnumkMGTP". See below for details.
kmglim	logical. If FALSE the conversion to SI units is not performed. Default is TRUE.
type	a string indicating the preferred format of the plot, choices are: <code>xyplot</code> : plot where y is plotted against the x-value. <code>linear</code> : plot where y values are plotted against equidistant x-values. <code>barplot</code> : plot where y values are represented as bars against equidistant x-values. <code>stackplot</code> : plot where y values are stacked for identical x-values and bars are equidistant.
col	a vector of colors for the bars or bar components.
prcol	the color to be used for the plot region.
border	the color to be used for the border of the bars.
main, sub	overall and sub titles for the plot.
xlab	a label for the x axis.
ylab	a label for the y axis.
xlim	limits for the x axis.
ylim	limits for the y axis.
xpd	logical. Should bars be allowed to go outside region?
log	a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic.
axes	logical. If TRUE, a vertical (or horizontal, if <code>horiz</code> is true) axis is drawn.
axisnames	logical. If TRUE, and if there are <code>names.arg</code> (see above), the other axis is drawn (with <code>lty=0</code> ) and labeled.
prval	logical. If TRUE, then values are plotted above all points and bars.
lm	logical. If TRUE, the linear fit is plotted.

<code>cex.axis</code> , <code>cex.names</code> , <code>cex.values</code>	character scaling factor for numeric axis labels, names, and displayed values, respectively.
<code>inside</code>	logical. If TRUE, the lines which divide adjacent (non-stacked!) bars will be drawn. Only applies when <code>space = 0</code> (which it partly is when <code>beside = TRUE</code> ).
<code>plot</code>	logical. If FALSE, nothing is plotted.
<code>axis.lty</code>	the graphics parameter <code>lty</code> applied to the axis and tick marks of the categorical (default horizontal) axis. Note that by default the axis is suppressed.
<code>plot.ci</code>	logical. If TRUE, confidence intervals are plotted over the bars. Note that if a stacked bar plot is generated, confidence intervals will not be plotted even if <code>plot.ci = TRUE</code>
<code>ci.l</code> , <code>ci.u</code>	The confidence intervals ( <code>ci.l</code> = lower bound, <code>ci.u</code> = upper bound) to be plotted if <code>plot.ci = TRUE</code> . Values must have the same dim structure as <code>height</code> .
<code>ci.color</code>	the color for the confidence interval line segments
<code>ci.lty</code>	the line type for the confidence interval line segments
<code>ci.lwd</code>	the line width for the confidence interval line segments
<code>plot.grid</code>	if TRUE a lined grid will be plotted behind the bars
<code>grid.inc</code>	the number of grid increments to be plotted
<code>grid.lty</code>	the line type for the grid
<code>grid.lwd</code>	the line width for the grid
<code>grid.col</code>	the line color for the grid
<code>add</code>	logical, if TRUE add barplot to current plot.
<code>by.row</code>	Logical value. If TRUE the data matrix is organized with variables along rows rather than down columns.
<code>...</code>	further graphical parameters ( <code>par</code> ) are passed to <code>plot.window()</code> , <code>title()</code> and <code>axis</code> .

## Details

Plot units are automatically scaled to SI units based on the maximum value present, according to the set of units specified by characters in the `kmg` parameter. These letters are interpreted as

**P** peta = 1E15  
**T** tera = 1E12  
**G** giga = 1E09  
**M** mega = 1E06  
**k** kilo = 1E03  
**m** milli= 1E-03  
**u** micro= 1E-06  
**n** nano = 1E-09  
**p** pico = 1E-12  
**f** femto= 1E-15

with the default being "fpnumkMGTP" (all of these units). For example, if the largest value plotted is 1243000, it would be presented as 1.234M.

**Value**

A numeric vector (or matrix, when `beside = TRUE`), say `mp`, giving the coordinates of *all* the bar midpoints drawn, useful for adding to the graph.

If `beside` is true, use `colMeans(mp)` for the midpoints of each *group* of bars, see example.

**Author(s)**

Lodewijk Bonebakker <bonebakker@comcast.net> with modifications by Gregory R. Warnes <greg@warnes.net>. Based on `barplot2()`.

**See Also**

[plot](#), [boxplot](#)

**Examples**

```
data(VADeaths, package = "datasets")

VADeaths <- cbind( Age=c(50,55,60,65,70), VADeaths)

mp <- ooplot(VADeaths) # default
mp <- ooplot(VADeaths, type="xyplot") # same as default
mp <- ooplot(VADeaths, type="linear") # linear scale
mp <- ooplot(VADeaths, type="linear", log="y") # log scale on y axis
mp <- ooplot(VADeaths, type="barplot") # barplot
mp <- ooplot(VADeaths, type="stackbar") # stacked

tot <- colMeans(VADeaths[,-1])
ooplot(VADeaths,
       col = c("lightblue", "mistyrose", "lightcyan", "lavender"),
       legend = colnames(VADeaths)[-1], ylim = c(0, 100),
       type="barplot", cex.values=0.75)
title(main = "Death Rates in Virginia", font.main = 4)

##
## Capability demo
##
## examples for the ooplot routine
##
## create some test data
test1 <- data.frame(x=c(0,1,2,3,4), lin=c(0,1,2,3,4))
test2 <- data.frame(x=c(0,1,2,3,4), par=c(0,1,4,9,16))
test3 <- data.frame(x=c(-2,-1,0,1,2), y2=c(4,1,0,1,4))
## single line test example
test1f <- test1
## two column example
test2f <- merge(test1,test2,by.x="x",all=TRUE,sort=TRUE)
## three column example
test3f <- merge(test2f,test3,by.x="x",all=TRUE,sort=TRUE)
```

```

## subset, single row, example
test5r <- test3f[5,]

##
## xyplot, linear, barplot, stackbar
mat <- matrix(c(1:16),4,4,byrow=TRUE)
layout(mat)

ooplot(test1f,type="barplot",col=c("red"))
title(main="barplot")
ooplot(test2f,type="barplot",col=c("red","blue"))
ooplot(test3f,type="barplot",col=c("red","blue","green"))
ooplot(test5r,type="barplot",col=c("red","blue","green"))

ooplot(test1f,type="xyplot",col=c("red"))
title(main="xyplot")
ooplot(test2f,type="xyplot",col=c("red","blue"))
ooplot(test3f,type="xyplot",col=c("red","blue","green"))
ooplot(test5r,type="xyplot",col=c("red","blue","green"))

ooplot(test1f,type="linear",col=c("red"))
title(main="linear")
ooplot(test2f,type="linear",col=c("red","blue"))
ooplot(test3f,type="linear",col=c("red","blue","green"))
ooplot(test5r,type="linear",col=c("red","blue","green"))

ooplot(test1f,type="stackbar",col=c("red"))
title(main="stackbar")
ooplot(test2f,type="stackbar",col=c("red","blue"))
ooplot(test3f,type="stackbar",col=c("red","blue","green"))
ooplot(test5r,type="stackbar",col=c("red","blue","green"))

# restore default layout (1 plot/page)
layout(1)

```

---

overplot

*Plot multiple variables on the same region, with appropriate axes*


---

## Description

overplot graphs a set of variables defined on the same x-range but which have varying y-ranges on the same plotting area. For each set of y-values it uses a different color and line-type and draws a correspondingly colored and line-typed axis. `panel.overplot` is used by `overplot` to draw the individual graphs.

## Usage

```

overplot(formula, data = parent.frame(), same.scale = FALSE, xlab, ylab,
         xlim, ylim, min.y, max.y, log = "", panel = "panel.overplot",
         subset, plot = TRUE, groups, main, f = 2/3, ...)

```

**Arguments**

formula	Formula describing the x and y variables. It should be of the form $x \sim y z$ . The conditioning variable (z) should be a factor.
same.scale	Logical value indicating whether the plot region should have the same range for all plots. Defaults to FALSE.
xlab, ylab, xlim, ylim, main	Standard plotting parameters. See <a href="#">plot</a> for details
min.y, max.y	Scalar or vector values used to specify the y plotting limits for individual plots. If a single scalar value is provided, it will be used for all plots. These parameters can be used specify one end of the individual plot ranges, while allowing the other end to vary with the data. EG, to force 0 to always be within the plot region.
log	character string "", 'x', 'y', or 'xy', indicating which axes should be plotted on a log scale. Defaults to "" (neither).
panel	a plotting function to be called to draw the individual plots. Defaults to <code>overplot.panel</code> , which plots the points and a lowess smooth.
plot	Logical value indicating whether to draw the plot.
groups	(optional) character vector giving the names of levels of the conditioning variable to plot. Defaults to all levels of the conditioning variable.
f	Smoothing parameter for lowess
data, subset, ...	parameters passed to <code>model.frame</code> to obtain the data to be plotted from the formula.

**Details**

This function essentially performs

```
tmp <- split(data, z)
for(i in levels(z))
  plot(x ~ y, data=tmp[[z]])
```

except that all of the plots are shown on the same plotting region and varying scales for each value of z are handled nicely.

**Value**

A copy of the data split by the conditioning variable.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

[interaction.plot](#), [coplot](#) for alternative visualizations of 3-way data.

## Examples

```
# Example teratogenicity rtPCR data
data(rtPCR)

# same scale
overplot( RQ ~ Conc..ug.ml. | Test.Substance,
          data=rtPCR,
          subset=Detector=="ProbeType 1" & Conc..ug.ml. > 0,
          same.scale=TRUE,
          log="xy",
          f=3/4,
          main="Detector=ProbeType 1",
          xlab="Concentration (ug/ml)",
          ylab="Relative Gene Quantification"
        )

# different scales, but force lower limit to 0.01
overplot( RQ ~ Conc..ug.ml. | Test.Substance,
          data=rtPCR,
          subset=Detector=="ProbeType 8" & Conc..ug.ml. > 0,
          log="xy",
          f=3/4,
          main="Detector=ProbeType 8",
          xlab="Concentration (ug/ml)",
          ylab="Relative Gene Quantification",
          min.y=0.01
        )
```

---

plotCI

*Plot Error Bars and Confidence Intervals*

---

## Description

Given a set of x and y values and interval width or upper and lower bounds, plot the points with error bars. This can be a useful tool for visualizing confidence intervals.

## Usage

```
plotCI(x, y = NULL, uiw, liw = uiw, ui, li, err='y', ylim=NULL,
       xlim=NULL, type="p", col=par("col"), barcol=col,
       pt.bg = par("bg"), sfrac = 0.01, gap=1, lwd=par("lwd"),
       lty=par("lty"), labels=FALSE, add=FALSE, xlab, ylab, minbar,
       maxbar, ... )
```

**Arguments**

<code>x,y</code>	coordinates for the center of error bars. <code>y</code> defaults to <code>1:n</code> .
<code>uiw</code>	width of the upper or right error bar. Set to <code>NULL</code> or <code>NA</code> to omit upper bars.
<code>liw</code>	width of the lower or left error bar. Defaults to same value as <code>uiw</code> . Set to <code>NULL</code> or <code>NA</code> to omit lower bars.
<code>ui</code>	upper end of error bars. Defaults to <code>y + uiw</code> or <code>x + uiw</code> depending on <code>err</code> . Set to <code>NULL</code> or <code>NA</code> to omit upper bars.
<code>li</code>	lower end of error bars. Defaults to <code>y - liw</code> or <code>x - liw</code> depending on <code>err</code> . Set to <code>NULL</code> or <code>NA</code> to omit lower bars.
<code>err</code>	direction for error bars. Set to <code>"y"</code> for vertical bars. Set to <code>"x"</code> for horizontal bars. Defaults to <code>"y"</code> .
<code>col</code>	color of plotting character used center marker of error bars. Default is <code>"black"</code> .
<code>xlim, ylim</code>	range of x/y values to include in the plotting area.
<code>type</code>	point/line type; passed to <a href="#">points</a>
<code>barcol</code>	color of the error bars. Defaults to the same value as <code>col</code>
<code>pt.bg</code>	background color of points (use <code>pch=21</code> , <code>pt.bg=par("bg")</code> to get open points superimposed on error bars).
<code>sfrac</code>	width of "crossbar" at the end of error bar as a fraction of the x plotting region. Defaults to 0.01.
<code>gap</code>	space left between the center of the error bar and the lines marking the error bar in units of the height (width) of the letter "O". Defaults to 1.0
<code>lwd</code>	width of bar lines.
<code>lty</code>	line type of bar lines.
<code>labels</code>	either a logical value indicating whether the circles representing the x values should be replaced with text giving the actual values or a vector containing labels to use instead. Defaults to <code>FALSE</code> .
<code>add</code>	logical indicating whether error bars should be added to the current plot. If <code>FALSE</code> (the default), a new plot will be created and symbols/labels for the x values will be plotted before drawing error bars.
<code>minbar</code>	minimum allowed value for bar ends. If specified, values smaller than <code>minbar</code> will be replaced with <code>minbar</code> .
<code>maxbar</code>	maximum allowed value for bar ends. If specified, values larger than <code>maxbar</code> will be replaced with <code>maxbar</code> .
<code>...</code>	optional plotting parameters
<code>xlab</code>	label for x axis.
<code>ylab</code>	label for y axis.

**Author(s)**

Original version by Bill Venables <wvenable@attunga.stats.adelaide.edu.au> posted to r-help on Sep. 20, 1997. Enhanced version posted to r-help by Ben Bolker <ben@zoo.ufl.edu> on Apr. 16, 2001. This version was modified and extended by Gregory R. Warnes <greg@warnes.net>. Additional changes suggested by Martin Maechler <maechler@stat.math.ethz.ch> integrated on July 29, 2004.

**See Also**

[plotmeans](#) provides an enhanced wrapper to `plotCI`.

**Examples**

```
# plot means and
data(state)
tmp <- split(state.area, state.region)
means <- sapply(tmp, mean)
stdev <- sqrt(sapply(tmp, var))
n <- sapply(tmp,length)
ciw <- qt(0.975, n) * stdev / sqrt(n)

# plain
plotCI(x=means, uiw=ciw)

# prettier
plotCI(x=means, uiw=ciw, col="black", barcol="blue", lwd=1)

# give mean values
plotCI(x=means, uiw=ciw, col="black", barcol="blue",
       labels=round(means,-3), xaxt="n", xlim=c(0,5) )
axis(side=1, at=1:4, labels=names(tmp), cex=0.7)

# better yet, just use plotmeans ... #
plotmeans( state.area ~ state.region )
```

---

plotmeans

*Plot Group Means and Confidence Intervals*

---

**Description**

Plot group means and confidence intervals.

**Usage**

```
plotmeans(formula, data=NULL, subset, na.action,
          bars=TRUE, p=0.95, minsd=0, minbar, maxbar,
          xlab=names(mf)[2], ylab=names(mf)[1], mean.labels=FALSE,
          ci.label=FALSE, n.label=TRUE, text.n.label="n=",
          digits=getOption("digits"), col="black", barwidth=1,
          barcol="blue", connect=TRUE, ccol=
          col, legends=names(means), xaxt, use.t=TRUE,
          lwd=par("lwd"), ...)
```



**Arguments**

formula	symbolic expression specifying the outcome (continuous) and grouping variable (factor). See <code>lm()</code> for details.
data	optional data frame containing the variables in the model.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain 'NA's. See <code>lm()</code> for details.
bars	a logical value indicating whether confidence interval bars should be plotted. Defaults to TRUE.
p	confidence level for error bars. Defaults to 0.95.
minsd	minimum permitted value for the standard deviation within each factor level. Any standard deviation estimates smaller than <code>minsd</code> will be replaced with <code>minsd</code> . Defaults to 0.
minbar	minimum allowed value for bar ends. If specified, values smaller than <code>minbar</code> will be replaced with <code>minbar</code> .
maxbar	maximum allowed value for bar ends. If specified, values larger than <code>maxbar</code> will be replaced with <code>maxbar</code> .
xlab	x-axis label.
ylab	y-axis label.
mean.labels	either a logical value indicating whether the circles representing the group means should be replaced with text giving the actual mean values or a vector containing labels to use instead. Defaults to FALSE.
ci.label	a logical value indicating whether text giving the actual interval end values should be placed at the end of each confidence interval bar. Defaults to FALSE.
n.label	a logical value indicating whether text giving the number of observations in each group should be added to the plot.
text.n.label	Prefix text for labeling observation counts. Defaults to "n=".
digits	number of significant digits to use when displaying mean or confidence limit values.
col	color of circles marking group means. Default is "black".
barwidth	linewidth of interval bars and end marks. Default is 1.
barcol	color of interval bars and end marks. Default is "blue".
connect	either a logical value indicating whether the means of each group should be connected by a line, or a list of vectors giving the index of bars that should be connected by a line. Defaults to TRUE.
ccol	color of lines used to connect means. Defaults to the same color as "col".
legends	vector containing strings used to label groups along the x axis. Defaults to group names.
xaxt	A character which specifies the axis type. Specifying "n" causes an axis to be set up, but not plotted.

`use.t` a logical value indicating whether the t distribution should be used to compute confidence intervals. If TRUE, the default, a t distribution will be used. If FALSE, a normal distribution will be used.

`lwd` Width of connecting lines

`...` optional plotting parameters.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

[plotCI](#), [boxplot](#)

**Examples**

```
# show comparison with boxplot
data(state)
plotmeans(state.area ~ state.region)

# show some color and mean labels
plotmeans(state.area ~ state.region,
           mean.labels=TRUE, digits=-3,
           col="red", connect=FALSE)

# show how to specify which means should be connected
plotmeans(state.area ~ state.region, connect=list(1:2, 3:4),
           ccol="red", pch=7 )

# more complicated example showing how to show an interaction
data(esoph)
par(las=2,
    mar=c(10.1,4.1,4.1,2.1), # use perpendicular axis labels
    mgp=c(8,1,0)           # create enough space for long x labels
                           # move x axis legend down to avoid overlap
)
plotmeans(ncases/ncontrols ~ interaction(agegp , alcgp, sep = "  "),
           connect=list(1:6,7:12,13:18,19:24),
           barwidth=2,
           col="dark green",
           data=esoph,
           xlab="Age Group and Alcohol Consumption",
           ylab="# Cases / # Controls",
           main=c("Fraction of Cases for by Age and Alcohol Consumption",
                  "Ile-et-Vilaine Esophageal Cancer Study")
)
abline(v=c(6.5, 12.5, 18.5), lty=2)
```

---

qqnorm.aov

*Makes a half or full normal plot for the effects from an aov model*


---

### Description

Makes a half or full normal plot for the effects from a model inheriting from class aov. One can interactively label the points in the plot.

### Usage

```
## S3 method for class 'aov'
qqnorm(y, full=FALSE, label=FALSE, omit=NULL,
        xlab=paste(if (full) "" else "Half", " Normal plot"),
        ylab="Effects", ...)
```

### Arguments

y	A model object inheriting from aov
full	Full or half normal plot (half is default)
label	If TRUE, function allows interactive labelling of points in plot, using the mouse
omit	Numeric or character vector of effects to omit, the intercept is always omitted
xlab	Horizontal axis label
ylab	Vertical axis label
...	Further arguments to be given to the plot function

### Details

Produces a (half) normal plot of the effects from an AOV model. The idea behind the plot is that most effects will be small or null, and this effects can be used as a basis for estimation of the experimental variance. This small effects will show up in the plot as a straight line, other effects can be judged against this as a background. Heavily used by Box, Hunter & Hunter, which attributes the idea to Daniel.

This is a simpler implementation than the one in S-Plus.

### Value

If label=TRUE, the vector of points identified, else nothing of interest.

### Author(s)

Kjetil Halvorsen <kjetil@entelnet.bo>

## References

- Box, Hunter and Hunter: Statistics for Experimenters. An Introduction to Design, Data Analysis and Model Building. Wiley.
- Daniel, C (1976): Applications of Statistics to Industrial Experimentation. Wiley.
- Daniel, C (1959): Use of half-normal plot in interpreting factorial two-level experiments. *Technometrics*.1, 149.

## Examples

```
library(MASS)
data(npk)
npk.aov <- aov(yield ~ block + N*P*K, npk)
qqnorm(npk.aov)

## interactive labeling of points. Click mouse on points to show label.
if (dev.interactive()) qqnorm(npk.aov, omit=2:6, label=TRUE)
```

---

residplot

*Undocumented functions*

---

## Description

These functions are undocumented. Some are internal and not intended for direct use. Others simply haven't been documented yet.

## Usage

```
residplot(model, formula, ...)
```

## Arguments

model	Undocumented
formula	Undocumented
...	arguments to be passed to fun

## Details

These functions are undocumented. Some are internal and not intended for direct use. Others simply haven't been documented yet.

## Author(s)

Gregory R. Warnes <greg@warnes.net>

---

 rich.colors *Rich Color Palettes*


---

**Description**

Create a vector of n colors that are perceptually equidistant and in an order that is easy to interpret.

**Usage**

```
rich.colors(n, palette="temperature", alpha=1.0, rgb=FALSE, plot=FALSE)
```

**Arguments**

n	number of colors to generate.
palette	palette to use: "temperature" contains blue-green-yellow-red, and "blues" contains black-blue-white.
alpha	alpha transparency, from 0 (fully transparent) to 1 (opaque).
rgb	if TRUE then a matrix of RGBA values is included as an attribute.
plot	whether to plot a descriptive color diagram.

**Value**

A character vector of color codes.

**Author(s)**

Arni Magnusson.

**See Also**

[rgb](#), [rainbow](#), [heat.colors](#).

**Examples**

```
m <- abs(matrix(1:120+rnorm(120), nrow=15, ncol=8))
opar <- par(bg="gray", mfrow=c(1,2))
matplot(m, type="l", lty=1, lwd=3, col=rich.colors(8))
matplot(m, type="l", lty=1, lwd=3, col=rich.colors(8,"blues"))
par(opar)

barplot(rep(1,100), col=rich.colors(100), space=0, border=0, axes=FALSE)
barplot(rep(1,20), col=rich.colors(40)[11:30]) # choose subset

plot(m, rev(m), ylim=c(120,0), pch=16, cex=2,
      col=rich.colors(200,"blues",alpha=0.6)[1:120]) # semitransparent

rich.colors(100, plot=TRUE) # describe rgb recipe
```

```

par(mfrow=c(2,2))
barplot(m, col=heat.colors(15), main="\nheat.colors")
barplot(m, col=1:15, main="\ndefault palette")
barplot(m, col=rich.colors(15), main="\nrich.colors")
barplot(m, col=rainbow(15), main="\nrainbow")
par(opar)

```

---

rtPCR

*Teratogenesis rtPCR data*


---

### Description

rtPCR data for experiments investigating a variety of markers for characterizing teratogenicity.

### Usage

```
data(rtPCR)
```

### Format

A data frame with 1672 observations on the following 21 variables.

**PlateID** a factor with levels A0027002 through A0054019

**Test.Substance** a factor with levels Compound A through Compound H

**Teratogenicity.in.vivo** a factor with levels Non Strong Weak / Moderate

**Sample** a factor with levels Sample 1 - Sample 152

**Rep..** a factor with levels Rep 1 - Rep 21

**Label** a factor with levels Ctrl, Neg. Ctrl P1 - P9, No Vehicle Ctrl, and Pos. Ctrl

**Conc..ug.ml.** a numeric vector

**Detector** a factor with levels ProbeType 1 - ProbeType 17

**Avg.delta.Ct** a numeric vector

**delta.Ct.SD** a numeric vector

**delta.delta.Ct** a numeric vector

**RQ** a numeric vector

**X..RQ** a numeric vector

**X100..Custom..** a numeric vector

**X100...Custom..** a numeric vector

**Custom..** a numeric vector

**Custom...1** a numeric vector

**RQ.Min** a numeric vector

**RQ.Max** a numeric vector

**Threshold** a numeric vector

**Details**

TBA

**Source**

Anonymized data.

**Examples**

```
data(rtPCR)

# same scale
overplot( RQ ~ Conc..ug.ml. | Test.Substance,
          data=rtPCR,
          subset=Detector=="ProbeType 7" & Conc..ug.ml. > 0,
          same.scale=TRUE,
          log="xy",
          f=3/4,
          main="Detector=ProbeType 7",
          xlab="Concentration (ug/ml)",
          ylab="Relative Gene Quantification"
        )

# different scales, but force lower limit to 0.01
overplot( RQ ~ Conc..ug.ml. | Test.Substance,
          data=rtPCR,
          subset=Detector=="ProbeType 7" & Conc..ug.ml. > 0,
          log="xy",
          f=3/4,
          main="Detector=ProbeType 7",
          xlab="Concentration (ug/ml)",
          ylab="Relative Gene Quantification",
          min.y=0.01
        )
```

---

sinkplot

*Send textual R output to a graphics device*

---

**Description**

Divert R's standard text output to a graphics device.

**Usage**

```
sinkplot(operation = c("start", "plot", "cancel"), ...)
```

**Arguments**

operation	See below
...	Plot arguments. (Ignored unless operation="plot").

## Details

This function allows the printed output of R commands to be captured and displayed on a graphics device.

The capture process is started by calling `sinkplot("start")`. Now R commands can be executed and all printed output (except errors) will be captured. When the desired text has been captured `sinkplot("plot")` can be called to actually display the output. `sinkplot("cancel")` can be used to abort the output capture without plotting.

The current implementation does not allow `sinkplot` to be nested.

## Value

Invisibly returns a character vector containing one element for each line of the captured output.

## Author(s)

Gregory R. Warnes <greg@warnes.net>

## References

Functionality requested by Kevin Wright <kwright@eskimo.com> in the R-devel newlist posting <https://stat.ethz.ch/pipermail/r-devel/2004-January/028483.html>.

## See Also

[capture.output](#), [textplot](#)

## Examples

```
set.seed(12456)
x <- factor(sample( LETTERS[1:5], 50, replace=TRUE))
y <- rnorm(50, mean=as.numeric(x), sd=1)

## construct a figure showing a box plot of the data, followed by an
## analysis of variance table for the data
layout(cbind(1:2), heights=c(2,1))

boxplot(y~x, col="darkgreen")

sinkplot()
anova(lm(y~x))
sinkplot("plot", col="darkgreen")
```



---

space	<i>Space points in an x-y plot so they don't overlap.</i>
-------	---

---

**Description**

Space points in an x-y plot so they don't overlap.

**Usage**

```
space(x, y, s=1/50, na.rm=TRUE, direction="x")
```

**Arguments**

x	numeric vector of x coordinates.
y	numeric vector of y coordinates.
s	either a single numeric value or 2 element vector specifying the minimum distance between points in the x and y dimensions as a fraction of the x and y range. Defaults to 1/50.
na.rm	logical indicating whether pairs where one or both elements are missing should be removed. Defaults to TRUE.
direction	"x" or "y", indicating which direction points should be moved to accomplish spacing.

**Details**

In an x-y plot where at least one variable has discrete levels several points may be plotted at or very near the same coordinates. This makes it difficult to gauge the number of points in a specific region. A common method of resolving this problem is to 'jitter' the points by adding random noise.

This function takes a different approach to the same problem.

When there are two or more points with the same (x,y) value (or within  $x \pm s[1]$  and  $x \pm s[2]$ ), it spaces these out in the x direction so that the points are separated by at least distance s.

Another method for dealing with overplotting is available in the [sunflowerplot](#) function.

**Value**

list with two components

x	(modified) x location for each input point
y	y location of each input point

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

[jitter](#), [sunflowerplot](#)

**Examples**

```
x <- rep(1:5, 10)
y <- round(rnorm(length(x),x))

prepar <- par("mfrow")
par(mfrow=c(1,3))

# standard x-y plot: noverlapping points are hidden
plot(x,y)
title("Standard Plot")

# 'spaced' plot: overlapping points are spread out and visible
plot(space(x,y))
title("Plot with 'space'")

# 'spaced' plot: overlapping points are spread out along y and visible
plot(space(x,y, direction='y'))
title("Plot with 'space', direction='y' ")

# 'sunflower' plot, another approach, overlapping points are
# indicated via petals
sunflowerplot(x,y)
title("Sunflower Plot")

par(mfrow=prepar)
```

---

textplot

*Display text information in a graphics plot.*

---

**Description**

This function displays text output in a graphics window. It is the equivalent of 'print' except that the output is displayed as a plot.

**Usage**

```
textplot(object, halign="center", valign="center", cex, ...)
## Default S3 method:
textplot(object, halign=c("center","left","right"),
         valign=c("center", "top", "bottom"), cex, ... )
## S3 method for class 'character'
```

```

textplot(object, halign = c("center", "left", "right"),
         valign = c("center", "top", "bottom"), cex, fixed.width=TRUE,
         cspace=1, lspace=1, mar=c(0, 0, 3, 0) + 0.1,
         tab.width = 8, ...)
## S3 method for class 'data.frame'
textplot(object, halign = c("center", "left", "right"),
         valign = c("center", "top", "bottom"), cex, ...)
## S3 method for class 'matrix'
textplot(object, halign = c("center", "left", "right"),
         valign = c("center", "top", "bottom"), cex, cmar = 2,
         rmar = 0.5, show.rownames = TRUE, show.colnames = TRUE,
         hadj = 1, vadj = 1, mar = c(1, 1, 4, 1) + 0.1,
         col.data = par("col"), col.rownames = par("col"),
         col.colnames = par("col"), ...)

```

### Arguments

object	Object to be displayed.
halign	Alignment in the x direction, one of "center", "left", or "right".
valign	Alignment in the y direction, one of "center", "top" , or "bottom"
cex	Character size, see <a href="#">par</a> for details. If unset, the code will attempt to use the largest value which allows the entire object to be displayed.
fixed.width	Logical value indicating whether to emulate a fixed-width font by aligning characters in each row of text. This is usually necessary for text-formatted tables display properly. Defaults to 'TRUE'.
cspace	Space between characters as a multiple of the width of the letter 'W'. This only applies when fixed.width==TRUE.
lspace	Line spacing. This only applies when fixed.width==TRUE.
mar	Figure margins, see the documentation for <a href="#">par</a> .
rmar, cmar	Space between rows or columns, in fractions of the size of the letter 'M'.
show.rownames, show.colnames	Logical value indicating whether row or column names will be displayed.
hadj, vadj	Vertical and horizontal location of elements within matrix cells. These have the same meaning as the <a href="#">adj</a> graphics parameter (see <a href="#">par</a> ).
col.data	Colors for data elements. If a single value is provided, all data elements will be the same color. If a matrix matching the dimensions of the data is provided, each data element will receive the specified color.
col.rownames, col.colnames	Colors for row names and column names, respectively. Either may be specified as a scalar or a vector of appropriate length.
tab.width	Width of a single tab stop, in characters
...	Optional arguments passed to the text plotting command or specialized object methods

**Details**

A new plot is created and the object is displayed using the largest font that will fit on in the plotting region. The `halign` and `valign` parameters can be used to control the location of the string within the plotting region.

For matrixes and vectors a specialized `textplot` function is available, which plots each of the cells individually, with column widths set according to the sizes of the column elements. If present, row and column labels will be displayed in a bold font.

**Value**

The character scaling factor (`cex`) used.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

[plot](#), [text](#), [capture.output](#)

**Examples**

```
## Not run:
### simple examples
# show R version information
textplot(version)

# show the alphabet as a single string
textplot( paste(letters[1:26], collapse=" ") )

# show the alphabet as a matrix
textplot( matrix(letters[1:26], ncol=2))

### Make a nice 4 way display with two plots and two text summaries

data(iris)
par(mfrow=c(2,2))
plot( Sepal.Length ~ Species, data=iris, border="blue", col="cyan",
      main="Boxplot of Sepal Length by Species" )
plotmeans( Sepal.Length ~ Species, data=iris, barwidth=2, connect=FALSE,
           main="Means and 95% Confidence Intervals\nof Sepal Length by Species")

info <- sapply( split(iris$Sepal.Length, iris$Species),
               function(x) round(c(Mean=mean(x), SD=sd(x), N=gdata::nobs(x)),2) )

textplot( info, valign="top" )
title("Sepal Length by Species")

reg <- lm( Sepal.Length ~ Species, data=iris )
textplot( capture.output(summary(reg)), valign="top")
title("Regression of Sepal Length by Species")
```

```

par(mfrow=c(1,1))

### Show how to control text color
cols <- c("red", "green", "magenta", "forestgreen")
mat <- cbind(name=cols, t(col2rgb(cols)), hex=col2hex(cols))

textplot(mat,
          col.data=matrix(cols, nrow=length(cols), byrow=FALSE, ncol=5),
          )

### Show how to manually tune the character size
data(iris)
reg <- lm( Sepal.Length ~ Species, data=iris )
text <- capture.output(summary(reg))

# do the plot and capture the character size used
textplot(text, valign="top")

# see what size was used
cex

# now redo the plot at 80% size
textplot( text, valign="top", cex=cex*0.80)

## End(Not run)

```

---

venn

*Plot a Venn diagram*


---

## Description

Plot a Venn diagrams for up to 5 sets

## Usage

```

venn(data, universe=NA, small=0.7, showSetLogicLabel=FALSE,
      simplify=FALSE, show.plot=TRUE, intersections=TRUE, names,
      ...)

## S3 method for class 'venn'
plot(x, y, ..., small=0.7, showSetLogicLabel=FALSE,
      simplify=FALSE)

```

**Arguments**

<code>data, x</code>	Either a list list containing vectors of names or indices of group intersections, or a data frame containing boolean indicators of group intersectionship (see below)
<code>universe</code>	Subset of valid name/index elements. Values ignore values in codedata not in this list will be ignored. Use NA to use all elements of data (the default).
<code>small</code>	Character scaling of the smallest group counts
<code>showSetLogicLabel</code>	Logical flag indicating whether the internal group label should be displayed
<code>simplify</code>	Logical flag indicating whether unobserved groups should be omitted.
<code>show.plot</code>	Logical flag indicating whether the plot should be displayed. If false, simply returns the group count matrix.
<code>intersections</code>	Logical flag indicating if the returned object should have the attribute "individuals.in.intersections" featuring for every set a list of individuals that are assigned to it.
<code>y</code>	Ignored
<code>...</code>	Optional graphical parameters.
<code>names</code>	Optional vector of group names.

**Details**

`data` should be either a named list of vectors containing character string names ("GeneAABBB", "GeneBBBCY", ..., "GeneXXZZ") or indexes of group intersections (1, 2, ..., N), or a data frame containing indicator variables (TRUE, FALSE, TRUE, ..) for group intersectionship. Group names will be taken from the component list element or column names.

**Value**

Invisibly returns an object of class "venn", containing:

- A matrix of all possible sets of groups, and the observed count of items belonging to each The first column contains observed counts, subsequent columns contain 0-1 indicators of group intersectionship.
- If `intersections=TRUE`, the attribute `intersections` will be a list of vectors containing the names of the elements belonging to each subset.

**Author(s)**

Steffen Moeller <steffen\\_moeller@gmx.de>, with cleanup and packaging by Gregory R. Warnes <greg@warnes.net>.

**Examples**

```
##
## Example using a list of item names belonging to the
## specified group.
##
```

```
## construct some fake gene names..
oneName <- function() paste(sample(LETTERS,5,replace=TRUE),collapse="")
geneNames <- replicate(1000, oneName())

##
GroupA <- sample(geneNames, 400, replace=FALSE)
GroupB <- sample(geneNames, 750, replace=FALSE)
GroupC <- sample(geneNames, 250, replace=FALSE)
GroupD <- sample(geneNames, 300, replace=FALSE)
input <-list(GroupA,GroupB,GroupC,GroupD)
input

tmp <- venn(input)
attr(tmp, "intersections")

##
## Example using a list of item indexes belonging to the
## specified group.
##
GroupA.i <- which(geneNames %in% GroupA)
GroupB.i <- which(geneNames %in% GroupB)
GroupC.i <- which(geneNames %in% GroupC)
GroupD.i <- which(geneNames %in% GroupD)
input.i <-list(A=GroupA.i,B=GroupB.i,C=GroupC.i,D=GroupD.i)
input.i

venn(input.i)

##
## Example using a data frame of indicator ('f'lag) columns
##
GroupA.f <- geneNames %in% GroupA
GroupB.f <- geneNames %in% GroupB
GroupC.f <- geneNames %in% GroupC
GroupD.f <- geneNames %in% GroupD
input.df <- data.frame(A=GroupA.f,B=GroupB.f,C=GroupC.f,D=GroupD.f)
head(input.df)
venn(input.df)

## smaller set to create empty groupings
small <- input.df[1:20,]

venn(small, simplify=FALSE) # with empty groupings
venn(small, simplify=TRUE) # without empty groupings

## Capture group counts, but don't plot
tmp <- venn(input, show.plot=FALSE)
tmp

## Show internal binary group labels
venn(input, showSetLogicLabel=TRUE)
```

```

## Limit universe
tmp <- venn(input, universe=geneNames[1:100])
tmp

##
## Example to determine which elements are in A and B but not in
## C and D using the 'intersections' attribute.
##
tmp <- venn(input, intersection=TRUE)
isect <- attr(tmp, "intersection")

# Look at all of the subsets
str(isect)

# Extract and combine the subsets of interest..
AandB <- unique(c(isect$A, isect$B, isect$`A:B`))

# and look at the results
str(AandB)

##
## The full set of elements of each intersection is provided in the
## "intersections" attribute.
##
a<-venn(list(1:5,3:8), show.plot=FALSE)
intersections<-attr(a,"intersections")
print(intersections)
# $A
# [1] "1" "2"
#
# $B
# [1] "6" "7" "8"
#
# $`A:B`
# [1] "3" "4" "5"

```

---

wapply

---

*Compute the Value of a Function Over a Local Region Of An X-Y Plot*


---

### Description

This function applies the specified function to the sets of y values that are defined by overlapping "windows" in the x-dimension. For example, setting fun=mean returns local means, while setting fun=function(x) sqrt(var(x)) returns local estimates of the standard deviation.

### Usage

```
wapply(x, y, fun=mean, method="range", width, n=50, drop.na=TRUE,
      pts, ...)
```



**Arguments**

x	vector of x values for (x,y) pairs
y	vector of y values for (x,y) pairs
fun	function to be applied
method	method of defining an x-neighborhood. One of "width", "nobs", "range", or "fraction". See details.
width	width of an x-neighborhood. See details.
n	Number of equally spaced points at which to compute local estimates. See details.
drop.na	should points which result in missing values NA be omitted from the return value. Defaults to true.
pts	x locations at which to compute the local mean when using the "width" or "range" methods. Ignored otherwise.
...	arguments to be passed to fun

**Details**

Two basic techniques are available for determining what points fall within the same x-neighborhood. The first technique uses a window with a fixed width in the x-dimension and is selected by setting `method="width"` or `method="range"`. For `method="width"` the `width` argument is an absolute distance in the x-dimension. For `method="range"`, the `width` is expressed as a fraction of the x-range. In both cases, `pts` specifies the points at which evaluation of `fun` occurs. When `pts` is omitted, `n` x values equally spaced along the x range are used.

The second technique uses windows containing `k` neighboring points. The (x,y) pairs are sorted by the x-values and the nearest `k/2` points with higher x values and the `k/2` nearest points with lower x values are included in the window. When `method="nobs"`, `k` equals `width` (actually `2*floor(width/2)`). When `method="fraction"`, `width` specifies what fraction of the total number of points should be included. The actual number of points included in each window will be `floor(n*frac/2)*2`. Regardless of the value of `pts`, the function `fun` will be evaluated at all x locations.

**Value**

Returns a list with components

x	x location'
y	Result of applying fun to the window about each x location

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**Examples**

```

#show local mean and inner 2-sd interval to help diagnose changing mean
#or variance structure
x <- 1:1000
y <- rnorm(1000, mean=1, sd=1 + x/1000 )

plot(x,y)
lines(wapply(x,y,mean),col="red")

CL <- function(x,sd) mean(x)+sd*sqrt(var(x))

lines(wapply(x,y,CL,sd= 1),col="blue")
lines(wapply(x,y,CL,sd=-1),col="blue")
lines(wapply(x,y,CL,sd= 2),col="green")
lines(wapply(x,y,CL,sd=-2),col="green")

#show local mean and inner 2-sd interval to help diagnose changing mean
#or variance structure
x <- 1:1000
y <- rnorm(1000, mean=x/1000, sd=1)

plot(x,y)
lines(wapply(x,y,mean),col="red")

CL <- function(x,sd) mean(x)+sd*sqrt(var(x))

lines(wapply(x,y,CL,sd= 1,method="fraction",width=1/20),col="blue")
lines(wapply(x,y,CL,sd=-1,method="fraction",width=1/20),col="blue")
lines(wapply(x,y,CL,sd= 2,method="nobs",width=250),col="green")
lines(wapply(x,y,CL,sd=-2,method="nobs",width=250),col="green")

```

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