

# Package ‘wrGraph’

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**Version** 1.0.5

**Title** Graphics in the Context of Analyzing High-Throughput Data

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**Description** Additional options for making graphics in the context of analyzing high-throughput data are available here.  
This includes automatic segmenting of the current device (eg window) to accommodate multiple new plots,  
automatic checking for optimal location of legends in plots, small histograms to insert as legends,  
histograms re-transforming axis labels to linear when plotting log2-transformed data,  
a violin-plot <doi:10.1080/00031305.1998.10480559> function for a wide variety of input-formats,  
principal components analysis (PCA) <doi:10.1080/14786440109462720> with bag-plots <doi:10.1080/00031305.1999.10474494> to highlight and compare the center areas for groups of samples,  
generic MA-plots (differential- versus average-value plots) <doi:10.1093/nar/30.4.e15>,  
staggered count plots and generation of mouse-over interactive html pages.

**Depends** R (>= 3.1.0)

**Imports** graphics, grDevices, RColorBrewer, stats, wrMisc

**Suggests** dplyr, factoextra, FactoMineR, knitr, limma, rmarkdown, sm

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addBagPlot	<i>Add bagplot to existing plot</i>
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## Description

This function adds a bagplot on an existing (scatter-)plot allowing to highlight the central area of the data. Briefly, a bagplot is a bivariate boxplot, see [Bagplot](#), following the basic idea of a boxplot in two dimensions. Of course, multimodal distributions - if not separated first - may likely lead to mis-interpretation, similarly as it is known for interpreting boxplots. If a group of data consists only of 2 data-points, they will be connected using a straight line. It is recommended using transparent colors to highlight the core part of a group (if only 2 points are available, they will be connected using a straight line), in addition, one could use the option to re-plot all (non-outlyrer) points (arguments `reCol`, `rePch` and `reCex` must be used).

## Usage

```
addBagPlot(
  x,
  lev1 = 0.5,
  outCoef = 2,
  bagCol = NULL,
  bagCont = bagCol,
  bagLwd = 1.5,
  nCore = 4,
  outlCol = 2,
  outlPch = NULL,
  outlCex = 0.6,
  reCol = NULL,
```

```

    rePch = NULL,
    reCex = NULL,
    ctrPch = NULL,
    ctrCol = NULL,
    ctrCex = NULL,
    returnOutL = FALSE,
    callFrom = NULL,
    silent = TRUE
)

```

### Arguments

x	(matrix, list or data.frame) main numeric input of data/points to plot
lev1	(numeric) min content of data for central area (default 0.5 for 50 percent)
outCoef	(numeric) parameter for defining outliers (equivalent to range in <a href="#">boxplot</a> )
bagCol	(character or integer) color for filling center part of bagplot (default light transparent grey); Note: It is highly suggested to use transparency, otherwise points underneath will be covered
bagCont	(character) color for inner and outer contours of bagplot
bagLwd	(numeric) line width for outer contour, set to NULL for not displaying outer contour (see also <a href="#">par</a> )
nCore	(integer) decide when center should be determined by median or mean: if number of points reach nCore the median will be used
outlCol	(character or integer) color for highlighting outliers (for text and replottig outliers points), set to NULL for not highlighting outliers at all
outlPch	(integer) symbol replottig highlighted outliers (for text and replottig outliers points), set to NULL for not replottig outlier-points (see also <a href="#">par</a> )
outlCex	(numeric) cex type expansion factor for labels of highlighted outliers, set to NULL for not printing (row)names of outliers (see also <a href="#">par</a> )
reCol	(character or integer) color for replottig (non-outlyer) points, default set to NULL for not replottig
rePch	(integer) symbol for replottig (non-outlyer) points, default set to NULL for not re-plotting (see also <a href="#">par</a> )
reCex	(numeric) cex type expansion factor for lfor replottig (non-outlyer) points, default set to NULL for not replottig
ctrPch	(integer) symbol for shwing group center (see also <a href="#">par</a> )
ctrCol	(character or integer) color for group center symbol
ctrCex	(numeric) cex type expansion factor for size of group center (see also <a href="#">par</a> )
returnOutL	(logical) decide if rownames of (potential) outlyer values should be returned when running the function
callFrom	(character) allow easier tracking of messages produced
silent	(logical) suppress messages

**Value**

plot, optional return of matrix with outliers

**See Also**

[plotPCAw](#), [princomp](#)

**Examples**

```
set.seed(2020); dat1 <- matrix(round(rnorm(2000),3),ncol=2); rownames(dat1) <- 1:nrow(dat1)
dat1 <- dat1+ 5*matrix(rep(c(0,1,1,0,0,0,1,1),nrow(dat1)/4),byrow=TRUE,ncol=2)
col1 <- rgb(red=c(153,90,203,255 ),green=c(143,195,211,125),blue=c(204,186,78,115),
  alpha=90,maxColorValue=255)
## suppose we know the repartition into 4 subgroups which we would like to highlight them
grp1 <- rep(1:4,nrow(dat1)/4)
plot(dat1,col=grey(0.8),xlab="x",ylab="y",las=1,pch=grp1)
for(i in 1:4) addBagPlot(dat1[which(grp1==i),],bagCol=col1[i])
## slightly improved
library(wrMisc)
col2 <- convColorToTransp(col1,255)
plot(dat1,col=grey(0.8),xlab="x",ylab="y",las=1,pch=grp1)
for(i in 1:4) addBagPlot(dat1[which(grp1==i),],bagCol=col1[i],outlPch=i,
  outlCol=col2[i],bagLwd=3)
```

---

checkForLegLoc

*Find best place on plot for placing legend*

---

**Description**

This function tries to find the best location for placing a legend of a bivariate plot, ie scatter-plot. All 4 corners of the data to plot are inspected for the least occupation by data plotted while displaying the content of sampleGrp. Alternatively, by setting the argument showLegend the user-defined legend will be returned

**Usage**

```
checkForLegLoc(
  matr,
  sampleGrp = NULL,
  showLegend = TRUE,
  suplSpace = 4,
  testCorner = 1:4,
  silent = TRUE,
  callFrom = NULL
)
```

**Arguments**

<code>matr</code>	(matrix, list or data.frame) main data of plot
<code>sampleGrp</code>	(character or factor) with this option the text to be displayed in the legend may be taken into consideration for its length
<code>showLegend</code>	(logical or character) decide if <code>matr</code> should be checked for best location; if <code>showLegend</code> contains any of the standard legend-location designations (eg 'topleft') it will be used in the output
<code>suplSpace</code>	(numeric) allows to consider extra room taken in legend by symbol and surrounding space, interpreted as n additional characters
<code>testCorner</code>	(integer) which corners should be considered (1=left-top, 2=right-top, right-bottom, left-bottom)
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

**Value**

list with `$showL` indicating if legend is desired and `$loc` for the proposition of the best location, `$nConflicts` gives the counts of conflicts

**See Also**

[legend](#)

**Examples**

```
dat1 <- matrix(c(1:5,1,1:5,5), ncol=2)
grp <- c("abc","efghijk")
(legLoc <- checkForLegLoc(dat1, grp))
plot(dat1, cex=3)
legend(legLoc$loc, legend=grp, text.col=2:3, pch=1, cex=0.8)
```

---

<code>convertPlotCoordPix</code>	<i>Convert points of plot to coordinates in pixels</i>
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---

**Description**

This function allows conversion the plotting positions ('x' and 'y' coordiantes) of points in a given plot into coordiantes in pixels (of the entire plotting region). It was designed to be used as coordinates in an html file for mouse-over interactivity (display of names of points and links). Of course, the size of the plotting region is crucial and may not be changed afterwards (if the plot is not written to file using png etc). In turn the function [mouseOverHtmlFile](#) will use the pixel-coordiantes, allowing to annotate given points of a plot for mouse-over interactive html.

**Usage**

```
convertPlotCoordPix(
  x,
  y,
  useMar = c(6.2, 4, 4, 2),
  plotDim = c(1400, 800),
  plotRes = 100,
  fromTop = TRUE,
  callFrom = NULL,
  silent = FALSE
)
```

**Arguments**

x	(numeric) initial plotting coordinates on x-axis, names of vector - if available - will be used as IDs
y	(numeric) initial plotting coordinates on y-axis
useMar	(numeric,length=4) margins defined with plot, see also <a href="#">par</a>
plotDim	(integer, length=2) dimension of the plotting device in pixels, see also <a href="#">par</a>
plotRes	(integer) resolution of plotting device, see also <a href="#">par</a>
fromTop	(logical) toggle if poordinates should start from top
callFrom	(character) allow easier tracking of message(s) produced
silent	(logical) suppress messages

**Value**

matrix with x- and y-coordinates in pixels

**See Also**

[mouseOverHtmlFile](#)

**Examples**

```
df1 <- data.frame(id=letters[1:10],x=1:10,y=rep(5,10),mou=paste("point",letters[1:10]),
  link=file.path(tempdir(),paste(LETTERS[1:10],".html",sep="")),stringsAsFactors=FALSE)
## Typically one wants to get pixel-coordinates for plots written to file.
## Here we'll use R's tempdir, later you may want to choose other locations
pngFile <- file.path(tempdir(),"test01.png")
png(pngFile,width=800, height=600,res=72)
## here we'll just plot a set of horional points at default parameters ...
plot(df1[,2:3],las=1,main="test01")
dev.off()
## Note: Special characters should be converted for proper display in html during mouse-over
library(wrMisc)
df1$mou <- htmlSpecCharConv(df1$mou)
## Let's add the x- and y-coordinates of the points in pixels to the data.frame
df1 <- cbind(df1,convertPlotCoordPix(x=df1[,2],y=df1[,3],plotD=c(800,600),plotRes=72))
```

```
head(df1)
## using mouseOverHtmlFile() one could now make an html document with interactive
## display of names and clockable links to the coordinates we determined here ...
```

---

cumFrqPlot	<i>Cumulative (or sorted) frequency plot (takes columns of 'dat' as separate series)</i>
------------	--

---

## Description

Display data as sorted or cumulative frequency plot. This type of plot represents an alternative to plotting data as histograms. Histograms are very universal and which are very intuitive. However, fine-tuning the bandwidth (ie width of the bars) may be very delicate, fine resolution details may often remain hidden. One of the advantages of directly displaying all data-points is that subtle differences may be revealed easier, compared to classical histograms. Furthermore, the plot presented here offers more options to display multiple series of data simultaneously. Thus, this type of plot may be useful to compare eg results of data normalization. Of course, with very large data-sets (eg > 3000 values) this gain of 'details' will be less important (compared to histograms) and will penalize speed. In such cases the argument `thisResol` will get useful as it allows to reduce the resolution and introduce binning. Alternatively for very large data-sets one may look into density-plots or vioplots (eg [vioplotW](#)). The argument `CVlimit` allows optionally excluding extreme values. If numeric (& > 2 columns), its value will be used [exclExtrValues](#) to identify series with column-median > 'CVlimit'. Of course, exclusion of extreme values should be done with great care, important features of the data may get lost.

## Usage

```
cumFrqPlot(
  dat,
  cumSum = FALSE,
  exclCol = NULL,
  colNames = NULL,
  displColNa = TRUE,
  tit = NULL,
  xLim = NULL,
  yLim = NULL,
  xLab = NULL,
  yLab = NULL,
  col = NULL,
  CVlimit = NULL,
  thisResol = NULL,
  supTxtAdj = 0,
  supTxtYOffs = 0,
  useLog = "",
  silent = FALSE,
  callFrom = NULL
)
```

**Arguments**

<code>dat</code>	(matrix or data.frame) data to plot/inspect
<code>cumSum</code>	(logical) for either plotting cumulates Sums (then <code>thisResol</code> for number of breaks) or (if <code>=FALSE</code> ) simply sorted values -> max resolution
<code>exclCol</code>	(integer) columns to exclude
<code>colNames</code>	(character) for alternative column/series names in display, as long as <code>displColNa=TRUE</code>
<code>displColNa</code>	(logical) display column-names
<code>tit</code>	(character) custom title
<code>xLim</code>	(numeric) custom limit for x-axis (see also <a href="#">par</a> )
<code>yLim</code>	(numeric) custom limit for y-axis (see also <a href="#">par</a> )
<code>xLab</code>	(character) custom x-axis label
<code>yLab</code>	(character) custom y-axis label
<code>col</code>	(integer or character) custom colors
<code>CVlimit</code>	(numeric) for the tag 'outlier column' (uses <a href="#">exclExtrValues</a> ) identify & mark column with median row-CV > CVlimit
<code>thisResol</code>	(integer) resolution <code>res</code> for binning large data-sets
<code>supTxtAdj</code>	(numeric) parameter <code>adj</code> for supplemental text
<code>supTxtYOffs</code>	(numeric) supplemental offset for text on y axis
<code>useLog</code>	(character) default="", otherwise for setting axis in log-scale "x", "y" or "xy"
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allows easier tracking of message(s) produced

**Value**

plot only

**See Also**

[layout](#), [exclExtrValues](#) for decision of potential outliers; [hist](#), [vioplotW](#)

**Examples**

```
set.seed(2017); dat0 <- matrix(rnorm(500), ncol=5, dimnames=list(NULL,1:5))
cumFrqPlot(dat0, tit="Sorted values")
cumFrqPlot(dat0, cumSum=TRUE, tit="Sum of sorted values")
```



histW

*Histogram (version by WR)***Description**

This function proposes a few special tweaks to the general [hist](#) function : In a number of settings data are treated and plotted as log-data. This function allows feeding directly data which are already log2 and displaying the x-axis (re-translated) in linear scale (see argument `isLog`). The default settings allow making (very) small histograms ('low resolution'), which may be used as a rough overview of bandwidth and distribution of values in `dat`. Similar to [hist](#), by changing the parameters `nBars` and/or `breaks` very 'high resolution' histograms can be produced. By default it displays `n` per set of data (on the top of the figure). Note that the argument for (custom) title `main` is now called `tit`.

**Usage**

```
histW(
  dat,
  fileName = "histW",
  output = "screen",
  nBars = 8,
  breaks = NULL,
  tit = NULL,
  subTi = NULL,
  xLab = NULL,
  yLab = NULL,
  imgxSize = 900,
  useCol = NULL,
  useBord = NULL,
  isLog = TRUE,
  cexSubTi = NULL,
  cropHist = TRUE,
  parDefault = TRUE,
  callFrom = NULL,
  silent = FALSE
)
```

**Arguments**

<code>dat</code>	(matrix, list or data.frame) data to plot
<code>fileName</code>	(character) name of file for saving graphics
<code>output</code>	(character, length=1) options for output on 'screen' or saving image in various formats (set to 'jpg', 'png' or 'tif')
<code>nBars</code>	(integer) number of bars in histogram (default for 'low resolution' plot to give rough overview)

breaks	(integer) for (partial) compatibility with hist() : use only for number of breaks (or 'FD'), gets priority over 'nBars'
tit	(character) custom title
subTi	(character) may be FALSE for NOT displaying, or any text, otherwise range
xLab	(character) custom x-axes label
yLab	(character) custom y-axes label
imgxSize	(integer) width of image when saving to file, see also <a href="#">par</a>
useCol	(character or integer) custom colors, see also <a href="#">par</a>
useBord	(character) custom histogram elements border color, see also <a href="#">par</a>
isLog	(logical) for lin scale signal intensity values where representation needs log, assume log2 if TRUE
cexSubTi	(numerical) subtitle size (expansion factor cex), see also <a href="#">par</a>
cropHist	(logical) -not implemented yet- designed for cutting off bars with very low ('insignificant') values
parDefault	(logical) to automatic adjusting par(marg=,cex.axis=0.8), see also <a href="#">par</a>
callFrom	(character) allow easier tracking of message(s) produced
silent	(logical) suppress messages

**See Also**[hist](#)**Examples**

```
set.seed(2016); dat1 <- round(c(rnorm(200,6,0.5),rlnorm(300,2,0.5),rnorm(100,17)),2)
dat1 <- dat1[which(dat1 <50 & dat1 > 0.2)]
histW(dat1,br="FD",isLog=FALSE)
histW(log2(dat1),br="FD",isLog=TRUE)

## quick overview of distributions
layout(partitionPlot(4))
for(i in 1:4) histW(iris[,i],isLog=FALSE,tit=colnames(iris)[i])
```

legendHist

*Add histogram to existing plot***Description**

Add histogram at place of legend using colors from 'colorRamp'.

**Usage**

```
legendHist(
  x,
  colRamp = NULL,
  location = "bottomright",
  legTit = NULL,
  cex = 0.7,
  srt = 67,
  offS = NULL,
  border = TRUE,
  silent = FALSE,
  callFrom = NULL
)
```

**Arguments**

<code>x</code>	(numeric) main input/component of plot
<code>colRamp</code>	(character or integer) set of colors, default is rainbow-like
<code>location</code>	(character) for location of histogram inside existing plot (may be 'br','bl','tl','tr','bottomright','bottomleft','topleft','topright')
<code>legTit</code>	(character, length=1) optional title for histogram-insert
<code>cex</code>	(numeric) expansion factor (see also <a href="#">par</a> )
<code>srt</code>	(numeric) angle for histogram text labels (90 will give vertical label) (see also <a href="#">par</a> )
<code>offS</code>	(NULL or numeric, length=5) fine-tuning of where histogram-insert will be placed and how elements therein are distributed (default c(xOff=0.2,yOff=0.25,leftOffS=0.05,upperBarEnd=1.05,txtOff=0.02), 1st and 2nd determine proportion of insert relative to entire plotting region, 3rd defines space left on bottom for text, 4th if bars hit ceiling of insert or proportion to leave, 5th for shifting text towards top when turned other than 90 degrees )
<code>border</code>	(logical) decide if draw gray rectangle or not around legend
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

**Value**

figure

**Examples**

```
dat <- rnorm(90); plot(dat)
legendHist(dat, col=1:5)
```

MAplotW

*MA-plot (differential intensity versus average intensity)***Description**

This type of plot is very common in high-throughput biology, see [MA-plot](#). Basically one would like to compare numerous independent measures (ie gene transcript or protein abundance values) of 2 samples/data-sets, it is usual to compare a change ('Minus'=M) versus absolute mean value ('Average'=A). In high-throughput biology data are typically already transformed to log2 and thus, the 'M'-value represents a relative change. Besides, output from statistical testing by [moderTest2grp](#) can be directly read to produce MA plots for diagnostic reasons. Please note, that plotting a very number of points in transparency (eg >10000) may take several seconds.

**Usage**

```
MAplotW(
  Mvalue,
  Avalue = NULL,
  filtFin = NULL,
  ProjNa = NULL,
  FCthrs = NULL,
  subTxt = NULL,
  grayIncr = TRUE,
  compNa = NULL,
  batchFig = FALSE,
  cexMa = 1.8,
  cexLa = 0.7,
  limM = NULL,
  limA = NULL,
  cexPt = NULL,
  cexSub = NULL,
  useMar = c(6.2, 4, 4, 2),
  callFrom = "",
  silent = FALSE,
  debug = FALSE
)
```

**Arguments**

Mvalue	(numeric or matrix) data to plot; M-values are typically calculated as difference of log2-abundance values and 'Avalue' the mean of log2-abundance values; M-values and A-values may be given as 2 columns of a matrix, in this case the argument Avalue should remain NULL
Avalue	(numeric, list or data.frame) if NULL it is assumed that 2nd column of 'Mvalue' contains the A-values to be used

filtFin	(matrix or logical) The data may get filtered before plotting: If FALSE no filtering will get applied; if matrix of TRUE/FALSE it will be used as optional custom filter, otherwise (if Mvalue if an MArrayLM-object eg from limma) a default filtering based on the filtFin element will be applied
ProjNa	(character) custom title
FCthrs	(numeric) Fold-Change threshold (display as line) give as Fold-change and NOT log2(FC)
subTxt	(character) custom sub-title
grayIncr	(logical) if TRUE, display overlay of points as increased shades of gray
compNa	(character) names of groups compared
batchFig	(logical) if TRUE figure title and axes legends will be kept shorter for display on fewer space
cexMa	(numeric) expansion factor for font-size of title (see also <a href="#">par</a> )
cexLa	(numeric) expansion factor cex for labels (see also <a href="#">par</a> )
limM	(numeric, length=2) range of axis M-values
limA	(numeric, length=2) range of axis A-values
cexPt	(numeric) expansion factor cex for points (see also <a href="#">par</a> )
cexSub	(numeric) expansion factor cex for subtitle (see also <a href="#">par</a> )
useMar	(numeric,length=4) custom margins (see also <a href="#">par</a> )
callFrom	(character) allow easier tracking of message(s) produced
silent	(logical) suppress messages
debug	(logical) additional messages for debugging

**Value**

MA-plot only

**See Also**

(for PCA) [plotPCAw](#)

**Examples**

```
library(wrMisc)
set.seed(2005); mat <- matrix(round(runif(600),1),ncol=6)
rownames(mat) <- c(rep(letters[1:25],each=3),letters[2:26])
MAplotW(mat[,2]-mat[,1], rowMeans(mat))
## assume 2 groups with 3 samples each
matMeans <- rowGrpMeans(mat, gr=gl(2,3,labels=LETTERS[3:4]))
MAplotW(matMeans[,2]-matMeans[,1], matMeans)
## assume 2 groups with 3 samples each and run moderated t-test (from package 'limma')
tRes <- moderTest2grp(mat,gl(2,3))
MAplotW(tRes$Mval, tRes$Amean)
MAplotW(M=tRes$Mval, A=tRes$means, FCth=1.3)
MAplotW(tRes)
MAplotW(tRes, limM=c(-2,2), FCth=1.3)
```

---

mouseOverHtmlFile      *Create mouse-over interactive html-pages (with links)*


---

## Description

This function allows generating html pages with interactive mouse-over to display information for the points of the plot and www-links when clicking based on embedded png file. Basically, an html page will be generated which contains a call to display to an image file specified in pngFileNa and in the body below pixel-coordinated will be given for display of information at mouse-over and embedded links.

## Usage

```
mouseOverHtmlFile(
  myCoor,
  pngFileNa,
  HtmFileNa = NULL,
  mouseOverTxt = NULL,
  displSi = c(800, 600),
  colNa = NULL,
  tit = "",
  myHtmTit = "",
  myComment = NULL,
  textAtStart = NULL,
  textAtEnd = NULL,
  pxDiam = 5,
  addLinks = NULL,
  linkExt = NULL,
  htmlExt = "htm",
  callFrom = NULL,
  silent = FALSE
)
```

## Arguments

myCoor	(matrix or data.frame) with initial x&y coordinates of points for plot; with IDs (1st column !!) & coordinates (2nd & 3rd col), data for mouse-over & link (4th & 5th); NOTE : if 'colNa' NOT given, colnames of 'myCoor' will be inspected & filtered (columns of non-conform names may get lost) !!! Associated with (already existing) figure file 'pngFileNa' and make html page where points may be indicated by mouse-over
pngFileNa	(character, length=1) filename for complementary png figure (must already exist)
HtmFileNa	(character, length=1) filename for html file produced
mouseOverTxt	(character, length=1) text for interactive mouse-over in html, if NULL, will use col specified by 1st 'colNa' or (if NULL) rownames of 'myCoor'

displSi	(integer, length=2) size of image ('pngFileNa') at display in html (width,height), see also <a href="#">par</a>
colNa	(character) if not NULL min length of 3 to custom specify the column-names to be used : 1st for mouse-over and 2nd+3rd for coordinates associated (and optional 4th for links)
tit	(character) title to be displayed on top of figure
myHtmTit	(character) title of Html page; 'htmlExt' .. checking and correcting filename-extension (only main Html page)
myComment	(character) modify comment embedded in html-document
textAtStart	(character) text in html before figure
textAtEnd	(character) text in html after figure
pxDiam	(integer, length=1) diameter for mouse-over tip to appear (single val or vector), simpler version/solution than with 'Tooltip' package
addLinks	(character) for clickable links, either 1) vector of links or 2) single character-chain to be used for pasting to rownames (eg <a href="https://www.uniprot.org/uniprot/">https://www.uniprot.org/uniprot/</a> ) or 3) TRUE to check presence of 4th name specified in 'colNa' to be used as columnname from 'myCoor' dominates over eventual presence of 4th name in 'colNa'
linkExt	(character) if specified : links will get specified ending, define as NULL or "" for taking 'addLinks' asIs
htmlExt	(character, length=1) extension used when making html files
callFrom	(character) allow easier tracking of message(s) produced
silent	(logical) suppress messages

### Details

Basically there are two options for defining the path to the image embedded : 1) Absolute path : In turn you can move the html to different locations, as long as it still can see the png-file the image can be displayed. However, this may not be any more the case when the html file is sent to another person. If the png-file is accessible as url, it should be easily visible. 2) Relative path : The simplest case would be to give only the file-name with no path at all, thus the png-file is supposed to be in the same directory as the html-file. This option is very 'transportable'. Basically the same applies to the clickable links which may be provided. In high-throughput biology one typically points here to data-bases accessible over the internet where urls to specific pages. With UniProt such links can easily be constructed when using protein identifiers as rownames.

### Value

plot

### See Also

[convertPlotCoordPix](#); use [htmlSpecCharConv](#) to convert special characters for proper html display

## Examples

```
## Note, this example writes files to R's tempdir,
## Otherwise, if you simply work in the current directory without specifying paths you'll
## get an html with relative paths, which simply needs the png file in the same path
df1 <- data.frame(id=letters[1:10],x=1:10,y=rep(5,10),mou=paste("point",letters[1:10]),
  link=file.path(tempdir(),paste(LETTERS[1:10],".html",sep="")),stringsAsFactors=FALSE)
## here we'll use R's tempdir, later you may want to choose other locations
pngFile <- file.path(tempdir(),"test01.png")
png(pngFile,width=800, height=600,res=72)
## here we'll just plot a set of horizontal points ...
plot(df1[,2:3],las=1,main="test01")
dev.off()
## Note : Special characters should be converted for display in html pages during mouse-over
library(wrMisc)
df1$mou <- htmlSpecCharConv(df1$mou)
## Let's add the x- and y-coordinates of the points in pixels to the data.frame
df1 <- cbind(df1,convertPlotCoordPix(x=df1[,2],y=df1[,3],plotD=c(800,600),plotRes=72))
head(df1)
## Now make the html-page allowing to display mouse-over to the png made before
htmFile <- file.path(tempdir(),"test01.html")
mouseOverHtmlFile(df1,pngFile,HtmFileName=htmFile,pxDiam=15,
  textAtStart="Points in the figure are interactive to mouse-over ...",
  textAtEnd="and/or may contain links")
## We still need to make some toy links
for(i in 1:nrow(df1)) cat(paste("point no ",i," : ",df1[i,1]," x=",df1[i,2]," y=",
  df1[i,3],sep=""), file=df1$link[i])
## Now we are ready to open the html file using any browser
## Not run:
browseURL(htmFile)

## End(Not run)
```

---

partitionPlot

---

*Make matrix for layout to partition plotting area*


---

## Description

This function proposes a matrix for use with [layout](#) to arrange given number of plots to be placed on a page/plotting area. In certain instances the proposed layout may accommodate slightly more plots, eg nFig=5 can not be arranged in 2 or 3 columns without an empty last spot. Portrait (vertical) or landscape (horizontal) layout proportions can be chosen. The user can also impose a given number of columns.

## Usage

```
partitionPlot(
  nFig,
  returnMatr = TRUE,
  horiz = TRUE,
```



```

    figNcol = NULL,
    byrow = TRUE,
    callFrom = NULL
  )

```

### Arguments

nFig	(integer) number of figures to be arrages on single plotting surface (ie window or plotting device)
returnMatr	(logical) will return matrix ready for use by <a href="#">layout</a> ; returns vector with nRow and nCol if =FALSE
horiz	(logical) will priviledge horizontal layout if TRUE
figNcol	(integer) optional number of columns
byrow	(logical) toggle if output is in order of rows or columns (equivament to <a href="#">matrix</a>
callFrom	(character) allows easier tracking of messages produced

### Value

matrix for use with layout or (if returnMatr=FALSE numeric vector with number of segements in x- an y-axis)

### See Also

[layout](#)

### Examples

```
partitionPlot(5); partitionPlot(14,horiz=TRUE)
```

---

plotBy2Groups

*Separate and plot data by 2 groups*

---

### Description

Plot series of data as membership of 2 different grouping vectors (eg by grp=patient and grp2=age-group).

### Usage

```

plotBy2Groups(
  dat,
  grp,
  grp2 = NULL,
  col = NULL,
  pch = NULL,
  tit = NULL,

```

```

    cex = 2,
    lwd = 0.5,
    lty = 2,
    yLab = NULL,
    cexLab = NULL,
    sepLines = FALSE,
    silent = FALSE,
    callFrom = NULL
  )

```

### Arguments

<code>dat</code>	(numeric) main data (may contain NA)
<code>grp</code>	(character or factor) grouping of columns of 'dat', eg replicate association
<code>grp2</code>	(character or factor) additional/secondary grouping of columns of 'dat'
<code>col</code>	(character or integer) use custom colors, see also <a href="#">par</a>
<code>pch</code>	(integer) symbol to mark group-center (see also <a href="#">par</a> )
<code>tit</code>	(character) custom title
<code>cex</code>	(numeric) expansion factor for text (see also <a href="#">par</a> )
<code>lwd</code>	(integer) line-width (see also <a href="#">par</a> )
<code>lty</code>	(integer) line-type (see also <a href="#">par</a> )
<code>yLab</code>	(character) custom y-axis label
<code>cexLab</code>	(numeric) expansion factor for labels: 1st value for main groups ( <code>grp</code> , eg genotypes), 2nd for detailed text ( <code>grp2</code> , eg animal IDs) (see also <a href="#">par</a> )
<code>sepLines</code>	(logical) optional drawing of horizontal lines aiming to separate groups (in analogy to support vectors)
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

### Value

list with `$annot`, `$abund` for initial/raw abundance values and `$quant` with final normalized quantitations, or returns `data.frame` with `annot` and `quant` if `separateAnnot=FALSE`

### See Also

[read.table](#), [normalizeThis](#))

### Examples

```

set.seed(2020); rand1 <- round(runif(12),2) +rep(1:3,each=4)
plotBy2Groups(rand1,gl(2,6,labels=LETTERS[5:6]),gl(4,3,labels=letters[1:4]))

```

plotLinReg

*Plot linear regression and confidence interval of regression***Description**

This function provides help to display a series of bivariate points given in 'dat' (multiple data formats possible), to model a linear regression and plot the results. Furthermore, a confidence interval to the regression may be added to the plot, regression parameters get be displayed.

**Usage**

```
plotLinReg(
  dat,
  indepVarLst = NULL,
  dependVar = NULL,
  cusTxt = NULL,
  regrLty = 1,
  regrLwd = 1,
  regrCol = 1,
  confInt = 0.95,
  confCol = NULL,
  xLab = NULL,
  yLab = NULL,
  xLim = NULL,
  yLim = NULL,
  tit = NULL,
  nSignif = 3,
  col = 1,
  pch = 1,
  silent = FALSE,
  callFrom = NULL
)
```

**Arguments**

dat	(numeric, data.frame or list) main data to plot/inspect. If numeric 'dat' will be used as dependent variable (y-data) together with numeric 'indepVarLst' (independent variable); if list, then list-elements indepVarLst and dependVar will be used; if matrix, the the 1st and 2nd column will be used
indepVarLst	(character) if 'dat' is list, this designs the list element with the explanatory or independent variable (ie the variable used for explaining, typically x-data)
dependVar	(character) if 'dat' is list, this designs the list element with dependent variable (ie the variable to be explained, typically y-data) to test
cusTxt	(character) optional custom text to display in subtitle (instead of p-value to H0: slope.regression=0)
regrLty	(integer) line type for regression

regrLwd	(integer) line width for regression
regrCol	(integer) color of regression-line
confInt	(numeric, between 0 and 1) the probability alpha for the regression interval, if NULL no confidence interval will be plotted/calculated
confCol	(character) (background) color for confidence-interval
xLab	(character) optional custom x-label
yLab	(character) optional custom y-label
xLim	(numeric) custom limit for x-axis (see also <a href="#">par</a> )
yLim	(numeric) custom limit for y-axis (see also <a href="#">par</a> )
tit	(character) optional title
nSignif	(integer) number of significant digits for regression parameters in subtitle of plot
col	(integer or character) custom color for points (choose NULL for not plotting the actual data)
pch	(integer or character) type of symbol for points (see also <a href="#">par</a> )
silent	(logical) suppress messages
callFrom	(character) allows easier tracking of message(s) produced

### Value

plot and invisible list containing \$data, \$linRegr, \$confInterval (if calculated)

### See Also

[exclExtrValues](#) for decision of potential outliers; [hist](#), [vioplotW](#)

### Examples

```
set.seed(2020); dat1 <- rep(1:6,each=2) +runif(12,0,1)
plotLinReg(dat1, gl(6,2))
# extract elements out of list :
li2 <- list(aa=gl(5,2), bb=dat1[1:10])
plotLinReg(li2, indepVarLst="aa", dependVar="bb")
```

## Description

Function to plot **principal components analysis (PCA)**, with options to show center and potential outliers for each of the groups (columns of data). One of the specificities of this implementation is the integration of bag-plots to better visualize different groups of points (if they can be organized so beforehand as distinct groups) : The main body of data is shown as 'bag-plots' (a bivariate boxplot, see **Bagplot**) with different transparent colors to highlight the core part of different groups (if they contain more than 2 values per group). Furthermore, group centers are shown as average or median (see 'nGrpForMedian') with stars & index-number (if <25 groups). Layout is automatically set to 2 or 4 subplots (if plotting more than 2 principal components makes sense). Note : This function uses for calculating PCA **prcomp** with default center=TRUE and scale.=FALSE, (different to princomp() which standardizes by default). Note: NA-values cannot (by definition) be processed by PCA - all lines with any non-finite values/content (eg NA) will be omitted ! Note : Package RColorBrewer may be used if available. Finally, note that several other packages dedicated to PCA exist, for example **FactoMineR** offers a very wide spectrum of possibilities, in particular for combined numeric and categorical data.

## Usage

```
plotPCAw(
  dat,
  sampleGrp,
  tit = NULL,
  useSymb = c(21:25, 9:12, 3:4),
  center = TRUE,
  scale. = TRUE,
  colBase = NULL,
  useSymb2 = NULL,
  displBagPl = TRUE,
  getOutL = FALSE,
  cexTxt = 1,
  showLegend = TRUE,
  nGrpForMedian = 6,
  pointLabelPar = NULL,
  rowTyName = "genes",
  rotatePC = NULL,
  suplFig = TRUE,
  callFrom = NULL,
  silent = FALSE
)
```

## Arguments

<code>dat</code>	(matrix, list or data.frame) data to plot. Note: NA-values cannot be processed - all lines with non-finite data (eg NA) will be omitted !
<code>sampleGrp</code>	(character or factor) should be factor describing groups of replicates, NAs are not supported
<code>tit</code>	(character) custom title
<code>useSymb</code>	(integer) symbols to use (see also <b>par</b> )

center	(logical or numeric) decide if variables should be shifted to be zero centered, argument passed to <a href="#">prcomp</a>
scale.	(logical or numeric) decide if scaling to obtain unit variance, argument passed to <a href="#">prcomp</a> Alternatively, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.
colBase	(character or integer) use custom colors
useSymb2	(integer) symbol to mark group-center (no mark of group-center if default NULL) (equivalent to pch, see also <a href="#">par</a> )
displBagPl	(logical) if TRUE, show bagPlot (group-center) if >3 points per group otherwise the average-confidence-interval
getOutL	(logical) return outlier samples/values
cexTxt	(integer) expansion factor for text (see also <a href="#">par</a> )
showLegend	(logical) toggle to display legend
nGrpForMedian	(integer) decide if group center should be displayed via its average or median value: If group has less than 'nGrpForMedian' values, the average will be used, otherwise the median; if NULL no group centers will be displayed
pointLabelPar	(character) define formatting for optional labels next to points in main figure (ie PC1 vs PC2); may be TRUE or list containing elements 'textLabel', 'textCol', 'textCex', 'textOffSet', 'textAdj' for fine-tuning
rowTyName	(character) for subtitle : specify nature of rows (genes, proteins, probesets,...)
rotatePC	(integer) optional rotation (by -1) for figure of the principal components specified by index
suplFig	(logical) to include plots vs 3rd principal component (PC) and Screeplot
callFrom	(character) allow easier tracking of message(s) produced
silent	(logical) suppress messages

**Value**

plot and optional matrix of outlier-data

**See Also**

(used in this function for the PCA underneath:) [prcomp](#), [princomp](#), the package [FactoMineR](#)

**Examples**

```
set.seed(2019); dat1 <- matrix(round(c(rnorm(1000), runif(1000,-0.9,0.9))),2),
  ncol=20, byrow=TRUE) + matrix(rep(rep(1:5,6:2), each=100), ncol=20)
biplot(prcomp(dat1))      # traditional plot
(grp = factor(rep(LETTERS[5:1],6:2)))
plotPCAw(dat1,grp)
```

---

staggerdCountsPlot	<i>Staggered Chart for Ploting Counts to Multiple Leveles of the Thresh- old used</i>
--------------------	---

---

## Description

The basic idea of this plot is to show how counts data change while shifting a threshold-criterium. At each given threshold the counts are plotted like a staggered bar-chart (or staggered histogram) but without vertical lines to illustrated the almost continuous change from preceedig or following threshold-value. Initially this plot was designed for showing the absolute count-data used when constructing roc-curves (eg using the function `summarizeForROC` of package `wrProteo`). The main input should furnish the panel of threshold as one column and the coresponding counts data as min 2 columns. The threshold coumns gets specified using the argument `threColumn`, the counts-data may either be specified using argument `countsCol` or be searched using `grep` using column-names containing the text given in argument `varCountNa` with may be combined with a fixed preceeding part given as argument `fixedCountPat`.

## Usage

```
staggerdCountsPlot(
  roc,
  threColumn = 1,
  countsCol = NULL,
  fixedCountPat = "n.pos.",
  varCountNa = NULL,
  sortAscending = TRUE,
  vertLine = NULL,
  col = NULL,
  tit = NULL,
  logScale = FALSE,
  las.alph = 2,
  displMaxSpec = TRUE,
  silent = FALSE,
  callFrom = NULL
)
```

## Arguments

<code>roc</code>	(numeric matrix or data.frame) main input: one column with thresholds and multiple columns of assoicated count data
<code>threColumn</code>	(integer or character) to specify the column with threshold-data, in typica proteomics benchmark studies this would be 'alph' (for the statistical test threshold)
<code>countsCol</code>	(character of integer, min length=2) choice of column(s) with count-data in 'roc' to be used for display, if not NULL will override alternative search of columns using 'varCountNa' and 'fixedCountPat'

fixedCountPat	(character) optional pattern to help identifying counts-data: if not NULL it will be used as fixed part in column names to get pasted to varCountNa. In proteomics benchmark studies this would typically be 'n.pos.'
varCountNa	(character) alternative way to select the columns from 'roc': searched using <a href="#">grep</a> using column-names containing the text given in argument varCountNa with may be combined with a fixed preceeding part given as argument fixedCountPat In proteomics benchmark studies this would typically be the species-abbreviations (eg 'H','S','E')
sortAscending	(logical) decide if data should be sorted ascending or descending
vertLine	(numeric) for optional vertical line, typically used to highlight alpha 0.05
col	(character) custom colors, see also <a href="#">par</a>
tit	(character) custom title
logScale	(logical) display threshld values (x-axis) on log-scale
las.alph	(numeric) orientation of label of alpha-cutoff, see also <a href="#">par</a>
displMaxSpec	(logical) display on right side of figure max count value of contributing group species
silent	(logical) suppress messages
callFrom	(character) allow easier tracking of message(s) produced

## Details

Investigate count data prepared for plotting ROC curves : cumulative counts plot by species (along different statistical test thresholds). Note : Package [wrProteo](#) may be used to prepare input (matrix of ROC data).

## Value

plot only

## See Also

[ecdf](#), for preparing input to ROC: function [summarizeForROC](#) in package [wrProteo](#)

## Examples

```
set.seed(2019); test1 <- cbind(a=sample.int(n=7,size=50,repl=TRUE),
  b=sample.int(n=11,size=50,repl=TRUE),c=sample.int(n=18,size=50,repl=TRUE))
test1 <- cbind(alph=seq(0,1,length.out=50),a=cumsum(test1[,1]),b=cumsum(test1[,2]),
  c=cumsum(test1[,3]))
staggerdCountsPlot(test1,countsCol=c("a","b","c"))
## example below requires the package wrProteo
```



## Description

This function allows generating **Violin plots**) using a variety of input formats and offers additional options for colors. Main input may be multiple vectors, a matrix or list of multiple data-elements (entries may be of variable length), individual colors for different sets of data or color-gradients can be specified, and the display of n per set of data was integtated (based on an inspiration from **Nabble**). It is also possible to plot pairwise half-violins for easier pairwise-comparisons (using halfViolin="pairwise"). Many arguments are kept similar to **vioplot** (here, the package vioplot is not required). Note : Arguments have to be given with full names, lazy evaluation of arguments will not work properly with this function (since '...' is used to capture additional data-sets). Note : **vioplot** offers better options for plotting formulas

## Usage

```
vioplotW(  
  x,  
  ...,  
  finiteOnly = TRUE,  
  halfViolin = FALSE,  
  boxCol = "def",  
  hh = NULL,  
  ylim = NULL,  
  nameSer = NULL,  
  cexNameSer = NULL,  
  horizontal = FALSE,  
  col = "rainbow",  
  border = "black",  
  xlab = NULL,  
  cexLab = NULL,  
  cexAxis = NULL,  
  lty = 1,  
  pointCol = NULL,  
  cexPt = NULL,  
  tit = NULL,  
  las = 1,  
  lwd = 1,  
  rectCol = "black",  
  at = 0,  
  add = FALSE,  
  wex = 1,  
  silent = FALSE,  
  callFrom = NULL  
)
```

**Arguments**

<code>x</code>	(matrix, list or data.frame) data to plot, or first series of data
<code>...</code>	(numeric) additional sets of data to plot
<code>finiteOnly</code>	(logical) eliminate non-finite elements to avoid potential errors (eg when encountering NA)
<code>halfViolin</code>	(logical or character) decide with TRUE or FALSE if full or only half of violins should be plotted, if "pairwise" always 2 data-sets will be plotted back-to-back
<code>boxCol</code>	(character) decide if boxplot should be added inside the violin, use "def" for default transparent grey
<code>hh</code>	(numeric, length <4) smoothing parameter (standard deviation to kernel function, if omitted an optimal smoothing parameter is used); equivalent to argument <code>h</code> in package <a href="#">vioplot</a> ; see also <a href="#">sm.density</a>
<code>ylim</code>	(NULL or numeric, length=2) custom limit on y-axis, see also <a href="#">par</a>
<code>nameSer</code>	(character) custom label for data-sets or columns (length must match number of data-sets)
<code>cexNameSer</code>	(numeric) size of individual data-series labels as cex-expansion factor (see also <a href="#">par</a> )
<code>horizontal</code>	(logical) orientation of plot
<code>col</code>	(character or integer) custom colors or gradients like 'rainbow', 'grayscale', 'heat.colors', 'topo.colors', 'Spectral' or 'Paired', or you may use colors made by the package <a href="#">colorRamps</a>
<code>border</code>	(character) custom color for figure border
<code>xlab</code>	(character) custom axis label
<code>cexLab</code>	(numeric) size of axis labels as cex-expansion factor (see also <a href="#">par</a> )
<code>cexAxis</code>	(numeric) size of numeric axis labels as cex-expansion factor (see also <a href="#">par</a> )
<code>lty</code>	(integer) line-type for linear regression line (see also <a href="#">par</a> )
<code>pointCol</code>	(character or numeric) display of median: color (default white)
<code>cexPt</code>	(numeric) display of median : size of point as cex-expansion factor (see also <a href="#">par</a> )
<code>tit</code>	(character) custom title to figure
<code>las</code>	(integer) orientation of axis labels (see also <a href="#">par</a> )
<code>lwd</code>	(integer) width of line(s) (see also <a href="#">par</a> )
<code>rectCol</code>	(character) color of rectangle
<code>at</code>	(numeric) custom location of data-series names, ie the points at which tick-marks are to be drawn, will be passed to <a href="#">axis</a> , its length must match the number of data-sets
<code>add</code>	(logical) add to existing plot if TRUE
<code>wex</code>	(integer) relative expansion factor of the violin
<code>silent</code>	(logical) suppress messages
<code>callFrom</code>	(character) allow easier tracking of message(s) produced

**Value**

figure only

**See Also**

the package [vioplot](#), [sm](#) is used for the density estimation

**Examples**

```
set.seed(2013)
dat6 <- matrix(round(rnorm(300)+3,1), ncol=6,
  dimnames=list(paste("li",1:50,sep=""), letters[19:24]))
vioplotW(dat6)
## variable number of elements (each n is displayed)
dat6b <- apply(dat6,2,function(x) x[which(x <5)])
dat6b[[4]] <- dat6b[[4]][dat6b[[4]] <4]
vioplotW(dat6b, col="Spectral")
vioplotW(dat6b, col="Spectral", halfViolin="pairwise", horizontal=TRUE)
vioplotW(dat6b, col="Spectral", halfViolin="pairwise", horizontal=FALSE)
```

---

VolcanoPlotW

*Volcano-plot (Statistical Test Outcome versus Relative Change)*


---

**Description**

This type of plot is very common in high-throughput biology, see [Volcano-plot](#). Basically, this plot allows comparing the outcome of a statistical test to the differential of the group means (ie log fold-change),

**Usage**

```
VolcanoPlotW(
  Mvalue,
  pValue = NULL,
  useComp = 1,
  filtFin = NULL,
  ProjNa = NULL,
  FCthrs = NULL,
  FdrList = NULL,
  FdrThrs = NULL,
  subTxt = NULL,
  grayIncr = TRUE,
  col = NULL,
  pch = 16,
  compNa = NULL,
  batchFig = FALSE,
  cexMa = 1.8,
  cexLa = 1.1,
```

```

limM = NULL,
limp = NULL,
annotColumn = c("SpecType", "ProteinName", "Accession", "Species", "Contam",
  "Description"),
annColor = NULL,
cexPt = NULL,
cexSub = NULL,
cexTxLab = 0.7,
namesNBest = NULL,
NbestCol = 1,
useMar = c(6.2, 4, 4, 2),
returnData = FALSE,
callFrom = NULL,
silent = FALSE,
debug = FALSE
)

```

### Arguments

Mvalue	(numeric or matrix) data to plot; M-values are typically calculated as difference of log2-abundance values and 'pValue' the mean of log2-abundance values; M-values and p-values may be given as 2 columns of a matrix, in this case the argument pValue should remain NULL
pValue	(numeric, list or data.frame) if NULL it is assumed that 2nd column of 'Mvalue' contains the p-values to be used
useComp	(integer) choice of one of multiple comparisons present in Mvalue (if generated using moderTestXgrp())
filtFin	(matrix or logical) The data may get filtered before plotting: If FALSE no filtering will get applied; if matrix of TRUE/FALSE it will be used as optional custom filter, otherwise (if Mvalue if an MArrayLM-object eg from limma) a default filtering based on the filtFin element will be applied
ProjNa	(character) custom title
FCthrs	(numeric) Fold-Change threshold (display as line) give as Fold-change and NOT log2(FC), default at 1.5, set to NA for omitting
FdrList	(numeric) FDR data or name of list-element
FdrThrs	(numeric) FDR threshold (display as line), default at 0.05, set to NA for omitting
subTxt	(character) custom sub-title
grayIncrem	(logical) if TRUE, display overlay of points as increased shades of gray
col	(character) custom color(s) for points of plot (see also <a href="#">par</a> )
pch	(integer) type of symbol(s) to plot (default=16) (see also <a href="#">par</a> )
compNa	(character) names of groups compared
batchFig	(logical) if TRUE figure title and axes legends will be kept shorter for display on fewer space
cexMa	(numeric) font-size of title, as expansion factor (see also cex in <a href="#">par</a> )

<code>cexLa</code>	(numeric) size of axis-labels, as expansion factor (see also <code>cex</code> in <a href="#">par</a> )
<code>limM</code>	(numeric, length=2) range of axis M-values
<code>limp</code>	(numeric, length=2) range of axis p-values
<code>annotColumn</code>	(character) column names of annotation to be extracted (only if <code>Mvalue</code> is <code>MArrayLM</code> -object containing matrix <code>\$annot</code> )
<code>annColor</code>	(character or integer) colors for specific groups of annotation (only if <code>Mvalue</code> is <code>MArrayLM</code> -object containing matrix <code>\$annot</code> )
<code>cexPt</code>	(numeric) size of points, as expansion factor (see also <code>cex</code> in <a href="#">par</a> )
<code>cexSub</code>	(numeric) size of subtitle, as expansion factor (see also <code>cex</code> in <a href="#">par</a> )
<code>cexTxLab</code>	(numeric) size of text-labels for points, as expansion factor (see also <code>cex</code> in <a href="#">par</a> )
<code>namesNBest</code>	(integer or character) number of best points (by <code>pValue</code> to display names in figure); if 'passThr' all points passing FDR and FC-filters will be selected
<code>NbestCol</code>	(character or integer) colors for text-labels of best points
<code>useMar</code>	(numeric,length=4) custom margins (see also <a href="#">par</a> )
<code>returnData</code>	(logical) optional returning data.frame with (ID, <code>Mvalue</code> , <code>pValue</code> , <code>FDRvalue</code> , <code>passFilt</code> )
<code>callFrom</code>	(character) allow easier tracking of message(s) produced
<code>silent</code>	(logical) suppress messages
<code>debug</code>	(logical) additional messages for debugging

## Details

In high-throughput biology data are typically already transformed to log2 and thus, the 'M'-value represents a relative change. Besides, output from statistical testing by [moderTest2grp](#) or [moderTestXgrp](#) can be directly read to produce Volcano plots for diagnostic reasons. Please note, that plotting a very number of points in transparency (eg >10000) may take several seconds.

## Value

MA-plot only

## See Also

(for PCA) [plotPCAw](#)

## Examples

```
library(wrMisc)
set.seed(2005); mat <- matrix(round(runif(900),2), ncol=9)
rownames(mat) <- paste0(rep(letters[1:25],each=4), rep(letters[2:26],4))
mat[1:50,4:6] <- mat[1:50,4:6] + rep(c(-1,1)*0.1,25)
mat[3:7,4:9] <- mat[3:7,4:9] + 0.7
mat[11:15,1:6] <- mat[11:15,1:6] - 0.7
## assume 2 groups with 3 samples each
gr3 <- gl(3,3,labels=c("C","A","B"))
tRes2 <- moderTest2grp(mat[,1:6], gl(2,3), addResults = c("FDR","means"))
```

```
# Note: due to the small number of lines only FDR chosen to calculate
VolcanoPlotW(tRes2)
VolcanoPlotW(tRes2, FCth=1.3, FdrThrs=0.2, namesNBest="passThr")

## assume 3 groups with 3 samples each
tRes <- moderTestXgrp(mat, gr3, addResults = c("FDR", "means"))
# Note: due to the small number of lines only FDR chosen to calculate
VolcanoPlotW(tRes)
VolcanoPlotW(tRes, FCth=1.3, FdrThrs=0.2)
VolcanoPlotW(tRes, FCth=1.3, FdrThrs=0.2, useComp=2)
```

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