

# Package ‘magicaxis’

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**Type** Package

**Title** Pretty Scientific Plotting with Minor-Tick and Log Minor-Tick Support

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**Description** Functions to make useful (and pretty) plots for scientific plotting. Additional plotting features are added for base plotting, with particular emphasis on making attractive log axis plots.

**License** GPL-3

**Suggests** imager, fst

**Imports** grDevices, graphics, stats, celestial (>= 1.4.1), MASS, plotrix, sm, mapproj, RColorBrewer, RANN

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magicaxis-package	<i>Pretty Scientific Plotting with Minor-Tick and Log Minor-Tick Support</i>
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## Description

Functions to make pretty axes (major and minor) on scientific plots. Particularly effort is made on producing nice log plot outputs. The core function produces pretty axis labelling in a number of circumstances that are often used in scientific plotting. There is a higher level interface to a generic plot function that will usually produce nice plots, even without much thought on the users part.

## Details

Package: magicaxis  
 Type: Package  
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 Depends: R (>= 2.13)  
 Suggests: imager, fst  
 Imports: grDevices, graphics, stats, celestial (>= 1.4.1), MASS, plotrix, sm, mapproj, RColorBrewer, RANN

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magaxis	<i>Magically pretty axes</i>
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## Description

This function generates nicely arranged axes for scientific plots, including minor tick marks. It supports log settings and can unclog axes that have been logged inline by the user. When the dynamic range is 50 or less and axis is logged, axis range factors of 10 times 1, 2 and 5 are used instead of powers of 10 alone.

**Usage**

```
magaxis(side = 1:2, majorn = 5, minorn = 'auto', tcl = 0.5, ratio = 0.5, labels = TRUE,
unlog = 'auto', mgp = c(2,0.5,0), mtline = 2, xlab = NULL, ylab = NULL, crunch = TRUE,
logpretty = TRUE, prettybase = 10, powbase = 10, hersh = FALSE, family = 'sans',
frame.plot = FALSE, usepar = FALSE, grid = FALSE, grid.col = 'grey', grid.lty = 1,
grid.lwd = 1, axis.lwd = 1, ticks.lwd = axis.lwd, axis.col = 'black', do.tick = TRUE,
...)
```

**Arguments**

side	The side to be used for axis labelling in the same sense as the base axis function (1=bottom, 2=left, 3=top, 4=right). A vector of multiple entries is allowed. By default, bottom and left axes are drawn (i.e. side 1 and 2).
majorn	The target number of major-axis sub-divisions for pretty plotting. If length is 1 and length of side is longer than this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. Obvious reason for varying this is different pretty labelling between a and y axes.
minorn	The exact number of minor-axis divisions (i.e. desired minor ticks + 1) to display in plotting. Auto will produce <a href="#">pretty</a> ticks for linear scaling, and powbase-2 minor ticks for logged (this might seem odd, but for base 10 this means ticks at 2/3/4/5/6/7/8/9, which is probably as desired). If set manually, must be greater than 1 to have a visible effect. Minor ticks are always calculated to be equally spaced in linear space, so tick spaces vary when using log plotting. If length is 1 and length of side is longer than this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. An obvious reason for varying this is different pretty labelling between x and y axes.
tcl	The length of major tick marks as a fraction of the height of a line of text. By default these face into the plot (in common with scientific plotting) with a value of 0.5, rather than the R default of -0.5. It is possible to force magaxis to inherit directly from par by setting usepar=TRUE (see below). See <a href="#">par</a> for more details.
ratio	Ratio of minor to major tick mark lengths.
labels	Specifies whether major-axis ticks should be labelled for each axis. If length is 1 and length of side is longer than this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. Default is to label all axes.
unlog	Determines if axis labels should be unlogged. If axis is found to be logged in par('usr') then the minor ticks are automatically log spaced, however "unlog" still controls how the labelling is done: either logged form (FALSE) or exponent form (TRUE). If axis has been explicitly logged (e.g. log10(x)) then this will can produce exponential axis marking/ labelling if set to TRUE. This case will also produce log minor tick marks. If length of unlog is 1 and length of side is longer than 1 then the assigned unlog value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. Can also take the text argument 'x', 'y', 'xy' or 'yx', where these refer to which

	axes have been logged. If left at the default of 'Auto' then unlog is assumed to be true when the axis in question is logged, and false otherwise.
mgp	The margin line (in mex units) for the axis title, axis labels and axis line. This has different (i.e. prettier) defaults than R of <code>c(2,0.5,0)</code> rather than <code>c(3,1,0)</code> . This pushes the numbers and labels nearer to the plot compared to the defaults. It is possible to force magaxis to inherit directly from par by setting <code>usepar=TRUE</code> (see below). See <a href="#">par</a> for more details.
mtline	Number of lines separating axis name from axis. If length 2 then specifies x and y axis separation respectively (else these are the same).
xlab	x axis name.
ylab	y axis name.
crunch	In cases where the scientific text would be written as $1 \times 10^8$ , should the $1 \times$ be removed so it reads $10^8$ . If length is 1 and length of side is longer then this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. TRUE by default.
logpretty	Should the major-ticks only be located at powers of 10. This changes cases where ticks are placed at 1, 3.1, 10, 31, 100 etc to 1, 10, 100. If length is 1 and length of side is longer then this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. TRUE by default.
prettybase	The unit of repetition desired. By default it is 10, implying a pretty plot is one with marks at 10, 20, 30 etc. If you are plotting degrees then it might be prettier to display 90, 180, 270 etc. In which case prettybase should be set to 90. If <code>log=TRUE</code> then the reference location of 10 is changed, so in the previous example the labels generated would be at 9, 90, 900 etc rather than the default of 1, 10, 100 etc. If length is 1 and length of side is longer then this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side.
powbase	Set the base to use for logarithmic axes. Default is to use 10.
hersh	To determines whether all plot text should be passed using Hershey vector fonts. This applies to the axis labels (which are handled automatically) and the axis names. In the case of axis names the user must be careful to use the correct plot utils escape characters: <a href="http://www.gnu.org/software/plotutils/manual/en/html_node/Text-String-Format.html">http://www.gnu.org/software/plotutils/manual/en/html_node/Text-String-Format.html</a> . magaxis will return back to the current plotting family after the function has executed.
family	Specifies the plotting family to be used. Allowed options are 'sans' and 'serif'. Depending on whether hersh is TRUE or FALSE these options are either applied to the Hershey vector fonts ( <code>hersh=TRUE</code> ) or the default R Helvetica font ( <code>hersh=FALSE</code> ). magaxis will return back to the current plotting family after the function has executed.
frame.plot	Logical indicating whether a box should be drawn around the plot.
usepar	Logical indicating whether tcl and mgp should be forced to inherit the global par values. This might be preferred when you want to define global plot settings at the start of a script.

<code>grid</code>	Logical indicating whether a background grid should be drawn onto the plotting area. This will only be done for <code>side=1</code> (i.e. vertical grid lines) and <code>side=2</code> (i.e. horizontal grid lines). If length is 1 and length of side is longer then this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. FALSE by default.
<code>grid.col</code>	The colour of the grid to be drawn.
<code>grid.lty</code>	The line type of the grid to be drawn.
<code>grid.lwd</code>	The line width of the grid to be drawn.
<code>axis.lwd</code>	The line width of the axis to be drawn. This is passed to 'lwd' argument in <a href="#">axis</a> .
<code>ticks.lwd</code>	The line width of the ticks to be drawn. This is passed to 'ticks.lwd' argument in <a href="#">axis</a> .
<code>axis.col</code>	Colour argument to pass directly to 'col' in axis. It is a bit clunky to have to specify this, but the option 'col' clashes too much with line and point colours.
<code>do.tick</code>	Logical; should ticks be drawn? Passed to <a href="#">axis</a> argument 'tick'.
<code>...</code>	Other arguments to be passed to base <a href="#">axis</a> and <a href="#">mtext</a> functions as relevant. Options for axis are as described in <a href="#">axis</a> , but note 'cex.lab', 'col.lab' and 'font.lab' are parsed as 'cex', 'col' and 'font' into <a href="#">mtext</a> as required.

### Details

This function tries hard to make nice plots for scientific papers.

### Value

No output. Run for the side effect of producing nice plotting axes.

### Author(s)

Aaron Robotham

### See Also

[magplot](#), [maglab](#), [magerr](#), [magmap](#), [magrun](#)

### Examples

```
x=10^{1:9}
y=1:9
plot(log10(x),y,axes=FALSE)
magaxis(unlog='x')

plot(log10(x),y,axes=FALSE)
magaxis(side=c(1,3),unlog=c(TRUE,FALSE))

plot(x,y,axes=FALSE,log='x')
magaxis()
```

---

 magbar

*Pretty colour bar*


---

### Description

This function is a high level interface to the plotrix 'color.legend' function. It makes reasonable assumptions on the plot window to place the colour and allows the user to specify log spacing for the colour gradient and labels, as well as add a title.

### Usage

```
magbar(position = "topright", range = c(0, 1), orient = "v", log = FALSE,
       col = hsv(h = seq(2/3, 0, len = 100)), scale = c(1/4, 1/20), inset = 1/40,
       labN = 5, title = "", titleshift = 0, centrealign = "rb", clip = '', cex=1, ...)
```

### Arguments

position	Relative position of the colour bar. This argument is used like the 'legend' function. Specify one of 'bottom', 'bottomleft', 'left', 'topleft', 'top', 'topright', 'right', 'bottomright' and 'centre'.
range	The text label limits used to label the colour bar.
orient	Orientation. Allowed options are 'v' for vertical and 'h' for horizontal.
log	Should the colour spacing and labelling be log spaced.
col	Colour palette to use for the colouring of the bar.
scale	The relative (to the plot window) length and width of the colour bar.
inset	Relative (to the plot window) inset of the colour bar.
labN	The number of text labels to draw on the colour bar.
title	Optional title (or axis label for the labels) to add to the colour bar.
titleshift	Extra shift to apply to the 'title' position.
centrealign	Option to control the labeling position used when the position='centre'.
clip	Setting clip='bg' will set values outside the 'range' values to be blank on the magbar (i.e. you can see through to the background).
cex	Character expansion factor for the labels.
...	Other arguments to pass to the <a href="#">color.legend</a> function.

### Details

This function creates pretty default colour bars by assessing the current plot window. It is a higher level implementation of the plotrix 'color.legend' function.

### Value

Called for the side effect of plotting a colour bar.

**Author(s)**

Aaron Robotham

**See Also**[magplot](#), [magaxis](#), [maglab](#), [magmap](#), [magrun](#)**Examples**

```

magplot(sin)
magbar('top')
magbar('right',title='Just looking',titleshift=0.5)
magbar('topleft',orient='h',title='Hello!')
magbar('bottom',range=c(0.3,30),orient='h',log=TRUE,title='Log test col')
magbar('bottomleft',range=c(0.3,30),orient='v',log=TRUE,title='Log test bg',clip='bg')

```

magbin

*2D Binning Routines***Description**

Allows for 2D binning (counts) and summary statistics on 2D bins (medians etc).

**Usage**

```

magbin(x, y, z = NULL, xlim = NULL, ylim = NULL, zlim = NULL, step = NULL,
log = '', unlog = log, clustering = 10, dustlim = 0.1, shape = "hex",
plot = TRUE, colramp = hcl.colors(1e4), colstretch = "lin", sizestretch = "lin",
colref = "count", sizeref = "none", funstat = function(x) median(x, na.rm=TRUE),
direction = 'h', offset = 0, jitterseed = 666, projden = FALSE, ...)

```

**Arguments**

x	Numeric vector or matrix/data.frame; x values to 2D bin. If x is a two (or more) column matrix or data.frame and y/z is missing as an argument, then the first column is used for x and the second/third column for y/z.
y	Numeric vector; the y coordinates of points in the plot, optional if 'x' is an appropriate structure.
z	Numeric vector; the z coordinates of points in the plot (optional), optional if 'x' is an appropriate structure.
xlim	Numeric vector; the x limits to use for the data. Default of NULL calculates the range based on the provided 'x' data vector. If length equals 1 then the argument is taken to mean the sigma range to select for plotting and the clipping is done by <a href="#">magclip</a> .

ylim	Numeric vector; the y limits to use for the data. Default of NULL calculates the range based on the provided 'y' data vector. If length equals 1 then the argument is taken to mean the sigma range to select for plotting and the clipping is done by <a href="#">magclip</a> .
zlim	Numeric vector; the z limits to use for the data. Default of NULL calculates the range based on the provided 'y' data vector. If length equals 1 then the argument is taken to mean the sigma range to select for plotting and the clipping is done by <a href="#">magclip</a> .
step	Numeric vector; grid steps in x and y directions. IF NULL then this is $c(\text{diff}(\text{xlim})/50, \text{diff}(\text{ylim})/50)$ . If length 1, then this value is repeated.
log	Character scalar; log axis arguments to be passed to used. E.g. use 'x', 'y', 'xy' or 'yx' as appropriate. Default "" assumes no logging of any axes. For convenience you can specify the 'z' axis too, which somewhat replaces the 'colstretch' argument. Note that in all cases the 'x'/'y'/'z' data is explicitly logged, which means the plotting window does not know it is in logged space (via the <code>par()\$xlog</code> and <code>par()\$ylog</code> structures). This means is you want to add points etc to the plot you will need to apply $\log_{10}$ yourself, so a point with coordinates $[10^2, 10^{-3}]$ should be plotted at $[2, -3]$ .
unlog	Character scalar; determines if x/y axis labels should be unlogged (z is ignored here). By default inherits 'log', since that is usually what you would want.
clustering	Numeric scalar; excess counts in densist bin relative to Uniform data. This is to optimise the binning, so can probably be ignored.
dustlim	Numeric scalar; if between 0 and 1 then the 2D bin count quantile to switch to showing the individual points (which visually look like 'dust'), if larger than 1 then the exact counts threshold. If this is NA or 0 then all cells are shown.
shape	Character scalar; type of binning, either hex/hexagon; sq/square; tri/triangle or trihex. 'trihex' is a triangle tessellation that is also arranged to have hexagonal packing (so 6 triangles can form a hexagon).
plot	Logical; create a plot? If FALSE then just the binning output list is created.
colramp	Vector; a colour scaling to use. Must be a vector and not a function.
colstretch	Character scalar; colour stretch, either linear (lin, default) or logarithmic (log, good for large dynamic ranges).
sizestretch	Character scalar; size stretch, either linear (lin, default) or logarithmic (log, good for large dynamic ranges).
colref	Character scalar; colour reference for call, either it should be based on the counts (count, default) or the z-axis statistic (zstat)?
sizeref	Character scalar; colour reference for call, either it should be ignored (none, so all are the same size and closely packed), based on the counts (count) or the z-axis statistic (zstat)?
funstat	Function; function to use to compute a statistic over the 'z' axis. The default is <a href="#">median</a> , but other good options might be <a href="#">mean</a> , <a href="#">sd</a> , <a href="#">mad</a> . Note, to change default arguments you might need to send through a new function, e.g. 'funstat' = <code>function(x) median(x, na.rm=TRUE)</code> and similar, but if you are happy with the defaults then you can use the simpler 'funstat' = <code>mean</code> etc.

direction	Character scalar; should there be a shape side aligned horizontally ('h', the default) or vertically ('v')? This is only relevant for hexagon and triangle bin shapes, and has the effect of leading the eye differently with some scatter structures.
offset	Numeric/character scalar; only relevant for 'shape'='sq' or 'shape'='tri'. Either a numeric value specifying the offset (relative to 'step') to apply to alternating rows ('direction'='h') or columns ('direction'='v'); or 'jitter' which means the rows or columns are randomly jittered (only used for 'shape'='sq' bins. This option is useful for visually breaking up strong patterns in certain types of data.
jitterseed	Integer scalar; the random seed to use for jittering (means you can recreate your plots exactly if the seed is the same). This argument is only used for 'shape'='sq' bins.
projden	Logical; do you want projected density PDFs to be displayed above and to the side of the standard plot.magbin plot? If so you also need to pass the same 'xdata' and 'ydata' that you originally sent to <a href="#">magbin</a> , since this is not stored in the object output from <a href="#">magbin</a> .
...	Dots to be passed to <a href="#">magplot</a> , <a href="#">magmap</a> and <a href="#">magmap</a> . Relevant arguments are matched, so look in those functions for optional arguments to pass.

### Details

Mostly run for the side effect of making a nice plot, but the output bin statistics might also be useful.

Re performance, magbin works pretty well on a modern computer for up to ~1e6 points, taking only a few seconds to run usually. Beyond this you might need to carefully tune the performance with 'clustering' otherwise it might run very slower and/or you run out of memory.

### Value

List of class 'magbin' containing:

bins	Bin x / y / count / and zstat info
dust	Dust x / y / z info
groups	Links input 'x' and 'y' data to the nearest grid cell by row number of 'bins'
xlim	x limits
ylim	y limits
step	'step' size
dustlim	'dustlim'
shape	'shape'

### See Also

[plot.magbin](#), [maghist](#)

## Examples

```

set.seed(666)
xydata = cbind(rnorm(1e4), rnorm(1e4))
magbin(xydata, shape='hexagon') #default
magbin(xydata, shape='square')
magbin(xydata, shape='triangle')
magbin(xydata, shape='trihex')
magbin(xydata, shape='hexagon', direction='v')
magbin(xydata, shape='triangle', direction='v')
magbin(xydata, shape='trihex', direction='v')
magbin(xydata, shape='hexagon', step=c(0.2,0.4)) #different aspect ratio hexagons

magbin(xydata, z=xydata[,1]^2-xydata[,2]^2, colref='zstat', sizeref='count')

magbin(xydata, z=xydata[,1]^2-xydata[,2]^2, colref='zstat', sizeref='count',
funstat=mad)
magbin(xydata, z=xydata[,1]^2-xydata[,2]^2, colref='zstat', sizeref='count',
funstat=function(x){quantile(x,0.9)})

xydata = cbind(10^rnorm(1e4), 10^rnorm(1e4))
magbin(xydata, log='xy')
magbin(xydata, z=xydata[,1]*xydata[,2], colref='zstat', sizeref='count',
log='xyz')
magbin(xydata, log='xy', unlog='xy', xlim=3, ylim=3)

```

---

magclip

*Magical sigma clipping*

---

## Description

This function does intelligent automatic sigma-clipping of data. This is optionally used by [magplot](#) and [maghist](#).

## Usage

```
magclip(x, sigma = 'auto', clipiters = 5, sigmasel = 1, estimate = 'both', extra = TRUE)
```

## Arguments

<code>x</code>	Numeric; the values to be clipped. This can reasonably be a vector, a matrix or a dataframe.
<code>sigma</code>	The level of sigma clipping to be done. If set to default of 'auto' it will dynamically choose a sigma level to cut at based on the length of <code>x</code> (or the clipped version once iterations have started), i.e.: $\text{sigma} = \text{qnorm}(1 - 2/\text{length}(x))$ . This has the effect of removing unlikely values based on the chance of them occurring, i.e. there is roughly a 50% chance of a 3.5 / 4.6 sigma Normal fluctuation occurring when you have 10,000 / 10,000,000 values, hence choosing this value dynamically is usually the best option.

clipiters	The maximum number of sigma clipping iterations to attempt. It will break out sooner than this if the iterations have converged. The default of 5 is usually plenty (up to the contamination being towards the 50% level). The number of actual iterations is returns as 'clipiters'.
sigmasel	The quantile to use when trying to estimate the true standard-deviation of the Normal distribution. if contamination is low then the default of 1 is about optimal in terms of S/N, but you might need to make the value lower when contamination is very high.
estimate	Character; determines which side/s of the distribution are used to estimate Normal properties. The default is to use both sides (both) giving better S/N, but if you know that your contamination only comes from positive flux sources (e.g., astronomical data when trying to select sky pixels) then you should only use the lower side to determine Normal statistics (lo). Similarly if the contamination is on the low side then you should use the higher side to determine Normal statistics (hi).
extra	Logical; if TRUE then 'clip' and 'range' are computed and returns, else these are set to NA to reduce computation and memory.

### Details

If you know more sepcific details about your data then you should probably carry out a thorough likelihood analysis, but the ad-hoc clipping done in magclip works pretty well in practice.

### Value

A list containing three items:

x	Numeric vector; the clipped 'x' values.
clip	Loical; logic of which values were clipped with the same type and shape attributes as the input 'x' (i.e. if the original 'x' was a matrix then 'clip' would also be a matrix that matches element to element).
range	The data range of clipped 'x' values returned.
clipiters	The number of iterations made, which might be less than the input 'clipiters' since it might converge faster.

### Author(s)

Aaron Robotham

### See Also

[maghist](#), [magplot](#)

### Examples

```
#A highly contaminated Normal distribution:
temp=c(rnorm(1e3),runif(500,-10,10))
magplot(density(temp))
```

```

lines(seq(-5,5,len=1e3),dnorm(seq(-5,5,len=1e3)),col='red')

magplot(density(magclip(temp)$x))
lines(seq(-5,5,len=1e3),dnorm(seq(-5,5,len=1e3)),col='red')

#Now we put the contamination on the high side:

temp=c(rnorm(1e3),runif(500,0,10))
magplot(density(magclip(temp)$x))
lines(seq(-5,5,len=1e3),dnorm(seq(-5,5,len=1e3)),col='red')

#Setting estimate to 'lo' in this case should work better:

magplot(density(magclip(temp, estimate='lo')$x))
lines(seq(-5,5,len=1e3),dnorm(seq(-5,5,len=1e3)),col='red')

```

---

magcon

2D quantile images and contours

---

## Description

This function generates pretty images and contours that reflect the 2D quantile levels of the data. This means the user can immediately assess the 2D regime that contains an arbitrary percentage of the data. This function was designed particularly with the output of MCMC posteriors in mind, where visualising the location of the 68% and 95% 2D quantiles for covariant parameters is a necessary part of the post MCMC analysis.

## Usage

```

magcon(x, y, h, doim = TRUE, docon = TRUE, dobar = TRUE, ngrid = 100, add = FALSE,
xlab = '', ylab = '', imcol = c(NA,rev(rainbow(1000, start = 0, end = 2/3))),
conlevels = c(0.5, pnorm(1) - pnorm(-1), 0.95), barposition = "topright",
barorient = "v", bartitle = "Contained %", bartitleshift = 0, xlim = NULL, ylim = NULL,
weights = NULL,...)

```

## Arguments

x	x values to contour. If x is a two (or more) column matrix or data.frame and y is missing as an argument, then the first column is used for x and the second column for y.
y	y values to contour.
h	Smoothing parameter to pass to kde2d. Can take 1 or 2 arguments for x and optionally y smoothing.
doim	Should an image be generated.
docon	Should contours be overlain.
dobar	Should a magbar colour bar be added describing the image levels (doim must also be true for this to appear).

ngrid	The ngrid to send to kde2d / sm.density to determine the resolution of the smoothing.
add	Should the output of this function be added to the current plot. If FALSE then a new plot is generated.
xlab	Label for x-axis, only used if add=FALSE.
ylab	Label for y-axis, only used if add=FALSE.
imcol	The colour palette to use for the image (this is also sent to magbar).
conlevels	Specific quantile contours to add. Default is for 50%, 68% and 95% contours, i.e. these contours contain that percentage of the data.
barposition	The position to use for magbar. See magbar help for more details.
barorient	The orientation to use for magbar. See magbar help for more details.
bartitle	Title to use for magbar.
bartitleshift	Control of how far the magbar title is shifted away from its default position.
xlim	The x limits to use for the data. Default of NULL calculates the range based on the provided x data vector. Data will be clipped between the extremes given. If xlim[1]>xlim[2] plotted axes will be flipped compared to default.
ylim	The y limits to use for the data. Default of NULL calculates the range based on the provided y data vector. Data will be clipped between the extremes given. If ylim[1]>ylim[2] plotted axes will be flipped compared to default.
weights	A vector of weights to pass onto sm.density (that does the 2D density estimate). This must be the same length as the x and y vectors if specified.
...	Other arguments to pass to the <a href="#">contour</a> function, e.g. lty=c(2,1,3).

### Details

This function is particularly designed to assess the output for MCMC posteriors since it highlights the confidence regimes quite clearly. More generally it can show the quantile distributions for any 2D data.

### Value

Called for the side effect of generating images and contours representing quantile in 2D data.

### Author(s)

Aaron Robotham

### See Also

[magplot](#), [magaxis](#), [maglab](#), [magmap](#), [magrun](#), [magbar](#)

### Examples

```
temp=cbind(rnorm(1e3),rnorm(1e3))
magcon(temp[,1],temp[,2])
```

magcurve

*Draw Function Plots***Description**

Draws a curve corresponding to a function over the interval [from, to] using [magplot](#). curve can plot also an expression in the variable xname, default 'x'. This is almost a direct port of [curve](#), with use of [magplot](#) rather than [plot](#).

**Usage**

```
magcurve(expr, from = NULL, to = NULL, n = 101, add = FALSE,
         type = "l", xname = "x", xlab = xname, ylab = NULL,
         log = NULL, xlim = NULL, ...)
```

**Arguments**

expr	The name of a function, or a <a href="#">call</a> or an <a href="#">expression</a> written as a function of x which will evaluate to an object of the same length as x.
x	a 'vectorizing' numeric R function.
from, to	the range over which the function will be plotted.
n	integer; the number of x values at which to evaluate.
add	logical; if TRUE add to an already existing plot; if NA start a new plot taking the defaults for the limits and log-scaling of the x-axis from the previous plot. Taken as FALSE (with a warning if a different value is supplied) if no graphics device is open.
xlim	NULL or a numeric vector of length 2; if non-NULL it provides the defaults for c(from, to) and, unless add = TRUE, selects the x-limits of the plot – see <a href="#">plot.window</a> .
type	magplot type: see <a href="#">plot.default</a> .
xname	character string giving the name to be used for the x axis.
xlab, ylab, log, ...	labels and <a href="#">graphical parameters</a> can also be specified as arguments. See 'Details' for the interpretation of the default for log. For the "function" method of magplot, ... can include any of the other arguments of magcurve, except expr.

**Details**

The function or expression expr (for magcurve) or function x (for magplot) is evaluated at n points equally spaced over the range [from, to]. The points determined in this way are then plotted.

If either from or to is NULL, it defaults to the corresponding element of xlim if that is not NULL.

What happens when neither from/to nor xlim specifies both x-limits is a complex story. For magplot(<function>) and for magcurve(add = FALSE) the defaults are (0, 1). For magcurve(add

= NA) and `magcurve(add = TRUE)` the defaults are taken from the x-limits used for the previous plot. (This differs from versions of R prior to 2.14.0.)

The value of `log` is used both to specify the plot axes (unless `add = TRUE`) and how ‘equally spaced’ is interpreted: if the x component indicates log-scaling, the points at which the expression or function is plotted are equally spaced on log scale.

The default value of `log` is taken from the current plot when `add = TRUE`, whereas if `add = NA` the x component is taken from the existing plot (if any) and the y component defaults to linear. For `add = FALSE` the default is ""

This used to be a quick hack which now seems to serve a useful purpose, but can give bad results for functions which are not smooth.

For expensive-to-compute expressions, you should use smarter tools.

The way `magcurve` handles `expr` has caused confusion. It first looks to see if `expr` is a [name](#) (also known as a symbol), in which case it is taken to be the name of a function, and `expr` is replaced by a call to `expr` with a single argument with name given by `xname`. Otherwise it checks that `expr` is either a [call](#) or an [expression](#), and that it contains a reference to the variable given by `xname` (using [all.vars](#)): anything else is an error. Then `expr` is evaluated in an environment which supplies a vector of name given by `xname` of length `n`, and should evaluate to an object of length `n`. Note that this means that `magcurve(x, ...)` is taken as a request to plot a function named `x` (and it is used as such in the function method for `magplot`).

### Value

A list with components `x` and `y` of the points that were drawn is returned invisibly.

### Warning

For historical reasons, `add` is allowed as an argument to the "function" method of `plot`, but its behaviour may surprise you. It is recommended to use `add` only with `magcurve`.

### See Also

[curve](#), [magplot](#)

### Examples

```
magcurve(sin, -2*pi, 2*pi, xname = "t")
magcurve(tan, xname = "t", add = NA,
  main = "magcurve(tan) --> same x-scale as previous plot")

op <- par(mfrow = c(2, 2))
magcurve(x^3 - 3*x, -2, 2, ylab='y')
magcurve(x^2 - 2, add = TRUE, col = "violet")

## simple and advanced versions, quite similar:
magcurve(cos, xlim = c(-pi, 3*pi), n = 1001, col = "blue", add = TRUE)

chippy <- function(x) sin(cos(x)*exp(-x/2))
magcurve(chippy, -8, 7, n = 2001)
```

```

for(ll in c("", "x", "y", "xy"))
  magcurve(log(1+x), 1, 100, log = ll,
           sub = paste("log= ", ll, "", sep = ""))
par(op)

```

---

magcutout

*Image Cutout Utilities*


---

## Description

Functions to subset both raw images and images with associated WCS systems.

## Usage

```

magcutout(image, loc = dim(image)/2, box = c(100, 100), shiftloc = FALSE, paddim = TRUE,
plot = FALSE, ...)
magcutoutWCS(image, header, loc, box = c(100, 100), shiftloc = FALSE, paddim = TRUE,
plot = FALSE, CRVAL1 = 0, CRVAL2 = 0, CRPIX1 = 0, CRPIX2 = 0, CD1_1 = 1, CD1_2 = 0,
CD2_1 = 0, CD2_2 = 1, coord.type = "deg", sep = ":", loc.type=c('coord','coord'),
approx.map = FALSE, ...)
magWCSradec2xy(RA, Dec, header, CRVAL1 = 0, CRVAL2 = 0, CRPIX1 = 0, CRPIX2 = 0, CD1_1 = 1,
CD1_2 = 0, CD2_1 = 0, CD2_2 = 1, CTYPE1 = 'RA--TAN', CTYPE2 = 'DEC--TAN',
loc.diff = c(0, 0), coord.type = "deg", sep = ":")
magWCSxy2radec(x, y, header, CRVAL1 = 0, CRVAL2 = 0, CRPIX1 = 0, CRPIX2 = 0, CD1_1 = 1,
CD1_2 = 0, CD2_1 = 0, CD2_2 = 1, CTYPE1 = 'RA--TAN', CTYPE2 = 'DEC--TAN',
loc.diff = c(0, 0))

```

## Arguments

image	Numeric matrix; required, the image we want to decorate. If ‘image’ is a list as created by readFITS, read.fits of magcutoutWCS then the image part of these lists is parsed to ‘image’ and the correct header part is parsed to ‘header’. If ‘image’ is a path to an fst format file then the cutout can be done on disk directly.
header	Full FITS header in table or vector format. Legal table format headers are provided by the read.fitshdr function or the ‘hdr’ list output of read.fits in the astro package; the ‘hdr’ output of readFITS in the FITSio package or the ‘header’ output of magcutoutWCS. If a header is provided then key words will be taken from here as a priority. Missing header keywords are printed out and other header option arguments are used in these cases.
loc	Numeric vector; the [x,y] (magcutout) or [x,y] / [RA,Dec] (magcutoutWCS) location where we want to cutout the image. For magcutoutWCS the unit type can be specified with the ‘loc.type’ option. Either it is WCS in degrees [RA,Dec] (coord) or pixel [x,y] of the ‘image’ (image).
box	Numeric vector; the dimensions of the box to cut out from ‘image’ centred on ‘loc’. For magcutout the ‘box’ unit is always pixels. For magcutoutWCS the unit type can be specified with the ‘loc.type’ option. Either it is pixels or asec (see ‘loc.type’).

RA	Vector or matrix; target right ascension in degrees. If matrix then the first column will be used as 'RA' and the second column as 'Dec'.
Dec	Vector; target declination in degrees. Ignored if 'RA' is a matrix.
x	Vector or matrix; target x-pixel. If Matrix then the first column will be used as the x-axis and the second column as y-axis. Note this is the R convention of [x,y] (see Notes) not FITS.
y	Vector; target y-pixel. Ignored if x is a matrix. Note this is the R convention of [x,y] not FITS (see Notes).
loc.diff	The pixel offset to apply. Only relevant if the image being plotted is a cutout from within a FITS legal image.
shiftloc	Logical; should the cutout centre shift from 'loc' away from the 'image' edge if the desired 'box' size extends beyond the edge of the 'image'?
paddim	Logical; should the cutout be padded with 'image' data until it meets the desired 'box' size (if 'shiftloc' is TRUE) or padded with NAs for data outside the 'image' boundary otherwise?
plot	Logical; should a <a href="#">magimage</a> (magcutout) or <a href="#">magimageWCS</a> (magcutoutWCS) plot of the output be generated?
CRVAL1	FITS header CRVAL1 for the 'CTYPE1' projection system. This is the RA in degrees at the location of 'CRPIX1'.
CRVAL2	FITS header CRVAL2 for the 'CTYPE2' projection system. This is the Dec in degrees at the location of 'CRPIX2'.
CRPIX1	FITS header CRPIX1 for the 'CTYPE1' projection system. This is the x pixel value at the location of 'CRVAL1'.
CRPIX2	FITS header CRPIX2 for the 'CTYPE2' projection system. This is the y pixel value at the location of 'CRVAL2'.
CD1_1	FITS header CD1_1 for the 'CTYPE1' projection system. Change in 'CTYPE1' in degrees along x-Axis.
CD1_2	FITS header CD1_2 for the 'CTYPE1' projection system. Change in 'CTYPE1' in degrees along y-Axis.
CD2_1	FITS header CD2_1 for the 'CTYPE2' projection system. Change in 'CTYPE2' in degrees along x-Axis.
CD2_2	FITS header CD2_2 for the 'CTYPE2' projection system. Change in 'CTYPE2' in degrees along y-Axis.
CTYPE1	The RA projection system type. Either 'RA-TAN' for Tan Gnomonic (default), or 'RA-SIN' for Sine Orthographic. 'RA-NCP' is approximated by Sine Orthographic with a warning. Over-ridden by the FITS header.
CTYPE2	The DEC projection system type. Either 'DEC-TAN' for Tan Gnomonic (default), or 'DEC-SIN' for Sine Orthographic. 'DEC-NCP' is approximated by Sine Orthographic with a warning. Over-ridden by the FITS header.
coord.type	The units of 'loc' for magcutoutWCS. Allowed options are 'deg' for degrees and 'sex' for sexagesimal (i.e. HMS for RA and DMS for Deg).
sep	When 'coord.type'='sex', 'sep' defines the type of separator used for the HMS and DMS strings (i.e. H:M:S and D:M:S would be sep=':', which is the default). See <a href="#">hms2deg</a> and <a href="#">dms2deg</a> for more details.

<code>loc.type</code>	Character vector; specifies what type of location is being provided. The first element specifies the coordinate type for 'loc' and the second element is the coordinate type for 'box'. Either it is WCS in degrees [RA,Dec] / asec ('coord') or pixel [x,y] of the 'image' ('image'). If only one element is provided then the same coordinate type is used for both 'loc' and 'box'.
<code>approx.map</code>	Logical; should an approximate coordinate mapping scheme be computed? This should be left as the default FALSE if saving the cut down object, and only TRUE if you are experimenting with the image cutouts within the same R session.
<code>...</code>	Dots are parsed to either <code>magimage</code> (magcutout) or <code>magimageWCS</code> (magcutoutWCS).

### Details

These functions are on a level trivial, since it is easy to subset matrices and therefore images within R. However these functions track important properties of the subset region that makes it easy to track its location with respect to the original image. Also, they allow direct plotting of the resultant cutout with the most appropriate image functions. In many cases these functions will be used purely for their plotting side effects.

The 'shiftloc' and 'paddim' control the behaviour of the function in the non-trivial case when the desired box size extends beyond the edge of the image. If 'shiftloc' is FALSE (the default behaviour), the cutout is guaranteed to be centred on the pixel specified by 'loc'. Then, if 'paddim' is FALSE, the cutout extends only as far as possible until it reaches the edge of the image; otherwise if 'paddim' is TRUE the cutout image is padded with NAs in regions outside the supplied 'image' (the default behaviour). If 'shiftloc' is TRUE, the centre of the cutout will be shifted. In this case, if 'paddim' is FALSE, the cutout will extend at most half of the supplied 'box' size from the given 'loc'; otherwise if 'paddim' is TRUE the cutout will be expanded until it reaches the desired 'box' size or spans the entire image.

Note that if 'shiftloc' is TRUE and 'paddim' is FALSE, the cutout can be larger than 'box'; otherwise, the cutout is guaranteed to be no larger than the specified 'box' size.

### Value

A list containing:

<code>image</code>	Numeric matrix; the cutout region of interest centred around 'loc'.
<code>loc</code>	The new 'loc' vector that transforms the input 'loc' x and y location to the new 'cutim' coordinates. This is in ProFit coordinates, so these values can be used when, e.g., constructing a ProFit modelist structure.
<code>loc.orig</code>	The original location is provided by the input 'loc'.
<code>loc.diff</code>	The x and y offsets of the cutout compared to the original image, where 'loc' + 'loc.diff' = 'loc.orig' exactly.
<code>xsel</code>	Integer vector; the extracted x pixels from the original 'image' that form 'cutim'.
<code>ysel</code>	Integer vector; the extracted y pixels from the original 'image' that form 'cutim'.
<code>loc.WCS</code>	Only output from magcutoutWCS. Numeric vector of the central RA and Dec of the cutout region in degrees.

scale.WCS	Only output from magcutoutWCS. Numeric scalar value of the pixel scale in asec/pixel.
usr.WCS	Only output from magcutoutWCS. Numeric matrix of the RA/Dec extremes of the image in order BL/TL/BR/TR.
approx.map	Only output from magcutoutWCS. A helper function that will usually approximately map RA and Dec numeric vector inputs to a matrix with columns x and y. This is less accurate than <a href="#">magWCSradec2xy</a> , so use that function if the projection is too extreme. Should work for most N-S aligned data pretty well though, and it saves having to correctly track the appropriate header.
header	Only output from magcutoutWCS. The updated header with the correct WCS for the cutout region. Basically this means CRPIX1.new=CRPIX1.org-loc.diff[1] and CRPIX2.new=CRPIX2.org-loc.diff[2].

### Note

By R convention the bottom-left part of the bottom-left pixel when plotting the image matrix is  $c(0,0)$  and the top-right part of the bottom-left pixel is  $c(1,1)$ , i.e. the mid-point of pixels are half integer values in x and y. This differs to the FITS convention of pixel mid points being integer values. As such the R  $[x,y] = \text{FITS} [x-0.5,y-0.5]$ . This rarely matters too much in practice, but for accurate overlays you will want to get it right (see Examples).

It is ambiguous what the desired outcome is in some cutting scenarios, e.g. what should be returned if a 3x3 cutout is requested at the "centre" of a 8x8 image? For this reason, and to avoid unexpected results due to numerical precision, you should only cut out even pixel dimensions if integer pixel coordinates are provided, and odd pixel dimensions if half-integer pixel coordinates are provided. Regardless, the 'loc' and 'loc.orig' outputs will always help you locate the absolute coordinates of your desired cut out centre in both the cut out and the original image coordinate system.

### Author(s)

Aaron Robotham & Dan Taranu

### See Also

[magimageWCS](#)

### Examples

```
## Not run:
temp=matrix(1:121,11)

#The central value is at:

temp[6,6]

print(magcutout(temp, dim(temp)/2, box=c(3,3))$image)

#Given we cutout around the centre of the central pixel [5.5,5.5], the new centre
#relative to the cutout image output should be at [1.5,1.5]:
```

```

print(magcutout(temp, dim(temp)/2, box=c(3,3))$loc.orig)
print(magcutout(temp, dim(temp)/2, box=c(3,3))$loc)

# A simple WCS cutout example:

image=readFITS(system.file("extdata", 'VIKING/mystery_VIKING_Z.fits', package="ProFound"))

par(mar=c(3.1,3.1,1.1,1.1))
magcutout(image$imDat, loc=c(50.5,50.5), plot=TRUE)
magcutoutWCS(image, loc=c(50.5,50.5), loc.type = 'image', plot=TRUE)

#We can cut out using the coordinates instead:
print({tempcoord=magWCSxy2radec(50.5,50.5,header=image$hdr)})
magcutoutWCS(image, loc=tempcoord, loc.type=c('coord','image'), plot=TRUE)

#You can select coordinates too:

magcutoutWCS(image, loc=c(352.29167, -31.827777), box=c(30,30), plot=TRUE)$loc.WCS
magcutoutWCS(image, loc=c("23:29:10", "-31:49:40"), box=c(30,30) , coord.type = 'sex',
plot=TRUE)$loc.WCS

#We can add RA Dec specific decorations easily:

cutim=magcutoutWCS(image, loc=c(352.2918, -31.82652), box=c(30,30), plot=TRUE,
approx.map=TRUE)

#Approx overlays:

points(cutim$approx.map(c(352.2918, 352.2897), c(-31.82652, -31.8252)), pch=3, col='blue')

#Exact overlays:

points(magWCSradec2xy(c(352.2918, 352.2897), c(-31.82652, -31.8252), header=cutim$header),
col='red')

#Given we correctly modify the header, we can actually use the cut down image directly:

magimageWCS(cutim)

# Now test the various cutout size options for a large cutout near the image boundary

loc = c(300,340)
box = c(200,200)
loc.type = c("image","image")

magimage(image$imDat)
points(loc[1], loc[2], col='red')

# Setting shiftloc=FALSE and paddim=TRUE pads the image with NAs (default):

cutim=magcutout(image$imDat, loc=loc, box=box, plot=TRUE, shiftloc=FALSE, paddim=TRUE)
points(cutim$loc[1], cutim$loc[2], col='red')

```

```

cutim=magcutoutWCS(image, loc=loc, box=box, coord.type="image", loc.type=loc.type,
plot=TRUE, shiftloc=FALSE, paddim=TRUE)
points(cutim$loc[1], cutim$loc[2], col='red')

# The cutout is exactly the request size, but the centre is shifted:

cutim=magcutout(image$imDat, loc=loc, box=box, plot=TRUE, shiftloc=TRUE, paddim=TRUE)
points(cutim$loc[1], cutim$loc[2], col='red')

cutim=magcutoutWCS(image, loc=loc, box=box, coord.type="image", loc.type=loc.type,
plot=TRUE, shiftloc=TRUE, paddim=TRUE)
points(cutim$loc[1], cutim$loc[2], col='red')

# Setting paddim=FALSE returns the largest possible cutout within the image bounds,
# without shifting the centre:

cutim=magcutout(image$imDat, loc=loc, box=box, plot=TRUE, shiftloc=FALSE, paddim=FALSE)
points(cutim$loc[1], cutim$loc[2], col='red')

cutim=magcutoutWCS(image, loc=loc, box=box, coord.type="image", loc.type=loc.type,
plot=TRUE, shiftloc=FALSE, paddim=FALSE)
points(cutim$loc[1], cutim$loc[2], col='red')

# Setting paddim=FALSE and shiftloc=TRUE returns a larger cutout, but with at most
# box/2 padding on either side:

cutim=magcutout(image$imDat, loc=loc, box=box, plot=TRUE, shiftloc=TRUE, paddim=FALSE)
points(cutim$loc[1], cutim$loc[2], col='red')

cutim=magcutoutWCS(image, loc=loc, box=box, coord.type="image", loc.type=loc.type,
plot=TRUE, shiftloc=TRUE, paddim=FALSE)
points(cutim$loc[1], cutim$loc[2], col='red')

# Setting shiftloc=FALSE and requesting a box size larger than the image returns a cutout
# with the requested box size:

box = c(400,400)
cutim=magcutoutWCS(image, loc=loc, box=box, coord.type="image", loc.type=loc.type,
plot=TRUE, shiftloc=FALSE, paddim=TRUE)
points(cutim$loc[1], cutim$loc[2], col='red')

## End(Not run)

```

**Description**

A function to add x and y error bars to plots. Low and high error bars can be generated.

**Usage**

```
magerr(x, y, xlo, ylo, xhi = xlo, yhi = ylo, corxy, length = 0.02,
col = 'black', fill = FALSE, poly = FALSE, ...)
```

**Arguments**

x	Numeric vector; x location of data.
y	Numeric vector; y location of data.
xlo	Numeric vector; error on the low side for x values. This can be positive or negative- the absolute vaue is used. If length 1, then will be repeated length('x') times.
ylo	Numeric vector; error on the low side for y values. This can be positive or negative- the absolute vaue is used. If length 1, then will be repeated length('x') times.
xhi	Numeric vector; error on the high side for x values. This can be positive or negative- the absolute vaue is used. By default this will inherit the xlo value. If length 1, then will be repeated length('x') times.
yhi	Numeric vector; error on the high side for y values. This can be positive or negative- the absolute vaue is used. By default this will inherit the ylo value. If length 1, then will be repeated length('x') times.
corxy	Numeric vector; if this parameter exists then error ellipses will be drawn instead of error bars. It takes the value of the sigma_x sigma_y correlation, i.e. $corxy=covxy/(xlo*ylo)$ . If length 1, then will be repeated length('x') times.
length	Numeric vector; length of error bar ends. If length 1, then will be repeated length('x') times.
col	Either the colour of the error bars or the outline colour of the error ellipses. If length 1, then will be repeated length('x') times.
fill	Logical; if TRUE then the error ellipses will be filled, if FALSE then only the border will be drawn.
poly	Logical; is FALSE then error bars or ellipses will be drawn, if TRUE then approximate error polygon will be shown instead.
...	Further arguments to be passed to the <a href="#">arrows</a> / <a href="#">draw.ellipse</a> / <a href="#">polygon</a> functions used to draw the error bars / error ellipses ('corxy' not missing) / error polygon ('poly'=TRUE).

**Details**

Note that with 'poly'=TRUE the x values are used igoring any error terms, and the point value y errors are used to define the limits of the polygon, with straight lines joining the points. The 'col' option is used to fill the polygon with a colour (so the default black is probably not a great choice). The [polygon](#) function takes the argument 'border' (parsed by dots from the magerr function) to colour the outer lines, so for a more subtle error polygon you might want to use 'col'=lightgrey, 'border'=NA, where NA means no outer border lines are drawn.

**Value**

Called for the side effect of plotting error bars.

**Author(s)**

Aaron Robotham

**See Also**

[magplot](#), [magaxis](#), [maglab](#), [magmap](#), [magrun](#), [arrows](#), [draw.ellipse](#), [polygon](#)

**Examples**

```
# Basic x and y errors added to plot
temp=cbind(x=runif(10),y=runif(10),xerr=runif(10,0.05,0.2),yerr=runif(10,0.1,0.3),
corxy=runif(10,-1,1))
magplot(temp[,1:2])
magerr(x=temp[,1],y=temp[,2],xlo=temp[,3],ylo=temp[,4])
# Example of errors on plots with log axes
magplot(temp[,1:2],log='xy')
magerr(x=temp[,1],y=temp[,2],xlo=temp[,3],ylo=temp[,4])

#Example of error ellipses

magplot(temp[,1:2])
magerr(x=temp[,1],y=temp[,2],xlo=temp[,3],ylo=temp[,4])
magerr(x=temp[,1],y=temp[,2],xlo=temp[,3],ylo=temp[,4],corxy=temp[,5])
```

---

maghist

*Magically pretty histograms*

---

**Description**

A fairly simple function that produces pretty histograms. The main difference to base [hist](#) is that it allows for easy truncation of the data provided via 'xlim' and useful logging options.

**Usage**

```
maghist(x, breaks = "Sturges", freq = TRUE, include.lowest = TRUE, right = TRUE,
density = NULL, angle = 45, col = NULL, border = NULL, xlim = NULL, ylim = NULL,
plot = TRUE, verbose = TRUE, add = FALSE, log = '', unlog = log, scale = 1,
cumsum = FALSE, p.test = NULL, ...)
```

**Arguments**

x	A vector of values for which the histogram is desired.
breaks	One of: <ul style="list-style-type: none"> <li>• A vector giving the breakpoints between histogram cells,</li> <li>• A function to compute the vector of breakpoints,</li> <li>• A single number giving the number of cells for the histogram,</li> <li>• A character string naming an algorithm to compute the number of cells,</li> <li>• A function to compute the number of cells.</li> </ul> <p>In the last three cases the number is a suggestion only; the breakpoints will be set to <code>pretty</code> values. If <code>breaks</code> is a function, the <code>x</code> vector is supplied to it as the only argument.</p>
freq	Logical; if TRUE, the histogram graphic is a representation of frequencies, the counts component of the result; if FALSE, probability densities, component density, are plotted (so that the histogram has a total area of one). Defaults to TRUE if and only if <code>breaks</code> are equidistant (and probability is not specified).
include.lowest	Logical; if TRUE, an <code>x[i]</code> equal to the <code>breaks</code> value will be included in the first (or last, for <code>right = FALSE</code> ) bar. This will be ignored (with a warning) unless <code>breaks</code> is a vector.
right	Logical; if TRUE, the histogram cells are right-closed (left open) intervals.
density	The density of shading lines, in lines per inch. 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).
col	A colour to be used to fill the bars. The default of NULL yields unfilled bars.
border	The color of the border around the bars. The default is to use the standard foreground color.
xlim	Vector; range of 'x' values to use for both counting and plotting. The default NULL will span the range of histogram breaks. If length equals 1 then the argument is taken to mean the sigma range to select for plotting and the clipping is done by <code>magclip</code> . If this is set to 'auto' then the limits will be estimated from the data dynamically. See examples.
ylim	Vector; range of y limits to show in the histogram plot.
plot	Logical; draw the histogram (otherwise it just returns the count data).
verbose	Logical; if TRUE and 'xlim' is used then the followign is printed out: summary of the data selected, standard-deviation the 1/2-sigma implied quantiles, and number and fraction of displayed data. Note all numbers are computed for the logged values of the 'x' input if 'log'= x   xy   yx.
add	Logical, if TRUE the histogram will be added to the current plot. Be careful to match 'log' properties if adding, else the comparison will be of little use and hard to interpret.
log	Log axis arguments to be passed to <code>hist</code> and <code>plot</code> . E.g. use 'x', 'y', 'xy' or 'yx' as appropriate. Default "" assumes no logging of any axes. If the x axis is logged then the histogram will be calculated in log-space.

unlog	Determines if axis labels should be unlogged. E.g. use 'x', 'y', 'xy' or 'yx' as appropriate. See <a href="#">magaxis</a> .
scale	Numeric scalar; an additional scaling parameter to apply to the frequency counts. This is useful if you want to get the y axis in to certain units, e.g. the counts represent objects in 10 square degrees of sky, so to get the y-axis into units of N/sq.deg you would set 'scale'=1/10.
cumsum	Logical; if FALSE (default) then 'counts' and 'density' are totals for the current bin (usual sense of a histogram), if TRUE then 'counts' and 'density' are cumulative totals of all counts up to and including the current bin (always from lowest 'x' upwards).
p.test	Function; optionally the user can provide a standard (or custom) p-test to be computed on the display (i.e. trimmed) data. This might be e.g. a Normality test with the <a href="#">shapiro.test</a> function etc. The results are printed to screen below the other standard summary information if 'verbose'=TRUE.
...	Arguments to be parsed to <a href="#">magplot</a> .

### Details

To better replicate the base [hist](#) plot you might consider setting 'frame.plot'=FALSE, which will be parsed to [magplot](#) and turn off the outer box. The default behaviour might change in the future.

### Value

An object of class "histogram", basically the same output as produced by [hist](#). Note where axes are logged, the corresponding hist list values will not be logged when returned. This is to make it easy to take a histogram object and plot it with different log scalings on the axes (see Examples). For the x axis this means the "breaks" and the "mids" items, and for the y axis this means the "counts" and the "density" items.

Appended to the end of the usual [hist](#) output are the summary of the sample (list element "summary") and the standard-deviation / 1 and 2-sigma quantile range (list element "ranges").

### Author(s)

Aaron Robotham

### See Also

[hist](#)

### Examples

```
maghist(rnorm(1e4))
maghist(rnorm(1e4), xlim=c(-2,4))

#Notice the x-limits are close to -3/3, since if we ask for xlim=3 (a 3-sigma range)
maghist(rnorm(1e4), xlim=3, verbose = FALSE)

#The 'auto' option allows magclip to dynamically estimate a clip value (which is similar
```

```

#in this case, but need not be in general).

maghist(rnorm(1e4), xlim='auto', verbose = FALSE)

#Test of log histograms:

testdata=10^(runif(1e3,0,4))
maghist(testdata)
maghist(testdata,log='x')
maghist(testdata,log='y')
maghist(testdata,log='xy')

maghist(testdata,freq=FALSE)
maghist(testdata,freq=FALSE,log='x')
maghist(testdata,freq=FALSE,log='y')
maghist(testdata,freq=FALSE,log='xy')

#Test of plotting histogram objects:

testhist=maghist(testdata,log='xy')
maghist(testhist)
maghist(testhist,log='x')
magplot(testhist,log='y')
magplot(testhist,log='xy')

#Nice to see a grid with large ranges:

maghist(rnorm(1e6), grid=TRUE)
maghist(rnorm(1e6), log='y', grid=TRUE)

```

---

magimage

*Magically pretty images*


---

## Description

magimage is a level replacement for base image with hooks into magaxis for the tick marks and magmap for the image scaling. The default behaviour is a bit different to base (e.g. x/y scales are automatically the number of pixels in the image matrix). magimageRGB is similar, but is for the creation colour images where the user can provide R G B input matrix channels (or similar).

## Usage

```

magimage(x, y, z, zlim, xlim, ylim, col = grey((0:1000)/1000), add = FALSE,
useRaster = TRUE, asp = 1, magmap = TRUE, locut = 0.4, hicut = 0.995, flip = FALSE,
range = c(0, 1), type = "quan", stretch = "asinh", stretchscale = 'auto', bad = NA,
clip = "", axes = TRUE, frame.plot = TRUE, sparse = 'auto', qdiff = FALSE,
rem_med = FALSE, ...)
magimageRGB(x, y, R, G, B, saturation = 1, zlim, xlim, ylim, add = FALSE,
useRaster = TRUE, asp = 1, magmap = TRUE, locut = 0.4, hicut = 0.995, flip = FALSE,
range = c(0, 1), type = "quan", stretch = "asinh", stretchscale = "auto", bad = range[1],
clip = "", axes = TRUE, frame.plot = TRUE, sparse = 'auto', ...)

```

**Arguments**

<code>x, y</code>	Locations of grid lines at which the values in <code>z</code> are measured. These must be finite and non-missing (order may be reversed). By default, equally spaced values from 0 to <code>dim(z)[1]</code> are used. If <code>x</code> is a list, its components <code>x\$x</code> and <code>x\$y</code> are used for <code>x</code> and <code>y</code> , respectively. If the list has component <code>z/R/G/B</code> this is used for <code>z/R/G/B</code> .
<code>z</code>	A numeric or logical matrix containing the values to be plotted (NAs are allowed). Note that <code>x</code> can be used instead of <code>z</code> for convenience.
<code>R</code>	A numeric or logical matrix containing the red colour values to be plotted (NAs are allowed). Note that ' <code>x</code> ' can be a 3D array or list (containing elements <code>R/G/B</code> ) instead of <code>R</code> for convenience, where <code>R=x[,1]</code> .
<code>G</code>	A numeric or logical matrix containing the green colour values to be plotted (NAs are allowed). Note that ' <code>x</code> ' can be a 3D array or list (containing elements <code>R/G/B</code> ) instead of <code>G</code> for convenience, where <code>G=x[,2]</code> .
<code>B</code>	A numeric or logical matrix containing the blue colour values to be plotted (NAs are allowed). Note that ' <code>x</code> ' can be a 3D array or list (containing elements <code>R/G/B</code> ) instead of <code>B</code> for convenience, where <code>B=x[,3]</code> .
<code>saturation</code>	The visual saturation of the colours, a bit like the dial on a TV. 1 is native, 0 is black and white, 2 is very intense nigh-on trippy.
<code>zlim</code>	The <code>z</code> limit with respect to the output of <code>magmap\$map</code> . If ' <code>magmap</code> '= <code>FALSE</code> (default) ' <code>zlim</code> ' should be with respect to the provided <code>z</code> matrix (like base <code>image</code> ). If ' <code>magmap</code> '= <code>TRUE</code> ' <code>zlim</code> ' should be with respect to the ' <code>range</code> ' output of <code>magmap</code> . By default the <code>magmap</code> function scales between 0 and 1, so to only show the brighter pixels ' <code>zlim</code> ' could be set to <code>c(0.5,1)</code> .
<code>xlim, ylim</code>	Ranges for the plotted <code>x</code> and <code>y</code> values, defaulting to the ranges of <code>x</code> and <code>y</code> .
<code>col</code>	A list of colours for the <code>magmap</code> re-mapping of <code>z</code> to be parsed into (e.g. <code>rainbow</code> , <code>heat.colors</code> , <code>topo.colors</code> , <code>terrain.colors</code> or similar).
<code>add</code>	If true add the new image to the current plot.
<code>useRaster</code>	If <code>TRUE</code> a bitmap raster is used to plot the image instead of polygons. The grid must be regular in that case, otherwise an error is raised. Raster is much faster, so use when pixels are equal sized.
<code>asp</code>	The <code>y/x</code> aspect ratio
<code>magmap</code>	If <code>TRUE</code> then <code>magmap</code> scaling is applied to the <code>z</code> dimension (default), if <code>FALSE</code> then it is not.
<code>locut</code>	The low limit to clip the <code>z</code> data at (what this means varies depending on the ' <code>type</code> ' option). For <code>magimageRGB</code> this can be a single value (used for ' <code>R</code> ', ' <code>G</code> ' and ' <code>B</code> ') or a vector of length 3 (used for ' <code>R</code> ', ' <code>G</code> ' and ' <code>B</code> ' respectively). See <code>magmap</code> for more information.
<code>hicut</code>	The high limit to clip the <code>z</code> data at (what this means varies depending on the ' <code>type</code> ' option). For <code>magimageRGB</code> this can be a single value (used for ' <code>R</code> ', ' <code>G</code> ' and ' <code>B</code> ') or a vector of length 3 (used for ' <code>R</code> ', ' <code>G</code> ' and ' <code>B</code> ' respectively). See <code>magmap</code> for more information.

flip	Should the z scaling be flipped. This allows numbers from 0 to 10 to be mapped from 1 to 0 (so ordered back to front with respect to the input). See <a href="#">magmap</a> for more information.
range	The numerical range of the output z mapping which should be a vector of length two specifying c(low,high). See <a href="#">magmap</a> for more information.
type	The type of z mapping attempted. Options are 'quan' (default), 'num', 'sig' and 'rank'. See <a href="#">magmap</a> for more information.
stretch	stretch='lin' gives linear mapping. stretch='log' gives logarithmic mapping. stretch='atan' gives atan mapping. stretch='asinh' gives asinh mapping. stretch='sqrt' gives sqrt mapping. See <a href="#">magmap</a> for more information.
stretchscale	A number to multiply the z data by before applying the stretch. This only has a user impact for stretch='atan' and stretch='asinh' since it controls what parts of the data is in the linear or logarithmic regime of the stretch procedure. If set to 'auto' (the default) it uses 1/median(abs(data)) to find a useful scale. See <a href="#">magmap</a> for more information. For magimageRGB this can be a single value (used for 'R', 'G' and 'B') or a vector of length 3 (used for 'R', 'G' and 'B' respectively). See <a href="#">magmap</a> for more information.
bad	Sets the value that NA, NaN and infinite input z data should be set to in the final map output. This should be thought of in the context of the range argument, i.e. if bad=range[1] then bad values will be the low range value and if bad=range[2] bad values will be the high range value. See <a href="#">magmap</a> for more information. For magimageRGB bad is set to range[1] by default since this removes RGB conversion errors that would be experienced with NA values (i.e. negative values when 'stretch'='log').
clip	By default clipped z values inherit the nearest lo/hi value (depending on which side they are clipped). Setting clip='NA' will set values outside the 'lo' and 'hi' values to be NA (currently this is the only other clip option). See <a href="#">magmap</a> for more information.
axes	Specify if any axes be drawn on the image. If FALSE then only the pixels (with appropriate magmap scaling) are shown.
frame.plot	Specify if a box be drawn around the image frame. Only happens if 'add'=TRUE and 'axes'=TRUE.
sparse	Determines whether the image pixels are sparse sampled to speed up plotting. If set to 2 it will only determine every 2nd pixel, and if 3 every 3rd etc. The default 'auto' means it will scale to produce a maximum number of 1,000 pixels on any side (on most monitors this is a fairly useful maximum, and ensures quick displaying of even very large images).
qdiff	Logical; if the z axis being plotted, this will set all the various parameters that make for a visually useful difference plot, where -ve difference values become blue, 0 difference values are yellow, and +ve difference values are red.
rem_med	Logical; should the median of the 'image' be subtracted or not? This is often useful in conjunction with 'qdiff' = TRUE.
...	Arguments to be parsed to image and magaxis as relevant (this is checked for internally by argument name). See <a href="#">image</a> and <a href="#">magaxis</a> for details.

## Details

See [image](#), [magmap](#) and [magaxis](#) for more details.

## Value

Outputs the final image list containing x,y and z (magimage) or R/G/B (magimageRGB). Generally run for the side effect of producing rapid and well-scaled image plots.

## Author(s)

Aaron Robotham

## See Also

[magimageWCS](#), [image](#), [magcutout](#), [magmap](#), [magaxis](#)

## Examples

```
#Basic
magimage(matrix(1:9,3))

#Mid pixel versus pixel edge:
magimage(3:0,1:3,matrix(1:9,3))

#Standard scaling is not very useful in this instance:
magimage(matrix(10^(1:9),3))
#Linear scaling is not very useful in this instance, though it does now map from [0,1]:
magimage(matrix(10^(1:9),3),magmap=TRUE,zlim=c(0,0.5))
#Log scaling with magmap makes it much clearer:
magimage(matrix(10^(1:9),3),magmap=TRUE,stretch='log')
#And it's easy just to show the lowest half now:
magimage(matrix(10^(1:9),3),magmap=TRUE,stretch='log',zlim=c(0,0.5))

## Not run:
#Some astro data:
image=readFITS(system.file("extdata", 'VIKING/mystery_VIKING_Z.fits', package="ProFound"))

#A monotone image:
magimage(image$imDat)
#A faked colour image (this won't look great):
magimageRGB(R=image$imDat^3, G=image$imDat^1.5, B=image$imDat^2)

## End(Not run)
```

---

magimageWCS

*Tan Gnomonic WCS Image Decoration*


---

## Description

These functions add various WCS information to R images. It is particularly designed to work in unison with ‘magimage’ that is used extensively in the wider ProFit package.

## Usage

```
magimageWCS(image, header, n, grid.col = "grey", grid.lty = 2, grid.lwd = 0.5,
lab.col = "green", coord.type = "sex", margin = TRUE, loc.diff = c(0, 0),
xlab = "Right Ascension", ylab = "Declination", mgp = c(2, 0.5, 0), mtline = 2,
position = "topright", com.col = "green", com.length = 0.05, coord.axis = 'auto',
pretty = 'auto', CRVAL1 = 0, CRVAL2 = 0, CRPIX1 = 0, CRPIX2 = 0, CD1_1 = 1, CD1_2 = 0,
CD2_1 = 0, CD2_2 = 1, CTYPE1 = 'RA--TAN', CTYPE2 = 'DEC--TAN', ...)
```

```
magimageWCSRGB(R, G, B, header_out, Rheader, Gheader, Bheader, dowarp='auto',
direction = "auto", boundary = "dirichlet", interpolation = "cubic", n, grid.col='grey',
grid.lty=2, grid.lwd=0.5, lab.col='green', coord.type='sex', margin=TRUE, loc.diff=c(0,0),
xlab='Right Ascension', ylab='Declination', mgp=c(2,0.5,0), mtline=2, position='topright',
com.col="green", com.length=0.05, coord.axis='auto', pretty='auto', CRVAL1=0, CRVAL2=0,
CRPIX1=0, CRPIX2=0, CD1_1=1, CD1_2=0, CD2_1=0, CD2_2=1, CTYPE1 = 'RA--TAN',
CTYPE2 = 'DEC--TAN', ...)
```

```
magimageWCSGrid(header, n, grid.col = "grey", grid.lty = 1, grid.lwd = 1,
coord.type = "sex", loc.diff = c(0, 0), pretty= 'auto', CRVAL1 = 0, CRVAL2 = 0,
CRPIX1 = 0, CRPIX2 = 0, CD1_1 = 1, CD1_2 = 0, CD2_1 = 0, CD2_2 = 1, CTYPE1 = 'RA--TAN',
CTYPE2 = 'DEC--TAN', ...)
```

```
magimageWCSLabels(header, n, lab.col = "green", coord.type = "sex", margin = TRUE,
loc.diff = c(0, 0), xlab = "Right Ascension", ylab = "Declination", mgp = c(2, 0.5, 0),
mtline = 2, coord.axis='auto', pretty= 'auto', CRVAL1 = 0, CRVAL2 = 0, CRPIX1 = 0,
CRPIX2 = 0, CD1_1 = 1, CD1_2 = 0, CD2_1 = 0, CD2_2 = 1, CTYPE1 = 'RA--TAN',
CTYPE2 = 'DEC--TAN', ...)
```

```
magimageWCSCompass(header, position = "topright", com.col = "green", com.length = 0.05,
loc.diff = c(0, 0), CRVAL1 = 0, CRVAL2 = 0, CRPIX1 = 0, CRPIX2 = 0, CD1_1 = 1, CD1_2 = 0,
CD2_1 = 0, CD2_2 = 1, CTYPE1 = 'RA--TAN', CTYPE2 = 'DEC--TAN', ...)
```

## Arguments

image	Numeric matrix; required, the image we want to decorate. If ‘image’ is a list as created by readFITS, read.fits of <a href="#">magcutoutWCS</a> then the image part of the list is parsed to ‘image’ and the correct header part is parsed to ‘header’.
header	Full FITS header in table or vector format. Legal table format headers are provided by the read.fitshdr function or the ‘hdr’ list output of read.fits in

the astro package; the 'hdr' output of readFITS in the FITSio package or the 'header' output of magcutoutWCS. If a header is provided then key words will be taken from here as a priority. Missing header keywords are printed out and other header option arguments are used in these cases.

R	Numeric matrix; containing the red colour values to be plotted (NAs are allowed). If 'R' is a list as created by readFITS, read.fits of magcutoutWCS then the image part of the list is parsed to 'R' and the correct header part is parsed to 'Rheader'.
G	Numeric matrix; containing the green colour values to be plotted (NAs are allowed). If 'G' is a list as created by readFITS, read.fits of magcutoutWCS then the image part of the list is parsed to 'G' and the correct header part is parsed to 'Gheader'.
B	Numeric matrix; containing the blue colour values to be plotted (NAs are allowed). If 'B' is a list as created by readFITS, read.fits of magcutoutWCS then the image part of the list is parsed to 'B' and the correct header part is parsed to 'Bheader'.
header_out	Full FITS header in table or vector format. This is the target WCS projection that the RGB image will be mapped onto. Legal table format headers are provided by the read.fitshdr function or the 'hdr' list output of read.fits in the astro package; the 'hdr' output of readFITS in the FITSio package or the 'header' output of magcutoutWCS. If a header is provided then key words will be taken from here as a priority. Missing header keywords are printed out and other header option arguments are used in these cases.
Rheader	Full 'R' FITS header in table or vector format. It is usually easier to include the header with the 'R' list input as described above.
Gheader	Full 'G' FITS header in table or vector format. It is usually easier to include the header with the 'G' list input as described above.
Bheader	Full 'B' FITS header in table or vector format. It is usually easier to include the header with the 'B' list input as described above.
dowarp	Image warping flag, either TRUE, FALSE or 'auto' (default). If TRUE then the images will be warped onto the 'header_out' WCS scheme, if FALSE they will not be (which will break if the WCSs are not truly the same and the iamges are pixel matched). 'auto' tries to detect if the headers are all the same, and if they are then it will set 'dowarp'=FALSE, otherwise it will set to TRUE. This can be fooled by small (and unimportant) differences in the headers, e.g. they have different SWarp dates etc, since it just checks if the text differs anywhere.
direction	Only used if re-mapping via magwarp. "auto" (default), "forward" or "backward", see imwarp. Since it is usally better to go from the higher resolution image and map this onto the lower resolution grid, "auto" selects the better direction given the pixel scales recovered from the header information.
boundary	Only used if re-mapping via magwarp. Boundary conditions: "dirichlet", "neumann", "periodic" (default "dirichlet"), see imwarp
interpolation	Only used if re-mapping via magwarp. "nearest", "linear", "cubic" (default "linear"), see imwarp
n	The target number of major-axis sub-divisions. Will not necessarily be achieved.

grid.col	The colour of the overlaid grid lines.
grid.lty	The line type of the overlaid grid lines.
grid.lwd	The line width of the overlaid grid lines.
lab.col	The colour of the labels when 'margin'=FALSE.
coord.type	Should the labels be drawn using degrees (deg) or colon delimited sexagesimal (sex).
margin	Should the labels be drawn in the outer margin region (default).
loc.diff	The pixel offset to apply. Only relevant if the image being plotted is a cutout from within a FITS legal image.
xlab	x axis name. If left as default either H:M:S or D:M:S ('coord.type'='sex') or deg ('coord.type'='deg') will be appended.
ylab	y axis name. If left as default either H:M:S or D:M:S ('coord.type'='sex') or deg ('coord.type'='deg') will be appended.
mgp	The margin line (in mex units) for the axis title, axis labels and axis line. This has different (i.e. prettier) defaults than R of c(2,0.5,0) rather than c(3,1,0). This pushes the numbers and labels nearer to the plot compared to the defaults. For 'margin'=FALSE 'mgp' = -'mgp' - 3, which has the effect of shifting the tick labels nicely inside the margin.
mtline	Number of lines separating axis name from axis. For 'margin'=FALSE 'mtline' = -'mtline', which has the effect of shifting the axis labels nicely inside the margin.
coord.axis	Integer vector; specifies whether the RA and Dec axes should be 1 or 2 (i.e. x or y axis). The default 'auto' tries to guess based on the header information (and this usually works okay). Otherwise 'coord.axis'=c(1,2) would be sensible for a N/S vertical aligned frame and 'coord.axis'=c(2,1) would be sensible for a E/W vertically aligned frame. When the orientation is between the two then it is not always obvious which will work better.
pretty	If 'auto' then it will try to compute the prettiest grid and label scaling *usually this is pretty good). Otherwise set to 1 to be degrees major ticks, 60 for minutes (DMS or HMS) and 3600 for seconds (DMS or HMS).
position	Relative position of the compass bar. This argument is used like the 'legend' function. Specify one of 'bottom', 'bottomleft', 'left', 'topleft', 'top', 'topright', 'right', 'bottomright' and 'centre'.
com.col	Colour of the compass.
com.length	Length of the edges of the arrow head.
CRVAL1	FITS header CRVAL1 for the 'CTYPE1' projection system. This is the RA in degrees at the location of 'CRPIX1'.
CRVAL2	FITS header CRVAL2 for the 'CTYPE2' projection system. This is the Dec in degrees at the location of 'CRPIX2'.
CRPIX1	FITS header CRPIX1 for the 'CTYPE1' projection system. This is the x pixel value at the location of 'CRVAL1'.
CRPIX2	FITS header CRPIX2 for the 'CTYPE2' projection system. This is the y pixel value at the location of 'CRVAL2'.

CD1_1	FITS header CD1_1 for the 'CTYPE1' projection system. Change in 'CTYPE1' in degrees along x-Axis.
CD1_2	FITS header CD1_2 for the 'CTYPE1' projection system. Change in 'CTYPE1' in degrees along y-Axis.
CD2_1	FITS header CD2_1 for the 'CTYPE2' projection system. Change in 'CTYPE2' in degrees along x-Axis.
CD2_2	FITS header CD2_2 for the 'CTYPE2' projection system. Change in 'CTYPE2' in degrees along y-Axis.
CTYPE1	The RA projection system type. Either 'RA-TAN' for Tan Gnomonic (default), or 'RA-SIN' for Sine Orthographic. 'RA-NCP' is approximated by Sine Orthographic with a warning. Over-ridden by the FITS header.
CTYPE2	The DEC projection system type. Either 'DEC-TAN' for Tan Gnomonic (default), or 'DEC-SIN' for Sine Orthographic. 'DEC-NCP' is approximated by Sine Orthographic with a warning. Over-ridden by the FITS header.
...	These are parsed to <a href="#">magimage</a> , ( <a href="#">magimageWCS</a> ), <a href="#">magimageRGB</a> , ( <a href="#">magimageWCSRGB</a> ), <a href="#">lines</a> ( <a href="#">magimageWCSGrid</a> ), <a href="#">axis</a> ( <a href="#">magimageWCSLabels</a> ) or <a href="#">arrows</a> ( <a href="#">magimageWCSCompass</a> ).

### Details

Most people will be content to use the higher level `magimageWCS` function, which calls (in order) `magimage`, `magimageWCSGrid`, `magimageWCSLabels` and `magimageWCSCompass`.

`magimageWCSRGB` can be used in a few different ways, but the recommended route is to supply combined image and header list objects to the 'R', 'G' and 'B' arguments. If 'header\_out' is not supplied then by default it will project the three images onto the first available WCS header it finds searching 'R', 'G' and 'B' in order. If you are happy to map the colour image into the 'R' WCS then you do not need to supply 'header\_out' at all. Note if image remapping is required (the images are different sizes or the headers differ) then the `imager` library will need to be installed in order to use `magwarp`.

### Value

Outputs the final image list containing x,y and z (`magimageWCS`) or R/G/B (`magimageWCSRGB`). Generally run for the side effect of producing rapid and well-scaled image plots.

### Note

For convenience users can use the header outputs produced by both the `readFITS` and `astro` package.

By R convention the bottom-left part of the bottom-left pixel when plotting the image matrix is  $c(0,0)$  and the top-right part of the bottom-left pixel is  $c(1,1)$ , i.e. the mid-point of pixels are half integer values in x and y. This differs to the FITS convention of pixel mid points being integer values. As such the R  $[x,y] = \text{FITS } [x-0.5,y-0.5]$ . This rarely matters too much in practice, but for accurate overlays you will want to get it right.

### Author(s)

Aaron Robotham

**See Also**

[magimage](#), [magcutoutWCS](#), [radec2xy](#), [xy2radec](#)

**Examples**

```
## Not run:
image=readFITS(system.file("extdata", 'VIKING/mystery_VIKING_Z.fits', package="ProFound"))

#Convenient image plotting for lists containing headers:

magimageWCS(image$imDat, header=image$hdr)
magimageWCS(image)

#First using the outer margins for tick labels:

par(mar=c(3.1,3.1,1.1,1.1))
magimageWCS(image)
magimageWCS(image, coord.type='deg')

#Now removing the margins and putting labels inside the image:

par(mar=c(0,0,0,0))
magimageWCS(image, margin=FALSE)
magimageWCS(image, margin=FALSE, coord.type='deg')

#We can make a WCS colour image of mismatched images:

VISTA_K=readFITS(system.file("extdata", 'VISTA_K.fits', package="magicaxis"))
VST_r=readFITS(system.file("extdata", 'VST_r.fits', package="magicaxis"))
GALEX_NUV=readFITS(system.file("extdata", 'GALEX_NUV.fits', package="magicaxis"))

magimageWCSRGB(VISTA_K, VST_r, GALEX_NUV)
magimageWCSRGB(VISTA_K, VST_r, GALEX_NUV, saturation=0.5)

#To make direct magimageRGB plots of the outputs you must turn off magmap scaling:

temp=magimageWCSRGB(VISTA_K, VST_r, GALEX_NUV)
magimageRGB(R=temp$R, G=temp$G, B=temp$B, magmap=FALSE)

#We can map onto various WCS schemes easily too:

magimageWCSRGB(VISTA_K, VST_r, GALEX_NUV, VISTA_K$hdr)
magimageWCSRGB(VISTA_K, VST_r, GALEX_NUV, VST_r$hdr)
magimageWCSRGB(VISTA_K, VST_r, GALEX_NUV, GALEX_NUV$hdr)

## End(Not run)
```

## Description

Utilises pretty for the major-tick locations, but makes prettier decisions if log axes are being used. Translates the default text into nicely formatted expressions- this is particularly successful when axes are logged and exponents are used since formats like  $1e5$  should not be used in scientific academic journals.

## Usage

```
maglab(lims, n, log=FALSE, exptext = TRUE, crunch = TRUE, logpretty = TRUE,
usemultloc = FALSE, multloc = c(1,2,5), prettybase = 10, powbase = 10, hersh = FALSE,
trim = FALSE)
```

## Arguments

lims	Limits over which pretty major-tick locations will be calculated.
n	The target number of major-axis sub-divisions. Will not necessarily be achieved.
log	Should the limits be evenly distributed over log space. Usually what you want if an axis has been logged.
exptext	Should log==TRUE then should the text be written in exponent form (e.g. $10^8$ , default when exptext==TRUE) or logged (e.g. 8 in this case).
crunch	In cases where the scientific text would be written as $1 \times 10^8$ , should the 1x be removed so it reads $10^8$ . TRUE by default.
logpretty	Should the major-ticks only be located at powers of 10, or when dynamic range is small (less than 50) powers of 10 times 1, 2 and 5. This changes cases where ticks are placed at 1, 3.1, 10, 31, 100 etc to 1, 10, 100.
usemultloc	For log=TRUE, if usemultloc=FALSE then label locations are only at powers of 10, if usemultloc=TRUE then they are at multiples of powers of 10 as defined by multloc.
multloc	If usemultloc is TRUE then multloc provides the multiples of powers of 10 for the location of labels. Default will give them at 0.1, 0.2, 0.5, 1 etc.
prettybase	The unit of repetition desired. By default it is 10, implying a pretty plot is one with marks at 10, 20, 30 etc. If you are plotting degrees then it might be prettier to display 90, 180, 270 etc. In which case prettybase should be set to 90. If log=TRUE then the reference location of 10 is changed, so in the previous example the labels generated would be at 9, 90, 900 etc rather than the default of 1, 10, 100 etc.
powbase	Set the base to use for logarithmic axes. Default is to use 10.
hersh	Determines whether the text format output by maglab should be Hershey vector font compatible text (TRUE), or normal plotmath style expressions (FALSE).
trim	If trim is TRUE the outputs are not allowed to exceed the stated limits, if FALSE then the whole range of pretty values calculated are used. This will usually extend beyond the limits to ensure the plots look pretty, but if maglab is being used for something other than plotting axis labels then trimmed values might be useful.

**Details**

This function is a mid level routine for producing nice ticks and text, with particularly effort on improving the outcome of logged axis cases. The end user will probably not require axis to it except in unusual circumstances. I note that my method of translating the default representation of the exponents is not very elegant, so any suggestions for improvement are welcome!

**Value**

tickat	Location of proposed major-tick marks.
labat	Location of proposed label locations (not necessarily the same as major-tick locations).
exp	Expressions to be used at label locations.

**Author(s)**

Aaron Robotham

**See Also**

[magplot](#), [magaxis](#), [magerr](#), [magmap](#), [magrun](#)

**Examples**

```
x=10^{1:9}
y=1:9
plot(log10(x),y,axes=FALSE)
ticks=maglab(range(x),log=TRUE)
print(ticks)
axis(1,at=log10(ticks$labat),labels=ticks$exp)

# Same outcome a different way:

plot(x,y,axes=FALSE,log='x')
ticks=maglab(range(x),log=TRUE)
print(ticks)
axis(1,at=ticks$labat,labels=ticks$exp)

# For small dynamic range

x=seq(1,40,len=9)
y=1:9
plot(x,y,axes=FALSE,log='x')
ticks=maglab(range(x),log=TRUE,usemultloc=TRUE)
axis(1,at=ticks$labat,labels=ticks$exp,tick=FALSE)
axis(1,at=ticks$tickat,labels=FALSE)

# Different base prettiness

x=0:270
y=sin(x*pi/180)
plot(x,y,axes=FALSE,type='l')
```

```

ticks=maglab(range(x))
axis(1,at=ticks$labat,labels=ticks$exp)
# Not very pretty for degree plotting
ticks=maglab(range(x),prettybase=45)
axis(3,at=ticks$labat,labels=ticks$exp)
# Much nicer!

```

---

magmap	<i>Value remapper</i>
--------	-----------------------

---

### Description

This function allows the use to remap a vector of values onto a different system. For instance you might have values stretching from -10 to 100 which you want mapped from 0 to 2/3 so you can then sue the output as an input for point colour or size. It allows clipping of values, rejection of bad values, and log stretching.

### Usage

```

magmap(data, locut = 0, hicut = 1, flip = FALSE, range = c(0, 2/3), type = "quan",
stretch = 'lin', stretchscale = 1, bad = NA, clip = '')

```

### Arguments

data	A vector of values. This can contain bad values (NA, NaN, infinite), but these will be ignored during mapping and set to the value of input parameter 'bad'.
locut	The low limit to clip the data at (what this means varies depending on the 'type' option). This should be a single value.
hicut	The high limit to clip the data at (what this means varies depending on the 'type' option). This should be a single value.
flip	Should the scaling be flipped. This allows numbers from 0 to 10 to be mapped from 1 to 0 (so ordered back to front with respect to the input).
range	The numerical range of the output mapping which should be a vector of length two specifying c(low,high).
type	The type of mapping attempted. Options are 'quan' (default), 'num', 'sig' and 'rank'.
stretch	'stretch'='lin' gives linear mapping. 'stretch'='log' gives logarithmic mapping. 'stretch'='atan' gives atan mapping. 'stretch'='asinh' gives asinh mapping. 'stretch'='sqrt' gives sqrt mapping. 'stretch'='cdf' gives CDF mapping onto the cumulative range 0-1
stretchscale	A number to multiply the data by before applying the stretch. This only has a user impact for stretch='atan' and stretch='asinh' since it controls what parts of the data is in the linear or logarithmic regime of the stretch procedure. If set to 'auto' it uses 1/median(abs(data)) to find a useful scale.

bad	Sets the value that NA, NaN and infinite input data should be set to in the final map output. This should be thought of in the context of the range argument, i.e. if bad=range[1] then bad values will be the low range value and if bad=range[2] bad values will be the high range value.
clip	By default clipped values inherit the nearest lo/hi value (depending on which side they are clipped). Setting clip='NA' will set values outside the 'lo' and 'hi' values to be NA (currently this is the only other clip option).

### Details

'type'='quan' means the 'lo' and 'hi' options are interpreted as the quantile limits to clip the data at (so lo=0.05 and hi 0.95 would clip the data at the 5% and 95% quantile limits and scale values between these). 'type'='num' interprets 'lo' and 'hi' as the exact values to clip the data at and scale between. 'type'='sig' treats 'lo' and 'hi' as the sigma offsets in a Normal distribution, with the probabilities at these positions used to clip and scale that data (so 'lo'=-1 and 'hi'=1 is interpreted as +/- 1 sigma, so the data is clipped and scaled at the 16% and 84% levels, i.e. the 1 sigma range). 'type'='rank' means the data mapping is done by rank value only, with 'lo' and 'hi' specifying the quantile limits used to clip and scale the ranks. In all cases lo and hi clipped values are set to the relevant extreme values of 'range'.

If range is between 1 and 100 and stretch='lin' the midpoint in the mapping will be 50.5. If stretch='log' the midpoint becomes 10. This enhances the local dynamic range of the mapping for data that has a logarithmic distribution.

### Value

map	The remapped data. This is the same length and order as the input data.
datalim	The a vector of the low and high limits actually applied to the data. Unless type='num' this will probably be different to the lo and hi arguments provided.
maplim	The output range (same as the requested input range, but included for book-keeping).
loclip	The fraction of objects clipped from the input data at the low end.
hiclip	The fraction of objects clipped from the input data at the high end.

### Author(s)

Aaron Robotham

### See Also

[magimage](#), [magbar](#)

### Examples

```
set.seed(650)
temp=cbind(runif(100),runif(100))
temp=cbind(temp,sqrt(temp[,1]^2+temp[,2]^2))
magplot(temp)
magplot(temp[,1:2],col=HSV(h=magmap(temp[,3])$map))
```

```

# A different mapping type:
magplot(temp[,1:2],col=HSV(h=magmap(temp[,3],type='rank')$map))

# Flipped:
magplot(temp[,1:2],col=HSV(h=magmap(temp[,3],flip=TRUE,type='rank')$map))

# Example of linear/log/atan/asinh mapping:
temp=cbind(temp,10^temp[,3])
magplot(temp[,1:2],col=HSV(h=magmap(temp[,4])$map))
magplot(temp[,1:2],col=HSV(h=magmap(temp[,4],stretch='log')$map))
magplot(temp[,1:2],col=HSV(h=magmap(temp[,4],stretch='atan')$map))
magplot(temp[,1:2],col=HSV(h=magmap(temp[,4],stretch='asinh')$map))

#atan and asinh can be useful when data spans negative to positive:
temp=cbind(temp,temp[,4]-10)
magplot(temp[,1:2],col=HSV(h=magmap(temp[,5],stretch='atan')$map))
magplot(temp[,1:2],col=HSV(h=magmap(temp[,5],stretch='asinh')$map))
#effect of stretchscale
magplot(temp[,1:2],col=HSV(h=magmap(temp[,5],stretch='atan',stretchscale=0.5)$map))
magplot(temp[,1:2],col=HSV(h=magmap(temp[,5],stretch='atan',stretchscale=2)$map))
magplot(temp[,1:2],col=HSV(h=magmap(temp[,5],stretch='asinh',stretchscale=0.5)$map))
magplot(temp[,1:2],col=HSV(h=magmap(temp[,5],stretch='asinh',stretchscale=2)$map))

#Using multiple mappings for plots:
magplot(temp[,1:2],col=HSV(h=magmap(temp[,4],stretch='log')$map),
cex=magmap(temp[,3],lo=0.5,hi=1,range=c(1,6),type='num')$map)

#Different combinations of mapping options:
magmap(c(-1,0.1,1,NA,0.3,3),lo=0,hi=2.5,type='num',stretch='lin',bad=0.5)$map
magmap(c(-1,0.1,1,NA,0.3,3),lo=0.1,hi=0.9,type='quan',stretch='log',bad=0.8)$map
magmap(c(-1,0.1,1,NA,0.3,3),lo=-1,hi=1,type='sig',stretch='asinh',bad=0,stretchscale=2)$map
magmap(c(-1,0.1,1,NA,0.3,3),type='rank',stretch='atan',bad=NA,stretchscale=2)$map

#Example showing using asinh to generate a different axis mapping:
datastretch=cbind(runif(1e3),10^runif(1e3,0,4)-10^runif(1e3,0,4))
#This isn't a very helpful view of the data
magplot(datastretch[,1:2])
#This only shows the positive half of the data:
magplot(datastretch[,1:2],log='y')
#We can do a better job by remapping using the asinh option in magmap:
datastretch=cbind(datastretch,magmap(datastretch[,2],lo=-1e4,hi=1e4,range=c(0,1),
type='num',stretch='asinh')$map)
asinh ticks=magmap(c(-10^(4:0),0,10^(0:4)),lo=-1e4,hi=1e4,range=c(0,1),type='num',
stretch='asinh')$map
magplot(datastretch[,1],datastretch[,3],side=1)
axis(2,asinh ticks,labels=c(-10^(4:0),0,10^(0:4)))
abline(h=magmap(0,lo=-1e4,hi=1e4,range=c(0,1),type='num',stretch='asinh')$map)

```

## Description

Makes scientific plots based on magaxis axes. Particularly designed for log plotting. Utilises base plot for the most part, but the axis drawing is replaced by a call to the magaxis fuction.

## Usage

```
magplot(x, y, z = NULL, log = "", main = "", side = 1:2, majorn = 5, minorn = 'auto',
tcl = 0.5, ratio = 0.5, labels = TRUE, unlog = "auto", mgp = c(2,0.5,0), mtline = 2,
xlab = '', ylab = '', crunch = TRUE, logpretty = TRUE, prettybase = 10, powbase = 10,
hersh = FALSE, family = "sans", frame.plot = TRUE, usepar = FALSE, grid = TRUE,
grid.col = 'grey90', grid.lty = 1, grid.lwd = 1, axes = TRUE, xlim = NULL,
ylim = NULL, lwd = 1, axis.lwd = 1, ticks.lwd = axis.lwd, axis.col = 'black',
zcol = hcl.colors(1e4), zstretch = 'lin', dobar = TRUE, ...)
```

## Arguments

x	The x coordinates of points/lines in the plot. Alternatively, a single plotting structure, function or any R object with a plot method can be provided.
y	The y coordinates of points/lines in the plot, optional if x is an appropriate structure.
z	The z coordinates for colour scaling of points in the plot. This will be passed through <a href="#">magmap</a> , with dots passed as relevant.
log	Log axis arguments to be passed to plot. E.g. use 'x', 'y', 'xy' or 'yx' as appropriate. Default "" assumes no logging of any axes.
main	Title for the plot. Default is no title.
side	The side to be used for axis labelling in the same sense as the base axis function (1=bottom, 2=left, 3=top, 4=right). A vector of multiple entries is allowed. By default, bottom and left axes are drawn (i.e. side 1 and 2). If 'side'=FALSE (or 'axes'=FALSE) then no sides or labels will be drawn.
majorn	The target number of major-axis sub-divisions for pretty plotting. If length is 1 and length of side is longer than this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. Obvious reason for varying this is different pretty labelling between a and y axes.
minorn	The exact number of minor-axis divisions (i.e. desired minor ticks + 1) to display in plotting. Auto will produce <a href="#">pretty</a> ticks for linear scaling, and powbase-2 minor ticks for logged (this might seem odd, but for base 10 this means ticks at 2/3/4/5/6/7/8/9, which is probably as desired). If set manually, must be greater than 1 to have a visible effect. Minor ticks are always calculated to be equally spaced in linear space, so tick spaces vary when using log plotting. If length is 1 and length of side is longer than this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. An obvious reason for varying this is different pretty labelling between x and y axes.
tcl	The length of major tick marks as a fraction of the height of a line of text. By default these face into the plot (in common with scientific plotting) with a value

	of 0.5, rather than the R default of -0.5. It is possible to force magaxis to inherit directly from par by setting usepar=TRUE (see below). See <a href="#">par</a> for more details.
ratio	Ratio of minor to major tick mark lengths.
labels	Specifies whether major-axis ticks should be labelled for each axis. If length is 1 and length of side is longer than this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. Default is to label all axes.
unlog	Determines if axis labels should be unlogged. If axis is found to be logged in par('usr') then the minor ticks are automatically log spaced, however "unlog" still controls how the labelling is done: either logged form (FALSE) or exponent form (TRUE). If axis has been explicitly logged (e.g. log10(x)) then this will can produce exponential axis marking/labelling if set to TRUE. This case will also produce log minor tick marks. If length of unlog is 1 and length of side is longer than 1 then the assigned unlog value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. Can also take the text argument 'x', 'y', 'xy' or 'yx', where these refer to which axes have been logged. If left at the default of 'auto' then unlog is assumed to be true when the axis in question is logged, and false otherwise.
mgp	The margin line (in mex units) for the axis title, axis labels and axis line. This has different (i.e. prettier) defaults than R of c(2,0.5,0) rather than c(3,1,0). This pushes the numbers and labels nearer to the plot compared to the defaults. It is possible to force magaxis to inherit directly from par by setting usepar=TRUE (see below). See <a href="#">par</a> for more details.
mtline	Number of lines separating axis name from axis. If length 2 then specifies x and y axis separation respectively (else these are the same).
xlab	x axis name.
ylab	y axis name.
crunch	In cases where the scientific text would be written as $1 \times 10^8$ , should the 1x be removed so it reads $10^8$ . If length is 1 and length of side is longer then this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. TRUE by default.
logpretty	Should the major-ticks only be located at powers of 10. This changes cases where ticks are placed at 1, 3.1, 10, 31, 100 etc to 1, 10, 100. If length is 1 and length of side is longer then this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side. TRUE by default.
prettybase	The unit of repetition desired. By default it is 10, implying a pretty plot is one with marks at 10, 20, 30 etc. If you are plotting degrees then it might be prettier to display 90, 180, 270 etc. In which case prettybase should be set to 90. If log=TRUE then the reference location of 10 is changed, so in the previous example the labels generated would be at 9, 90, 900 etc rather than the default of 1, 10, 100 etc. If length is 1 and length of side is longer then this value is used for all axes. If length of arguments is longer than 1 then these should tally with the relevant axes in side.
powbase	Set the base to use for logarithmic axes. Default is to use 10.

hersh	To determines whether all plot text should be passed using Hershey vector fonts. This applies to the axis labels (which are handled automatically) and the axis names. In the case of axis names the user must be careful to use the correct plot utils escape characters: <a href="http://www.gnu.org/software/plotutils/manual/en/html_node/Text-String-Format.html">http://www.gnu.org/software/plotutils/manual/en/html_node/Text-String-Format.html</a> . magaxis will return back to the current plotting family after the function has executed.
family	Specifies the plotting family to be used. Allowed options are 'sans' and 'serif'. Depending on whetherersh is TRUE or FALSE these options are either applied to the Hershey vector fonts (hersh=TRUE) or the default R Helvetica font (hersh=FALSE). magaxis will return back to the current plotting family after the function has executed.
frame.plot	Logical indicating whether a box should be drawn around the plot.
usepar	Logical indicating whether tcl and mgp should be forced to inherit the global par values. This might be preferred when you want to define global plot settings at the start of a script.
grid	Logical indicating whether a background grid should be drawn onto the plotting area. If true this will generate vertical and horizontal grid lines. For more control (i.e. to only draw horizontal or vertical lines) see <code>link{magaxis}</code> .
grid.col	The colour of the grid to be drawn.
grid.lty	The line type of the grid to be drawn.
grid.lwd	The line width of the grid to be drawn.
axes	If 'axes'=FALSE (or 'side'=FALSE) then no sides or labels will be drawn.
xlim	Vector; range of data to display. Default of NULL shows the full range. If length equals 1 then the argument is taken to mean the sigma range to select for plotting and the clipping is done by <code>magclip</code> . If this is set to 'auto' then the limits will be estimated from the data dynamically.
ylim	Vector; range of data to display. Default of NULL shows the full range. If length equals 1 then the argument is taken to mean the sigma range to select for plotting and the clipping is done by <code>magclip</code> . If this is set to 'auto' then the limits will be estimated from the data dynamically.
lwd	The width of plot lines to be drawn. This has different behaviour depending on the plot type.
axis.lwd	The line width of the axis to be drawn. This is passed to 'lwd' argument in <code>axis</code> .
ticks.lwd	The line width of the ticks to be drawn. This is passed to 'ticks.lwd' argument in <code>axis</code> .
axis.col	Colour argument to pass directly to 'col' in axis. It is a bit clunky to have to specify this, but the option 'col' clashes too much with line and point colours.
zcol	Vector; a colour palette to use for 'z' mapped colours. Must be a vector and not a function.. Only relevant if data has been passed to 'z'
zstretch	Character scalar; 'z' colour stretch, either linear (lin, default) or logarithmic (log, good for large dynamic ranges).
dobar	Logical; should a colour bar be added to the plot?
...	Further arguments to be passed to: base <code>plot</code> ; <code>magaxis</code> -> <code>axis</code> ; <code>magmap</code> and <code>magbar</code> if 'z' scaling is being used.

**Details**

This is a simple function that just turns off most of the plotting output of base plot, and replaces where possible those present in magaxis.

If 'x' is a data.frame with more than 2 columns then the utility base `plot` data.frame plotting function is used to create a full plotting grid. This ignores `magaxis` settings entirely.

Setting 'xlim' and 'ylim'

**Value**

No output. Run for the side effect of producing nice plotting axes.

**Author(s)**

Aaron Robotham

**See Also**

[magaxis](#), [maglab](#), [magerr](#), [magmap](#), [magrun](#)

**Examples**

```
x=10^{1:9}
y=1:9
magplot(log10(x),y,unlog='x')
magplot(x,y,log='x')

#Not ideal to have two decades between major labels:

magplot(x,y,log='x',majorn=c(10,5))
magplot(x,y,log='xy',majorn=c(10,5,5,5),side=1:4)

#Sometimes it is helpful to focus on where most of the data actually is.
#Using a single value for xlim and ylim sigma clips the data to that range.
#Here a value of 2 means we only show the inner 2-sigma (2% to 98%) range.
#The 'auto' option allows magclip to dynamically estimate a clip value.

temp=cbind(rt(1e3,1.5),rt(1e3,1.5))
magplot(temp)
magplot(temp, xlim=2, ylim=2)
magplot(temp, xlim='auto', ylim='auto')

#Some astronomy related examples (and how to display the solar symbol):

temp=cbind(runif(10,8,12),runif(10,0,5))

magplot(temp[,1:2], xlab=expression(M['\u0298']), ylab=expression(M['\u0298']/Yr), unlog='xy')

#With z scaling

z=sqrt(9:1)
magplot(x, y, z, log='x', position='topleft')
```

---

magproj *Magic longitude / latitude projection function*

---

### Description

High level methods for producing pretty plot of projected data. Particularly useful in astronomy or geography, where many datasets are in longitude (right ascension) / latitude (declination) format. magproj is the highest level function, creating a projected image grid with labels and data. magprojgrid and magprojlabels are functions to simply overplot a grid and add labels respectively.

### Usage

```
magproj(long, lat, type = "b", plottext, longlim = c(-180, 180), latlim = c(-90, 90),
projection = "aitoff", parameters = NULL, centre = c(0, 0), add = FALSE, fliplong = FALSE,
nlat = 6, nlong = 6, prettybase = 30, labels = TRUE, grid = TRUE, grid.col = "grey",
grid.lty = 2, auto = FALSE, upres = 100, box = TRUE, labloc = c(90, -45),
labeltype = "deg", crunch = FALSE, ...)
magprojgrid(nlat = 6, nlong = 6, prettybase = 30, box = TRUE, ...)
magprojlabels(nlat = 6, nlong = 6, prettybase = 30, labloc = c(90, -45),
labeltype = 'deg', crunch=FALSE, ...)
```

### Arguments

long	Vector of longitude values to use. If this is a matrix or data.frame with two columns and 'lat' is missing then column 1 is taken to be longitude values and column 2 is taken to be latitude values. long should have 2 elements only when 'type'="b".
lat	Vector of latitude values to use. If the input for 'long' is a matrix or data.frame with two columns and lat is missing then column 1 is taken to be longitude values and column 2 is taken to be latitude values. lat should have 2 elements only when type="b".
type	The display type, either points (p), lines (l), polygon (pl), text (t), or box (b, the default). Points simply projects longitude and latitude positions into particle positions. Lines will join the positions together into a line, using approxfun to interpolate between positions at resolution 'upres'. Polygon will join the positions together into a polygon, using approxfun to interpolate between positions at resolution 'upres'. Text will display the text provided in plottext at the positions. Box will draw a polygon box, where the limits are given as a two element vector for 'long' and a two element vector for 'lat'.
plottext	A vector of text to display at the provided longitude and latitude positions. Only used if 'type='t'.
longlim	The longitude limits to use in the plot. Vector of length 2.
latlim	The latitude limits to use in the plot. Vector of length 2.
projection	Map projection to use. This function directly uses <a href="#">mapproject</a> , and all of the inputs allowed for the 'projection' argument in that function are also allowed here.

parameters	Map parameters to use. For details see the ‘parameters’ argument in <a href="#">mapproject</a> .
centre	For most popular projections this argument specifies the longitude and latitude that is centred in the plot. Strictly ‘orientation’ in <a href="#">mapproject</a> is set to $c(90+centre[2],centre[1],0)$ .
add	Should a fresh plot be drawn (‘add=FALSE’), or should the new data be added to the current plot (‘add=TRUE’).
fliplong	Should the the longitude axis be flipped so that low values are on the right hand side (normal for celestial sphere plots in astronomy).
nlong	The target number of gridlines in the longitude direction. Uses <a href="#">pretty</a> , so the result may not be what is requested.
nlat	The target number of gridlines in the latitude direction. Uses <a href="#">pretty</a> , so the result may not be what is requested.
prettybase	The unit of repetition desired for the grid lines and labels. See ‘prettybase’ in <a href="#">maglab</a> . By default it is 30, implying a pretty plot is one with marks at 30, 60, 90 etc (i.e. attractive for large scale plots covering large longitude and latitude limits).
labels	Should text coordinate labels be added to the plot.
grid	Should a background grid be drawn.
grid.col	The colour of the background grid.
grid.lty	The line type for the background grid.
auto	If ‘auto=FALSE’ the plot is set up using all options specified. If ‘auto=TRUE’ then ‘longlim’, ‘latlim’, ‘centre’ and ‘labloc’ is estimated from the data. This mostly behaves sensibly, but do not be too surprised if the automatic plot is not ideal, and some manual tweaking is required.
upres	The resolution at which to do internal interpolation when drawing lines and boxes.
box	Should a black outline be drawn following the ‘longlim’ and ‘latlim’ limits.
labloc	The longitude and latitude at which labels should be drawn.
labeltype	Should the labels be drawn using degrees (deg) or colon delimited sexagesimal (sex).
crunch	If set to FALSE the full output of <a href="#">deg2hms</a> and <a href="#">deg2dms</a> is printed. If set to TRUE a simplified output is used, where only the hours and degrees parts are extracted and appended with a ‘h’ and a degree symbol respectively.
...	For magproj, Extra options that are either passed to <a href="#">points</a> (‘type=’p’), <a href="#">lines</a> (‘type=’l’), <a href="#">polygon</a> (‘type=’pl’), <a href="#">text</a> (‘type=’t’), or <a href="#">polygon</a> (‘type=’b’). For magprojgrid dots are passed to <a href="#">lines</a> for drawing the grid lines. For magprojlabels dots are passed to <a href="#">text</a> for adding text labels.

**Value**

No output. Run for the side effect of producing nice projected plots.

**Author(s)**

Aaron Robotham

**See Also**

[magplot](#), [magaxis](#), [maglab](#), [magmap](#), [magrun](#), [magbar](#), [magprojextra](#)

**Examples**

```
# GAMA fields:
par(mar=c(0.1,0.1,0.1,0.1))
magproj(c(129,141), c(-2,3), type='b', projection='aitoff', centre=c(180,0),
fliplong=TRUE, labloc=c(90,-45), col='red', labeltype = 'sex', crunch=TRUE)
magproj(c(211.5,223.5), c(-2,3), col='red', add=TRUE)
magproj(c(30.2,38.8), c(-10.25,-3.72), col='red', add=TRUE)
magproj(c(30.2,38.8), -6, type='l', add=TRUE, col='grey')
magproj(c(339,351), c(-35,-30), col='red', add=TRUE)

magecliptic(width=10,col=HSV(1/12,alpha=0.3),border=NA)
magecliptic(width=0,col='orange')
magMWplane(width=20,col=HSV(v=0,alpha=0.1),border=NA)
magMWplane(width=0,col='darkgrey')
magMW(pch=16, cex=2, col='darkgrey')
magsun(c(7,26), pch=16, cex=2, col='orange2') #An important date!

magproj(c(174,186), c(-3,2), col='red', add=TRUE)

#Plus SDSS:
magproj(c(110,260), c(-4,70), border='blue', add=TRUE)

magproj(c(35,135,180,217.5,345), c(-3.72,3,2,3,-30)+10, type='t',
plottext=c('G02','G09','G12','G15','G23'), add=TRUE)

legend('topleft', legend=c('GAMA Regions','SDSS Main Survey'), col=c('red','blue'),
pch=c(15,NA), lty=c(NA,1), bty='n')
legend('topright', legend=c('Ecliptic','MW Plane'), col=c(HSV(c(1/12,0), v=c(1,0),
alpha=0.5)), pch=c(15,15), lty=c(1,1), bty='n')
legend('bottomleft', legend=c('Sun', 'MW Centre'), col=c('orange2','darkgrey'), pch=16,
bty='n')
```

---

magprojextra

*Attractive great circles and thick bands on magproj plots*


---

**Description**

High level functions to add great circles and thick bands on projections plots. In astronomy these are popular for indicating regions of exclusion surrounding the ecliptic or the Milky-Way plane. Also simple functions to add either the MW bluge to the current projection (magMW) or the sun on a given date (magsun).

**Usage**

```

magring(crosseq = 0, peaklat = 0, offset = 0, res = 1000, ...)
magband(crosseq = 0, peaklat = 0, width = 10, res = 1000, ...)
magecliptic(width = 10, ...)
magMWplane(width = 10, ...)
magsun(Ydate = 'get', anti = FALSE, ...)
magMW(...)

```

**Arguments**

crosseq	The longitude below the latitude peak of the great circle (or centre of the band) where the centre crosses the equator. See examples to see how this is used in practice.
peaklat	The positive maximum latitude obtained by the great circle (or centre of the band). See examples to see how this is used in practice.
offset	Whether the ring drawn is systematically offset from the great circle defined by 'crosseq' and 'peaklat'. Leave at 0 to draw a great circle.
width	How wide should the band be in degrees. For magecliptic and magMWplane, if this is zero it will draw a line instead.
res	Number of elements making up each side of the band (default should be fine for most plots).
Ydate	The date for the location of the Sun on the spherical grid. Vector in c(M,D) format. If set to 'get' then the function will return the Sun's location for today.
anti	Should the anti-sun position be computed (i.e. the RA and Dec of the position diametrically opposed to the Sun).
...	Arguments passed on to <a href="#">lines</a> ( <a href="#">magring</a> ), <a href="#">polygon</a> ( <a href="#">magband</a> ), <a href="#">points</a> ( <a href="#">magMW</a> and <a href="#">magsun</a> ).

**Value**

No output. Run for the side effect of producing nice projected plots.

**Author(s)**

Aaron Robotham

**See Also**

[magplot](#), [magaxis](#), [maglab](#), [magmap](#), [magrun](#), [magbar](#), [magproj](#)

**Examples**

```

# GAMA fields:
par(mar=c(0.1,0.1,0.1,0.1))
magproj(c(129,141), c(-2,3), type='b', projection='aitoff', centre=c(180,0),
fliplong=TRUE, labloc=c(90,-45), col='red', labeltype = 'sex', crunch=TRUE)
magproj(c(211.5,223.5), c(-2,3), col='red', add=TRUE)

```

```

magproj(c(30.2,38.8), c(-10.25,-3.72), col='red', add=TRUE)
magproj(c(30.2,38.8), -6, type='l', add=TRUE, col='grey')
magproj(c(339,351), c(-35,-30), col='red', add=TRUE)

magecliptic(width=10,col=HSV(1/12,alpha=0.3),border=NA)
magecliptic(width=0,col='orange')
# Note this a shortcut for: magring(0,23.4,col='orange')
magMWplane(width=20,col=HSV(v=0,alpha=0.1),border=NA)
magMWplane(width=0,col='darkgrey')
# Note this a shortcut for: magring(76.75,62.6,col='darkgrey')
magMW(pch=16, cex=2, col='darkgrey')
magsun(c(7,26), pch=16, cex=2, col='orange2') #An important date!

magproj(c(174,186), c(-3,2), col='red', add=TRUE)

#Plus SDSS:
magproj(c(110,260), c(-4,70), border='blue', add=TRUE)

magproj(c(35,135,180,217.5,345), c(-3.72,3,2,3,-30)+10, type='t',
plottext=c('G02','G09','G12','G15','G23'), add=TRUE)

legend('topleft', legend=c('GAMA Regions','SDSS Main Survey'), col=c('red','blue'),
pch=c(15,NA), lty=c(NA,1), bty='n')
legend('topright', legend=c('Ecliptic','MW Plane'), col=c(HSV(c(1/12,0), v=c(1,0),
alpha=0.5)), pch=c(15,15), lty=c(1,1), bty='n')
legend('bottomleft', legend=c('Sun', 'MW Centre'), col=c('orange2','darkgrey'), pch=16,
bty='n')

```

---

magrun

*Running averages*


---

## Description

Computes running averages (medians / means / modes), user defined quantiles and standard deviations for x and y scatter data.

## Usage

```

magrun(x, y, bins = 10, type='median', ranges = pnorm(c(-1, 1)), binaxis = "x",
equalN = TRUE, xcut, ycut, log = '', Nscale = FALSE, diff = FALSE)

```

## Arguments

x	Data x coordinates. This can be a 1D vector (in which case y is required) or a 2D matrix or data frame, where the first two columns will be treated as x and y.
y	Data y coordinates, optional if x is an appropriate structure.
bins	If a single integer value, how many bins the data should be split into. If a vector is provided then these values are treated as the explicit bin limits to use.

type	The type of running average to determine. Options are 'median' (the default), 'mean', 'mode' and 'mode2d'. 'median' calculates the median for binned x and y values. 'mean' calculates the mean for binned x and y values. 'mode' uses the default R 'density' function, and finds the mode of the resulting smoothed 1D distributions for binned x and y values. 'mode2d' uses the MASS package 'kde2d' function, and finds the mode of the resulting smoothed 2d distribution for binned x and y values. 'cen' just calculates the geometric centre of the bin in x and y directions and is useful for using in conjunction with another 'type' option for plotting purposes. 'mean', 'mode' and 'mode2d' should be used with some thought if 'log' is used, since the central values will be determined for the logged data, which may or may not be desired.
ranges	The quantile ranges desired, can set to NULL if quantiles are not desired. The default adds 1-sigma equivalent quantile ranges.
binaxis	Which axis to bin across. Must be set to 'x' or 'y'.
equalN	Should the data be split into bins with equal numbers of objects (default, TRUE), or into regular spaces from min to max (FALSE). Only relevant if 'bins' parameter is set to a single integer value and 'magrun' is determining the explicit bin limits automatically.
xcut	A two element vector containing optional lower and upper x limits to apply to the data.
ycut	A two element vector containing optional lower and upper y limits to apply to the data.
log	Specify axes that should be logged. Allowed arguments are 'x'
Nscale	Sets whether the quantile ranges and standard deviations calculated are reduced with respect to the median by the square-root of the number of contributing data within each bin. The result of setting Nscale to TRUE is to scale the data like you are calculating the error-in-the-mean, rather than the scatter. For describing the 'significance' of trends in scatter data this is often what you want to show.
diff	Should the output quantiles and standard deviations be expressed as differences from the chosen type of running average (TRUE) or the actual values (default, FALSE). The advantage of the former is plotting the results as errorbars using magerr, which expects differences (so error like values). If set to TRUE then the output of 'xsd' and 'ysd' is a 1D vector rather than a data.frame with x/y-sd and x/y+sd columns. See the examples below for usage guidance.

### Details

This function will by default calculate the running median along the x axis for y values, it is intended to be used to trace the spread in scattered data.

### Value

x	The chosen averages (default median) of the x bins.
y	The chosen averages (default median) of the y bins.
xquan	Matrix containing the extra user defined x quantile ranges (columns are in the same order as the requested quantiles). If Nscale is set to TRUE then this is also divided by sqrt the contributing objects in each bin.

yquan	Matrix containing the extra user defined y quantile ranges (columns are in the same order as the requested quantiles). If Nscale is set to TRUE then this is also divided by sqrt the contributing objects in each bin.
xsd	The standard deviations in the x bins. This is a two column data.frame if 'diff' is set to FALSE, giving the x-sd and x+sd values, or a single vector if 'diff' is set to TRUE. If Nscale is set to TRUE then this is also divided by sqrt the contributing objects in each bin.
ysd	The standard deviations in the y bins. This is a two column data.frame if 'diff' is set to FALSE, giving the y-sd and y+sd values, or a single vector if 'diff' is set to TRUE. If Nscale is set to TRUE then this is also divided by sqrt the contributing objects in each bin.
bincen	The bin centres used in the chosen binning direction.
binlim	The bin limits used in the chosen binning direction.
Nbins	The number of items contributing to each running bin. This effectively produces a histogram counts output for the final bin limits.

**Author(s)**

Aaron Robotham

**See Also**

[magplot](#), [magaxis](#), [maglab](#), [magerr](#), [magmap](#)

**Examples**

```
#Simple example

temp=cbind(seq(0,2,len=1e4),rnorm(1e4))
temprun=magrun(temp)
magplot(temp,col='lightgreen',pch='.')
lines(temprun,col='red')
lines(temprun$x,temprun$yquan[,1],lty=2,col='red')
lines(temprun$x,temprun$yquan[,2],lty=2,col='red')
temprun=magrun(temp,binaxis='y')
lines(temprun,col='blue')
lines(temprun$xquan[,1],temprun$y,lty=2,col='blue')
lines(temprun$xquan[,2],temprun$y,lty=2,col='blue')

#Now with a gradient- makes it clear why the axis choice matters for simple line fitting.

temp=cbind(seq(0,2,len=1e4),rnorm(1e4)+1+seq(0,2,len=1e4))
temprun=magrun(temp)
magplot(temp,col='lightgreen',pch='.')
lines(temprun,col='red')
lines(temprun$x,temprun$yquan[,1],lty=2,col='red')
lines(temprun$x,temprun$yquan[,2],lty=2,col='red')
temprun=magrun(temp,binaxis='y')
lines(temprun,col='blue')
lines(temprun$xquan[,1],temprun$y,lty=2,col='blue')
```

```

lines(temprun$xquan[,2], temprun$y, lty=2, col='blue')

#Compare the different centres.

temp=cbind(seq(0,2,len=1e4), rnorm(1e4)^2+seq(0,2,len=1e4))
temprunmedian=magrun(temp, type='median')
temprunmean=magrun(temp, type='mean')
temprunmode=magrun(temp, type='mode')
temprunmode2d=magrun(temp, type='mode2d')
magplot(temp, col='grey', pch='.', ylim=c(-2,5))
lines(temprunmedian, col='red')
lines(temprunmean, col='green')
lines(temprunmode, col='blue')
lines(temprunmode2d, col='orange')

#Choose your own bins.

temp=cbind(seq(0,2,len=1e4), rnorm(1e4)+1+seq(0,2,len=1e4))
temprun=magrun(temp, bins=c(0.1,0.5,0.7,1.2,1.3,2))
magplot(temp, col='lightgreen', pch='.')
points(temprun, col='red')

#Show the 'error in the mean' type data points. Comparing to the best fit line,
#it is clear they are much more meaningful at reflecting the error in the trend seen,
#but not the distribution (or scatter) of data around this.

temp=cbind(seq(0,2,len=1e3), rnorm(1e3)+1+seq(0,2,len=1e3))
temprun=magrun(temp, bins=5)
temprunNscale=magrun(temp, bins=5, Nscale=TRUE)
magplot(temp, col='lightgreen', pch='.')
magerr(temprun$x, temprun$y, temprun$x-temprun$xquan[,1], temprun$y-temprun$yquan[,1],
temprun$xquan[,2]-temprun$x, temprun$yquan[,2]-temprun$y, lty=2, length=0, col='blue')
magerr(temprunNscale$x, temprunNscale$y, temprunNscale$x-temprunNscale$xquan[,1],
temprunNscale$y-temprunNscale$yquan[,1], temprunNscale$xquan[,2]-temprunNscale$x,
temprunNscale$yquan[,2]-temprunNscale$y, col='red')
abline(lm(temp[,2]~temp[,1]), col='black')

#Or the above type of plot can be done more simply using the 'diff' flag.

temprun=magrun(temp, bins=5, diff=TRUE)
temprunNscale=magrun(temp, bins=5, Nscale=TRUE, diff=TRUE)
magplot(temp, col='lightgreen', pch='.')
magerr(temprun$x, temprun$y, temprun$xquan[,1], temprun$yquan[,1], temprun$xquan[,2],
temprun$yquan[,2], lty=2, length=0, col='blue')
magerr(temprunNscale$x, temprunNscale$y, temprunNscale$xquan[,1], temprunNscale$yquan[,1],
temprunNscale$xquan[,2], temprunNscale$yquan[,2], col='red')
abline(lm(temp[,2]~temp[,1]), col='black')

#Similar, but using the 'sd' output.

magplot(temp, col='lightgreen', pch='.')
magerr(temprun$x, temprun$y, temprun$x$sd, temprun$y$sd, lty=2, length=0, col='blue')
magerr(temprunNscale$x, temprunNscale$y, temprunNscale$x$sd, temprunNscale$y$sd, col='red')

```

```
abline(lm(temp[,2]~temp[,1]),col='black')
```

---

 magtri

*High level triangle plotting code for MCMC chains*


---

### Description

A very high level (minimal options) MCMC chain triangle (AKA corner) plot function. The default is deliberately spartan in terms of options, but the result should be a clear set of covariance plots that should give quick insight into the stationary sampling quality of a set of MCMC posterior chains.

### Usage

```
magtri(chains, samples = 1000, thin = 1, samptype = 'end', grid = FALSE, do.tick = FALSE,
refvals = NULL, lab = NULL, ...)
```

### Arguments

chains	A matrix or data.frame of the posterior chains, arranged so that the columns are the parameters and rows are the individual chain samples. The column names are inherited as the parameter names from the input to chains.
samples	Specify the number of sub-samples desired. To speed up plotting it is often a good idea not to plot all chain samples (the reduced set is plotted as the top-left points and used to generate the bottom-right contours). The default plot 1000 samples.
thin	Specify the thinning of chain samples, default (1) processes the whole chain.
samptype	Specifies whether to take all of the samples from the end of the supplied chains ('end', the default since samples are usually better towards the end of a set of psoterior chain samples), randomly selected ('ran', should only be used if you are confident the posterior chains supplied are true stationary samples) or evenly selected ('thin', which behaves much like thinning except we specify the target number of outputs, not the fraction of samples kept).
grid	Should a background grid be added to the sub-panels? See <a href="#">magaxis</a> for details.
do.tick	Logical; should ticks be drawn on each sub-panel? Passed to <a href="#">axis</a> argument 'tick'.
refvals	Numeric vector; this gives reference values to overdraw. If provided it must be the same length as dim(chains)[2], i.e. this would usually be the number of parameters being compared in the triangle plot.
lab	Character vector; optional over-ride for column names when plotting the grid of scatter plots.
...	Extra arguments are passed to ' <a href="#">\link{magcon}</a> ' for plotting.

**Details**

This interface is deliberately very high level with few options. It is really designed to allow quick exploratory views of posterior samples from MCMC chains, and publication grade plots should be designed by the user. That said, in many situations the plots generated are of pleasant, clear and publishable quality.

Other types of data can be plotted using this function of course, but the default setup is tuned towards being useful for MCMC posterior chain samples.

The contour levels shown are the defaults for magcon, i.e. they contain 50% (lty=2), 68% (lty=1) and 95% (lty=3) of the posterior chains.

The red cross shows the mean for the sampled posterior chain. The red vertical dashed line traces this over the contour plots. The red dotted line shows the +/- SD range of the sampled posterior chain.

**Value**

Outputs a two column matrix containing the means and standard deviations for the parameters. Generally run for the side effect of producing nice projected plots.

**Author(s)**

Aaron Robotham

**See Also**

[magcon](#)

**Examples**

```
Sigma=matrix(c(10,3,-5,3,12,8,-5,8,20),3,3)
chains=MASS::mvrnorm(n=1000, mu=1:3, Sigma=Sigma)
magtri(chains,tick=TRUE)
```

---

magwarp

*Remap Image WCS via Warping*

---

**Description**

Remaps an input Tan Gnomonic or Sine Orthographic projection system to a different target WCS.

**Usage**

```
magwarp(image_in, header_out = NULL, header_in = NULL, dim_out, direction = "auto",
boundary = "dirichlet", interpolation = "cubic", doscale = TRUE, CRVAL1_in = 0,
CRVAL2_in = 0, CRPIX1_in = 0, CRPIX2_in = 0, CD1_1_in = 1, CD1_2_in = 0, CD2_1_in = 0,
CD2_2_in = 1, CRVAL1_out = 0, CRVAL2_out = 0, CRPIX1_out = 0, CRPIX2_out = 0,
CD1_1_out = 1, CD1_2_out = 0, CD2_1_out = 0, CD2_2_out = 1, plot = FALSE, ...)
```

**Arguments**

image_in	Numeric matrix; required, the image we want to remap. If 'image_in' is a list as created by readFITS, read.fits of <a href="#">magcutoutWCS</a> then the image part of the list is parsed to 'image_in' and the correct header part is parsed to 'header_in'.
header_out	Full FITS header in table or vector format. This is the target WCS projection that 'image_in' will be mapped onto. Legal table format headers are provided by the read.fitshdr function or the 'hdr' list output of read.fits in the astro package; the 'hdr' output of readFITS in the FITSio package or the 'header' output of magcutoutWCS. If 'header_out' is provided then key words will be taken from here as a priority. Missing header keywords are printed out and other header option arguments are used in these cases.
header_in	Full FITS header in table or vector format. This should be the header WCS that matches 'image_in'. Legal table format headers are provided by the read.fitshdr function or the 'hdr' list output of read.fits in the astro package; the 'hdr' output of readFITS in the FITSio package or the 'header' output of magcutoutWCS. If 'header_in' is provided then key words will be taken from here as a priority. Missing header keywords are printed out and other header option arguments are used in these cases.
dim_out	Integer vector; this defines the desired dimensions of the output image. If this is not provided then the output image is made to be the same size as the NAXIS1 and NAXIS2 arguments taken from 'header_out' (which is usually what you will want TBH).
direction	"auto" (default), "forward" or "backward", see imwarp. Since it is usually better to go from the higher resolution image and map this onto the lower resolution grid, "auto" selects the better direction given the pixel scales recovered from the header information.
boundary	boundary conditions: "dirichlet", "neumann", "periodic" (default "dirichlet"), see imwarp
interpolation	"nearest", "linear", "cubic" (default "linear"), see imwarp
doscale	Logical; if TRUE (default) then the image is scaled by the relative change in the pixel scale. This is usually what you want when converting images between different WCS (since we really want to make sure we conserve overall flux). If FALSE then nothing is done to rescale the image. This is useful when the input 'image_in' is something like a segmentation map, where the actual values matter.
CRVAL1_in	FITS header CRVAL1 for the Tan Gnomonic projection system of the input WCS. This is the RA in degrees at the location of 'CRPIX1'.
CRVAL2_in	FITS header CRVAL2 for the Tan Gnomonic projection system of the input WCS. This is the Dec in degrees at the location of 'CRPIX2'.
CRPIX1_in	FITS header CRPIX1 for the Tan Gnomonic projection system of the input WCS. This is the x pixel value at the location of 'CRVAL1'.
CRPIX2_in	FITS header CRPIX2 for the Tan Gnomonic projection system of the input WCS. This is the y pixel value at the location of 'CRVAL2'.
CD1_1_in	FITS header CD1_1 for the Tan Gnomonic projection system of the input WCS. Change in RA-Tan in degrees along x-Axis.

CD1_2_in	FITS header CD1_2 for the Tan Gnomonic projection system of the input WCS. Change in RA-Tan in degrees along y-Axis.
CD2_1_in	FITS header CD2_1 for the Tan Gnomonic projection system of the input WCS. Change in Dec-Tan in degrees along x-Axis.
CD2_2_in	FITS header CD2_2 for the Tan Gnomonic projection system of the input WCS. Change in Dec-Tan in degrees along y-Axis.
CRVAL1_out	FITS header CRVAL1 for the Tan Gnomonic projection system of the output WCS. This is the RA in degrees at the location of 'CRPIX1'.
CRVAL2_out	FITS header CRVAL2 for the Tan Gnomonic projection system of the output WCS. This is the Dec in degrees at the location of 'CRPIX2'.
CRPIX1_out	FITS header CRPIX1 for the Tan Gnomonic projection system of the output WCS. This is the x pixel value at the location of 'CRVAL1'.
CRPIX2_out	FITS header CRPIX2 for the Tan Gnomonic projection system of the output WCS. This is the y pixel value at the location of 'CRVAL2'.
CD1_1_out	FITS header CD1_1 for the Tan Gnomonic projection system of the output WCS. Change in RA-Tan in degrees along x-Axis.
CD1_2_out	FITS header CD1_2 for the Tan Gnomonic projection system of the output WCS. Change in RA-Tan in degrees along y-Axis.
CD2_1_out	FITS header CD2_1 for the Tan Gnomonic projection system of the output WCS. Change in Dec-Tan in degrees along x-Axis.
CD2_2_out	FITS header CD2_2 for the Tan Gnomonic projection system of the output WCS. Change in Dec-Tan in degrees along y-Axis.
plot	Logical; should a <code>magimageWCS</code> plot of the output be generated?
...	Dots are parsed to either <code>magimageWCS</code> (only relevant if 'plot'=TRUE).

## Details

The function allows for arbitrary WCS remapping, as long as the input and output WCS both use the Tan Gnomonic projection system (which is by far the most common with modern survey imaging data). The process internally does the following:

- `xy2radec`; maps the input image to RA and Dec per pixel using the input header
- `radec2xy`; maps the pixel RA and Dec coordinates onto the desired output pixel grid using the output header

There are a few different ways to consider doing pixel remapping (or warping). The main question is usually whether to operate on a forward or backwards manner (see `imwarp`). Backwards mapping (the default) finds the best interpolation of every output pixel in the input image, whereas forward mapping finds the best interpolation of every input pixel on the output image. Backwards mapping usually provides the fewest artefacts (hence it is the default), but in general if the input image is higher resolution then you might prefer forward mapping and vica-versa.

The actual warping is done using the `imwarp` function in the `imager` package, so this will need to be installed prior to use (it is available on CRAN).

**Value**

A list containing:

image	Numeric matrix; the remapped image using the target WCS.
header	The target 'header_out'.

**Note**

This function uses a bi-cubic interpolation scheme by default. It should approximately conserve the flux in 'image\_in', but this is not guaranteed. The 'linear' interpolation scheme may be closer to conserving flux in images with sharp features. The conservation is usually good to about 0.1% (i.e. 0.01 mag). If you require better conservation than this then alternative schemes (e.g. SWarp) will be required.

**Author(s)**

Aaron Robotham

**See Also**

[magimageWCSRGB](#)

**Examples**

```
## Not run:
VISTA_K=readFITS(system.file("extdata", 'VISTA_K.fits', package="magicaxis"))
VST_r=readFITS(system.file("extdata", 'VST_r.fits', package="magicaxis"))
GALEX_NUV=readFITS(system.file("extdata", 'GALEX_NUV.fits', package="magicaxis"))

magwarp(VST_r, GALEX_NUV$hdr, plot=TRUE)
magwarp(VISTA_K, GALEX_NUV$hdr, plot=TRUE)

magwarp(GALEX_NUV, VST_r$hdr, plot=TRUE)
magwarp(VISTA_K, VST_r$hdr, plot=TRUE)

magwarp(GALEX_NUV, VISTA_K$hdr, plot=TRUE)
magwarp(VST_r, VISTA_K$hdr, plot=TRUE)

#Check we can warp forwards and backwards correctly:

magimageWCS(GALEX_NUV)
magwarp(GALEX_NUV, GALEX_NUV$hdr, plot=TRUE)
magwarp(magwarp(GALEX_NUV, VST_r$hdr, interpolation='nearest'),
        GALEX_NUV$hdr, interpolation='nearest', plot=TRUE)

## End(Not run)
```

plot.magbin

*Plot 2D Histogram or Bin Data***Description**

Plot 2D histogram counts or a third (z) axis summary statistic in 2D cells of different shapes.

**Usage**

```
## S3 method for class 'magbin'
plot(x, colramp = hcl.colors(10000), colstretch = "lin",
     sizestretch = "lin", colref = "count", sizeref = "none", add = FALSE,
     dobar = TRUE, title = colref, colnorm = FALSE, projden = FALSE, xdata = NULL,
     ydata = NULL, pch.dust = '.', cex.dust = 1, ...)
```

**Arguments**

x	Object of class 'magbin'.
colramp	Vector; a colour palette to use. Must be a vector and not a function.
colstretch	Character scalar; colour stretch, either linear (lin, default) or logarithmic (log, good for large dynamic ranges).
sizestretch	Character scalar; size stretch, either linear (lin, default) or logarithmic (log, good for large dynamic ranges).
colref	Character scalar; colour reference for call, either it should be based on the counts (count) or the z-axis statistic (zstat)?
sizeref	Character scalar; colour reference for call, either it should be ignored (none, so all are the same size and closely packed), based on the counts (count) or the z-axis statistic (zstat)?
add	Logical; should bins be added to the current plot? If FALSE then a new plot will be made.
dobar	Logical; should a colour bar be added to the plot?
title	Character scalar; title to use for the '\link{magbar}' label.
colnorm	Logical; should the colour bar be normalised so the maximum value equals 1?
projden	Logical; do you want projected density PDFs to be displayed above and to the side of the standard plot.magbin plot? If so you also need to pass the same 'xdata' and 'ydata' that you originally sent to <a href="#">magbin</a> , since this is not stored in the object output from <a href="#">magbin</a> .
xdata	Numeric vector; the original x data sent to <a href="#">magbin</a> . Only relevant if 'projden'=TRUE.
ydata	Numeric vector; the original y data sent to <a href="#">magbin</a> . Only relevant if 'projden'=TRUE.
pch.dust	Scalar; pch symbol to use for the dust points.
cex.dust	Scalar; cex size to use for the dust points.
...	Dots to be passed to <a href="#">magplot</a> , <a href="#">magmap</a> and <a href="#">magmap</a> . Relevant arguments are matched, so look in those functions for optional arguments to pass.

**Value**

Run for the side effect of making a nice plot.

**Author(s)**

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**See Also**

[magbin](#)

**Examples**

```
temp = magbin(rnorm(1e4), rnorm(1e4), plot=FALSE)
plot(temp, xlab='x', ylab='y')
```

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