

Package: smatr (via r-universe)

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Title (Standardised) Major Axis Estimation and Testing Routines

Description Methods for fitting bivariate lines in allometry using the major axis (MA) or standardised major axis (SMA), and for making inferences about such lines. The available methods of inference include confidence intervals and one-sample tests for slope and elevation, testing for a common slope or elevation amongst several allometric lines, constructing a confidence interval for a common slope or elevation, and testing for no shift along a common axis, amongst several samples. See Warton et al. 2012 <[doi:10.1111/j.2041-210X.2011.00153.x](https://doi.org/10.1111/j.2041-210X.2011.00153.x)> for methods description.

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URL <https://github.com/traitecoevo/smatr>,
<https://traitecoevo.github.io/smatr/>

Imports dplyr, tidyr, stringr, rlang, magrittr, ggplot2

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'confint.sma.R' 'defineAxis.R' 'elev.com.R' 'elev.test.R'
'fitted.sma.R' 'ggplot.sma.R' 'huber.M.R' 'leaflife.R'
'leafmeas.R' 'line.cis.R' 'logLik.sma.R' 'lr.b.com.R' 'ma.R'
'makeLogMinor.R' 'meas.est.R' 'multcompmatrix.R' 'nicePlot.R'
'plot.sma.R' 'predict.sma.R' 'print.sma.R' 'residuals.sma.R'
'robust.factor.R' 'seqLog.R' 'shift.com.R' 'slope.com.R'
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coef.sma	<i>Extract coefficients from a 'sma' or 'ma' fit</i>
----------	--

Description

Extracts elevation and slope of a standardized major axis (sma) or major axis (ma) fit, for each of the groups if the fit was by group.

Usage

```
## S3 method for class 'sma'  
coef(object, ...)
```

Arguments

object Object of class 'sma'.
... Further arguments ignored.

Value

A dataframe with the slope(s) and elevation(s), and their confidence intervals. If the fit was by multiple groups, fits by all groups are returned.

Author(s)

R.A. Duursma

See Also

[sma](#)

confint.sma	<i>Returns confidence intervals for sma object</i>
-------------	--

Description

Returns confidence intervals for sma object

Usage

```
## S3 method for class 'sma'  
confint(object, ...)
```

Arguments

object a sma object
... arguments passed

Value

dataframe containing confidence interval

defineAxis	<i>Utility plotting functions</i>
------------	-----------------------------------

Description

Functions used in conjunction with `plot.sma` to customize spacing of ticks on plot axes. `defineAxis` creates an 'axis' object, including tick spacing, limits, and labels, that can be passed into `plot.sma` or `nicePlot`. `nicePlot` creates an empty plot using x and y axis objects.

Usage

```
defineAxis(
  major.ticks,
  limits = NULL,
  minor.ticks = NULL,
  major.tick.labels = major.ticks,
  both.sides = FALSE
)

nicePlot(
  xaxis,
  yaxis,
  log = "",
  ann = par("ann"),
  xlab = NULL,
  ylab = NULL,
  tck = par("tck"),
  frame.plot = TRUE,
  ...
)
```

Arguments

<code>major.ticks</code> , <code>minor.ticks</code>	Where to draw major and minor ticks (vectors).
<code>limits</code>	the x or y limits of the plot, (x1, x2) or (y1,y2).
<code>major.tick.labels</code>	Labels to draw at the ticks (optional).
<code>both.sides</code>	a logical value indicating whether tickmarks should also be drawn on opposite sides of the plot, i.e. right or top
<code>xaxis</code> , <code>yaxis</code>	'axis' objects, the result of calling 'defineAxis'.
<code>log</code>	One of 'x', 'y' or 'xy', specifying which axes draw in log10 scale.
<code>ann</code>	a logical value indicating whether the default annotation (x and y axis labels) should appear on the plot.
<code>xlab</code>	a label for the x axis, defaults to a description of x.

<code>ylab</code>	a label for the y axis, defaults to a description of y.
<code>tck</code>	The length of tick marks as a fraction of the smaller of the width or height of the plotting region. If <code>tck >= 0.5</code> it is interpreted as a fraction of the relevant side, so if <code>tck = 1</code> grid lines are drawn. By default set to current system defaults (<code>tck = par("tck")</code>).
<code>frame.plot</code>	a logical indicating whether a box should be drawn around the plot, by default = TRUE.
<code>...</code>	Arguments to be passed to <code>nicePlot</code> , and therein to <code>'axis'</code> .

Details

By default, calls to `plot.sma` use the values given by `plot.default` to determine axis limits and spacing of major and minor ticks. Users can override these values by passing two `'axis'` objects created by `defineAxis` to `plot.sma`. When both x and y axis objects are passed to `plot.sma`, the function uses `nicePlot` to construct the axes according to the specified values, instead of `plot.default`. As a minimum, users must at least one argument (`major.ticks`) to `defineAxis` when passing these to `plot.sma`.

The function `nicePlot` can also be called to construct a new set of axes according to the specified values. For this to work, axis objects must contain both `major.ticks` and `limits`.

See Also

[sma](#), [plot.sma](#)

Examples

```
# Load leaf lifetime dataset:
data(leaflife)

#First example of axis spacing
ft <- sma(longev~lma*rain,log="xy",data=leaflife)
xax <- defineAxis(major.ticks=c(50, 100, 200, 400))
yax <- defineAxis(major.ticks=c(0.25, 0.5, 1,2,4,8))
plot(ft, xaxis=xax, yaxis=yax)

#As above, marking axes on both sides
xax <- defineAxis(major.ticks=c(50, 100, 200, 400), both.sides=TRUE)
yax <- defineAxis(major.ticks=c(0.25, 0.5, 1,2,4,8), both.sides=TRUE)
plot(ft, xaxis=xax, yaxis=yax)

#Using labels with log10 spacing and minor tick marks
xax <- defineAxis(limits=c(10, 1E3), major.ticks=seqLog(1, 1000),
  minor.ticks=makeLogMinor(seqLog(1, 1000)))
yax <- defineAxis(limits=c(1E-1, 1E1), major.ticks=seqLog(1E-2, 10),
  minor.ticks=makeLogMinor(seqLog(1E-2, 10)))
plot(ft, xaxis=xax, yaxis=yax)

#As above, but using expressions as labels
xax <- defineAxis(limits=c(10, 1E3), major.ticks=seqLog(10, 1000),
  minor.ticks=makeLogMinor(seqLog(10, 1000)),
```

```

major.tick.labels = parse(text=paste("10^", c( 1,2,3), sep="")),
  both.sides=FALSE)
yax <- defineAxis(limits=c(1E-1, 1E1), major.ticks=seqLog(1E-1, 10),
  minor.ticks=makeLogMinor(seqLog(1E-1, 10)),
major.tick.labels = parse(text=paste("10^", c( -1,0,1), sep="")),
  both.sides=FALSE)
plot(ft, xaxis=xax, yaxis=yax)

#start an empty plot using nicePlot
xax <- defineAxis(limits=c(8, 1.2E3), major.ticks=seqLog(1, 1000))
yax <- defineAxis(limits=c(0.8E-1, 1.2E1), major.ticks=seqLog(1E-2, 10))
nicePlot(xax,yax,log='xy')

```

elev.com

Test for equal elevation among several lines fitted with (standardised) major axes of common slope.

Description

Test if several major axis or standardised major axis lines share a common elevation. This can now be done via `sma(y~x+groups)`, see help on the [sma](#) function.

Usage

```

elev.com(
  y,
  x,
  groups,
  data = NULL,
  method = "SMA",
  alpha = 0.05,
  robust = FALSE,
  V = array(0, c(2, 2, length(unique(groups)))),
  group.names = sort(unique(groups))
)

```

Arguments

y	The Y-variable for all observations (as a vector).
x	The X-variable for all observations (as a vector).
groups	Coding variable identifying which group each observation belongs to (as a factor or vector).
data	Deprecated. Use <code>with()</code> instead (see Examples).
method	The line fitting method: 'SMA' or 1 standardised major axis (this is the default) 'MA' or 2 major axis

alpha	The desired confidence level for the 100(1-alpha)% confidence interval for the common elevation. (Default value is 0.05, which returns a 95% confidence interval.)
robust	If TRUE, uses a robust method to fit the lines and construct the test statistic.
V	The estimated variance matrices of measurement error, for each group. This is a 3-dimensional array with measurement error in Y in the first row and column, error in X in the second row and column, and groups running along the third dimension. Default is that there is no measurement error.
group.names	(optional: rarely required). A vector containing the labels for 'groups'. (Only actually useful for reducing computation time in simulation work).

Details

Calculates a Wald statistic to test for equal elevation of several MA's or SMA's with a common slope. This is done by testing for equal mean residual scores across groups.

Note that this test is only valid if it is reasonable to assume that the axes for the different groups all have the same slope.

The test assumes the following:

- each group of observations was independently sampled
- the axes fitted to all groups have a common slope
- y and x are linearly related within each group
- residual scores independently follow a normal distribution with equal variance at all points along the line, within each group

Note that we do not need to assume equal variance across groups, unlike in tests comparing several linear regression lines.

The assumptions can be visually checked by plotting residual scores against fitted axis scores, and by constructing a Q-Q plot of residuals against a normal distribution, available using the [plot.sma](#) function. On a residual plot, if there is a distinct increasing or decreasing trend within any of the groups, this suggests that all groups do not share a common slope.

Setting robust=TRUE fits lines using Huber's M estimation, and modifies the test statistic as proposed in Taskinen & Warton (in review).

The common slope ($\hat{\beta}$) is estimated from a maximum of 100 iterations, convergence is reached when the change in $\hat{\beta} < 10^{-6}$.

Value

stat	The Wald statistic testing for no shift along the common axis
p	The P-value of the test. This is calculated assuming that stat has a chi-square distribution with (g-1) df, if there are g groups
a	The estimated common elevation
ci	A 100(1-alpha)% confidence interval for the true common elevation
as	Separate elevation estimates for each group

Author(s)

Warton, D.I.<David.Warton@unsw.edu.au>, J. Ormerod, & S. Taskinen

References

Warton D. I., Wright I. J., Falster D. S. and Westoby M. (2006) A review of bivariate line-fitting methods for allometry. *Biological Reviews* **81**, 259–291.

Taskinen, S. and D.I. Warton. in review. Robust tests for one or more allometric lines.

See Also

[sma](#), [plot.sma](#), [line.cis](#), [slope.com](#), [shift.com](#)

Examples

```
# Load leaf longevity data
data(leaflife)

# Test for common SMA slope amongst species at low soil nutrient sites
# with different rainfall:
leaf.low.soilp <- subset(leaflife, soilp == 'low')
with(leaf.low.soilp, slope.com(log10(longev), log10(lma), rain))

# Now test for common elevation of the groups fitted with an axis
# of common slope, at low soil nutrient sites:
with(leaf.low.soilp, elev.com(log10(longev), log10(lma), rain))

# Or test for common elevation amongst the MA's of common slope,
# for low soil nutrient sites, and construct 99% a confidence interval
# for the common elevation:
with(leaf.low.soilp, elev.com(log10(longev), log10(lma), rain, method='MA',
  alpha=0.01))
```

elev.test

One-sample test of a (standardised) major axis elevation

Description

Test if the elevation of a major axis or standardised major axis equals a specific value. This can now be done via `sma(y~x,elev.test=0)`, see help on the [sma](#) function.

Usage

```
elev.test(
  y,
  x,
  test.value = 0,
```

```

    data = NULL,
    alpha = 0.05,
    method = "SMA",
    robust = FALSE,
    V = matrix(0, 2, 2)
)

```

Arguments

y	The Y-variable
x	The X-variable
test.value	The hypothesised value of the elevation (default value is 0)
data	Deprecated. Use with() instead (see Examples).
alpha	The desired confidence level for the 100(1-alpha)% confidence interval for the common slope. (Default value is 0.05, which returns a 95% confidence interval.)
method	The line fitting method: 'OLS' or 0 linear regression 'SMA' or 1 standardised major axis (this is the default) 'MA' or 2 major axis
robust	If TRUE, uses a robust method to fit the lines and construct the test statistic.
V	The estimated variance matrix of measurement error. Default is that there is no measurement error.

Details

Tests if the line relating y to x has an elevation equal to test.value (which has a default value of 0). The line can be a linear regression line, major axis or standardised major axis (as selected using the input argument choice). The test is carried out using a t-statistic, comparing the difference between estimated and hypothesised elevation to the standard error of elevation. As described in Warton et al (2006).

A confidence interval for the elevation is also returned, again using the t-distribution.

If measurement error is present, it can be corrected for through use of the input argument V, which makes adjustments to the estimated sample variances and covariances then proceeds with the same method of inference. Note, however, that this method is only approximate (see Warton et al 2006 for more details).

The test assumes the following:

1. y and x are linearly related
2. residuals independently follow a normal distribution with equal variance at all points along the line

The assumptions can be visually checked by plotting residual scores against fitted axis scores, and by constructing a Q-Q plot of residuals against a normal distribution, available using the [plot.sma](#) function.

Setting robust=TRUE fits lines using Huber's M estimation, and modifies the test statistic as proposed in Taskinen & Warton (in review).

fitted.sma	Returns fitted values
------------	-----------------------

Description

Returns "fitted values" of a (standardized) major axis fit.

Usage

```
## S3 method for class 'sma'  
fitted(object, type = "fitted", newdata = NULL, centered = TRUE, ...)
```

Arguments

object	Object of class sma.
type	Either 'residuals', or 'fitted'.
newdata	New data for which to provide fitted values.
centered	Logical. If TRUE (the default) returns the zero-centered fitted values.
...	Further arguments are currently ignored.

Details

"Fitted values" are calculated using $y+bx$ for SMA or $by+x$ for MA (see Warton et al. 2006, especially Table 4). Note these values are calculated differently to ordinary linear regression, and they cannot be interpreted as predicted values. The "fitted values" should be interpreted as measuring how far along the fitted axis each point lies, and are used in checking assumptions (via residual vs. fitted value plots).

Fitted values may be computed for new data, using the newdata arguments. Be aware that the names of the variables need to be the same as in the data used in the original model fit. Also, if the original fit used $\log='xy'$, for example, this transformation will also be applied to your newdata (so don't do the transformation yourself).

References

Warton D. I., Wright I. J., Falster D. S. and Westoby M. (2006) A review of bivariate line-fitting methods for allometry. *Biological Reviews* **81**, 259-291.

See Also

[sma](#), [residuals.sma](#)

ggplot.sma

*Plot a (S)MA fit using ggplot2***Description**

Produce a ggplot2 version of the default x-y plot for an sma fit: the data points plus the fitted (standardised) major axis line(s), with separate colours for each group where present. This is a ggplot2-based alternative to the base-graphics [plot.sma](#).

Usage

```
## S3 method for class 'sma'
ggplot(data = NULL, mapping = aes(), ..., environment = parent.frame())
```

Arguments

data	An object of class sma, as returned by sma or ma . (Named data for consistency with the ggplot2::ggplot generic.)
mapping, environment	Present for consistency with the ggplot2::ggplot generic; not used.
...	Further arguments passed to geom_line for the fitted lines (for example linewidth or linetype).

Details

Data and fitted lines are drawn on the natural (back-transformed) scale of the original variables. Where the fit used a log transformation (log was one of "x", "y" or "xy"), the corresponding axis is drawn on a log10 scale via [scale_x_log10](#) / [scale_y_log10](#). The fitted line geometry mirrors the curve logic used by [plot.sma](#), so both plotting methods agree.

The returned object is a standard ggplot object and can be further customised with additional layers, themes, scales and facets in the usual way.

Value

A ggplot object.

Author(s)

F. Kar, D. Falster

See Also

[plot.sma](#)

Examples

```
## Not run:
data(leaflife)
leaf.low.soilp <- subset(leaflife, soilp == "low")

# Single fit
ft1 <- sma(longev ~ lma, data = leaf.low.soilp, log = "xy")
ggplot2::ggplot(ft1)

# Grouped fit with common-slope test
ft2 <- sma(longev ~ lma * rain, data = leaf.low.soilp, log = "xy")
ggplot2::ggplot(ft2)

# ggplot object can be extended as usual
ggplot2::ggplot(ft2) + ggplot2::theme_minimal()

## End(Not run)
```

leaflife	<i>Leaf longevity and leaf mass per area for plant species from different sites</i>
----------	---

Description

This dataset contains the leaf longevity and leaf mass per area of 75 plant species from four sites in south-eastern Australia. Sites represent contrasts along rainfall and soil phosphorous gradients.

Usage

```
leaflife
```

Format

A data frame containing 75 rows and 5 variables:

site the site at which this species was sampled (coded as 1, 2, 3, or 4)

rain The level of annual rainfall at the site (coded as "high" or "low")

soilp The level of soil phosphate concentration at the site (coded as "high" or "low")

longev Leaf longevity (years)

lma Leaf mass per area (m²/kg)

Source

Wright I. J., Westoby M. and Reich P. B. (2002) Convergence towards higher leaf mass per area in dry and nutrient-poor habitats has different consequences for leaf life span. *Journal of Ecology* **90**, 534–543.

leafmeas	<i>Leaf mass per area and photosynthetic rate for plant species from different sites</i>
----------	--

Description

This dataset contains the leaf mass per area (LMA) and photosynthetic rate per leaf mass (A_{mass}) of individual plants from 81 plant species at four sites in south-eastern Australia. Sites represent contrasts along rainfall and soil phosphorous gradients.

Usage

```
leafmeas
```

Format

A data frame containing 529 rows and 4 variables:

site (factor) The site at which this species was sampled (coded as Murrumbidgee, WH, RHM, RHW)

spp (factor) Species of the observed plant species

A_{mass} (numeric) Photosynthetic rate per leaf mass (g/g/h)

lma (numeric) Leaf mass per area (mg/kg)

Source

Wright I. J., Reich P. B. and Westoby M. (2001) Strategy shifts in leaf physiology, structure and nutrient content between species of high- and low-rainfall and high- and low-nutrient habitats. *Functional Ecology* **15**, 423–434.

line.cis	<i>Slope and elevation of a (standardised) major axis, with confidence intervals</i>
----------	--

Description

Calculates the slope and elevation of a major axis or standardised major axis, and constructs confidence intervals for the true slope and elevation. This can now be fitted via calls of the form `sma(y~x, ...)`, see [sma](#).

Usage

```

line.cis(
  y,
  x,
  alpha = 0.05,
  data = NULL,
  method = "SMA",
  intercept = TRUE,
  V = matrix(0, 2, 2),
  f.crit = 0,
  robust = FALSE,
  ...
)

```

Arguments

y	The Y-variable
x	The X-variable
alpha	The desired confidence level for the 100(1-alpha)% confidence interval for the common slope. (Default value is 0.05, which returns a 95% confidence interval.)
data	Deprecated. Use with() instead (see Examples).
method	The line fitting method: 'OLS' or 0 linear regression 'SMA' or 1 standardised major axis (this is the default) 'MA' or 2 major axis
intercept	(logical) Whether or not the line includes an intercept. FALSE no intercept, so the line is forced through the origin TRUE an intercept is fitted (this is the default)
V	The estimated variance matrix of measurement error. Average measurement error for Y is in the first row and column, and average measurement error for X is in the second row and column. The default is that there is no measurement error.
f.crit	(optional - rarely required). The critical value to be used from the F distribution. (Only actually useful for reducing computation time in simulation work - otherwise, do not change.)
robust	If TRUE, uses a robust method to fit the lines and construct confidence intervals.
...	Further parameters (not passed anywhere at the moment).

Details

Fits a linear regression line, major axis, or standardised major axis, to a bivariate dataset. The slope and elevation are returned with confidence intervals, using any user-specified confidence level.

Confidence intervals are constructed by inverting the standard one-sample tests for elevation and slope (see slope.test and elev.test for more details). Only the primary confidence interval is returned

- this is valid as long as it is known a priori that the (standardised) major axis is estimating the true slope rather than the (standardised) minor axis. For SMA, this means that the sign of the true slope needs to be known a priori, and the sample slope must have the same sign as the true slope.

The test assumes the following:

1. y and x are linearly related
2. residuals independently follow a normal distribution with equal variance at all points along the line

These assumptions can be visually checked by plotting residuals against fitted axis scores, and by constructing a Q-Q plot of residuals against a normal distribution. An appropriate residual variable is $y - bx$, and for fitted axis scores use x (for linear regression), $y + bx$ (for SMA) or $by + x$ (for MA), where b represents the estimated slope.

If measurement error is present, it can be corrected for through use of the input argument `V`, which makes adjustments to the estimated sample variances and covariances then proceeds with the same method of inference. Note, however, that this method is only approximate (see Warton et al in review for more details).

Setting `robust=TRUE` fits lines using Huber's M estimation, and modifies confidence interval formulae along the lines discussed in Taskinen & Warton (in review).

Value

`coeff` A matrix containing the estimated elevation and slope (first column), and the lower and upper limits of confidence intervals for the true elevation and slope (second and third columns). Output for the elevation and slope are in the first and second rows, respectively.

Author(s)

Warton, D.I.<David.Warton@unsw.edu.au>, J. Ormerod, & S. Taskinen

References

Warton, D.I., I.J. Wright, D.S. Falster and M. Westoby. 2006. Bivariate line-fitting methods for allometry. *Biological Reviews* **81**, 259–291.

Taskinen, S. and D.I. Warton. in review. Robust tests for one or more allometric lines.

See Also

[sma](#), [slope.test](#), [elev.test](#)

Examples

```
#load the leaflife data
data(leaflife)

#consider only the low rainfall sites:
leaf.low.rain=leaflife[leaflife$rain=='low',]
```

```
#estimate the SMA line for reserve vs coat
with(leaf.low.rain, line.cis(log10(longev),log10(lma)))

#produce CI's for MA slope and elevation:
with(leaf.low.rain, line.cis(log10(longev),log10(lma),method='MA'))
```

ma	<i>Major axis estimation and testing for one or several samples</i>
----	---

Description

Major axis estimation and testing for one or several samples

Usage

```
ma(...)
```

Arguments

... arguments passed to sma()

makeLogMinor	<i>Generate spacing for minor tick marks on a plot with log-scaled axes</i>
--------------	---

Description

Generates a sequence of numbers providing minor tick marks on log scaled axes.

A vector is created according to the following algorithm. For each pair of adjacent values (x1, x2) in major, the function adds the values (x1, 2*x1, 3*x1, ..., x2) to the vector of return values.

This is useful for generating spacing of minor tick-values on log-transformed axes.

Usage

```
makeLogMinor(major)
```

Arguments

major a vector of values giving major tick marks.

Value

vector of minor tick spacings appropriate for log 10 scaled axis with major ticks given by 'major'

See Also

[plotutils](#)

Examples

```
#Sequence suitable for log base 10 labels
makeLogMinor(seqLog(1E-5, 1E5))
```

meas.est

Measurement error variance estimation from repeated measures

Description

Estimates the average variance matrix of measurement error for a set of subjects with repeated measures.

Usage

```
meas.est(datameas, id, data = NULL)
```

Arguments

datameas	A data matrix containing the repeated measures of observations, with each variable in a different column and all observations on all subjects in different rows of the same column.
id	An id vector identifying the subject being measured for each observation in the data matrix.
data	Deprecated. Use with() instead (see Examples).

Details

This function allows the estimation of measurement error variance, given a set of repeated measures on different subjects. Measurement error variance is estimated separately for each subject, then averaged across subjects. This provides terms that can be used to correct for measurement error in allometric analyses.

Any number of variables can be specified in the data matrix for measurement error calculation. If more than one variable is specified, the covariance of measurement error is estimated from the repeated measures as well as the variance.

As well as the estimated measurement error variance, a data matrix is returned which contains the averages of the repeated measures for each subject.

Value

V	A matrix containing the average variances and average covariances of the repeated measures of subjects.
dat.mean	A matrix containing the values for each subject, averages across repeated measures. Subjects are in rows, variables in columns.

Author(s)

Warton, D. <David.Warton@unsw.edu.au>, translated to R by Ormerod, J. 2005-12-08

References

Warton, D.I., I.J. Wright, D.S. Falster and M. Westoby. 2006. Bivariate line-fitting methods for allometry. *Biological Reviews* **81**, 259–291.

See Also

[line.cis](#), [slope.test](#)

Examples

```
#load the individual level leaf example dataset
data(leafmeas)

#Estimate measurement error variance matrix, store in "meas.vr"
meas.vr <- meas.est(leafmeas[,3:4], leafmeas$spp)
```

multcompmatrix	<i>Multiple comparisons graphical matrix</i>
----------------	--

Description

Print a matrix of pair-wise comparisons based on an 'sma' fit.

A matrix of comparisons is drawn, based on the P values of the pair-wise tests between levels of the grouping variable. An 'X' indicates $P < 0.05$, 'o' indicates $0.05 < P < 0.1$.

Usage

```
multcompmatrix(smfit, sort = TRUE)
```

Arguments

smfit	An object of class 'sma', fit with sma .
sort	Logical. Specifies whether or not to sort groups from smallest to largest value based on the parameter of interest (slope, elevation or mean fitted value).

Value

Invisibly returns the (character) matrix.

Author(s)

Remko Duursma and Daniel Falster.

See Also

[sma](#)

Examples

```
# Print the matrix of comparisons:
data(leaflife)
sm1 <- sma(lma ~ longev + site, data=leaflife, multcomp=TRUE)
multcompmatrix(sm1)

# Write the matrix to a file like this:
## Not run:
capture.output(multcompmatrix(sm1), file="sm1matrix.txt")

## End(Not run)
```

plot.sma

Draw an X-Y plot

Description

Plot a (standardized) major axis fit, including the data and the fitted lines. There are many options for changing the appearance of the plot and generating high-quality publishable graphs.

Usage

```
## S3 method for class 'sma'
plot(
  x,
  which = c("default", "residual", "qq"),
  use.null = FALSE,
  add = FALSE,
  type = "o",
  xaxis = NULL,
  yaxis = NULL,
  xlab = NULL,
  ylab = NULL,
  pch = NULL,
  col = NULL,
  lty = NULL,
  from = NULL,
  to = NULL,
  log = x$log,
  frame.plot = TRUE,
  tck = par("tck"),
  p.lines.transparent = NA,
  axes = TRUE,
  ...
)
```

Arguments

x	Object of class 'sma'.
which	If 'residual', plots a residual plot; if 'qq', plots a qq plot; otherwise an x-y plot.
use.null	Logical. If FALSE, plots the fitted lines (the default), otherwise those corresponding to the null hypothesis.
add	Logical. If TRUE, adds lines or points to an existing plot.
type	As in 'lm.default' : 'p' plots points only, 'l' only lines, and 'o' or 'b' plot both.
xaxis, yaxis	Special axis objects. See Details and examples.
xlab, ylab	Labels for X and Y axes.
pch	Plotting symbols (see points).
col	Color of points and lines.
lty	Line type (see lines).
from, to	Min and max X values for the lines (defaults to values given by sma , which are the X values corresponding the maximum and minimum fitted values in the data.).
log	One of 'x', 'y' or 'xy', to denote which axes to log-scale.
frame.plot	a logical indicating whether a box should be drawn around the plot, by default = TRUE.
tck	The length of tick marks as a fraction of the smaller of the width or height of the plotting region. If tck >= 0.5 it is interpreted as a fraction of the relevant side, so if tck = 1 grid lines are drawn. By default set to current system defaults (tck = par("tck")).
p.lines.transparent	Adjusts transparency level of fitted lines according to p-value of correlation between X and Y, via formula opacity = 1-p/p.lines.transparent). Setting to a value 0.1 means the line for any group with p = 0.1 would be fully transparent, while line for a group with p = 0.05 would be 50 percent transparent. by default set to NA, which means lines are fully visible.
axes	If FALSE, suppress plotting of the axes (Default TRUE)
...	Further arguments passed to plot.default .

Details

The `plot.sma` function produces one of three different types of plot, depending on the `which` argument.

The default plot, `which="default"`, produced a plot of y vs x , with separate symbols for each group if appropriate, and MA or SMA lines fitted through each group. The formula used in the `sma` object that is input to the `plot` function determines whether there is a group structure, whether fitted lines have common slope, etc.

A residual plot can be obtained via `which="residual"` - this is a plot of residuals against fitted values. This can be used to check assumptions - if assumptions are satisfied there should be no pattern.

A normal quantile plot can be obtained via `which="qq"` - this is a normal quantile plot of residuals. This can be used to check the normality assumption - if data are close to a straight line, normality is plausible. Note that non-normality is only important to the validity of the test in small samples. In larger samples, non-normality will not effect validity, but strong non-normality will reduce the power of tests.

If `use.null=TRUE` then the lines added to the plot use the coefficients estimated under the null hypothesis. For example, if the `sma` object `x` was produced using a common slopes test (via `y~x*groups` or similar) then `use.null=TRUE` will plot lines that apply the common slope to each group.

The arguments `pch`, `col`, `lty`, `from` & `to`, are used to modify characteristics of the plotted points and lines. If a vector of values for anyone of these arguments is passed to `plot.sma`, then successive values are applied to each group, provided group structure is included in `x` and the vector length is at least as long as the number of groups.

By default, `plot.sma` uses the default tick spacing given by `plot.default`. To customise axes, users can pass special axis objects to `plot.sma`, obtained using the `defineAxis` command as in the example below. This enables high quality publishable plots to be produced. See `utils` for more information.

Author(s)

D. Falster, R.A. Duursma, D.I. Warton

Examples

```
## Not run:
# Load leaf lifetime dataset:
data(leaflife)

# Only consider low-nutrient sites:
leaf.low.soilp <- subset(leaflife, soilp == 'low')

# Fit SMA's separately at each of high and low
# rainfall sites and test for common slope:
ft <- sma(longev~lma*rain, data=leaf.low.soilp, log="xy")

# Plot leaf longevity (longev) vs leaf mass per area (lma)
# separately for each of high and low rainfall:
plot(ft)

# As before but add lines which have a common slope:
plot(ft, use.null=TRUE)

#As above, but adding the common slope lines to an existing plot
plot(ft, type='p', col="black")
plot(ft, use.null=TRUE, add=TRUE, type='l')

# Plot with equally spaced tick marks:
plot(ft, xaxis=defineAxis(major.ticks=c(40,80,160,320,640)),
      yaxis=defineAxis(major.ticks=c(0.5,1,2,4,8)) )
```

```
# Produce a residual plot to check assumptions:
plot(ft,which="res")

# Produce a normal quantile plot:
plot(ft,which="qq")

## End(Not run)
```

predict.sma

*Predicting from an (Standardized) major axis estimation***Description**

Predicting from an (Standardized) major axis estimation

Usage

```
## S3 method for class 'sma'
predict(object, ...)
```

Arguments

object	sma obj
...	arguments passed

Value

A cautionary message

print.sma

*Print an object of class 'sma'.***Description**

Prints the coefficients and the results of the various hypothesis tests of an sma object.

Usage

```
## S3 method for class 'sma'
print(x, ..., coefbygroup = FALSE)
```

Arguments

x	Object of class 'sma'.
...	Further arguments ignored.
coefbygroup	Whether or not to print the coefficients by group.

Author(s)

R.A. Duursma, D. Falster, D.I. Warton

See Also

[sma](#)

residuals.sma

Extract model residuals

Description

Extracts the residuals of a (standardized) major axis fit.

Usage

```
## S3 method for class 'sma'  
residuals(object, ...)
```

Arguments

object	Object of class 'sma'.
...	Further arguments ignored.

Details

Residuals are calculated as $y - bx - a$ for each group. These values are useful in assumption checking, especially in constructing residual vs fitted value plots.

Value

A vector of residuals.

See Also

[sma](#), [plot.sma](#)

seqLog	<i>Sequence Generation</i>
--------	----------------------------

Description

Generate multiplicative sequences, or series.

Usage

```
seqLog(from, to, base = 10)
```

Arguments

from, to	the starting and (maximal) end value of a sequence.
base	multiplication value.

Details

Starting at from, seq multiplies successively by base until the maximal value is reached. This is useful for generating tick-spacing on log-transformed axes.

Value

vector from lo to hi with multiplication steps of incr. Used for making ticks to a log-scaled axis

See Also

[plotutils](#)

Examples

```
#Sequence suitable for log base 10 labels  
seqLog(1E-5, 1E5)
```

```
#Sequence suitable for log base 2 labels  
seqLog(2, 128, base=2)
```

shift.com

*Test for no mean shift along a common (standardised) major axis***Description**

Test if several groups of observations have no shift in location along major axis or standardised major axis lines with a common slope. This can now be done via `sma(y~x+groups, type="shift")`, see help on the [sma](#) function.

Usage

```
shift.com(
  y,
  x,
  groups,
  data = NULL,
  method = "SMA",
  intercept = TRUE,
  robust = FALSE,
  V = array(0, c(2, 2, length(unique(groups)))),
  group.names = sort(unique(groups))
)
```

Arguments

y	The Y-variable for all observations (as a vector)
x	The X-variable for all observations (as a vector)
groups	Coding variable identifying which group each observation belongs to (as a factor or vector)
data	Deprecated. Use <code>with()</code> instead (see Examples).
method	The line fitting method: 'SMA' or 1 standardised major axis (this is the default) 'MA' or 2 major axis
intercept	(logical) Whether or not the line includes an intercept. FALSE no intercept, so the line is forced through the origin TRUE an intercept is fitted (this is the default)
robust	If TRUE, uses a robust method to fit the lines and construct the test statistic.
V	The estimated variance matrices of measurement error, for each group. This is a 3-dimensional array with measurement error in Y in the first row and column, error in X in the second row and column, and groups running along the third dimension. Default is that there is no measurement error.
group.names	(optional: rarely required). A vector containing the labels for 'groups'. (Only actually useful for reducing computation time in simulation work).

Details

Calculates a Wald statistic to test for no shift along several MA's or SMA's of common slope. This is done by testing for equal fitted axis means across groups.

Note that this test is only valid if it is reasonable to assume that the axes for the different groups all have the same slope.

The test assumes the following:

1. each group of observations was independently sampled
2. the axes fitted to all groups have a common slope
3. y and x are linearly related within each group
4. fitted axis scores independently follow a normal distribution with equal variance at all points along the line, within each group

Note that we do not need to assume equal variance across groups, unlike in tests comparing several linear regression lines.

The assumptions can be visually checked by plotting residuals against fitted axis scores, and by constructing a Q-Q plot of residuals against a normal distribution, available using

```
plot.sma(sma.object,which="residual").
```

On a residual plot, if there is a distinct increasing or decreasing trend within any of the groups, this suggests that all groups do not share a common slope.

A plot of residual scores against fitted axis scores can also be used as a visual test for no shift. If fitted axis scores systematically differ across groups then this is evidence of a shift along the common axis.

Setting `robust=TRUE` fits lines using Huber's M estimation, and modifies the test statistic as proposed in Taskinen & Warton (in review).

The common slope ($\hat{\beta}$) is estimated from a maximum of 100 iterations, convergence is reached when the change in $\hat{\beta}$ is $< 10^{-6}$.

Value

stat	The Wald statistic testing for no shift along the common axis
p	The P-value of the test. This is calculated assuming that stat has a chi-square distribution with (g-1) df, if there are g groups
f.mean	The fitted axis means for each group

Author(s)

Warton, D.I.<David.Warton@unsw.edu.au>, J. Ormerod, & S. Taskinen

References

Warton D. I., Wright I. J., Falster D. S. and Westoby M. (2006) A review of bivariate line-fitting methods for allometry. *Biological Reviews* **81**, 259–291.

Taskinen, S. and D.I. Warton. in review. Robust tests for one or more allometric lines.

See Also

[sma](#), [plot.sma](#), [line.cis](#), [elev.com](#), [shift.com](#)

Examples

```
#load leaf longevity data
data(leaflife)

#Test for common SMA slope amongst species at low rainfall sites
#with different levels of soil nutrients
leaf.low.rain=leaflife[leaflife$rain=='low',]
with(leaf.low.rain, slope.com(log10(longev), log10(lma), soilp))

#Now test for no shift along the axes of common slope, for sites
#with different soil nutrient levels but low rainfall:
with(leaf.low.rain, shift.com(log10(longev), log10(lma), soilp))

#Now test for no shift along the axes of common slope, for sites
#with different soil nutrient levels but low rainfall:
with(leaf.low.rain, shift.com(log10(longev), log10(lma), soilp, method='MA'))
```

slope.com

Common slope test amongst several allometric lines

Description

Test if several major axis or standardised major axis lines share a common slope. This can now be done via `sma(y~x*groups)`, see help on the [sma](#) function.

Usage

```
slope.com(
  y,
  x,
  groups,
  method = "SMA",
  alpha = 0.05,
  data = NULL,
  intercept = TRUE,
  robust = FALSE,
  V = array(0, c(2, 2, length(unique(groups)))),
  group.names = sort(unique(groups)),
  ci = TRUE,
  bs = TRUE,
  slope.test = NULL
)
```

Arguments

y	The Y-variable for all observations (as a vector)
x	The X-variable for all observations (as a vector)
groups	Coding variable identifying which group each observation belongs to (as a factor or vector)
method	The line fitting method: 'SMA' or 1 standardised major axis (this is the default) 'MA' or 2 major axis 'lamest' or 3 Error variance ratio is estimated from the data
alpha	The desired confidence level for the 100(1-alpha)% confidence interval for the common slope. (Default value is 0.05, which returns a 95% confidence interval.)
data	Deprecated. Use with() instead (see Examples).
intercept	(logical) Whether or not the line includes an intercept. FALSE no intercept, so the line is forced through the origin TRUE an intercept is fitted (this is the default)
robust	If TRUE, uses a robust method to fit the lines and construct the test statistic.
V	The estimated variance matrices of measurement error, for each group. This is a 3-dimensional array with measurement error in Y in the first row and column, error in X in the second row and column, and groups running along the third dimension. Default is that there is no measurement error.
group.names	(optional: rarely required). A vector containing the labels for 'groups'. (Only actually useful for reducing computation time in simulation work).
ci	(logical) Whether or not to return a confidence interval for the common slope.
bs	(logical) Whether or not to return the slopes for the separate groups, with confidence intervals.
slope.test	If a value provided, tests the common slope fit against this value.

Details

For several bivariate groups of observations, this function tests if the line-of-best-fit has a common slope for all samples, when the line-of-best-fit is estimated using the major axis, standardised major axis, or a more general version of these methods in which the error variance ratio is estimated from the data.

The test assumes the following:

1. each group of observations was independently sampled
2. y and x are linearly related within each group
3. residuals independently follow a normal distribution with equal variance at all points along the line, within each group

Note that we do not need to assume equal variance across groups, unlike in the standard test for common slope for linear regression.

The assumptions can be visually checked by plotting residual scores against fitted axis scores, and by constructing a Q-Q plot of residuals against a normal distribution, available using the [plot.sma](#) function.

Setting `robust=TRUE` fits lines using Huber's M estimation, and modifies the test statistic as proposed in Taskinen & Warton (in review).

The common slope is estimated from a maximum of 100 iterations, convergence is reached when the change in b is $< 10^{-6}$.

Value

<code>lr</code>	The (Bartlett-corrected) likelihood ratio statistic testing for common slope
<code>p</code>	The P-value of the test. This is calculated assuming that <code>lr</code> has a chi-square distribution with $(g-1)$ df, if there are g groups
<code>b</code>	The common slope estimate
<code>varb</code>	The sample variance of the common slope
<code>ci</code>	A $100(1-\alpha)\%$ confidence interval for the common slope
<code>lambda</code>	The error variance ratio - the ratio of error variance in y to error variance in x . For MA, this is assumed to be 1. for SMA, this is assumed to be b^2 . For the 'lamest' method, the error variance ratio is estimated from the data under the common slope assumption.
<code>bs</code>	The slopes and confidence intervals for data from each group.

Author(s)

Warton, D.I.<David.Warton@unsw.edu.au>, J. Ormerod, & S. Taskinen

References

- Warton D. I. and Weber N. C. (2002) Common slope tests for bivariate structural relationships. *Biometrical Journal* **44**, 161–174.
- Warton D. I., Wright I. J., Falster D. S. and Westoby M. (2006) A review of bivariate line-fitting methods for allometry. *Biological Reviews* **81**, 259–291.
- Taskinen, S. and D.I. Warton. in review. Robust tests for one or more allometric lines.

See Also

[sma](#), [line.cis](#), [elev.com](#), [shift.com](#)

Examples

```
#load leaf longevity data
data(leaflife)

#plot the data, with different symbols for different groups.
plot(leaflife$lma, leaflife$longev, type='n', log='xy', xlab=
  'leaf mass per area [log scale]', ylab='leaf longevity [log scale]')
colours <- c('blue', 'red', 'green', 'yellow')
```

```

points(leaflife$lma, leaflife$longev,
       col=colours[as.numeric(leaflife$site)])
legend(55, 5, as.character(unique(leaflife$site)), col=colours,
       pch=rep(1,4))

#test for common SMA slope of log(leaf longevity) vs log(LMA),
#across species sampled at different sites:
fit <- with(leaflife, slope.com(log10(longev), log10(lma), site))
fit

#Residual vs fits plots for SMA fit of each site
y <- log10(leaflife$longev)
x <- log10(leaflife$lma)
site <- leaflife$site
par( mfrow=c(2,2) )
plot(y[site==1] + fit$bs[1,1] * x[site==1], y[site==1] - fit$bs[1,1]
     * x[site==1], xlab='fits (site 1)', ylab='residuals (site 1)')
plot(y[site==2] + fit$bs[1,2] * x[site==2], y[site==2] - fit$bs[1,2]
     * x[site==2], xlab='fits (site 2)', ylab='residuals (site 2)')
plot(y[site==3] + fit$bs[1,3] * x[site==3], y[site==3] - fit$bs[1,3]
     * x[site==3], xlab='fits (site 3)', ylab='residuals (site 3)')
plot(y[site==4] + fit$bs[1,4] * x[site==4], y[site==4] - fit$bs[1,4]
     * x[site==4], xlab='fits (site 4)', ylab='residuals (site 4)')

#Test for common SMA slope amongst species at low rainfall sites
#with different levels of soil nutrients
leaf.low.rain <- leaflife[leaflife$rain=='low',]
with(leaf.low.rain, slope.com(log10(longev), log10(lma), soilp))

#test for common MA slope:
with(leaflife, slope.com(log10(longev), log10(lma), site, method='MA'))

#test for common MA slope, and produce a 90% CI for the common slope:
with(leaflife, slope.com(log10(longev), log10(lma), site, method='MA', alpha=0.1))

```

slope.test

One-sample test of a (standardised) major axis slope

Description

Test if the slope of a major axis or standardised major axis equals a specific value. This can now be done via `sma(y~x, slope.test=1)`, see help on [sma](#).

Usage

```

slope.test(
  y,
  x,

```

```

    test.value = 1,
    data = NULL,
    method = "SMA",
    alpha = 0.05,
    V = matrix(0, 2, 2),
    intercept = TRUE,
    robust = FALSE
)

```

Arguments

y	The Y-variable
x	The X-variable
test.value	The hypothesised value of the slope (default value is 1)
data	Deprecated. Use with() instead (see Examples).
method	The line fitting method: 'OLS' or 0 linear regression 'SMA' or 1 standardised major axis (this is the default) 'MA' or 2 major axis
alpha	The desired confidence level for the 100(1-alpha)% confidence interval for the common slope. (Default value is 0.05, which returns a 95% confidence interval.)
V	The estimated variance matrix of measurement error. Average measurement error for Y is in the first row and column, and average measurement error for X is in the second row and column. The default is that there is no measurement error.
intercept	(logical) Whether or not the line includes an intercept. FALSE no intercept, so the line is forced through the origin TRUE an intercept is fitted (this is the default)
robust	If TRUE, uses a robust method to fit the lines and construct the test statistic.

Details

Tests if the line relating y to x has a slope equal to test.value (which has a default value of 1). The line can be a linear regression line, major axis or standardised major axis (as selected using the input argument choice). The test is carried out by testing for correlation between residual and fitted values, as described in Warton et al (in review).

A confidence interval for the slope is also returned, which is the primary confidence interval found by inverting the one-sample test statistic.

If measurement error is present, it can be corrected for through use of the input argument V, which makes adjustments to the estimated sample variances and covariances then proceeds with the same method of inference. Note, however, that this method is only approximate (see Warton et al in review for more details).

The test assumes the following:

1. y and x are linearly related

2. residuals independently follow a normal distribution with equal variance at all points along the line

The assumptions can be visually checked by plotting residual scores against fitted axis scores, and by constructing a Q-Q plot of residuals against a normal distribution, available using the [plot.sma](#) function.

Setting `robust=TRUE` fits lines using Huber's M estimation, and modifies the test statistic as proposed in Taskinen & Warton (in review).

Value

<code>r</code>	The test statistic - the sample correlation between residuals and fitted values
<code>p</code>	The P-value, taken from the F-distribution. This is an exact test if residuals are normally distributed.
<code>test.value</code>	The hypothesised value of the slope
<code>b</code>	The estimated slope
<code>ci</code>	A 100(1-alpha)% CI for the slope.

Author(s)

Warton, D.I.<David.Warton@unsw.edu.au>, J. Ormerod, & S. Taskinen

References

Warton D. I., Wright I. J., Falster D. S. and Westoby M. (2006) A review of bivariate line-fitting methods for allometry. *Biological Reviews* **81**, 259–291.

Taskinen, S. and D.I. Warton. in review. Robust tests for one or more allometric lines.

See Also

[sma](#), [line.cis](#), [elev.test](#)

Examples

```
#load the leaflife dataset:
data(leaflife)

#consider only the low rainfall sites:
leaf.low.rain <- leaflife[leaflife$rain=='low',]

#test if the SMA slope amongst species at low rainfall sites is 1,
#for log (base 10) transformed data:
with(leaf.low.rain, slope.test(log10(longev), log10(lma)))

#test if the MA slope is 2/3
with(leaf.low.rain, slope.test(log10(longev), log10(lma), test.value = 2/3, method = 'MA'))
```

sma	<i>(Standardized) major axis estimation and testing for one or several samples</i>
-----	--

Description

The `sma` and `ma` functions fit SMA and MA respectively, and construct confidence intervals or test hypotheses about slope or elevation in one or several samples, depending on how the arguments are specified. Options exist to force lines through the origin, (approximately) correct for measurement error if the measurement error variance is known, and use robust estimation to ensure that inferences are valid in the presence of outliers (currently implemented for single samples only).

Usage

```
sma(
  formula,
  data,
  subset,
  na.action,
  log = "",
  method = c("SMA", "MA", "OLS"),
  type = c("elevation", "shift"),
  alpha = 0.05,
  slope.test = NA,
  elev.test = NA,
  multcomp = FALSE,
  multcompmethod = c("default", "adjusted"),
  robust = FALSE,
  V = matrix(0, 2, 2),
  n_min = 3,
  quiet = FALSE,
  ...
)
```

Arguments

<code>formula</code>	Formula of the form $y \sim x$ etc. This determines whether a single (S)MA is fitted, or whether several lines are fitted and compared. See Details.
<code>data</code>	A dataframe with the x and y variables.
<code>subset</code>	A subset of the dataframe for fitting; optional.
<code>na.action</code>	What to do with missing values (<code>na.omit</code> , <code>na.fail</code> , etc).
<code>log</code>	One of 'x', 'y', or 'xy' to log10-transform variables.
<code>method</code>	If SMA, standardized major axis, if MA, major axis, and if OLS, ordinary least squares.
<code>type</code>	If several lines with common slope are to be compared, do you want to test for a change in 'elevation' or for a 'shift' along a common (S)MA. See Details.

<code>alpha</code>	The error rate for confidence intervals. Typically 0.05.
<code>slope.test</code>	The hypothesised value to be used, if testing for evidence that (S)MA slope(s) are significantly different from a hypothesised value.
<code>elev.test</code>	The hypothesised value to be used, if testing for evidence that (S)MA elevation(s) are significantly different from a hypothesised value.
<code>multcomp</code>	Logical. If TRUE, performs pair-wise comparisons between levels of the grouping variable.
<code>multcompmethod</code>	Whether to adjust the P values for multiple comparisons ('adjusted') or not ('default').
<code>robust</code>	If TRUE, uses a new method of robust line fitting. (Currently available for single-sample testing only.)
<code>V</code>	The estimated variance matrix of measurement error. Average measurement error for Y is in the first row and column, and average measurement error for X is in the second row and column. The default is that there is no measurement error.
<code>n_min</code>	The minimum sample size for a group.
<code>quiet</code>	If TRUE, suppresses all messages.
<code>...</code>	Further arguments passed to internal functions (none at the moment?)

Details

This is the key function in the [smatr-package](#); all the key estimation and testing functionality in the package can all be accessed using this function, via different usages of the formula and other arguments, as described below.

One-sample testing The below options allow estimation of a (S)MA, confidence intervals for parameters, and hypothesis testing of parameters, from a single sample of two variables y and x . Use the `sma` function to fit a standardised major axis (SMA), or use `ma` in combination with the below options in order to fit major axis (MA) instead.

`list("sma(y~x)")` Fits a SMA and constructs confidence intervals for the true slope and elevation. Replaces the `line.cis` function from previous versions of `smatr`.

`list("ma(y~x)")` Fits a MA and constructs confidence intervals for the true slope and elevation. All the below functions also work for MA, if the `ma` function is called instead of the `sma` function.

`list("sma(y~x, slope.test=B)")` Tests if the slope of a SMA equals B.

`list("sma(y~x, elev.test=A)")` Tests if the elevation of a SMA equals A.

`list("sma(y~x, robust=T)")` Fits a SMA using Huber's M estimation and constructs confidence intervals for the true slope and elevation. This offers robustness to outliers in estimation and inference, and can be used in combination with the `slope.test` and `elev.test` arguments.

`list("sma(y~x-1)")` Fits a SMA where the line is forced through the origin, and constructs confidence intervals for the true slope. This type of formula can be used in combination with the `slope.test` argument.

For several samples: The below options allow estimation of several (S)MA lines, confidence intervals for parameters, and hypothesis testing of parameters, from two variables y and x for observations that have been classified into several different samples using the factor groups. Use the `sma` function to fit a standardised major axis (SMA), or use the `ma` in combination with the below options in order to fit major axis (MA) instead.

- list("sma(y~x*groups)")** Test if several SMA lines share a common slope, and construct a confidence interval for the true common slope.
- list("sma(y~x+groups, type='elevation')")** Test if several common slope SMA lines also share a common elevation, and construct a confidence interval for the true common elevation.
- list("sma(y~x+groups, type='shift')")** Test if several groups of observations have no shift in location along common slope SMA lines.
- list("sma(y~x*groups, slope.test=B)")** Test if several SMA lines share a common slope whose true value is exactly equal to B.
- list("sma(y~x+groups, elev.test=A)")** Test if several common-slope SMA lines share a common elevation whose true value is exactly equal to A.
- list("sma(y~x*groups-1)")** Test if several SMA lines forced through the origin share a common slope. This can also be used in combination with the `slope.test` argument or when testing for no shift along common (S)MA lines.

In all cases, estimates and confidence intervals for key parameters are returned, and if a hypothesis test is done, results will be returned and stored in the `slope.test` or `elev.test` output arguments.

The `plot` function can be applied to objects produced using the `sma` and `ma` functions, which is highly recommended to visualise results and check assumptions.

Multiple comparisons If `multcomp=TRUE`, pair-wise comparisons are made between levels of the grouping variable for differences in slope, elevation or shift, depending on the formula used. The P values can be adjusted for multiple comparisons (using the Sidak correction). See also `multcompmatrix` for visualization of the results. **Warning:** When using the multiple comparisons (`multcomp=TRUE`), you must specify a data statement. If your variables are not in a dataframe, simply combine them in a dataframe before calling `sma`.

Value

An object of class `sma` or `ma`, which contains the following output arguments:

- coef** The coefficients of the fitted (standardised) major axes. If several samples are being compared, this will return parameters from the alternative model, e.g. assuming separate slopes if testing for common slope, or assuming common slope but separate elevations if testing for common elevation.
- nullcoef** The coefficients under the null hypothesis
- alpha** As above.
- method** The method used in fitting lines: 'MA' or 'SMA'
- intercept** Whether or not (S)MA lines were forced through the origin (True or False).
- call** The call to the `ma` or `sma` function.
- data** As above.
- log** As above.
- variables** A list of the variables used in fitting (S)MA lines.
- origvariables** A list of the variables prior to transformation (if any) for use in fitting (S)MA lines.
- groups** Levels of the grouping variable, if present in the fit.
- gt** Type of group test ("slopecom", "elevcom", or "shiftcom"), if it was carried out, or "none" if none.

- gtr** The result of that `groupTest`.
- slopetest** Output from the hypothesis test of slope(s), if any. Returned as a list of objects, including the P-value (p), the test statistic (r or LR), the (common) slope (b) and its confidence interval (ci).
- elevtest** Output from the hypothesis test of elevation(s), if any. Returned as a list of objects, including the P-value (p), the test statistic (t or stat), the (common) elevation (a) and its confidence interval (ci).
- slopetestdone** Whether a `slopetest` was actually carried out.
- elevtestdone** Whether an elevation test was actually carried out.
- n** Sample size(s).
- r2** Squared correlation coefficient.
- pval** P-value of the test of correlation coefficient against zero.
- from,to** X values corresponding the maximum and minimum fitted values in each group. Used by `plot.sma` to determine endpoints for fitted lines).
- groupsummary** Neatly organized dataframe with coefficients by group.

Author(s)

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References

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- Warton D. I. and Weber N. C. (2002) Common slope tests for bivariate structural relationships. *Biometrical Journal* **44**, 161–174.
- Warton D. I., Wright I. J., Falster D. S. and Westoby M. (2006) A review of bivariate line-fitting methods for allometry. *Biological Reviews* **81**, 259–291.
- Taskinen S. and Warton D. I. (in press) Robust estimation and inference for bivariate line-fitting in allometry. *Biometrical Journal*.

See Also

[plot.sma](#)

Examples

```
# Load leaf lifetime dataset:
data(leaflife)

### One sample analyses ###
# Extract only low-nutrient, low-rainfall data:
leaf.low <- subset(leaflife, soilp == 'low' & rain == 'low')

# Fit a MA for log(leaf longevity) vs log(leaf mass per area):
```

```

ma(longev ~ lma, log='xy', data=leaflife)

# Test if the MA slope is not significantly different from 1:
ma.test <- ma(longev ~ lma, log='xy', slope.test=1, data=leaflife)
summary(ma.test)

# Construct a residual plot to check assumptions:
plot(ma.test,type="residual")

### Several sample analyses ###

# Now consider low-nutrient sites (high and low rainfall):
leaf.low.soilp <- subset(leaflife, soilp == 'low')

# Fit SMA's separately at each of high and low rainfall sites,
# and test for common slope:
com.test <- sma(longev~lma*rain, log="xy", data=leaf.low.soilp)
com.test

# Plot longevity vs LMA separately for each group:
plot(com.test)

# Fit SMA's separately at each of high and low rainfall sites,
# and test if there is a common slope equal to 1:
sma(longev~lma*rain, log="xy", slope.test=1, data=leaf.low.soilp)

# Fit SMA's with common slope across each of high and low rainfall sites,
# and test for common elevation:
sma(longev~lma+rain, log="xy", data=leaf.low.soilp)

# Fit SMA's with common slope across each of high and low rainfall sites,
# and test for no shift along common SMA:
sma(longev~lma+rain, log="xy", type="shift", data=leaf.low.soilp)

```

summary.sma

Print a summary

Description

Writes a summary of a (standardized) major axis fit.

See [sma](#) for examples.

Usage

```

## S3 method for class 'sma'
summary(object, ...)

```

Arguments

object	Object of class 'sma'.
...	Further arguments ignored.

Author(s)

Remko Duursma, Daniel Falster, David Warton

See Also

[sma, print.sma](#)

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