Package ‘smatr’

April 19, 2009

Version 2.1

Date 2007-01-11

Title (Standardised) Major Axis Estimation and Testing Routines

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Description This package provides methods of 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.

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URL http://web.maths.unsw.edu.au/~dwarton

Repository CRAN

Date/Publication 2007-01-12 08:33:19

R topics documented:

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.

Usage

```
elev.com(y, x, groups, data = NULL, method = 'SMA', alpha = 0.05,
  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`	(optional) data frame containing the data
`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.)
`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. Residual scores can be obtained as y-bx, and for fitted axis scores y+bx (for SMA) or by+lx (for MA or 'lamest'), where b represents the common slope estimate, and l the error variance ratio. 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 common elevation. If residual scores generally differ across groups (with some groups generally having larger residual scores than others) then this is evidence that the groups do not share a common elevation.

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. ⟨David.Warton@unsw.edu.au⟩, translated to R by Ormerod, J. 2005-12-08

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* (in press)

See Also

`line.cis`, `slope.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',]
```

```
slope.com(log10(longev), log10(lma), soilp, data=leaf.low.rain)

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

#Or test for common elevation amongst the MA's of common slope,
#for low rainfall sites, and construct 99
#for the common elevation:
elev.com(log10(longev), log10(lma), soilp, method='MA',
    data = leaf.low.rain, 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

Usage

```
elev.test(y, x, test.value = 0, data = NULL, alpha = 0.05,
    method = 'SMA', 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`	(optional) data frame containing 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.)
`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
`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 usinga t-statistic, comparing the difference between estimated and hypothesised elevation to the standard error of elevation. As described in Warton et al (in review).

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 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

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.

Value

`t`	The test statistic - a t statistic.
`p`	The P-value, taken from the t_{n-2}-distribution. This is an exact test if residuals are normally distributed.
`test.value`	The hypothesised value of the elevation
`a`	The estimated elevation
`ci`	A 100(1-alpha)% CI for the slope.

Author(s)

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

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* (in press)

See Also

`line.cis`, `slope.test`

Examples

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

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

#construct a plot
plot(log10(leaf.low.rain$lma), log10(leaf.low.rain$longev),
   xlab="leaf mass per area [log scale]", ylab="leaf longevity [log scale]")
```

```
#test if the SMA elevation is 0 for leaf longevity vs LMA
elev.test(log10(leaf.low.rain$lma), log10(leaf.low.rain$longev),
   data = leaf.low.rain )

#test if the MA elevation is 2
elev.test(log10(leaf.low.rain$lma), log10(leaf.low.rain$longev),
   data = leaf.low.rain, test.value = 2, method = "MA")
```

`leaflife` *Leaf longevity and leaf mass per area for plant species from different sites*

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

```
data(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` *Leaf mass per area and photosynthetic rate for plant species from different sites*

Description

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

Usage

```
data(leafmeas)
```

Format

A data frame containing 529 rows and 4 variables:

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

spp (factor) Species of the observed plant species

Amass (numeric) Photosynthetic rate per leaf mass ()

lma (numeric) Leaf mass per area (m2/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` *Slope and elevation of a (standardised) major axis, with confidence intervals*

Description

Calculates the slope and elevation of a major axis or standardised major axis, and constructs confidence intervals for the true slope and elevation

Usage

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

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`	(optional) data frame containing the data
`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
`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)
`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.)

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 elvation 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.

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

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.

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. ⟨David.Warton@unsw.edu.au⟩, translated to R by Ormerod, J. 2005-12-08

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* (in press)

See Also

`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
line.cis(log10(longev),log10(lma),data=leaf.low.rain)

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

---

meas.est *Measurement error variance estiamtion 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` — A data frame containing the variables listed in data.meas and id.

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 convariances 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., Wright I. J., Falster D. S. and Westoby M. (2006) A review of bivariate line-fitting methods for allometry. *Biological Reviews* (in press)

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)
```

`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.

Usage

```
shift.com( y, x, groups, data = NULL, method = 'SMA', intercept = TRUE,
   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` (optional) data frame containing the data

`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)

`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. An appropriate residual variable is y-bx, and for fitted axis scores y+bx (for SMA) or by+lx (for MA or 'lamest'), where b represents the common slope estimate, and l the error variance ratio. 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 common elevation. If fitted axis scores systematically differ across groups then this is evidence of a shift along the common axis.

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. ⟨David.Warton@unsw.edu.au⟩, translated to R by Ormerod, J. 2005-12-08

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* (in press)

See Also

`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',]
slope.com(log10(longev), log10(lma), soilp, data=leaf.low.rain)

#Now test for no shift along the axes of common slope, for sites
```

```
#with different soil nutrient levels but low rainfall:
shift.com(log10(longev), log10(lma), soilp, data = leaf.low.rain)

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

Usage

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

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`	(optional) data frame containing the data
`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 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.

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 residuals against fitted axis scores, and by constructing a Q-Q plot* of residuals against a normal distribution. An appropriate residual variable is $y - \hat{\beta}_i \times x$, and for fitted axis scores $y + \hat{\beta}_i x$ (for SMA) or $\hat{\beta}_i y + lx$ (for MA or 'lamest'), where $\hat{\beta}_i$ represents the estimated slope for group i, and l the error variance ratio.

If a plot of residuals against fitted axis scores is produced in which the estimated common slope (b) is used rather than the slopes estimated within each group ($\hat{\beta}_i$), this can be used as a visual test for common slope. 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.

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

Value

`lr`	The (Bartlett-corrected) likelihood ratio statistic testing for common slope
`p`	The P-value of the test. This is calculated assuming that lr has a chi-square distribution with (g-1) df, if there are g groups
`b`	The common slope estimate
`varb`	The sample variance of the common slope
`ci`	A 100(1-alpha)% confidence interval for the common slope
`lambda`	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.
`bs`	The slopes and confidence intervals for data from each group.

Author(s)

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

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* (in press)

See Also

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 <- slope.com(log10(longev), log10(lma), site, data = leaflife)
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',]
slope.com(log10(longev), log10(lma), soilp, data=leaf.low.rain)

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

```
#test for common MA slope, and produce a 90
slope.com(log10(longev), log10(lma), site, data = leaflife,
   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

Usage

```
slope.test(y, x, test.value = 1, data=NULL, method = SMA,
     alpha = 0.05, V = matrix(0,2,2), intercept = TRUE )
```

Arguments

`y` The Y-variable

`x` The X-variable

`test.value` The hypothesised value of the slope (default value is 1)

`data` (optional) data frame containing the data

`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)

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

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.

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

Value

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

Author(s)

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

See Also

`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:
slope.test(log10(longev), log10(lma), data=leaf.low.rain)

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

`smatr` *(Standardised) Major Axis Estimation and Testing Routines*

Description

This package provides methods of 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.

Details

The key functions available in this package are the following.

For one sample:

line.cis fit allometric lines and construct confidence intervals for the true slope and elevation

slope.test test if the slope of an allometric line equals a specific value

elev.test test if the elevation of an allometric line equals a specific value

For several samples:

slope.com test if several major axis or standardised major axis lines share a common slope, and construct a confidence interval for the true common slope

elev.com test if several major axis or standardised major axis lines share a common elevation, and construct a confidence interval for the true common elevation

shift.com test if several groups of observations have no shift in location along major axis or standardised major axis lines with a common slope

Options are available for forcing lines through the origin (where appropriate), and all procedures have the option of correcting for measurement error (although only in an approximate fashion, valid in large samples).

Additional features of this package are listed below.

Measurement error estimation:

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

Example datasets:

leaflife leaf longevity and leaf mass per area for plant species from different sites. Used to demonstrate the functionality of one-sample and multi-sample procedures

leafmeas leaf mass per area and photosynthetic rate for plant species from different sites. Used to demonstrate the meas.est function

For more details, see the documentation for any of the individual functions listed above.

Author(s)

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

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* (in press)

See Also

`line.cis`, `slope.test`, `elev.test`, `slope.com`, `elev.com`, `shift.com`, `meas.est`, `leaflife`, `leafmeas`

Examples

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

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

#construct a plot
plot(log10(leaf.low.rain$lma), log10(leaf.low.rain$longev), xlab='leaf mass per area [lo

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

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

#produce CI's for MA slope and elevation:
line.cis(log10(longev),log10(lma),data=leaf.low.rain, method=2)

#now construct a scatterplot, with different colours for different sites
plot(leaflife$lma,leaflife$longev,type="n",xlab="leaf mass per area [log scale]",ylab="l
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 a common SMA slope amongst species from sites with different rainfall/nutrient
```

```
fit.slopes <- slope.com(log10(longev), log10(lma), site, data = leaflife)

#Test for common SMA slope amongst species at low rainfall sites with different levels c
slope.com(log10(longev), log10(lma), soilp, data=leaf.low.rain)

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

#Now test for no shift along the axes of common slope, for sites with different soil nut
shift.com(log10(longev), log10(lma), soilp, data=leaf.low.rain)

#Test for common major axis slope, and construct 90
slope.com(log10(longev), log10(lma), site, data=leaflife, method="MA", alpha=0.1)

#Test for common elevation amongst the MA's of common slope, for low rainfall sites, and
elev.com(log10(longev), log10(lma), soilp, method="MA", data = leaf.low.rain, alpha=0.01
```

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