

Package ‘deming’

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Title Deming, Theil-Sen, Passing-Bablok and Total Least Squares Regression

Maintainer Terry Therneau <therneau.terry@mayo.edu>

Description

Generalized Deming regression, Theil-Sen regression and Passing-Bablok regression functions.

Imports boot

Priority optional

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LazyData Yes

Author Terry Therneau

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| | |
|----------|---|
| arsenate | <i>Comparison of two assays for arsenate.</i> |
|----------|---|

Description

Arsenate(V) ion in natural river waters, as determined by two assay methods.

Usage

```
data(arsenate)
```

Format

A data frame with 30 observations on the following 4 variables.

aas micrograms/liter, by continuous selective reduction and atomic absorption spectrometry

se.aas estimated standard error of the result

aes micrograms/liter, by non-selective reduction, cold trapping, and atomic emission spectroscopy

se.aes estimated standard error of the result

Source

The data is found in BD Ripley and M Thompson, Regression techniques for the detection of analytical bias, Analyst 112:377-383, 1987.

| | |
|--------|--|
| deming | <i>Fit a generalized Deming regression</i> |
|--------|--|

Description

Find the MLE line relating x and y when both are measured with error. When the variances of x and y are constant and equal, this is the special case of Deming regression.

Usage

```
deming(formula, data, subset, weights, na.action, cv=FALSE,
       xstd, ystd, stdpat, conf=.95, jackknife=TRUE, dfbeta=FALSE,
       id, x=FALSE, y=FALSE, model=TRUE)
```

Arguments

| | |
|-------------|--|
| formula | a model formula with a single continuous response on the left and a single continuous predictor on the right. |
| data | an optional data frame, list or environment containing the variables in the model. |
| subset | an optional vector specifying a subset of observations to be used in the fitting process. |
| weights | an optional vector of weights to be used in the fitting process. Should be NULL or a numeric vector. |
| I | |
| na.action | a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options. The 'factory fresh' default is na.omit, the na.exclude option is often useful. |
| xstd | optional, the variable name of a vector that contains explicit error values for each of the predictor values. This data overrides the cv option if both are present. |
| ystd | optional, the variable name of a vector that contains explicit error values for each of the response values. This data overrides the cv option if both are present. |
| cv | constant coefficient of variation? The default of false corresponds to ordinary Deming regression, i.e., an assumption of constant error. A value of cv=TRUE corresponds to the assumption of constant coefficient of variation. |
| stdpat | pattern for the standard deviation, see comments below. If this is missing the default is based on the cv option. |
| conf | confidence level for the confidence interval |
| jackknife | compute a jackknife estimate of variance. |
| dfbeta | return the dfbeta matrix from the jackknife computation. |
| id | grouping values for the grouped jackknife |
| x, y, model | logicals. If TRUE the corresponding components of the fit (the model frame, the model matrix, or the response) is returned. |

Details

Ordinary least squares regression minimizes the sum of distances between the y values and the regression line, Deming regression minimizes the sum of distances in both the x and y direction. As such it is often appropriate when both x and y are measured with error. A common use is in comparing two assays, each of which is designed to quantify the same compound.

The standard deviation of the x variate will often be of the form $\sigma(c + dx)$ for c and d some constants, where σ is the overall scale factor; similarly for y with constants e and f. Ordinary Deming regression corresponds to c=1 and d=0, i.e., constant variation over the range of the data. A more realistic assumption for many laboratory measurements is c=0 and d=1, i.e., constant coefficient of variation. Laboratory tests are often assumed to have constant coefficient of variation rather than constant variance.

There are 3 ways to specify the variation. The first is to directly set the pattern of (c,d,e,f) for the \$x\$ and \$y\$ standard deviations. If this is omitted, a default of (0,1,0,1) or (1,0,1,0) is chosen, based on whether the cv option is TRUE or FALSE, respectively. As a third option, the user can

specify `xstd` and `ystd` directly as vectors of data values. In this last case any values for the `stdpat` or `ccs` options are ignored. Note that the two calls `deming(y ~ x, cv=TRUE)` and `deming(y ~ x, xstd=x, ystd=y)` are subtly different. In the second the standard deviation values are based on the data, and in the first they will be based on the fitted values. The two outcomes will often be nearly identical.

Although a `cv` option of `TRUE` is often much better justified than an assumption of constant variance, assuming a perfectly constant CV can also be questionable. Most actual biologic assays will have both a constant and a proportional component of error, with the former becoming dominant for values near zero and the latter dominant elsewhere. If all of the results are far from zero, however, the constant part may be ignored.

Many times an assay will be done in duplicate, in which case the paired results can have correlated errors due to sample handling or manipulation that preceeds splitting it into separate aliquots for assay, and the ordinary variance will be too small (as it also is when the duplicate values are averaged together before fitting the regression line.) A correct grouped jackknife estimate of variance is obtained in this case by setting `id` to a vector of sample identifiers.

Value

a object of class 'deming' containing the components:

| | |
|--------------------------|--|
| <code>coefficient</code> | the coefficient vector, containing the intercept and slope. |
| <code>variance</code> | The jackknife or bootstrap estimate of variance |
| <code>ci</code> | bootstrap confidence intervals, if <code>nboot > 0</code> |
| <code>dfbeta</code> | optionally, the <code>dfbeta</code> residuals. A 2 column matrix, each row is the change in the coefficient vector if that observation is removed from the data. |

Author(s)

Terry Therneau

References

BD Ripley and M Thompson, Regression techniques for the detection of analytical bias, *Analyst* 112:377-383, 1987.

K Linnet, Estimation of the linear relationship between the measurements of two methods with proportional errors. *Statistics in Medicine* 9:1463-1473, 1990.

Examples

```
# Data from Ripley and Thompson
fit <- deming(aes ~ aas, data=arsenate, xstd=se.aas, ystd=se.aes)
print(fit)
## Not run:
      Coef se(coef) lower 0.95 upper 0.95
Intercept 0.1064  0.2477  -0.3790   0.5919
Slope      0.9730  0.1430   0.6928   1.2532

Scale= 1.358
```

```
## End(Not run)
plot(1:30, fit$dfbeta[,2]) #subject 22 has a large effect on the slope

# Constant proportional error fit (constant CV)
fit2 <- deming(new.lot ~ old.lot, ferritin, cv=TRUE,
               subset=(period==3))
```

ferritin

Validation of a ferritin assay

Description

For each of seven periods in which there was a new batch of reagent, a small set of patient samples was assayed for ferritin content using both the old and new batches.

Usage

```
data(ferritin)
```

Format

A data frame with 162 observations on the following 4 variables.

```
sample  sample identifier
period  the transition number, 1 to 7
old.lot  assay result using the old lot of the reagent
new.lot  assay result using the new lot
```

Details

The samples from each period are distinct. In the second data set `ferritin2` outliers have been added to the data for period 2, excess noise added to one lot in period 4, and deterministic laboratory error to period 6.

Source

Blinded data from a clinical laboratory.

Examples

```
data(ferritin)
temp <- ferritin[ferritin$period < 4,]
plot(temp$old.lot, temp$new.lot, type='n', log='xy',
      xlab="Old lot", ylab="New Lot")
text(temp$old.lot, temp$new.lot, temp$period,
      col=temp$period)
```

pbreg

*Passing-Bablok regressin***Description**

Passing-Bablok regression is a robust regression method for two variables that is symmetric in x and y .

Usage

```
pbreg(formula, data, subset, weights, na.action, conf=.95,
      nboot = 0, method=1, eps=sqrt(.Machine$double.eps),
      x = FALSE, y = FALSE, model = TRUE)
```

Arguments

| | |
|-------------|---|
| formula | a model formula with a single continuous response on the left and a single continuous predictor on the right. |
| data | an optional data frame, list or environment containing the variables in the model. |
| subset | an optional vector specifying a subset of observations to be used in the fitting process. |
| weights | an optional vector of weights to be used in the fitting process. Should be NULL or a numeric vector. |
| I | |
| na.action | a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options. The 'factory fresh' default for R is na.omit, the na.exclude option is often useful. |
| conf | the width of the computed confidence limit |
| nboot | number of bootstrap samples used to compute standard errors and/or confidence limits. |
| method | which of 3 related methods to use for the computation |
| eps | the tolerance used to detect tied values in x and y |
| x, y, model | logicals. If TRUE the corresponding components of the fit (the model frame, the model matrix, or the response) is returned. |

Details

There are 3 related estimators under this heading. Method 1 is the original Passing-Bablok (1983) method, which is equal to a Theil-Sen estimate symmetric about the $y=x$ line. Method 2 is the first extended method of the 1988 paper, designed to be scale invariant. Method 3 is the second extended method from the 1985 paper, the "scissors" estimate which is symmetric about both the x and y axes, and is also scale invariant.

The default confidence interval estimate is based on that derived by Sen, which is in turn based on the relationship to Kendall's tau. A theoretical justification of this approach for methods 2 and 3 is lacking, and we recommend a bootstrap based confidence interval based on 500-1000 replications.

Value

pbreg returns an object of class "pbreg". The generic accessor functions `coef`, `fitted` and `residuals` extract the relevant components.

Author(s)

Terry Therneau

References

Passing, H. and Bablock, W. (1983). A new biometrical procedure for testing the equality of measurements from two different analytical methods. Application of linear regression procedures for method comparison studies in Clinical Chemistry, Part I. J. Clin. Chem. Clin. Biochem. 21:709-720.

Passing, H. and Bablock, W. (1984). Comparison of several regression procedures for method comparison studies and determination of sample size. Application of linear regression procedures for method comparison studies in Clinical Chemistry, Part II. J. Clin. Chem. Clin. Biochem. 22:431-435.

Bablock, W., Passing, H., Bender, R. and Schneider, B. (1988). A general regression procedure for method transformations. Application of linear regression procedures for method comparison studies in Clinical Chemistry, Part III. J. Clin. Chem. Clin. Biochem. 26:783-790.

See Also

[deming](#)

Examples

```
afit1 <- pbreg(aes ~ aas, data= arsenate)
afit2 <- pbreg(aas ~ aes, data= arsenate)
rbind(coef(afit1), coef(afit2)) # symmetric results
1/coef(afit1)[2]
```

theilsen

Theil-Sen regression

Description

Thiel-Sen regression is a robust regression method for two variables. The symmetric option gives a variant that is symmetric in x and y.

Usage

```
theilsen(formula, data, subset, weights, na.action, conf=.95,
  nboot = 0, symmetric=FALSE, eps=sqrt(.Machine$double.eps),
  x = FALSE, y = FALSE, model = TRUE)
```

Arguments

| | |
|-------------|---|
| formula | a model formula with a single continuous response on the left and a single continuous predictor on the right. |
| data | an optional data frame, list or environment containing the variables in the model. |
| subset | an optional vector specifying a subset of observations to be used in the fitting process. |
| weights | an optional vector of weights to be used in the fitting process. |
| na.action | a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options. |
| conf | the width of the computed confidence limit. |
| nboot | number of bootstrap samples used to compute standard errors and/or confidence limits. If this is 0 or missing then an asymptotic formula is used. |
| symmetric | compute an estimate whose slope is symmetric in x and y. |
| eps | the tolerance used to detect tied values in x and y |
| x, y, model | logicals. If TRUE the corresponding components of the fit (the model frame, the model matrix, or the response) is returned. |

Details

One way to characterize the slope of an ordinary least squares line is that $\rho(x, r) = 0$, where ρ is the correlation coefficient and r is the vector of residuals from the fitted line. Thiel-Sen regression replaces ρ with Kendall's τ , a non-parametric alternative. It is resistant to outliers while retaining good statistical efficiency.

The symmetric form of the estimate is based on solving the inverse equation: find that rotation of the original data such that $\tau(x, y) = 0$ for the rotated data. (In a similar fashion, the rotation such that the least squares slope is zero yields Deming regression.) In this case it is possible to have multiple solutions, i.e., slopes that yield a 0 correlation, although this is rare unless the deviations from the fitted line are large.

The default confidence interval estimate is based on the result of Sen, which is in turn based on the relationship to Kendall's tau and is essentially an inversion of the confidence interval for tau. The argument does not extend to the symmetric case, for which we recommend using a bootstrap confidence interval based on 500-1000 replications.

Value

theilsen returns an object of class "theilsen" with components

| | |
|--------------|--|
| coefficients | the intercept and slope |
| residuals | residuals from the fitted line |
| angle | if the symmetric option is chosen, this contains all of the solutions for the angle of the regression line |
| n | number of data points |
| model, x, y | optional components as specified by the x, y, and model arguments |
| terms | the terms object corresponding to the formula |

na.action na.action information, if applicable
call a copy of the call to the function

The generic accessor functions `coef`, `residuals`, and `terms` extract the relevant components.

Author(s)

Terry Therneau

References

Thiel, H. (1950), A rank-invariant method of linear and polynomial regression analysis. I, II, III, *Nederl. Akad. Wetensch., Proc.* 53: 386-392, 521-525, 1397-1412.

Sen, P.B. (1968), Estimates of the regression coefficient based on Kendall's tau, *Journal of the American Statistical Association* 63: 1379-1389.

See Also

[deming](#), [pbreg](#)

Examples

```
afit1 <- theilsen(aes ~ aas, symmetric=TRUE, data= arsenate)
afit2 <- theilsen(aas ~ aes, symmetric=TRUE, data= arsenate)
rbind(coef(afit1), coef(afit2)) # symmetric results
1/coef(afit1)[2]
```

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