

pcor.test

R Documentation

Partial Correlation

Description

Calculate the partial correlation coefficient of both of parametric ("Pearson") and non-parametric ("Spearman" and "Kendall") statistics.

Usage

```
pcor.test(x, y, z, use = c("mat", "rec"), method = c("pearson", "spearman", "kendall
```

Arguments

x a numeric vector. Missing values are allowed.
y a numeric vector. Missing values are allowed.
z a numeric vector, matrix or data frame. Missing values are allowed.
use an optional character string giving a method for computing the partial correlation coefficients. This must be one of the strings "mat" (default) or "rec".
method a character string indicating which partial correlation coefficient is to be computed. One of "pearson" (default), "kendall", or "spearman", can be abbreviated.
na.rm logical. Should missing values be removed? Default is `True`

Values

`estimate` gives the partial correlation coefficient between `x` and `y` given `z`, `p.value` gives the p-value of the test, `statistic` gives the value of the test statistic, `n` gives the number of samples after deleting all the missing samples, `gn` gives the number of given variables, `Method` gives the correlation method used, and `Use` gives the computation method used.

Details

Partial correlation is the correlation of two variables while controlling for a third or more other variables. There are two methods to compute the partial correlation coefficient in `pcor.test`. One is by using variance-covariance matrix ("mat") and the other recursive formula ("rec"). Both of "mat" and "rec" give the same result in case of `na.rm = T`. Otherwise, the `estimate` may be slightly different from each other due to the way dealing with the missing samples, if there are the missing samples.

References

Kim, S-H. and Yi, S. (2007) [Understanding relationship between sequence and functional evolution in yeast proteins](#). *Genetica*, In press.

Kim, S-H. and Yi, S. (2006) [Correlated asymmetry between sequence and functional divergence of duplicate proteins in *Saccharomyces cerevisiae*](#). *Molecular Biology and Evolution*, **23**: 1068–1075.

Johnson, Richard A. and Dean W. Wichern (2002) *Applied multivariate statistical analysis*. Prentice Hall.

Whittaker, Joe (1990) *Graphical models in applied multivariate statistics*. John Wiley & Sons.

See Also

`cor`, `cov2cor`, `eigen`, `cor.test`

Example

```
# load the R code "pcor.test"
source("pcor.R")

# data
y.data <- data.frame(
  hl=c(7,15,19,15,21,22,57,15,20,18),
  disp=c(0.000,0.964,0.000,0.000,0.921,0.000,0.000,
  deg=c(9,2,3,4,1,3,1,3,6,1),
  BC=c(1.78e-02,1.05e-06,1.37e-05,7.18e-03,0.00e+00
)

# partial correlation between "hl" and "disp" given "deg" and "BC"
pcor.test(y.data$hl,y.data$disp,y.data[,c("deg","BC")])
pcor.test(y.data[,1],y.data[,2],y.data[,c(3:4)])
pcor.test(y.data[,1],y.data[,2],y.data[, -c(1:2)])
```

Download

[pcor.R](#)

[R code *pcor.test*]