

Package ‘nopaco’

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Type Package

Title Non-Parametric Concordance Coefficient

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Description A non-parametric test for multi-observer concordance and differences between concordances in (un)balanced data.

License GPL (>= 3)

Depends R (>= 3.5.0)

Imports methods, Matrix (>= 1.1.5), parallel, stats

Suggests MASS

RoxygenNote 7.3.2

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coef	<i>Extract test results from the results of a concordance.test</i>
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Description

coef extract the test results from the results of a concordance.test

Usage

```
## S4 method for signature 'ConcordanceTest'
coef(object, ...)
```

Arguments

object	An object of ConcordanceTest-class
...	Not used

Value

A matrix

See Also

Other concordance functions: [concordance.test\(\)](#), [getPsi\(\)](#), [rfromPsi\(\)](#)

Examples

```
matRandom <- matrix(rnorm(3*20),20,3)
testResult <- concordance.test(matRandom)
getPsi(testResult)
coef(testResult)
```

concordance.test *Perform a nonparametric concordance test.*

Description

concordance.test performs a test for a random concordance (if a single matrix is given) or tests for equal concordance between two matrices.

Usage

```
concordance.test(x, y = NULL, alternative = NULL, alpha = 0.05, ...)
```

Arguments

x	a numeric matrix, subjects in the rows, repeated measurements in the columns
y	(optional) a numeric matrix of equal size as argument x
alternative	"less", "greater" or "two.sided". Only used when y is given.
alpha	significance level (default = 0.05)
...	see details

Details

- Testing the deviation from random concordance: if only one matrix is given (i.e. argument x), its concordance will be tested against the alternative hypothesis of finding a higher concordance under random sampling conditions. For small matrices (depending on number of replicate measurements) an exact method will be used to determine a p-value. In case of larger matrices, where the exact approach is not feasible, either the revised-beta approach (default), a beta approximation, or a normal approximation is used. To enforce the use of either one method, the method argument can be used with value "exact", "Rbeta", "beta" or "normal".
- Testing for a difference between concordances: if both arguments x and y have been given, the equality of concordances of both matrices is tested. The default alternative hypothesis is 'two.sided'. Both matrices must be of equal size and have corresponding missing entries (NA values). In case of missing data in one matrix, the same entries in the other matrix will also be set to missing. This method involves bootstrapping to estimate variance and confidence estimates, with adjustable options via the global R options "nopaco.nCPU" (default=2), "nopaco.nDraws.CI" (default=1e4) and "nopaco.seed" (default = 1).

Unbalanced data due to randomly missing data or an unequal number of repeated measurements per subject is allowed. In that case, missing or unknown values must be set to NA.

Value

An object of [ConcordanceTest-class](#)

References

P.Rothery (1979) *Biometrika* 66(3):629-639

See Also

Other concordance functions: [coef\(\)](#), [getPsi\(\)](#), [rfromPsi\(\)](#)

Examples

```
require(MASS) ##to use the 'mvrnorm' function

#Generate a matrix without concordance
# for three observers in two samples
matRandom <- matrix(rnorm(3*20),20,3)
concordance.test(matRandom)

#Generate a corresponding matrix with strong concordance
sigma<-matrix(0.8,3,3)
diag(sigma)<-1
matConcordant <- mvrnorm(20,mu=rep(0,3),Sigma=sigma)
concordance.test(matConcordant)

#Test concordances between the two matrices
aTest <- concordance.test(matConcordant, matRandom)

getPsi(aTest)
coef(aTest)
```

ConcordanceTest-class *Class ConcordanceTest*

Description

This class stores results obtained from a concordance test.

Details

Class ConcordanceTest stores results from a concordance test.

Slots

pvalue The pvalue
 psi1 The concordance in matrix x
 psi2 The concordance in matrix y
 method The method used to obtain the pvalue
 alternative The alternative hypothesis
 ci.lower The lower confidence boudary
 ci.upper The upper confidence boudary
 ci.method The method used to obtain the confidence interval
 alpha The significance level
 call The call made to the [concordance.test](#) function

getPsi *Obtain concordance coefficients.*

Description

getPsi returns the concordance coefficient(s) from a matrix or a result obtained by the [concordance.test](#) function.

Usage

```
getPsi(x, y, ...)  
  
## S4 method for signature 'ConcordanceTest,missing'  
getPsi(x)  
  
## S4 method for signature 'matrix,missing'  
getPsi(x, y, ...)  
  
## S4 method for signature 'data.frame,missing'  
getPsi(x, y, ...)  
  
## S4 method for signature 'data.frame,data.frame'  
getPsi(x, y, ...)  
  
## S4 method for signature 'matrix,NULL'  
getPsi(x, y, ...)  
  
## S4 method for signature 'matrix,matrix'  
getPsi(x, y, ...)
```

Arguments

x	A numeric matrix or an object ConcordanceTest-class
y	A numeric matrix (optional)
...	Not used

Value

A numeric vector with coefficient(s)

References

P.Rothery (1979) *Biometrika* 66(3):629-639

See Also

Other concordance functions: [coef\(\)](#), [concordance.test\(\)](#), [rfromPsi\(\)](#)

Examples

```
matRandom <- matrix(rnorm(30),10,3)
testResult <- concordance.test(matRandom)
getPsi(testResult)
getPsi(matRandom)
```

names,ConcordanceTest-method

Extract argument names from a ConcordanceTest object

Description

names extracts argument names from a [ConcordanceTest-class](#) object

Usage

```
## S4 method for signature 'ConcordanceTest'
names(x)
```

Arguments

x An object of [ConcordanceTest-class](#)

Value

A character vector

Examples

```
matRandom <- matrix(rnorm(3*20),20,3)
testResult <- concordance.test(matRandom)
names(testResult)
```

rfromPsi

Conversion between Pearson correlation and the non paramtric concordance coefficient

Description

Conversion between Pearson correlation and the non paramtric concordance coefficient

Usage

```
rfromPsi(psi)

psifromR(r)
```

Arguments

psi a (vector of) non paramtric concordance coefficient(s)
 r a (vector of) Pearson correlation coefficient(s)

Details

The conversion is performed following the relationship described by Rothery (1979). $2*\cos(\pi*(1-\psi))-1$

Value

A (vector of) corresponding Pearson correlation coefficient(s).

References

Rothery, P. 'A nonparametric measure of intraclass correlation', *Biometrika*, 66, 3, 629-639 (1979).

See Also

Other concordance functions: [coef\(\)](#), [concordance.test\(\)](#), [getPsi\(\)](#)

Examples

```
#Generate a matrix without concordance
matRandom <- matrix(rnorm(30),10,3)
result<-concordance.test(matRandom)
getPsi(result) #concordance coefficient
result$ci      #95% confidence interval

#Corresponding Pearson correlation
rfromPsi(getPsi(result))
rfromPsi(result$ci)

#Plot the relation between Pearson correlation and the nonparamatric concordance coefficient.
r<-seq(-1,1,0.01)
psi<-psifromR(r)
plot(r,psi,type='l',xlab="Pearson correlation", ylab="nonparametric concordance")
```

 scores

Hypothetical data of outcomes for two risk models

Description

This data is generated as explained in the nopaco vignette. It represents the outcomes of the risk models (model A and model B). Both models were applied to gene expression profiles 100 subjects, each run in duplo.

Usage

```
data(scores)
```

Format

A list with two elements named 'modelA' and 'modelB' both containing a dataframe with outcome scores for 100 subjects in the rows each having two replicate measurements in the columns.

Source

```
vignette("nopaco", package = "nopaco")
```

Examples

```
data(scores)
str(scores)
plot(scores[['modelA']])
plot(scores[['modelB']])
```

\$, *ConcordanceTest*-method

Extract argument values from a ConcordanceTest object

Description

Extracts argument values from a [ConcordanceTest-class](#) object

Usage

```
## S4 method for signature 'ConcordanceTest'
x$name
```

Arguments

x	An object of ConcordanceTest-class
name	The argument to get the value of

Value

The value of the requested argument

Examples

```
matRandom <- matrix(rnorm(3*20),20,3)
testResult <- concordance.test(matRandom)
names(testResult)
testResult$psi
```

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