Package: Interatrix (via r-universe)

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Type Package

Title Compute Chi-Square Measures with Corrections

Version 1.1.5

Description Chi-square tests are computed with corrections.

Depends R (>= 2.14)

Imports graphics, grDevices, MASS, stats, tcltk, tools, utils

Suggests doParallel, foreach, quarto

License GPL (>= 2)

Encoding UTF-8

URL https://github.com/lbbe-software/Interatrix

BugReports https://github.com/lbbe-software/Interatrix/issues

VignetteBuilder quarto

Repository https://lbbe-software.r-universe.dev

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Contents

chi2Corr 2
chi2CorrAge 3
dataInteratrix 5
Interatrix-internal 5
InteratrixGUI 6

Index **7**

chi2Corr *Searches for parasite interactions taking risk factors into account.*

Description

This function implements a method to correct for shared risk factors in the search for interactions. It provides the observed chi-square value, a measure of association between two parasites, and simulates bootstrapped data taking risk factors into account.

Usage

```
chi2Corr(formula, data.obs, namepara1, namepara2, nsimu)
```

Arguments

formula	a string of characters indicating a symbolic description of the model of shared risk factors to be fitted without any response variable
data.obs	the name of the data set to be used
namepara1	the name of the column giving the status to the first parasite
namepara2	the name of the column giving the status to the second parasite
nsimu	an integer indicating the number of repetitions for the bootstrap simulation

Value

The value returned is a list containing:

formula	the model fitted without any response variable
time	duration in seconds of the simulations
chi2.corr.obs	the Pearson's chi2 statistic calculated on data.obs
dispcoeff	the estimated coefficient of over- (or under-) dispersion, defined as the mean of the bootstrapped values of the corrected chi-square.
pval1	p-value of the corrected chi-square test under the null hypothesis of independence of the two parasites. pval1 was estimated assuming that the corrected chi-square is proportional to a chi-square with one degree of freedom.
pval2	p-value of the corrected chi-square test under the null hypothesis of independence of the two parasites. pval2 was given by the proportion of bootstrapped corrected chi-squares smaller than the observed value (chi2.corr.obs).
tab.th	expected frequencies, ie. the contingency table calculated on the theoretical (bootstrapped) data
tab.obs	observed frequencies, ie. the contingency table calculated on data.obs
chi2.corr.sim	a vector containing the nsimu Pearson's chi2 statistics calculated on simulated data.

The distribution of the bootstrapped corrected chi-squares (an histogram) is also provided.

Note

pval2 is better than pval1 but requires running enough simulations, wich may be long in some cases. pval1 allows working with smaller numbers of simualtions when simulation times are too long.

References

True versus False Parasite Interactions: A Robust Method to Take Risk Factors into Account and Its Application to Feline Viruses. Hellard E., Pontier D., Sauvage F., Poulet H. and Fouchet D. (2012). PLoS ONE 7(1): e29618. doi:10.1371/journal.pone.0029618.

Examples

```
## Not run:
  library(Interatrix)
  data(dataInteratrix)
  res1 <- chi2Corr("F1+F2*F3+F4", dataInteratrix, "Parasite1", "Parasite2", 500)

## End(Not run)
```

---

chi2CorrAge *Searches for parasite interactions taking the cumulative effect of age and other risk factors into account.*

Description

This function implements a method to correct for the cumulative effect of age and for other potentially confounding risk factors in the search for interactions. It provides the observed chi-square value, a measure of the association between two parasites, and simulates bootstrapped data taking risk factors into account.

Usage

```
chi2CorrAge(formula, data.obs, namepara1, namepara2, nameage, w1, w2, mort, a,
nsimu, nbcore = 3)
```

Arguments

formula	a string of characters indicating a symbolic description of the model of shared risk factors (including age) to be fitted without any response variable
data.obs	the name of the data set to be used
namepara1	the name of the column giving the status to the first parasite
namepara2	the name of the column giving the status to the second parasite
nameage	the column name of the age classes
w1	a real number between 0 and 1 indicating the antibodies' disappearance rate of the first studied parasite

w2	a real number between 0 and 1 indicating the antibodies' disappearance rate of the second studied parasite
mort	a vector of real numbers between 0 and 1 giving the mortality rates of all age classes
a	a vector of integers giving the bounds of the age classes
nsimu	an integer indicating the number of repetitions for the bootstrap simulation
nbcore	an integer indicating the number of cores available on the computer to set up a parallel calculation

Value

The value returned is a list containing:

formula	the model fitted without any response variable
time	duration in seconds of the simulations
nbcore	the number of cores used for parallel simulations
chi2.corr.obs	the Pearson's chi2 statistic calculated on data.obs
pval	p-value of the corrected chi-square test under the null hypothesis of independence of the two parasites. pval was given by the proportion of bootstrapped corrected chi-squares smaller than the observed value (chi2.corr.obs).
tab.th	expected frequencies, ie. the contingency table calculated on the theoretical (bootstrapped) data
tab.obs	observed frequencies, ie. the contingency table calculated on data.obs
chi2.corr.sim	a vector containing the nsimu Pearson's chi2 statistics calculated on simulated data.

The distribution of the bootstrapped corrected chi-squares (an histogram) is also provided.

References

Unknown age in health disorders: a method to account for its cumulative effect and an application to feline viruses interactions. Hellard E., Pontier D., Siberchicot A., Sauvage F. and Fouchet D. (2015). Epidemics 11: 48-55. doi:10.1016/j.epidem.2015.02.004.

Examples

```
## Not run:
  library(Interatrix)
  data(dataInteratrix)
 res2 <- chi2CorrAge("F1+F2+AGE", dataInteratrix, "Parasite1", "Parasite2", "AGE", w1 = 0,
    w2 = 0, mort = c(0.2, 0.2, 0.2), a = c(0, 1, 2, 10), nsimu = 500, nbcore = 2)

## End(Not run)
```

dataInteratrix *A generated data set for test*

Description

A generated data set provided to test the `Interatrix` package.

Usage

```
data(dataInteratrix)
```

Format

A data frame with 100 observations for the following variables:

`F1` a numeric vector containing a factor with three modalities

`F2` a numeric vector containing a continuous variable

`F3` a numeric vector containing a factor with two modalities

`F4` a numeric vector containing a continuous variable

`Parasite1` a numeric vector containing the serological status to the first parasite

`Parasite2` a numeric vector containing the serological status to the second parasite

`AGE` a numeric vector containing a factor with three modalities indicating the age classes

Examples

```
data(dataInteratrix)
```

Interatrix-internal *Internal functions for the Interatrix package.*

Description

Internal functions for the Interatrix package.

Details

list2ascii(x,file = paste(deparse(substitute(x)), ".txt", sep = ""))

internal functions for chi2Corr() and chi2CorrGUI()
obsdata_chi2corr(formula, data, name1, name2)
chi2corrboot(data, formula, sero1, sero2)
simudata_chi2corr(formula, data, name1, name2, nbsimu, pvir1, pvir2, chi2corrobs)

internal functions for chi2CorrAge() and chi2CorrAgeGUI()

SensTransMatrix(para, listmodel, rate, agenum, a)
EstimParam(paranum, rate, listmodel, agenum, v0, tol = 0.00000001, maxit = 50000, a, mort)
ModelClass(para, formula, data, agemax, nameage)
calcInfectProba(data, formula, namepara1, namepara2, nameage, w1, w2, mort, a, v0para1, v0para2)
obsdata_chi2corrage(formula, data, name1, name2, nameage, w1, w2, mort, a, v0para1, v0para2)
simudata_chi2corrage(formula, data, name1, name2, nameage, w1, w2, mort, a, v0para1, v0para2, matprobainfect)

`InteratrixGUI` *Function to start the graphical interface*

Description

This function opens a graphical interface and helps step by step to compute corrected chi-square tests.

Usage

```
InteratrixGUI()
```

Value

A first interactive graphical interface is opened to choose between two methods. When all parameters are defined by the user, simulation results are printed to the R console, saved in a file and plotted as an histogram.

Index

∗ **datasets**
dataInteratrix, 5
∗ **hplot**
chi2Corr, 2
chi2CorrAge, 3
InteratrixGUI, 6
∗ **htest**
chi2Corr, 2
chi2CorrAge, 3
InteratrixGUI, 6
∗ **interface**
chi2Corr, 2
chi2CorrAge, 3
InteratrixGUI, 6
∗ **print**
chi2Corr, 2
chi2CorrAge, 3
InteratrixGUI, 6
∗ **utilities**
Interatrix-internal, 5

calcInfectProba *(*Interatrix-internal*)*, 5
chi2Corr, 2
chi2CorrAge, 3
chi2corrboot *(*Interatrix-internal*)*, 5

dataInteratrix, 5

EstimParam *(*Interatrix-internal*)*, 5

Interatrix-internal, 5
InteratrixGUI, 6

list2ascii *(*Interatrix-internal*)*, 5

ModelClass *(*Interatrix-internal*)*, 5

obsdata_chi2corr *(*Interatrix-internal*)*, 5
obsdata_chi2corrage *(*Interatrix-internal*)*, 5

SensTransMatrix *(*Interatrix-internal*)*, 5
simudata_chi2corr *(*Interatrix-internal*)*, 5
simudata_chi2corrage *(*Interatrix-internal*)*, 5