Package ‘Interatrix’

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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

NeedsCompilation no

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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