Package 'CPCAT'

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Title The Closure Principle Computational Approach Test

Version 1.0.0

Description P-values and no/lowest observed (adverse) effect concentration values derived from the closure principle computational approach test (Lehmann, R. et al. (2015) <doi:10.1007/s00477-015-1079-4>) are provided. The package contains functions to generate intersection hypotheses according to the closure principle (Bretz, F., Hothorn, T., Westfall, P. (2010) <doi:10.1201/9781420010909>), an implementation of the computational approach test (Ching-Hui, C., Nabendu, P., Jyh-Jiuan, L. (2010) <doi:10.1080/03610918.2010.508860>) and the combination of both, that is, the closure principle computational approach test.

License GPL (>= 3)

Depends R (>= 2.10)

Imports stats

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Encoding UTF-8

LazyData true

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Contents

CPCAT   *Performs the closure principle computational approach test (CPCAT).*

Description

Performs the closure principle computational approach test (CPCAT).

Usage

```
CPCAT(z, M = 10000)
```

Arguments

z   The data set to be used. One column of z must contain the numeric Poisson
             data and one must contain the factor variable. The first level of the factor vari-
             able is assumed to be the control group. Factor levels (i.e., groups) should be in
             ascending order (e.g. increasing concentration of a test substance). If the data
             frame contains more than one numeric column and/or more than one factor vari-
             able the CPCAT is applied to the first numeric column and the corresponding
             Poisson data are grouped according the first factor variable.

M   The number of parametric bootstrap simulations. Defaults to M=10000.

Value

A p-value for each main hypotheses H_0i: mu_0=mu_i "control vs. treatment i".

Examples

```
data(testdata)
CPCAT(testdata)
CPCAT(z=testdata)
CPCAT(z=testdata, M=1000)
```

---

hypotheses	*Create main hypotheses and intersection hypotheses.*

Description

Create main hypotheses and intersection hypotheses.

Usage

```
hypotheses(n)
```

Arguments

n	The number of treatments exclusive of the control group. That is, if we have, e.g., a control group and 3 treatments choose n=3.

Value

A contrast matrix reflecting all main and intersection hypotheses induced by the closure principle (CP). Please note that the leading column of treatment 0 (i.e., the control group) is not displayed because it always contains only ones.

Examples

```
hypotheses(3)
hypotheses(n=2)
```

---

poisson.sub.test	*Perform a computational approach test (CAT).*

Description

Perform a computational approach test (CAT).

Usage

```
poisson.sub.test(dat, contrast, M = 10000)
```

Arguments

dat	A list. The first list element contains the Poisson data of the control group, the second list element contains the Poisson data of the first treatment group etc..
contrast	A matrix consisting of one row and ncol=number of treatments. The values must be either 0 or 1. 1 (0) includes (excludes) the corresponding treatment from the CAT procedure. For example consider 1 control group and 4 treatment groups. For testing H0: mu_0=mu_1=mu_4 choose contrast=matrix(c(1,0,0,1),nrow = 1).
M	The number of parametric bootstrap simulations. Defaults to M=10000.

Value

A p-value for testing one intersection hypothesis.

Examples

```
data(testdata)
#Extract the group names from testdata.
conc<-unique(testdata[,2]) #concentration levels of the test data
#Extract the number of treatment groups.
N=length(conc)-1
#Devide the testdata into a list where the first element contains
#the Poisson data of the control group and the following contain
#the Poisson data of the treatment groups, respectively.
dat<-list()
#Create the final list.
for(j in 1:length(conc)){
index<-which(testdata[,2]==conc[j])
dat[[j]]<-testdata[index,]
}
#Show the data list.
dat
#Generate the intersection hypotheses of H01: mu_0=mu_1 using the
#hypotheses function.
C=hypotheses(N)[[1]]
#Show the first intersection hypothesis.
C[1,]
#Test the first intersection hypothesis.
poisson.sub.test(dat=dat,contrast=C[1,],M=10000)
```

---

poisson.test	*Perform the closure principle computational approach test (CPCAT)* *for one main hypothesis H0i: mu_0=mu_i.*

Description

Perform the closure principle computational approach test (CPCAT) for one main hypothesis H0i: mu_0=mu_i.

Usage

```
poisson.test(Data, contrastmatrix, M = 10000)
```

Arguments

Data	The data matrix.
contrastmatrix	The contrasts according to the closure principle induced intersection hypotheses.
M	The number of parametric bootstrap simulations. Defaults to M=10000.

Value

The set of p-values according to the intersection hypotheses and the maximum p-value.

Examples

```
#Consider a data set of one control group and 3 treatment groups
data(testdata2)
#Test the main hypothesis H0: mu_0=mu_1 using M=10000
#simulation runs
C=hypotheses(3)[[1]] #Generate the set of intersection hypotheses
#according to H0
poisson.test(testdata2,contrastmatrix=C,M=10000)
```

---

testdata *Description of testdata*

Description

The data set testdata contains two variables.

Usage

```
testdata
```

Format

A data frame with 20 rows and 2 variables:

Poissondata Contains 20 realizations of Poisson distributed random variables.

group Contains the group names of the Poisson data.

Source

Artificial example data.

Examples

```
data(testdata)    #Lazy loading of the test data. To view the data type testdata.
```

---

testdata2   *Description of testdata2*

Description

The data set testdata2 contains two variables.

Usage

```
testdata2
```

Format

A data frame with 16 rows and 2 variables:

Poissondata Contains 16 realizations of Poisson distributed random variables.

group Contains the group names of the Poisson data.

Source

Artificial example data.

Examples

```
data(testdata2)    #Lazy loading of the test data. To view the data type testdata.
```

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