Package 'scccna'

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Type Package

Title Sufficient Condition Conjunction Algorithm Based on CNA

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Description Pkg{scccna} is a package to perform the Sufficient Condition Conjunction Algorithm Based on CNA.

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Imports plyr,purrr,stringr,cna,admisc,dplyr

NeedsCompilation no

R topics documented:

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scccna-package	*Sufficient Condition Conjunction Algorithm Based on CNA*

Description

Pkgscccna is a package to perform the Sufficient Condition Conjunction Algorithm Based on CNA.

Author(s)

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References

Baumgartner, Michael.(2009). Inferring Causal Complexity. Sociological Methods &amp Research. 38. 10.1177/0049124109339369.

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bocorrection	*Bonferroni correction for the Chi-squared test.*

Description

This function corrects Pearson's Chi-squared test by bonferroni correction.

Usage

```
bocorrection(screencom,pvaluevec,numofsnps)
```

Arguments

screencom	the snp combination.
pvaluevec	the p-value of Pearson's Chi-squared test.
numofsnps	the number of SNPs.

Value

A numeric value of pvalue in the pearsons chisquared by bonferroni correction..

References

Benjamini, Y. and D. Yekutieli (2001). The control of the false discovery rate in multiple testing under dependency. The Annals of Statistics. 29: 1165-1188.

Examples

```
library(purrr)
library(plyr)
library(stringr)
snps<-data.frame(
V1=c(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1),
V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3)
)
class<-c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
screencom<-c(3,4)
pvalue<-chi2test(screencom,snps,class)
numofsnps<-ncol(snps)
pvaluewithbc<-bocorrection(screencom,pvalue,numofsnps)
```

---

chi2test   *Chisquaretest for the Pattern in the Source Data*

Description

This function tests whether the pattern is related to the depend variable in the source dataset by Pearson's Chi-squared test.

Usage

```
chi2test(factor,snps,class)
```

Arguments

factor   the snp combination.

snps   the snps matrix,0 denotes the missing data,1 denotes homozygous wild-type al-
                    leles, 2 denotes homozygous wild-type alleles,3 denotes homozygous mutant
                    alleles.

class   the disease vector,1 denotes case and 2 denotes control.

Value

A numeric value of pvalue in the Pearsons Chi-squared test.

References

Haviland MG. Yates's correction for continuity and the analysis of 2 x 2 contingency tables. Stat Med. 1990 Apr;9(4):363-7; discussion 369-83. doi: 10.1002/sim.4780090403. PMID: 2362976.

Examples

```
library(purrr)
library(plyr)
library(stringr)
snps<-data.frame(
V1=c(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1),
V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3)
)
class<-c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
factor<-c(2,3,4)
pvalue<-chi2test(factor,snps,class)
```

samplescount	*Generate a contingency table for the Source Data*

Description

This function generate a contingency table for the source data.

Usage

```
samplescount(snps,factor,class)
```

Arguments

snps	the snps matrix,0 denotes the missing data,1 denotes homozygous wild-type alleles, 2 denotes homozygous wild-type alleles,3 denotes homozygous mutant alleles.
factor	the snp combination.
class	the disease vector,1 denotes case and 2 denotes control.

Value

A contingency table for the source data as matrix.

References

Gravetter, F. J., & Wallnau, L. B. (2010). Essentials of Statistics for the Behavioral Sciences (PSY 200 (300) Quantitative Methods in Psychology). Boston: Cengage Learning.

Examples

```
library(purrr)
library(plyr)
library(stringr)
snps<-data.frame(
V1=c(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1),
V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3)
)
class<-c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
factor<-c(2,3)
contingencytable<-samplescount(snps,factor,class)
```

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scccna   *Sufficient Condition Conjunction Algorithm Based on CNA*

Description

This function completes the calculation of scccna analysis.

Usage

```
scccna(sccsamples,mvsccsamples,consistencythreshold,maxinumofconditions)
```

Arguments

sccsamples   Dataset.

mvsccsamples   Dataset with multivalue coding.

consistencythreshold

                  Threadhold of consistency.

maxinumofconditions

                  Maximum order of combinations.

Value

The scccna solution.

References

Baumgartner, Michael.(2009). Inferring Causal Complexity. Sociological Methods &amp Research. 38. 10.1177/0049124109339369.

Examples

```
#library(cna)
library(purrr)
library(plyr)
library(stringr)
consistencythreshold=0;
maxnumofconditions=2;
sccsamples<-data.frame(
V1=c(1,0,1,0,1,0,1,1,0,1,1,0,1,1,0,0,1,0,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V2=c(1,0,0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,1,0,0,0,0),
V3=c(1,1,1,1,1,0,1,1,1,0,0,0,1,1,0,0,1,1,0,1,1,0,0,0,0,0,0,0,1,0,0,0,1,0,0,0,1,0,0,0),
V4=c(0,1,1,1,1,0,1,1,1,1,0,0,1,1,0,0,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
mvsccsamples<-data.frame(
V1=c(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1),
V5=c(1,1,2,1,1,1,1,1,1,2,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,2,1,1)
)
#sccsamples<-read.csv(sccsamples1,header=F,skip=1)
scccnasolution<-scccna(sccsamples,mvsccsamples,consistencythreshold,maxnumofconditions)
```

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