

Package ‘asccdpsht’

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Type Package

Title Accelerated Sufficient Condition Conjunction Algorithm Based on
Dual Particle Swarm with High Order by Contingency Table

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Description Pkg{asccdpsht} is a package to perform the Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm with High Order by Contingency Table.

License GPL (>= 2)

Encoding UTF-8

LinkingTo Rcpp

Imports Rcpp,plyr,purrr,stringr,admisc,dplyr

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asccdpshct-package	<i>Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm with High Order by Contingency Table</i>
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Description

Pkgasccdpshct is a package to perform the Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm with High Order by Contingency Table.

Author(s)

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References

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

asccdpshct	<i>Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm with High Order by Contingency Table</i>
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Description

This function completes the asccdpshct analysis.

Usage

```
asccdpshct(sccsamples,mvsccsamples,MaxOrder=MaxOrder,Pop=Pop,Iter=Iter,c1=c1,c2=c2,TopSNP=TopSNP)
```

Arguments

sccsamples	Dataset.
mvsccsamples	Dataset.
MaxOrder	The maxorer of combination.
Pop	Polulation.
Iter	Iteration.
c1	The acceleration factor of individual experience.
c2	The acceleration factor of global experience.
TopSNP	The selected SNPs with top indexes.
alphacon	The threshod of consistecny.
alphacov	The threshod of coverage.

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)
mvscsamples<-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),
V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1),
V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3),
V6=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)
)
screencom<-c(3,4)
pvalue<-chi2test(screencom,mvscsamples)
numofsnps<-ncol(mvscsamples)-1
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(pattern, samples)
```

Arguments

pattern	the pathogenic pattern,for example,"[2,3]" denotes the mutation of the sceond and the third snp.
samples	the data of samples.

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)
mvscsamples<-data.frame(
  V1=c(1,2,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
  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(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
  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),
  V5=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)
pattern<-c(2,3)
pvalue<-chi2test(pattern,mvscsamples)
```

consistency

Consistency calculation for the Pattern in the Source Data

Description

This function calculates the consistency in the source dataset.

Usage

```
consistency(pattern, samples)
```

Arguments

pattern	the pathogenic pattern,for example,"[2,3]" denotes the mutation of the sceond and the third snp.
samples	the data of samples.

Value

A numeric value between 0 and 1.

References

Ragin,C.C.(2008).Redesigning social inquiry: Fuzzy sets and beyond: University of Chicago Press.

```
samples<-data.frame(
V1=c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V2=c(0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
V3=c(0,0,1,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,0,1,0,0,0,0,0,0,0,1,1,1,1,1,1,0,1,0,1,0,1,0,0,1,0,1,0,1,0,1,0,1,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
pattern<-c(2,3)
consistencyresult<-consistency(pattern=pattern,samples=samples)
```

coverage
Coverage calculation for the Pattern in the Source Data

This function calculates the coverage in the source dataset.

```
coverage(pattern, samples)
```

pattern	the pathogenic pattern,for example,"[2,3]" denotes the mutation of the sceond and the third snp.
samples	the data of samples.

A numeric value between 0 and 1.

Ragin, C.C. (2008). *Redesigning social inquiry: Fuzzy sets and beyond*: University of Chicago Press.

```
samples<-data.frame(
V1=c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V2=c(0,0,1,0,1,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V3=c(0,0,1,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,0,1,0,0,0,0,0,0,0,1,1,1,1,1,1,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
pattern<-c(2,3)
coverageresult<-coverage(pattern=pattern,samples=samples)
```

samplescount	<i>Generate a contingency table for the Source Data</i>
--------------	---

Description

This function generate a contingency table for the source data.

Usage

```
samplescount(pattern,mvscsamples)
```

Arguments

pattern	the snp combination.
mvscsamples	the mv matrix,0 denotes the missing data,1 denotes homozygous wild-type alleles, 2 denotes homozygous wild-type alleles,3 denotes homozygous mutant alleles.

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

```
mvscsamples<-data.frame(
V1=c(1,2,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1),
V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,1,3,1,1,2,1,3),
V6=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)
)
pattern<-c(2,3)
contingencytable<-samplescount(pattern,mvscsamples)
```

sccdpscon	<i>Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm according to Consistency</i>
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Description

This function completes the sccdpscon analysis.

Usage

```
sccdpscon(snpd,disease,MaxOrder,Population,Iteration,c1,c2,TopSNP,sccsamples,alpha)
```


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