Package 'asccdps'

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Description Pkg{asccdps} is a package to perform the Accelerated Sufficient Condition Conjunction Algorith Based on Dual Particle Swarm with High Order.

License GPL (>= 2)

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asccdpsh-package *Accelerated Sufficient Condition Conjunction Algorith Based on Dual Particle Swarm with High Order*

Description

Pkgasccdpsh is a package to perform the Accelerated Sufficient Condition Conjunction Algorith Based on Dual Particle Swarm with High Order.

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References

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

asccdpsh *Accelerated Sufficient Condition Conjunction Algorith Based on Dual Particle Swarm with High Order*

Description

This function completes the asccdpsh analysis.

Usage

```
asccdpsh(sccsamples,mvsccsamples,MaxOrder=MaxOrder,Pop=Pop,Iter=Iter,c1=c1,c2=c2,TopSNP=TopSNP,a
```

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.

Value

The asccdpsh solution.

References

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

Examples

```
library(stringr)
sccsamples<-data.frame(
V1=c(0,1,0,0,0,0,0,0,0,1,0,0,0,1,1,0,1,0,0,0,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,0,0),
V2=c(0,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,1,0,1,0,0,1,0),
V3=c(0,0,0,0,1,0,0,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,1,0,1,0),
V4=c(1,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0),
V5=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V6=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V7=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V8=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0)
)
mvsccsamples<-data.frame(
V1=c(1,2,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1,1),
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(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
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),
V5=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V6=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V7=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V8=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)
MaxOrder=5
Pop=100
Iter=10
c1=2
c2=2
TopSNP=10
alphacon=0.5
alphacov=0.02
asccdpshsolution<-asccdpsh(sccsamples,mvsccsamples,MaxOrder=MaxOrder,Pop=Pop,Iter=Iter,c1=c1,c2=c2,TopSNP=T
```

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

`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.

Examples

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

`coverage` *Coverage calculation for the Pattern in the Source Data*

Description

This function calculates the coverage in the source dataset.

Usage

```
coverage(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.

Examples

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

judgecompatible *Judge Whether a Sample is Compatible with the Pattern*

Description

This function judges whether a sample is compatible with the pattern or not.

Usage

```
judgecompatible(pattern, samples)
```

Arguments

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

Value

Logical value.

Examples

```
library(purrr)
library(plyr)
library(stringr)
samples<-data.frame(
V1=c(0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
V2=c(0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
V3=c(0,0,1,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,1,0,0,0,0,0,1,1,1,1,1,1,1,0,1,0,1,0,1,0,0,1,0,1,0,1,1,0,1,0),
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)
)
splitsamples<-llply(transpose(samples), do.call, what = rbind)
sample<-splitsamples[[3]]
pattern<-c(2,3,4)
result<-judgecompatible(pattern=pattern,sample=sample)
```

samplescount *Generate a contingency table for the Source Data*

Description

This function generate a contingency table for the source data.

Usage

```
samplescount(pattern,mvsccsamples)
```

Arguments

pattern	the snp combination.
mvsccsamples	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

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

---

sccdpscon *Sufficient Condition Conjunction Algorith Based on Dual Particle Swarm according to Consistency*

Description

This function completes the sccdpscon analysis.

Usage

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

Arguments

snps	Snps dataset.
disease	Diesease vector.
MaxOrder	Max Order of combination.
Population	Population of Particle.
Iteration	Iteration.
c1	The acceleration factor of individual experience.
c2	The acceleration factor of global experience.
TopSNP	TopSNP.
sccsamples	Dataset.
alpha	Threshold.

Value

The sccdpscon solution.

References

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

Examples

```
library(stringr)
sccsamples<-data.frame(
V1=c(1,0,1,0,1,0,1,1,0,1,1,0,1,1,0,0,1,0,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V2=c(1,0,0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
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(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V6=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)
)
snps<-sccsamples[,1:(ncol(sccsamples)-1)]
disease<-sccsamples[,ncol(sccsamples)]
sccdpsconsolution<-sccdpscon(snps,disease,MaxOrder=3,Population=100,Iteration=10,
           c1=2,c2=2,TopSNP=10,sccsamples=sccsamples,alpha=0.5)
```

`sccdpscov` *Sufficient Condition Conjunction Algorith Based on Dual Particle Swarm according to Coverage*

Description

This function completes the sccdpscov analysis.

Usage

```
sccdpscov(snps,disease,MaxOrder,Population,Iteration,c1,c2,TopSNP,sccsamples,alpha)
```

Arguments

`snps`	Snps dataset.
`disease`	Diesease vector.
`MaxOrder`	Max Order of combination.
`Population`	Population of Particle.
`Iteration`	Iteration.
`c1`	The acceleration factor of individual experience.
`c2`	The acceleration factor of global experience.
`TopSNP`	TopSNP.
`sccsamples`	Dataset.
`alpha`	Threshold.

Value

The sccdpscov solution.

References

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

Examples

```
library(stringr)
sccsamples<-data.frame(
V1=c(1,0,1,0,1,0,1,1,0,1,1,0,1,1,0,0,1,0,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V2=c(1,0,0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
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(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V6=c(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)
)
snps<-sccsamples[,1:(ncol(sccsamples)-1)]
disease<-sccsamples[,ncol(sccsamples)]
sccdpscovsolution<-sccdpscov(snps,disease,MaxOrder=3,Population=100,Iteration=10,
          c1=2,c2=2,TopSNP=10,sccsamples=sccsamples,alpha=0.02)
```

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