

Package ‘asccdhmct’

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Type Package

Title Accelerated Sufficient Condition Conjunction Algorithm Based on
Dual Harmony Memories by Contingency Table

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Description Pkg{asccdhmct} is a package to perform the Sufficient Condition Conjunction Algo-
rithm Based on Dual Harmony Memories by Contingency Table.

License GPL (>= 2)

Encoding UTF-8

LinkingTo Rcpp

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

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NeedsCompilation yes

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asccdhmct-package	<i>Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories by Contingency Table</i>
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Description

Pkgasccdhmct is a package to perform the Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories by Contingency Table.

Author(s)

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References

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

asccdhmct	<i>Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories by Contingency Table</i>
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Description

This function completes the asccdhmct analysis.

Usage

```
asccdhmct(HMS,max_iter,HMCR,PAR,sccsamples,mvsccsamples)
```

Arguments

HMS	Harmony Memories Size.
max_iter	Max iteration.
HMCR	Harmony memory consideration rate.
PAR	Pitch-adjustment rate.
sccsamples	Dataset.
mvsccsamples	Dataset.

Value

The asccdhmct solution.

References

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

Examples

```
library(stringr)
sccssamples<-data.frame(
V1=c(2,1,2,2,2,2,2,2,2,1,2,2,2,1,1,2,1,2,2,2,2,2,2,1,2,2,2,1,2,2,2,2,2,2,2,2),
V2=c(2,1,2,2,2,1,2,2,2,2,2,2,2,2,2,2,2,2,2,1,2,2,2,2,2,2,1,2,2,2,1,2,1,2,2,1,2),
V3=c(2,2,2,2,1,2,2,2,2,1,2,1,2,2,2,2,1,2,2,2,2,2,2,2,2,2,1,2,2,2,2,2,2,2,1,2,1,2),
V4=c(1,2,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,1,2,2,2,2,2,2,1,2,2,2,2,2,2,2,2,2,2),
V5=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V6=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V7=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V8=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)
mvscsamples<-data.frame(
V1=c(1,2,1,1,1,1,1,1,1,1,3,3,1,1,1,3,3,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
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),
V5=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V6=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V7=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V8=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)
HMS = 10;
max_iter=50;
HMCR=0.95;
PAR=0.35;
ascddhmctsolutioncon<-ascddhmct(HMS=HMS,max_iter=max_iter,HMCR=HMCR,PAR=PAR,sccssamples=sccssamples,mvscsamples=mvscsamples)
```

bocorrection	<i>Bonferroni correction for the Chi-squared test.</i>
--------------	--

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)
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(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1),
V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3),
V6=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
)
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,mvscsamples)
```

Arguments

pattern	the pathogenic pattern,for example,"[2,3]" denotes the mutation of the sceond and the third snp.
mvscsamples	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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
  V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
  V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,3,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
  V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1),
  V5=c(1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)
pattern<-c(2,3)
pvalue<-chi2test(pattern,mvscsamples)
```

consistency	<i>Consistency calculation for the Pattern in the Source Data</i>
-------------	---

Description

This function calculates the consistency in the source dataset.

Usage

```
consistency(pattern, sccsamples)
```

Arguments

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

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

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

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 condition combination.
mvsccsamples Dataset.

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)
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(1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1),
V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3),
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)
```

sccdhmcon

*Sufficient Condition Conjunction algorithm Base on Dual Harmony
Memories According to consistency*

Description

This function completes the sccdhmcon analysis.

Usage

```
sccdhmcon(HMS,max_iter,HMCR,PAR,sccsamples)
```

Arguments

HMS	Harmony Memories Size.
max_iter	Max iteration.
HMCR	Harmony memory consideration rate.
PAR	Pitch-adjustment rate.
sccsamples	Dataset.

Value

The sccdhmcon solution.

References

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

Examples

```
library(stringr)
sccsamples<-data.frame(
V1=c(2,1,2,2,2,2,2,2,2,1,2,2,2,1,1,2,1,2,2,2,2,2,2,2,1,2,2,2,1,2,2,2,2,2,2,2),
V2=c(2,1,2,2,2,1,2,2,2,2,2,2,2,2,2,2,2,2,2,1,2,2,2,2,2,2,1,2,2,2,1,2,1,2,2,1,2),
V3=c(2,2,2,2,1,2,2,2,1,2,1,2,2,2,2,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,1,2,1,2),
V4=c(1,2,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2),
V5=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V6=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V7=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V8=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)

HMS = 10;
max_iter =50;
HMCR=0.95;
PAR=0.35;
sccdacsolutioncon<-sccdhmcon(HMS=HMS,max_iter=max_iter,HMCR=HMCR,PAR=PAR,sccsamples=sccsamples)
```

sccdhmconv

Sufficient Condition Conjunction algorithm Base on Dual Harmony Memories According to coverage

Description

This function completes the sccdhmconv analysis.

Usage

```
sccdhmconv(HMS,max_iter,HMCR,PAR,sccsamples)
```


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