Package 'asccdhm'

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Type Package

Title Accelerated Sufficient Condition Conjunction Algorithm Based on
Dual Harmony Memories

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Description Pkg{asccdhm} is a package to perform the Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories.

License GPL (>= 2)

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LinkingTo Rcpp

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

RoxygenNote 7.1.0

NeedsCompilation yes

ExperimentalWindowsRuntime ucrt

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asccdhm-package	*Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories*

Description

Pkgasccdhm is a package to perform the Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories.

Author(s)

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References

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

asccdhm	*Accelerated Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories*

Description

This function completes the asccdhm analysis.

Usage

```
asccdhm(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 asccdhm 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),
V2=c(0,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,1,0,1,0,0,1,0),
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(1,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0),
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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1,1),
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(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V6=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V7=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2),
V8=c(1,1,2,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)
HMS = 10;
max_iter =50;
HMCR=0.95;
PAR=0.35;
asccdhmsolutioncon<-asccdhm(HMS=HMS,max_iter=max_iter,HMCR=HMCR,PAR=PAR,sccsamples=sccsamples,mvsccsamples=
```

| 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(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
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(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3),
V6=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
)
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,mvsccsamples)
```

Arguments

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

mvsccsamples   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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1,1),
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(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
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, 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(0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
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),
V4=c(1,1,1,1,1,0,0,0,1,0,0,0,0,0,1,1,1,1,1,1,1,1,0,1,0,1,0,1,0,0,1,0,1,0,1,1,0,1,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
pattern<-c(2,3)
consistencyresult<-consistency(pattern=pattern,sccsamples=sccsamples)
```

---

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

Description

This function calculates the coverage in the source dataset.

Usage

```
coverage(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(0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
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),
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(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
pattern<-c(2,3)
coverageresult<-coverage(pattern=pattern,sccsamples=sccsamples)
```

---

is2kmember   *Judge whether the pattern is the member of 2-order set*

Description

This function judges whether the pattern is the member of 2-order set.

Usage

```
is2kmember(pattern,set)
```

Arguments

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

Value

A logical value.

Examples

```
set<-array(1:20,dim=c(10,2))
pattern<-list(2,12)
is2kmemberresult<-is2kmember(pattern,set)
```

---

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, sample)
```

Arguments

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

Value

Logical value.

Examples

```
library(purrr)
library(plyr)
library(stringr)
samples<-data.frame(
V1=c(0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
V2=c(0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
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),
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(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
splitsamples<-llply(transpose(samples), do.call, what = rbind)
sample<-splitsamples[[3]]
pattern<-c(2,3)
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 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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1,1),
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(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3),
V6=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
)
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 &amp Research. 38. 10.1177/0049124109339369.

Examples

```
library(stringr)
sccsamples<-data.frame(
V1=c(0,1,0,0,0,0,0,0,0,1,0,0,0,1,1,0,1,0,0,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,0),
V2=c(0,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,1,0,1,0,0,1,0),
V3=c(0,0,0,0,1,0,0,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,1,0,1,0),
V4=c(1,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0),
V5=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V6=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V7=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V8=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0)
)

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)
```

---

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

Description

This function completes the sccdhmcov analysis.

Usage

```
sccdhmcov(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 sccdhmcov solution.

References

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

Examples

```
library(stringr)
sccsamples<-data.frame(
V1=c(0,1,0,0,0,0,0,0,0,1,0,0,0,1,1,0,1,0,0,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,0),
V2=c(0,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,1,0,0,0,1,0,1,0,0,1,0),
V3=c(0,0,0,0,1,0,0,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,1,0,1,0),
V4=c(1,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0),
V5=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V6=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V7=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0),
V8=c(1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0)
)

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

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