

# Package ‘sccdps’

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**Type** Package

**Title** Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm with High Order

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**Description** Pkg{sccdps} is a package to perform the Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm with High Order.

**License** GPL (>= 2)

**Encoding** UTF-8

**Imports** plyr, purrr, stringr, admisc, dplyr

**NeedsCompilation** yes

**ExperimentalWindowsRuntime** ucrt

## R topics documented:

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sccdpsh-package	<i>Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm with High Order</i>
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### Description

Pkgscdpsh is a package to perform the Sufficient Condition Conjunction Algorithm Based on Dual Particle Swarm with High Order.

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### References

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

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bocorrection	<i>Bonferroni correction for the Chi-squared test.</i>
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### 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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,1,3,1,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,3,1),
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),
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(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
)
screencom<-c(3,4)
pvalue<-chi2test(screencom,mvscsamples)
numofsnps<-ncol(mvscsamples)-1
pvaluewithhbc<-bocorrection(screencom,pvalue,numofsnps)
```

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chi2test	<i>Chisquaretest for the Pattern in the Source Data</i>
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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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,1,3,1,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
```

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consistency	<i>Consistency calculation for the Pattern in the Source Data</i>
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This function calculates the consistency in the source dataset.

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





## Examples

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

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

This function completes the sccdpcon analysis.

## Usage

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

## Arguments

snps	Snps dataset.
disease	Disease 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 sccdpcon solution.

## References

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









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