# Package 'sccdpsh'

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Type Package

Swarm with High Order	
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<b>Description</b> Pkg{sccdps} is a package to perform the Sufficient Condition Conjunction Algorith Based on Dual Particle Swarm with High Order.	
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R topics documented:	
sccdpsh-package	2
bocorrection	2
chi2test	3
consistency	4
coverage	5
judgecompatible	5
samplescount	6
sccdpscon	7
sccdpscov	8
scedpsh	9
Index 1	1

2 bocorrection

sccdpsh-package Sufficient Condition Conjunction Algorith Based on Dual Particle
Swarm with High Order

# Description

Pkgsccdpsh is a package to perform the 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 & Research. 38. 10.1177/0049124109339369.

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.

chi2test 3

#### **Examples**

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 second

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**

4 consistency

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**

coverage 5

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 second

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**

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)
```

6 samplescount

#### **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**

samplescount

Generate a contingency table for the Source Data

# Description

This function generate a contingency table for the source data.

#### Usage

```
samplescount(snps,factor,class)
```

## **Arguments**

snps the snps matrix,0 denotes the missing data,1 denotes homozygous wild-type al-

leles, 2 denotes homozygous wild-type alleles,3 denotes homozygous mutant

alleles.

factor the snp combination.

class the disease vector, 1 denotes case and 2 denotes control.

# 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.

7 sccdpscon

#### **Examples**

```
library(purrr)
library(plyr)
library(stringr)
snps<-data.frame(</pre>
factor<-c(2,3)
contingencytable<-samplescount(snps,factor,class)</pre>
```

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**

c2

Snps dataset. snps disease Diesease vector.

MaxOrder Max Order of combination. Population Population of Particle.

Iteration Iteration.

The acceleration factor of individual experience. c1 The acceleration factor of global experience.

TopSNP. **TopSNP** Dataset. sccsamples alpha Threshold.

#### Value

The sccdpscon solution.

#### References

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

8 sccdpscov

#### **Examples**

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.

Max Order of combination.

Population Population of Particle.

Iteration Iteration.

The acceleration factor of individual experience.
 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 & Research. 38. 10.1177/0049124109339369.

9 sccdpsh

#### **Examples**

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

sccdpsh

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

#### **Description**

This function completes the sccdpsh analysis.

## Usage

sccdpsh(sccsamples, mvsccsamples, MaxOrder=MaxOrder, Pop=Pop, Iter=Iter, c1=c1, c2=c2, TopSNP=TopSNP, al

## **Arguments**

c2

sccsamples Dataset. mvsccsamples Dataset.

The maxorer of combination. MaxOrder

Polulation. Pop Iter Iteration.

c1 The acceleration factor of individual experience. The acceleration factor of global experience.

The selected SNPs with top indexes. **TopSNP** 

alphacon The threshod of consistecny. alphacov The threshod of coverage.

#### Value

The sccdpsh solution.

#### References

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

10 sccdpsh

#### **Examples**

```
library(stringr)
sccsamples<-data.frame(</pre>
mvsccsamples<-data.frame(</pre>
)
MaxOrder=5
Pop=100
Iter=10
c1=2
c2=2
TopSNP=10
alphacon=0.5
alphacov=0.02
sccdpsh solution <-sccdpsh (sccsamples, MaxOrder=MaxOrder, Pop=Pop, Iter=Iter, c1=c1, c2=c2, TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSNP=TopSN
```

# **Index**

```
bocorrection, 2

chi2test, 3
consistency, 4
coverage, 5

judgecompatible, 5

samplescount, 6
sccdpscon, 7
sccdpscov, 8
sccdpsh, 9
sccdpsh-package, 2
```