

Package ‘sccdac’

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Type Package

Title Sufficient Condition Conjunction Algorithm Based on Ant Colony Optimization

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Description Pkg{asccdac} is a package to perform the Sufficient Condition Conjunction Algorithm based on Ant Colony Optimization.

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Imports plyr, purrr, stringr, admisc, dplyr

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sccdac-package	<i>Sufficient Condition Conjunction Algorithm Based on Ant Colony Optimization</i>
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Description

Pkgsscdac is a package to perform the Sufficient Condition Conjunction Algorithm based on Ant Colony Optimization.

Author(s)

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References

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

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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,1,3,1,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
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(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3),
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,mvscsamples)
numofsnps<-ncol(mvscsamples)-1
pvaluewithbc<-bocorrection(screencom,pvalue,numofsnps)
```

chi2test	<i>Chisquaretest for the Pattern in the Source Data</i>
----------	---

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(1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
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),
```

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

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


Arguments

`conditionalvarvec`
the vector of the conditional variables.

`maxorder` the maximum order specified.

Value

A list of the combinations.

References

Lockwood, Elise, Gibson, Bryan R..Combinatorial tasks and outcome listing: Examining productive listing among undergraduate students[J].Educational Studies in Mathematics.2016,91(2).

Examples

```
library(purrr)
library(plyr)
library(stringr)
conditionalvarvec<-c(1:8)
maxorder=3
combinations<-generatecombine(conditionalvarvec,maxorder)
```

generatecombineall	<i>Generate all the combinations less than or equal to the max order</i>
--------------------	--

Description

This function generates all the combinations less than or equal to the max order.

Usage

```
generatecombineall(conditionalvarvec,maxorder)
```

Arguments

`conditionalvarvec`
the vector of the conditional variables.

`maxorder` the maximum order specified.

Value

A list of the combinations.

References

Lockwood, Elise, Gibson, Bryan R..Combinatorial tasks and outcome listing: Examining productive listing among undergraduate students[J].Educational Studies in Mathematics.2016,91(2).

Examples

```
library(purrr)
library(plyr)
library(stringr)
conditionalvarvec<-c(1:8)
maxorder=3
allcombinations<-generatecombineall(conditionalvarvec,maxorder)
```

`generatecombinebetweengroups`*Generate the combinations between two groups*

Description

This function generates all the combinations between two groups.

Usage

```
generatecombinebetweengroups(group1,group2)
```

Arguments

group1	the vector of the conditional variables in group1.
group2	the vector of the conditional variables in group2.

Value

A list of the combinations.

References

Lockwood, Elise,Gibson, Bryan R..Combinatorial tasks and outcome listing: Examining productive listing among undergraduate students[J].Educational Studies in Mathematics.2016,91(2).

Examples

```
library(purrr)
library(plyr)
library(stringr)
group1<-c(6,1,5,8,10,12)
group2<-c(15,9,3,4)
combinationsbetweengroups<-generatecombinebetweengroups(group1,group2)
```


Arguments

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

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),
V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,3,1),
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),
V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,3,1,1,2,1,3)
)
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)
factor<-c(2,3)
contingencytable<-samplescount(snps,factor,class)
```

sccdac	<i>Sufficient Condition Conjunction Algorithm Based on Ant Colony Optimization</i>
--------	--

Description

This function completes the sccdac analysis.

Usage

```
sccdac(conthreshold,covthreshold,antnum,group,rou,rate,rule,sccsamples,mvsccsamples)
```

Arguments

conthreshold	The threshold of consistency.
covthreshold	The threshold of coverage.
antnum	Ant population.
group	The number of group,the group number corresponds to the order.
rou	Volatility coefficient.

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