

Package ‘aisscc’

February 1, 2024

Type Package

Title Accelerated Iterative Screening Method Based on Sufficient
Condition Conjunction

Version 1.0

Date 2024-1-20

Author Wei Xu

Maintainer Wei Xu <eric.wxu@hotmail.com>

Description Pkg{aisscc} is a package to perform the Accelerated Iterative Screen-
ing Method Based on Sufficient Condition Conjunction(aisscc) Analysis of data.

License GPL (>= 2)

Encoding UTF-8

LinkingTo Rcpp

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

RoxygenNote 7.1.0

NeedsCompilation yes

ExperimentalWindowsRuntime ucrt

Archs x64

R topics documented:

aisscc-package	2
aantscc	2
abgscc	3
aesascc	4
aisscc	5
bocorrection	6
chi2test	7
consistency	8
coverage	9
generatecombine	9
generatecombineall	10
generatecombinebetweengroups	11
judgecompatible	12
samplescount	12
Index	14

aisscc-package	<i>Accelerated Iterative Screening Method Based on Sufficient Condition Conjunction</i>
----------------	---

Description

Pkgaiscc is a package to perform the Iterative Screening method based on Sufficient Condition Conjunction.

Author(s)

Author:
Wei Xu

Maintainer:
Wei Xu <eric.wxu@hotmail.com>

References

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

aantscc	<i>Accelerated Ant colony optimization Algorithm Based on Sufficient Condition Conjunction</i>
---------	--

Description

This function completes the aantscc analysis.

Usage

```
aantscc(Ant_Num,group,BaseIter,rou,rate,rule,covthreshold,sccsamples)
```

Arguments

Ant_Num	Ant population.
group	The number of group,the group number corresponds to the order.
BaseIter	The base value of the number of iterations.
rou	Volatility coefficient.
rate	What percentage of the ants don't follow the rules.
rule	Set rules for the number of iterations, 0: the number of ants in all order is the same; 1: According to the increase of order, the number of ants increases
covthreshold	The threshold of coverage.
sccsamples	Dataset.

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


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

`pattern` the snp combination.

`mvscsamples` the mv matrix, 0 denotes the missing data, 1 denotes homozygous wild-type alleles, 2 denotes homozygous wild-type alleles, 3 denotes homozygous mutant alleles.

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

```
mvscsamples<-data.frame(
  V1=c(1,2,1,1,1,1,1,1,1,3,3,1,1,1,3,3,1,3,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
  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(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1),
  V5=c(1,1,2,1,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,1,1,3,1,1,2,1,3),
  V6=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
)
pattern<-c(2,3)
contingencytable<-samplescount(pattern,mvscsamples)
```

Index

aantscc, [2](#)
abgscc, [3](#)
aesascc, [4](#)
aisscc, [5](#)
aisscc-package, [2](#)

bocorrection, [6](#)

chi2test, [7](#)
consistency, [8](#)
coverage, [9](#)

generatecombine, [9](#)
generatecombineall, [10](#)
generatecombinebetweengroups, [11](#)

judgecompatible, [12](#)

samplescount, [12](#)