# Package 'aisscc'

February 1, 2024

Title Accelerated Iterative Screening Method Based on Sufficient

Type Package

**Condition Conjunction** 

Version 1.0
<b>Date</b> 2024-1-20
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<b>Description</b> Pkg{aisscc} is a package to perform the Accelerated Iterative Screening 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:
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# Description

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

# Author(s)

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# References

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

aantscc	Accelerated Ant colony optimization Algorithm Based on Sufficient
	Condition Conjunction

# Description

This function completes the aantscc analysis.

Dataset.

# Usage

aantscc(Ant\_Num,group,BaseIter,rou,rate,rule,covthreshold,sccsamples)

# Arguments

sccsamples

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.

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#### Value

The aantscc solution.

#### References

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

## **Examples**

abgscc

Accelerated Exhaustive Search Algorithm between two groups Based on Sufficient Condition Conjunction

## **Description**

This function completes the abgscc analysis.

# Usage

abgscc(consistencythreshold,sccsamples,mvsccsamples,group1,group2)

#### **Arguments**

consistencythreshold

Threadhold of consistency.

sccsamples Dataset.

mvsccsamples Dataset with multivalue coding.
group1 A vector of variables in Group1.
group2 A vector of variables in Group2.

#### Value

The abgscc solution.

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#### References

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

## **Examples**

```
library(purrr)
library(plyr)
library(stringr)
consistencythreshold=0.1;
sccsamples<-data.frame(</pre>
\forall 3 = c(\emptyset, \emptyset, \emptyset, \emptyset, 1, \emptyset, 0, \emptyset, 1, \emptyset, 1, \emptyset, 1, \emptyset, 0, 0, 0, 1, \emptyset, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0),
mvsccsamples<-data.frame(</pre>
)
group1 < -c(3,1)
group2 < -c(2)
abgsccsolution<-abgscc(consistencythreshold,sccsamples,mvsccsamples,group1,group2)
```

aesascc

Accelerated Exhaustive Search Algorithm Based on Sufficient Condition Conjunction

## **Description**

This function completes the aesascc analysis.

# Usage

aesascc(consistencythreshold,maximumofconditions,sccsamples,mvsccsamples)

#### **Arguments**

```
consistencythreshold
Threadhold of consistency.

maximumofconditions
Maximum order of combinations.

sccsamples
Dataset.

mvsccsamples
Multi-value Dataset.
```

#### Value

The aesascc solution.

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#### References

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

## **Examples**

aisscc

Accelerated Iterative Screening Method Based on Sufficient Condition Conjunction

# Description

This function completes the single step calculation of aissec analysis.

#### Usage

aisscc(consistencythreshold, maxnumofconditions, sccsamples, mvsccsamples)

### **Arguments**

consistencythreshold

Threadhold of consistency.

maxnumofconditions

Maximum order of combinations.

sccsamples Dataset.

mvsccsamples Dataset with multivalue coding.

## Value

The aissec solution.

### References

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

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#### **Examples**

```
library(purrr)
library(plyr)
library(stringr)
consistencythreshold=0.5;
maxnumofconditions=2;
sccsamples<-data.frame(</pre>
mvsccsamples<-data.frame(</pre>
aisscconestep<-aisscc(consistencythreshold,maxnumofconditions,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.

chi2test 7

#### **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, 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 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.

8 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.

coverage 9

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 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**

generatecombine

Generate the combinations equal to the max order

# Description

This function generates all the combinations equal to the max order.

# Usage

```
generatecombine(conditionalvarvec, maxorder)
```

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## **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)</pre>
```

generatecombineall

Generate all the combinations less than or equal to the max order

# **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)</pre>
```

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).

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

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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, samples)
```

## **Arguments**

pattern the pathogenic pattern, for example, "[2,3]" denotes that the mutation of the second

and third snp.

samples 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(pattern, mvsccsamples)
```

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## **Arguments**

pattern the snp combination.

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

leles, 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.

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