

# Package ‘asccdacct’

February 14, 2024

**Type** Package

**Title** Accelerated Sufficient Condition Conjunction Algorithm based on  
Dual Ant Colony by Contingency Table

**Version** 1.0

**Date** 2024-2-1

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**Description** Pkg{asccdacct} is a package to perform the Accelerated Sufficient Condition Conjunction Algorithm based on Dual Ant Colony by Contingency Table.

**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**

Pkgasccdacct is a package to perform the Accelerated Sufficient Condition Conjunction Algorithm based on Dual Ant Colony by Contingency Table.

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**References**

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

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

















**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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
  V2=c(1,3,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
  V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,3,1),
  V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1),
  V5=c(1,1,2,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3),
  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

*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 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(1,1,1,1,3,1,1,1,2,1,3,1,1,1,3,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
  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(1,1,2,1,1,1,1,1,1,1,1,2,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)
pattern<-c(2,3)
pvalue<-chi2test(pattern,mvscsamples)
```

---

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

```
samples<-data.frame(
  V1=c(0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
  V2=c(0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,1,0,0,0),
  V3=c(0,0,1,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
  V4=c(1,1,1,1,1,0,0,0,1,0,0,0,0,0,1,1,1,1,1,1,0,1,0,1,0,1,0,1,0,1,1,0,1,0),
  V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
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>
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---

**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(1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
  V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,3,1,3,1),
  V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1),
  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(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
)
pattern<-c(2,3)
contingencytable<-samplescount(pattern,mvscsamples)
```



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