

Package ‘esascc’

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Type Package

Title Exhaustive Search Algorithm Based on Sufficient Condition
Conjunction

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Author Wei Xu

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

Description Pkg{esascc} is a package to perform the Exhaustive Search Algorithm based on Sufficient Condition Conjunction(hsascc) Analysis of data.

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Imports plyr, purrr, stringr, admisc, dplyr

NeedsCompilation yes

ExperimentalWindowsRuntime ucrt

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esascc-package	<i>Exhaustive Search Algorithm Based on Sufficient Condition Conjunction Analysis of the Data</i>
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Description

Pkgesascc is a package to perform the Exhaustive Search Algorithm based on Sufficient Condition Conjunction(esascc) Analysis of data.

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.

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(1,2,1,1,1,1,1,1,1,3,1,1,1,1,3,3,1,3,1,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
V2=c(1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
V3=c(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
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),
V5=c(1,1,2,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2)
)
```


conditionalvarvec	the vector of the conditional variables.
maxorder	the maxorder of combinations.

A list of all combinations.

```
conditionalvarvec<-unlist(1:20)
maxorder<-2
allcombinations<-generatecombine(conditionalvarvec,maxorder)
```

judgecompatible	<i>Judge Whether a Sample is Compatible with the Pattern</i>
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This function judges whether a sample is compatible with the pattern or not.

```
judgecompatible(pattern, sample)
```

pattern	the pathogenic pattern,for example,"[2,3]" denotes that the mutation of the sceond and third snp.
sample	the data of one sample.

Logical value.

```
library(purrr)
library(plyr)
samples<-data.frame(
V1=c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V2=c(0,0,1,0,1,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V3=c(0,0,1,0,0,0,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,0,0,1,0,0,0,0,0,0,1,1,1,1,1,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,0,0,0,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0))
)
splitsamples<-llply(transpose(samples), do.call, what = rbind)
sample<-splitsamples[[3]]
pattern<-list(2,3,4)
result<-judgecompatible(pattern=pattern,sample=sample)
```

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 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(1,2,1,1,1,1,1,1,1,3,1,1,1,3,3,1,3,1,1,1,1,1,1,2,1,1,1,3,1,1,1,1,1,1,1,1),
  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(1,1,1,1,3,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
  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)
)
class<-c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
factor<-c(2,3)
contingencytable<-samplescount(snps, factor, class)
```

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