

Package ‘sccdhm’

February 5, 2024

Type Package

Title Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories

Version 1.0

Date 2024-2-1

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Description Pkg{sccdhm} is a package to perform the Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories.

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Encoding UTF-8

Imports plyr,purrr,stringr,admisc,dplyr

NeedsCompilation yes

ExperimentalWindowsRuntime ucrt

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sccdhm-package	<i>Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories</i>
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Description

Pkgsccdhm is a package to perform the Sufficient Condition Conjunction Algorithm Based on Dual Harmony Memories.

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>
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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
pvaluewithhbc<-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(1,1,1,1,1,3,1,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
```

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

Arguments

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

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

```
sccsamples<-data.frame(
V1=c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
V2=c(0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
V3=c(0,0,1,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,1,0,0,0,0,0,1,1,1,1,1,1,1,0,1,0,1,0,1,0,1,0,1,0,1,1,0,1,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
pattern<-c(2,3)
consistencyresult<-consistency(pattern=pattern,sccsamples=sccsamples)
```


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

A logical value.

```
set<-array(1:20,dim=c(10,2))
pattern<-list(2,12)
is2kmemberresult<-is2kmember(pattern,set)
```

judgecompatible	<i>Judge Whether a Sample is Compatible with the Pattern</i>
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

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.

[illegible]

samplescount	<i>Generate a contingency table for the Source Data</i>
--------------	---

Description

This function generate a contingency table for the source data.

Usage

```
samplescount(snp, factor, class)
```

Arguments

snp	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)
snp<-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(1,3,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,3,1,1,1,2,1,3,1,1,3,1),
  V3=c(1,1,1,1,3,1,1,1,1,2,1,3,1,1,1,1,3,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,1,3,1,3,1),
  V4=c(2,1,3,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,1,1,1,1,1,1,2,1,1,1,1,1,1,1,1,1,1,1),
  V5=c(1,1,2,1,1,1,1,1,1,1,3,1,1,2,1,1,1,1,1,1,1,3,1,1,1,1,1,1,1,1,1,1,3,1,1,1,2,1,3)
)
class<-c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
factor<-c(2,3)
contingencytable<-samplescount(snp,factor,class)
```


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