Package 'iev'

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Type Package

Title Iterative Exclusion of Varibles Analysis of the Data

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Description Pkg{iev} is a package to perform the Iterative Exclusion of Varibles(iev) Analysis and Necessary Conditons Analysis of data.

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Imports plyr,purrr,QCA,admisc,dplyr

NeedsCompilation no

R topics documented:

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iev-package   *Iterative Exclusion of Variables Analysis of the Data*

Description

pkgiev is a package to perform the Iterative Exclusion of Variables (iev) Analysis and Necessary Conditons Analysis of data.

Author(s)

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References

Charles C. Ragin.The Comparative Method. Moving Beyond Qualitative and Quantitative Strategies, University of California Press, Berkeley and Los Angeles (1987)

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chisquare   *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 with yates' continuity correction.

Usage

```
chisquare(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 Pearson's Chi-squared test with yates' continuity correction

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

```
samples<-data.frame(
V1=c(0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
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(0,0,1,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,1,0,0,0,0,0,1,1,1,1,1,1,1,0,1,0,1,0,1,0,0,1,0,1,0,1,1,0,1,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
)
pattern<-list(2,3)
chisquaretest<-chisquare(pattern=pattern,samples=samples)
```

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excludevariables	*Exclude the variables Compatible with the Pattern*

Description

The function excludes all variables that is compatible with the pattern.

Usage

```
excludevariables(pattern, samples)
```

Arguments

pattern   pathogenic pattern,for example,"[a,b]" denotes the mutation of the SNP a and
                 SNP b.

samples   the data of samples.

Value

The .csv file which contains remaining variables and samples in list format in current work dictio-
nary.

Examples

```
samples<-data.frame(
a=c(0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
b=c(0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
c=c(0,0,1,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
d=c(1,1,1,1,1,0,0,0,1,0,0,0,0,0,1,1,1,1,1,1,1,0,1,0,1,0,1,0,0,1,0,1,0,1,1,0,1,0),
e=c(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)
)
write.table(samples,file = "data.csv")
pattern<-list("a","c")
excludevariables(pattern=pattern,samples=samples)
file.remove("data.csv")
```

---

extractpattern	*Extract the Pattern of the Solution with the Highest Coverage*

Description

This function generates pattern marked by number from the solution with the highest coverage in
the qcaresult.

Usage

```
extractpattern(qcaresult, samples)
```

Arguments

qcaresult	the result of qca calculation
samples	the data of samples

Value

A list of the pattern marked by number

References

Gagliano SA, Sengupta S, Sidore C, Maschio A, Cucca F, Schlessinger D, Abecasis GR. Relative impact of indels versus SNPs on complex disease. Genet Epidemiol. 2019 Feb;43(1):112-117. doi: 10.1002/gepi.22175. Epub 2018 Nov 22. PMID: 30565766; PMCID: PMC6330128.

See Also

[qcacalculation](#)

Examples

```
samples<-data.frame(
V1=c(0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
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(0,0,1,0,0,1,0,0,1,0,0,1,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,1,1,0,0,0,0,1,1,1,1,1,1,1,0,1,0,1,0,1,0,0,1,0,1,0,1,1,0,1,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,1,0)
)
qcaresultlist<-qcacalculation(consistencythreshold=0.8,samples) # qca calculation for the data
if (length(qcaresultlist)==1){break  # no solution of qca
}else{
if (length(qcaresultlist)==7){solutionlist<-qcaresultlist[[1]][[1]]}else{
solutionlist<-qcaresultlist[[1]]}
} # no prime implicants are tied
extractpattern<-extractpattern(qcaresult=solutionlist,samples=samples)
```

---

iev *Iterative Exclusion of Variables Analysis of the Data*

Description

This function completes the iev analysis.

Usage

```
iev(k,consistencythreshold,samples)
```

Arguments

k	the iterations.
consistencythreshold	
	the threshold of consistency.
samples	the data of samples.

Value

The iev solution.

References

Fiss,P.C.2011,Building Better Causal Theories: A Fuzzy Set Approach to Typologies in Organization Research,Academy of Management Journal, Vol.54, pp. 393~420

See Also

qcacalculation

Examples

```
samples<-data.frame(
a=c(1,0,1,0,1,0,1,1,0,1,1,0,1,1,0,0,1,0,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
b=c(1,0,0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,0,0),
c=c(1,1,1,1,1,0,1,1,1,0,0,0,1,1,0,0,1,1,0,1,1,0,0,0,0,0,0,1,0,0,0,1,0,0,0,1,0,0,0,0),
d=c(0,1,1,1,1,0,1,1,1,1,0,0,1,1,0,0,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
e=c(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)
)
ievsolution<-iev(k=3,consistencythreshold=0.8,samples=samples)
file.remove("data.csv")
```

---

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, sample)
```

Arguments

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

sample   the data of one sample.

Value

Logical value.

Examples

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

---

necessaryconditions   *Necessary Conditions Analysis*

Description

This function analysis the necessary conditions and calculate the pvalue of Pearson's Chi-squared test with yates' continuity correction.

Usage

```
necessaryconditions(inclthreshold,covthreshold,samples)
```

Arguments

inclthreshold	threshold of incl.
covthreshold	threshold of cov.
samples	data of samples.

Value

inclN	The inclusion score
RoN	The relevance of necessity
covN	The coverage score
pvalue	The pvalue of chisquare

References

Greckhamer, Thomas & Misangyi, Vilmos & Fiss, Peer. (2013). The two QCAs: From a small-N to a large-N set-theoretic approach. Configurational Theory and Methods in Organizational Research. 38. 49-75. 10.1108/S0733-558X(2013)0000038007.

See Also

qcacalculation

Examples

```
samples<-data.frame(
V1=c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
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(1,0,1,1,0,0,0,0,1,0,0,1,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,1,0,0,0,0,0,1,1,1,1,1,1,1,0,1,0,1,0,1,0,0,1,0,1,0,1,1,0,1,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,0,1,0,0,1,0,0)
)
necessaryconditionsanalysis<-necessaryconditions(inclthreshold=0.9,covthreshold=0.5,samples=samples)
```

---

qcacalculation	*Qca Calculation*

Description

This function completes the qca calculation.

Usage

```
qcacalculation(consistencythreshold,samples)
```

Arguments

consistencythreshold

> the threshold of consistency.

samples   data of samples

Value

The qca solution.

References

RAGIN C.The comparative method: moving beyond qualitative and quantitative strategies[M].California: University of California Press,1987:1-20

See Also

[iev](#)

Examples

```
samples<-data.frame(
V1=c(1,0,0,1,1,0,0,0,0,0,1,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1),
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(1,0,1,1,0,0,0,0,1,0,0,1,0,0,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
V4=c(1,1,1,1,1,0,0,0,1,0,0,0,0,0,1,1,1,1,1,1,1,0,1,0,1,0,1,0,0,1,0,1,0,1,1,0,1,0),
V5=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,1,0,1,0,0,1,0,0)
)
qcasolution<-qcacalculation(consistencythreshold=0.8,samples=samples)
```

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