

Package ‘MaXact’

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Type Package

Title Exact max-type Cochran-Armitage trend test(CATT)

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Author Jianan Tian <jiant17@gmail.com>, Chenliang Xu <lucky.random@gmail.com>

Maintainer Chenliang Xu <lucky.random@gmail.com>

Depends R (>= 2.2.0), mnormt

Description Perform exact MAX3 or MAX2 test for one-locus genetic association analysis and trend test for dominant, recessive and additive models. It can also calculate approximated p-value with the normal approximation method.

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Exact Max CATT Test *MAX CATT test in case-control genetic association analysis*

Description

Perform exact MAX3 test, MAX2 test or Cochran-Armitage trend test for one-locus genetic association analysis and trend test for dominant, recessive and additive models. It can also calculate approximated p-value of a MAX test using the normal approximation method. MAX3 is the maximized chi-squares of Cochran-Armitage trend tests for dominant, recessive and additive models. MAX2 is the maximization of the former two chi-squares.

Usage

```
maxact.test(data, max3 = TRUE, exact=TRUE, alternative = "two.sided")
catt.test(data, theta, exact=TRUE, alternative = "two.sided")
```

Arguments

data	2x3 contingency table(rows are case/control, columns are the three genotypes)
max3	a logical. If 'TRUE'(the default) the MAX3 is returned; if 'FALSE' MAX2 is computed
theta	parameter theta of Cochran-Armitage trend test
exact	a logical indicating if an exact method should be used (default is 'TRUE')
alternative	indicates the alternative hypothesis and must be one of "'two.sided'", "'greater'" or "'less'"

Value

A list with class "'hctest'" containing the following components:

data.name	a character string giving the names of the data.
p.value	the p-value of the test.
method	a character string describing the method used.
statistic	the value of the MAX test statistic.
alternative	a character string describing the alternative hypothesis.

Note

The normal approximation method(exact=FALSE) is not recommended, unless you have really good reason for that. It is not exact, and it would not be faster than the exact method for normal sample size (such as thousands).

Author(s)

Jianan Tian <jiant17@gmail.com>, Chenliang Xu <lucky.random@gmail.com>

References

Tian, J., Xu, C., Zhan, H., Yang, Y. (2009) "Exact MAX tests in case-control association analysis (Manuscript)."

Examples

```
data.sladek<-matrix(c(129,326,229,198,325,143),2,3,byrow=TRUE)

## MAX3 test (exact p-value)
maxact.test(data.sladek)

## MAX2 test (exact p-value):
maxact.test(data.sladek,max3=FALSE,exact=TRUE)

## MAX test (p-value calculated from the normal approximation method), it
## is not recommends, see NOTE for more information
maxact.test(data.sladek,max3=TRUE,exact=FALSE)
maxact.test(data.sladek,max3=FALSE,exact=FALSE)

## Cochran-Armitage trend test, assuming we know the model
catt.test(data.sladek, theta=0) #recessive model
catt.test(data.sladek, theta=0.5) #additive model
catt.test(data.sladek, theta=1) #dominant model

#the alternative hypothesis is less
catt.test(data.sladek, theta=0, alternative="less")
```

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