Package ‘MaXact’

February 19, 2015

Type Package
Title Exact max-type Cochran-Armitage trend test (CATT)
Version 0.2.1
Date 2013-12-01
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.
License GPL-2
Repository CRAN
NeedsCompilation yes
Date/Publication 2013-12-05 00:42:52

R topics documented:

Exact Max CATT Test

Description

Perform exact MAX3 test, MAX2 test and Cochran-Armitage trend test for one-locus genetic association analysis. MAX3 is the maximum of the Cochran-Armitage trend test statistic for dominant, recessive and additive models, and MAX2 is the maximum of dominant and recessive models. It also provides approximated p-value of a MAX test with the normal approximation method.
Exact Max CATT Test

Usage

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

Arguments

data 2x3 contingency table of data values, with rows representing case/control, and columns representing the three genotypes

maxS a logical indicating whether MAX3 or MAX2 test statistic should be used

theta parameter of the Cochran-Armitage trend test

exact a logical indicating whether an exact p-value should be computed

alternative a character string describing the alternative hypothesis, which must be one of "two.sided", "greater" or "less"

Value

A list with class "htest" 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 test statistic.
alternative a character string describing the alternative hypothesis.

Note

The normal approximation method(exact=FALSE) is provided for comparison purpose, and is not recommended for data analysis. The exact method is faster than the normal approximation method in most of cases, and it is fast enough for most of applications.

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

```r
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, maxS=FALSE, exact=TRUE)
```
## Exact Max CATT Test

### MAX test (p-value calculated from the normal approximation method), it is not recommended, see NOTE for more information

```r
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

```r
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

```r
catt.test(data.sladek, theta=0, alternative="less")
```
Index

*Topic htest
   Exact Max CATT Test, 1

catt.test (Exact Max CATT Test), 1

Exact Max CATT Test, 1

MaXact (Exact Max CATT Test), 1
maxact.test (Exact Max CATT Test), 1