

# Package ‘MaXact’

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**Type** Package

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

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**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

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

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## 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.

**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 of data values, with rows representing case/control, and columns representing the three genotypes
max3	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)**

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**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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