

# Package ‘exact2x2’

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**Type** Package

**Title** Exact Conditional Tests and Confidence Intervals for 2x2 tables

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**Depends** stats, exactci

**Description** Calculates Fisher’s exact test, Blaker’s exact test, or the exact McNemar’s test with appropriate matching confidence intervals.

**License** GPL-2

**LazyLoad** yes

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**Description**

Performs exact conditional tests for two by two tables. For independent binary responses, performs either Fisher's exact test or Blaker's exact test for testing hypotheses about the odds ratio. The commands follow the style of `fisher.test`, the difference is that for two-sided tests there are three methods for calculating the exact test, and for each of the three methods its matching confidence interval is returned (see details). For paired binary data resulting in a two by two table, performs an exact McNemar's test.

**Usage**

```
exact2x2(x, y = NULL, or = 1, alternative = "two.sided", tsmethod = NULL, conf.int = TRUE, conf.level = 0.95, tol = 0.00001, conditional = TRUE, paired=FALSE, plot=FALSE)
fisher.exact(x, y = NULL, or = 1, alternative = "two.sided", tsmethod = "minlike", conf.int = TRUE, conf.level = 0.95, tol = 0.00001, conditional = TRUE, paired=FALSE, plot=FALSE)
blaker.exact(x, y = NULL, or = 1, alternative = "two.sided", conf.int = TRUE, conf.level = 0.95, tol = 0.00001, conditional = TRUE, paired=FALSE, plot=FALSE)
mcnemar.exact(x,y=NULL, conf.level=.95)
```

**Arguments**

<code>x</code>	either a two-dimensional contingency table in matrix form, or a factor object.
<code>y</code>	a factor object; ignored if <code>x</code> is a matrix.
<code>or</code>	the hypothesized odds ratio. Must be a single numeric.
<code>alternative</code>	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". if "two.sided" uses method defined by <code>tsmethod</code> .
<code>tsmethod</code>	one of "minlike", "central", or "blaker". NULL defaults to "minlike" when <code>paired=FALSE</code> and "central" when <code>paired=TRUE</code> . Defines type of two-sided method (see details). Ignored if <code>alternative="less"</code> or "greater".
<code>conf.int</code>	logical indicating if a confidence interval should be computed.
<code>conf.level</code>	confidence level for the returned confidence interval. Only used if <code>conf.int = TRUE</code> .
<code>tol</code>	tolerance for confidence interval estimation.
<code>conditional</code>	TRUE. Unconditional exact tests not supported at this time.
<code>paired</code>	logical. TRUE gives exact McNemar's test, FALSE are all other tests
<code>plot</code>	logical. TRUE gives basic plot of point null odds ratios by p-values, for greater plot control use <a href="#">exact2x2Plot</a>

## Details

The motivation for this package is to match the different two-sided conditional exact tests for 2x2 tables with the appropriate confidence intervals.

There are three ways to calculate the two-sided conditional exact tests, motivated by three different ways to define the p-value. The usual two-sided Fisher's exact test defines the p-value as the sum of probability of tables with smaller likelihood than the observed table (`tsmethod="minlike"`). The central Fisher's exact test defines the p-value as twice the one-sided p-values (but with a maximum p-value of 1). Blaker's (2000) exact test defines the p-value as the sum of the tail probability in the observed tail plus the largest tail probability in the opposite tail that is not greater than the observed tail probability.

In `fisher.test` the p-value uses the two-sample method associated with `tsmethod="minlike"`, but the confidence interval method associated with `tsmethod="central"`. The probability that the lower central confidence limit is less than the true odds ratio is bounded by  $1-(1-\text{conf.level})/2$  for the central intervals, but not for the other two two-sided methods. The confidence intervals in `exact2x2` match the test associated with `alternative`. In other words, the confidence interval is the smallest interval that contains the confidence set that is the inversion of the associated test (see Fay, 2010). The functions `fisher.exact` and `blaker.exact` are just wrappers for certain options in `exact2x2`.

If `x` is a matrix, it is taken as a two-dimensional contingency table, and hence its entries should be nonnegative integers. Otherwise, both `x` and `y` must be vectors of the same length. Incomplete cases are removed, the vectors are coerced into factor objects, and the contingency table is computed from these.

P-values are obtained directly using the (central or non-central) hypergeometric distribution.

The null of conditional independence is equivalent to the hypothesis that the odds ratio equals one. 'Exact' inference can be based on observing that in general, given all marginal totals fixed, the first element of the contingency table has a non-central hypergeometric distribution with non-centrality parameter given by the odds ratio (Fisher, 1935). The alternative for a one-sided test is based on the odds ratio, so `alternative = "greater"` is a test of the odds ratio being bigger than or.

When `paired=TRUE`, this denotes there is some pairing of the data. For example, instead of Group A and Group B, we may have pretest and posttest binary responses. The proper two-sided test for such a setup is McNemar's Test, which only uses the off-diagonal elements of the 2x2 table, and tests that both are equal or not. The exact version is based on the binomial distribution on one of the off-diagonal values conditioned on the total of both off-diagonal values. We use `binom.exact` from the `exactci` package, and convert the p estimates and confidence intervals (see note) to odds ratios (see Breslow and Day, 1980, p. 165). The function `mcnemar.exact` is just a wrapper to call `exact2x2` with `paired=TRUE`, `alternative="two.sided"`, `tsmethod="central"`. One-sided exact McNemar-type tests may be calculated using the `exact2x2` function with `paired=TRUE`. For details of McNemar-type tests see Fay (2010, R Journal).

## Value

A list with class "htest" containing the following components:

<code>p.value</code>	the p-value of the test
<code>conf.int</code>	a confidence interval for the odds ratio

<code>estimate</code>	an estimate of the odds ratio. Note that the <i>conditional</i> Maximum Likelihood Estimate (MLE) rather than the unconditional MLE (the sample odds ratio) is used.
<code>null.value</code>	the odds ratio under the null, or.
<code>alternative</code>	a character string describing the alternative hypothesis
<code>method</code>	a character string, changes depending on alternative and tsmethod
<code>data.name</code>	a character string giving the names of the data

### Note

The default exact confidence intervals for the odds ratio when `paired=TRUE` (those matching the exact McNemar's test) are transformations of the Clopper-Pearson exact confidence intervals for a single binomial parameter which are central intervals. See note for `binom.exact` for discussion of exact binomial confidence intervals.

### Author(s)

Michael Fay

### References

Blaker, H. (2000) Confidence curves and improved exact confidence intervals for discrete distributions. *Canadian Journal of Statistics* 28: 783-798.

Breslow, NE and Day NE (1980). *Statistical Methods in Cancer Research: Vol 1-The analysis of Case-Control Studies*. IARC Scientific Publications. IARC, Lyon.

Fay, M. P. (2010). Confidence intervals that Match Fisher's exact and Blaker's exact tests. *Bio-statistics*, 11: 373-374 (go to doc directory for earlier version or <http://www3.niaid.nih.gov/about/organization/dcr/BRB/staff/michael.htm> for link to official version).

Fay M.P. (2010). Two-sided Exact Tests and Matching Confidence Intervals for Discrete Data. *R Journal* 2(1):53-58.

Fisher, R.A. (1935) The logic of inductive inference. *Journal of the Royal Statistical Society Series A* 98:39-54.

### See Also

[fisher.test](#) or [mcnemar.test](#)

### Examples

```
## In example 1, notice how fisher.test rejects the null at the 5 percent level,
## but the 95 percent confidence interval on the odds ratio contains 1
## The intervals do not match the p-value.
## In fisher.exact you get p-values and the matching confidence intervals
example1<-matrix(c(6,12,12,5),2,2,dimnames=list(c("Group A", "Group B"),c("Event", "No Event")))
example1
fisher.test(example1)
fisher.exact(example1, tsmethod="minlike")
fisher.exact(example1, tsmethod="central")
```

```

blaker.exact(example1)
## In example 2, this same thing happens, for tsmethod="minlike"... this cannot be avoided because of the
## holes in the confidence set.
##
example2<-matrix(c(7,255,30,464),2,2,dimnames=list(c("Group A", "Group B"),c("Event", "No Event")))
example2
fisher.test(example2)
exact2x2(example2,tsmethod="minlike")
## you can never get a test-CI inconsistency when tsmethod="central"
exact2x2(example2,tsmethod="central")

```

---

exact2x2Plot

*Plot p-value function for one 2 by 2 table.*


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### Description

Plots two-sided p-values as a function of odds ratios. Can plot three types of p-values: the two-sided Fisher's exact, the central Fisher's exact (i.e., twice the one-sided Fisher's exact), and Blaker's exact.

### Usage

```

exact2x2Plot(x, y=NULL, OR = NULL, ndiv = 1000, tsmethod=NULL, method = NULL, paired=FALSE,
orRange = NULL, dolog = TRUE, dolines = FALSE, dopoints = TRUE,
doci=TRUE, alternative=c("two.sided", "less", "greater"),
conf.level=.95, alphaline=TRUE, newplot = TRUE, ...)

```

### Arguments

x	matrix representing the 2 by 2 table
y	a factor object; ignored if x is a matrix.
OR	odds ratio values for plot, if NULL divides orRange into ndiv pieces
ndiv	number of pieces to divide up odds ratio range
tsmethod	either "minlike", "blaker" or "central"
method	same as tsmethod, kept for backward compatability
paired	logical, do paired analysis giving McNemar's test p-values
orRange	range for calculating odds ratios
dolog	logical, plot odds ratios on log scale?
dolines	logical, add lines to a plot?
dopoints	logical, add points to a plot?
doci	logical, add vertical lines at confidence interval?
alternative	one of "two.sided", "less", "greater", type of alternative for p-values
conf.level	when doci=TRUE, level for confidence interval to be plotted
alphaline	logical, if doci=TRUE should a line be drawn at the significance level?
newplot	logical, start a new plot?
...	values passed to plot, points, or lines statement

**See Also**[exact2x2](#)**Examples**

```
example1<-matrix(c(6,12,12,5),2,2,dimnames=list(c("Group A", "Group B"),c("Event", "No Event")))
example1
exact2x2Plot(example1)
## add lines from central Fisher's exact
exact2x2Plot(example1,method="central",dolines=TRUE,newplot=FALSE,col="red")
```

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