

# Package ‘exactmeta’

February 19, 2015

**Type** Package

**Title** Exact fixed effect meta analysis

**Version** 1.0-2

**Date** 2014-9-1

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**Description** Perform exact fixed effect meta analysis for rare events data without the need of artificial continuity correction.

**License** GPL-2

**LazyLoad** yes

**NeedsCompilation** no

**Repository** CRAN

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metaexact-package	<i>Exact Meta Analysis for Rare Events Data</i>
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## Description

Compute the exact confidence interval and p-value for risk difference, risk ratio, rate difference and rate ratio in meta analysis using fixed effect model without artificial continuity correction. The validity of the output does not depend on asymptotical approximation and thus the method is suitable for analyzing rare event data. \

The current version corrected the computations of the asymptotical MH confidence intervals for risk ratio and rate ratio.

## Details

Package: metaexact  
Type: Package  
Version: 1.0-1  
Date: 2013-11-15  
License: GLP-2

The package includes the main functions "meta.exact" and "study.exact". When the data from individual study consists of simple two by two table, the parameter of interest is the risk difference or ratio, where the risks refer to the binomial probabilities in two groups. When the data from individual study consists of the number of events and total follow-up time by arm, the parameter of interest is the rate difference or ratio, where the rates refer to the poisson rates in two groups.

## Author(s)

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## References

Tian, L., Cai, T., Pfeffer, M., Piankov, N., Cremieux, P., and Wei, LJ. (2008). Exact and efficient inference procedure for meta-analysis and its application to the analysis of independent two by two tables with all available data but without artificial continuity correction. *Biostatistics*, 10(2):275-281.

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meta.exact

*Exact fixed effect meta analysis*

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## Description

Compute the exact confidence interval and p-value for risk difference, risk ratio, rate difference or rate ratio in meta analysis using fixed effect model.

## Usage

```
meta.exact(data, type="risk difference", BB.grdnum=2000, B.sim=20000, cov.prob=0.95,  
midp=T, print=T, studyCI=T, ratio.upper=1000)
```

**Arguments**

data	The data matrix summarizing information from multiple studies needed in the meta analysis. The first column consists of the numbers of events in arm 1; the second column consists of the numbers of events in arm 2; the third column consists of the sample sizes or total follow up times in arm 1 and the fourth column consists of the sample sizes or total follow up times in arm 2. Each row contains data from a study.
type	The parameter of interest. It can be "risk difference" (the difference of two binomial proportions); "risk ratio" (the ratio of two binomial proportions); "rate difference" (the difference of two Poisson rates) and "rate ratio" (the ratio of two Poisson rates).
BB.grdnum	The number of grid points used in searching the ends of the confidence interval. A bigger value increases the precision of the constructed confidence interval.
B.sim	The number of Monte-carlo simulations used to generate the null-distribution based on which the confidence interval and p-value are obtained.
cov.prob	The coverage probability of the confidence interval to be constructed.
midp	The binary indicator for if the mid-p values are used in calculating the exact p-values and constructing the exact confidence intervals. The results are more conservative without using mid-p values.
print	The binary indicator for if the computing progress is printed during the computation.
studyCI	The binary indicator for if the confidence interval and p-value for individual study are reported.
ratio.upper	A value indicating the limits in computing the confidence interval for either the risk ratio or rate ratio. The default value of 1000 means that the widest confidence interval for the ratio is (0.001, 1000).

**Value**

ci.fixed	A matrix reporting the point estimators, confidence intervals, and p-values from three methods: constant weighting, inverse-variance weighting and Fisher's weighting. Normally, the result from the inverse-variance weighting method is recommended. It also reports the corresponding result from the asymptotical MH method with or without continuity correction as specified by users. When type is either "risk ratio" or "rate ratio", the continuity correction are automatically made for zero event. The last column of the matrix provides the range used for searching the confidence limits. When a confidence limit is the same as the range limit, the true confidence interval goes beyond the specified range.
study.ci	When "studyCI=T", "study.ci" is a matrix reporting the point estimators (the first column), confidence intervals (the second and third columns), p values (the fourth column) and if the confidence interval goes beyond the pre-specified range: 1 if within the range and 0 otherwise (the fifth column).
precision	The precision used to search the limit of the confidence interval. It can be improved by increasing "BB.grdnum" in the arguments.

**Author(s)**

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**References**

Tian, L., Cai, T., Pfeffer, M., Piankov, N., Cremieux, P., and Wei, LJ. (2008). Exact and efficient inference procedure for meta-analysis and its application to the analysis of independent two by two tables with all available data but without artificial continuity correction. *Biostatistics*, 10(2):275-281.

**Examples**

```
data=cbind(c(2, 1), c(1, 1), c(10, 10), c(12, 12))

meta.exact(data, type="risk difference", BB.grdnum=100, studyCI=FALSE)
meta.exact(data, type="rate difference", BB.grdnum=100, studyCI=FALSE)
meta.exact(data, type="risk ratio", BB.grdnum=100, studyCI=FALSE)
meta.exact(data, type="rate ratio", BB.grdnum=100)
```

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study.exact	<i>Compute the exact confidence interval and p-value based on a single study</i>
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**Description**

Compute the exact confidence interval and p-value for risk difference, risk ratio, rate difference and rate ratio based on data from an individual study.

**Usage**

```
study.exact(x1, x2, n1, n2, type="risk difference", BB.grdnum=2000, cov.prob=0.95,
midp=T)
```

**Arguments**

x1	The number of events in arm 1.
x2	The number of events in arm 2.
n1	The sample size of arm 1 when type="risk difference" or "risk ratio"; The total follow-up time for patients in arm 1 when type="rate difference" or "rate ratio".
n2	The sample size of arm 2 when type="risk difference" or "risk ratio"; The total follow-up time for patients in arm 2 when type="rate difference" or "rate ratio".
type	Indicate the parameter of interest: it can be "risk difference" (the difference of two binomial proportions); "risk ratio" (the ratio of two binomial proportions); "rate difference" (the difference of two Poission rates) and "rate ratio" (the ratio of two Poisson rates).

BB.grdnum	The number of grid points used in searching the limits of the confidence interval
cov.prob	The coverage level of the constructed confidence interval
midp	The binary indicator for if the mid-p value is used in constructing the exact confidence interval.

**Value**

est	the point estimator
lower	the lower end of the confidence interval
upper	the upper end of the confidence interval
status	1 if the confidence interval is within the pre-specified range and 0 otherwise
p	the p value

**Author(s)**

Yilei Yu

**Examples**

```
study.exact(1, 2, 12, 10, BB.grdnum=100, type="risk difference")
study.exact(1, 2, 12, 10, BB.grdnum=100, type="rate difference")
study.exact(1, 2, 12, 10, BB.grdnum=100, type="risk ratio")
study.exact(1, 2, 12, 10, BB.grdnum=100, type="rate ratio")
```

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\*Topic **meta analysis, exact inference,  
fixed effect, rare event,  
continuity correction**  
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