

# Package ‘mmeta’

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**Type** Package

**Title** Multivariate Meta-Analysis

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**Description** This package implements a novel multivariate meta-analysis.

**Depends** R (>= 2.10.0)

**Imports** aod,HI

**License** GPL (>= 2)

**LazyLoad** no

**NeedsCompilation** yes

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colorectal

*Studies on the Association of N-acetyltransferase 2 (NAT2) Acetylation Status and Colorectal Cancer*

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### Description

Results from 20 case-control studies investigating the association between rapid NAT2 acetylator status and colorectal cancer

### Format

The data frame contains the following columns:

**y1** number of subjects with rapid NAT2 acetylator status in the control group

**n1** number of subjects in the control group (without colorectal cancer)

**y2** number of subjects with rapid NAT2 acetylator status in the case group

**n2** number of subjects in the case group (with colorectal cancer)

**studynames** The study names indicating the last name of the first author of each study

### Note

The dataset `colorectal` is used to conduct exact posterior inference of odds ratio for multiple 2X2 tables.

### References

Chen, Y., Chu, H., Luo, S., Nie, L., and Chen, S. (2011b). Bayesian analysis on meta-analysis of case-control studies accounting for within-study correlation. *Statistical Methods in Medical Research*, Published online on Dec 4, 2011, PMID: 22143403. doi: 10.1177/0962280211430889

Ye, Z. and Parry, J. (2002) Meta-analysis of 20 case-control studies on the N -acetyltransferase 2 acetylation status and colorectal cancer risk. *Med Sci Monit* 8, CR558-65.

### See Also

[multipletables](#), [summary.multipletables](#), [plot.multipletables](#),

### Examples

```
library(mmeta)
data(colorectal)
summary(colorectal)
```

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diabetes	<i>Studies on the Association of Gestational Diabetes Mellitus (GDM) and Type 2 Diabetes Mellitus (T2DM)</i>
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---

### Description

Results from 20 cohort studies investigating the association between GDM and T2DM

### Format

The data frame contains the following columns:

**y1** number of subjects who developed T2DM among the unexposed subjects (without GDM)

**n1** number of unexposed subjects (without GDM)

**y2** number of subjects who developed T2DM among the exposed subjects (with GDM)

**n2** number of exposed subjects (with GDM)

**studynames** The study names indicating the last name of the first author and the year of each study

### Note

The dataset `diabetes` is used to conduct exact posterior inference of relative risk and risk difference for multiple 2X2 tables.

### References

Chen, Y., Luo, S., Chu, H., Su, X., and Nie, L. (2012a). An empirical Bayes method for multivariate meta-analysis with an application in clinical trials. in press, *Communication in Statistics: Theory and Methods*.

Bellamy, L, Casas, J.P., Hingorani, A.D., Williams, D. (2009) Type 2 diabetes mellitus after gestational diabetes: a systematic review and meta-analysis. *The Lancet* 373(9677):1773-1779

### See Also

[multipletables](#), [summary.multipletables](#), [plot.multipletables](#),

### Examples

```
library(mmeta)
data(diabetes)
summary(diabetes)
```

multipletables

*Exact posterior inference based on multiple 2x2 tables***Description**

This function conducts exact posterior inference based on multiple 2x2 tables.

**Usage**

```
multipletables(data=NULL, measure=NULL, model="Sarmanov",
               method="sampling", nsam=10000, alpha=0.05)
```

**Arguments**

data	a data frame that contains y1, n1, y2, n2, studynames. See details
measure	a character string specifying a measure. Options are OR, RR, and RD. OR is odds ratio, RR is relative risk, and RD is risk difference.
model	a character string specifying the model. Options are independent and Sarmanov. Independent is independent beta-binomial model. Sarmanov is Sarmanov beta-binomial model.
method	a character string specifying the method. Options are exact and sampling. sampling (default) is a method based on Monte Carlo sampling. exact is exact method.
alpha	a numeric value specifying the significant level. Default value sets to 0.05.
nsam	a numeric value specifying the number of samples if method is sampling. Default value sets to 10000

**Details**

There are two kinds of study design, i.e., prospective study or clinical trial, and retrospective or case-control study. In a prospective study or clinical trial, data is a data frame that contains y1, n1, y2, n2, studynames. y1 is the number of subjects experienced a certain event in the unexposed group. n1 is the number of subjects in the unexposed group. y2 is the number of subjects experienced a certain event in the exposed group. n2 is the number of subjects in the exposed group. In this study, OR is odds ratio of event comparing exposed group with unexposed group. RR is relative risk of event comparing exposed group with unexposed group. RD is risk difference of event comparing exposed group with unexposed group.

For case-control study, y1 is the number of subjects with exposure in the control group. n1 is the number of subjects in the control group. y2 is the number of subjects with exposure in the case group. n2 is the number of subjects in the case group. In this study, OR is odds ratio of event comparing case group with control group. RR is relative risk of event comparing case group with control group. RD is risk difference of event comparing case group with control group.

Empirical Bayes method is used to maximize the marginal likelihood combining all studies to obtain the estimates of the hyperparameters a1, b1, a2, b2, and rho. When method="independent",

only the estimated hyperparameters of  $a_1$ ,  $b_1$ ,  $a_2$ , and  $b_2$  are used. When `model="Sarmanov"`,  $\rho$  is subject to constraints. See Chen et al (2011) for details.

The output `cov.matrix` and `hessian` are the estimated covariance matrix and hessian matrix of the estimated parameters in the transformed scales. The estimated parameters are  $\log(a_1)$ ,  $\log(b_1)$ ,  $\log(a_2)$ ,  $\log(b_2)$ ,  $\omega$ , where the correlation coefficient  $\rho$  is a function of  $a_1$ ,  $b_1$ ,  $a_2$ ,  $b_2$ , and  $\omega$ . Please see details on page 7 of Chen et al (2012 b).

## Value

An object is returned, inheriting from class `multipletables`. Objects of this class have methods for the generic functions `summary` and `plot`. The following components must be included in a legitimate `multipletables` object.

<code>measure</code>	the value of <code>measure</code> argument.
<code>model</code>	the value of <code>model</code> argument.
<code>method</code>	the value of <code>method</code> argument.
<code>dataset</code>	a data matrix with rows being $y_1$ , $n_1$ , $y_2$ , and $n_2$ .
<code>studynames</code>	a character string indicating all the study names
<code>measurename</code>	a character string specifying the full names of value of <code>measure</code> argument. Can be Odds Ratio, Relative Risk, and Risk Difference.
<code>alpha</code>	the value of <code>alpha</code> argument.
<code>chi2</code>	the chi-square test statistics of the likelihood ratio test
<code>pvalue</code>	the p-value of the likelihood ratio test
<code>MLE</code>	a numeric vector of the estimated hyperparameters in the following order: $a_1$ , $b_1$ , $a_2$ , $b_2$ , $\rho$ .
<code>cov.matrix</code>	the estimated covariance matrix of the estimated parameters in the transformed scales
<code>hessian</code>	the estimated hessian matrix of the estimated parameters in the transformed scales
<code>overall</code>	a list of two components that contain the overall measure (e.g., overall OR) and its 95% equal-tail credible interval.
<code>sample</code>	a list of length the number of studies with components numerical vectors of the samples of the each study-specific measure.
<code>density</code>	a list of length the number of studies with components lists of density of each study-specific measure.
<code>dataset</code>	a numeric vector of input data with components: $y_1$ , $n_1$ , $y_2$ , $n_2$
<code>parameter</code>	a numeric vector specifying the hyperparameters with components $a_1$ , $b_1$ , $a_2$ , $b_2$ , and $\rho$ .
<code>alpha</code>	a numeric value specifying the significant level. Default value sets to 0.05.
<code>sample</code>	a list of samples for the posterior and prior distributions
<code>density</code>	a list of the density of the posterior and prior distributions
<code>studynames</code>	a character vector being "Posterior" and "Prior".

## References

Luo, S., Chen, Y., Su, X., Chu, H., (2014). mmeta: An R Package for Multivariate Meta-Analysis. *Journal of Statistical Software*, 56(11), 1-26.

Chen, Y., Luo, S., (2011a). A Few Remarks on "Statistical Distribution of the Difference of Two Proportions" by Nadarajah and Kotz, *Statistics in Medicine* 2007; 26(18):3518-3523" . *Statistics in Medicine*, 30(15), 1913-1915.

Chen, Y., Chu, H., Luo, S., Nie, L., and Chen, S. (2014a). Bayesian analysis on meta-analysis of case-control studies accounting for within-study correlation. *Statistical Methods in Medical Research*, doi: 10.1177/0962280211430889. In press.

Chen, Y., Luo, S., Chu, H., Su, X., and Nie, L. (2014b). An empirical Bayes method for multivariate meta-analysis with an application in clinical trials. *Communication in Statistics: Theory and Methods*. In press.

Chen, Y., Luo, S., Chu, H., Wei, P. (2013). Bayesian inference on risk differences: an application to multivariate meta-analysis of adverse events in clinical trials. *Statistics in Biopharmaceutical Research*, 5(2), 142-155.

## See Also

[plot.multipletables](#) [summary.multipletables](#)

## Examples

```
#library(mmeta)
#Analyze the dataset colorectal to conduct exact inference of the odds ratios
#data(colorectal)
#multiple.OR <- multipletables(data=colorectal, measure="OR",
# model="Sarmanov", method="exact")
#summary(multiple.OR)
# Generate the forest plot with 95% CIs of study-specific odds ratios
#and 95% CI of overall odds ratio
#plot(multiple.OR, type="forest", addline=1,file="forestOR")
# Plot the posterior density functions of some target studies in an overlaying manner
#plot(multiple.OR, type="overlap", select=c(4,14,16,20),file="overlapOR")
# Plot the posterior density functions of some target studies in a
#side-by-side manner
#plot(multiple.OR, type="sidebyside", select=c(4,14,16,20), ylim=c(0,2.7),
# xlim=c(0.5,1.5),file="sidebysideOR")
#print(multiple.OR.table)
#print(multiple.OR.table, type="html")

# Analyze the dataset withdrawal to conduct inference of the relative risks
#data(withdrawal)
#multiple.RR <- multipletables(data=withdrawal, measure="RR",
#                               model="Sarmanov")
#summary(multiple.RR)
#plot(multiple.RR, type="forest", addline=1)
#plot(multiple.RR, type="overlap", select=c(3,8,14,16))
#plot(multiple.RR, type="sidebyside", select=c(3,8,14,16),
#ylim=c(0,1.2), xlim=c(0.4,3))
```

```

#print(multiple.RR.table)
#print(multiple.RR.table, type="html")

# Analyze the dataset withdrawal to conduct inference of the risk differences
#data(withdrawal)
#multiple.RD <- multipletables(data=withdrawal, measure="RD",
#                               model="Sarmanov")
#summary(multiple.RD)
#plot(multiple.RD, type="forest", addline=0)
#plot(multiple.RD, type="overlap", select=c(3,8,14,16))
#plot(multiple.RD, type="sidebyside", select=c(3,8,14,16))
#plot(multiple.RD, type="sidebyside", select=c(3,8,14,16),
#      ylim=c(0,6), xlim=c(-0.2,0.4))
#print(multiple.RD.table)
#print(multiple.RD.table, type="html")

```

---

plot.multipletables     *Plot Method for multipletables objects*

---

## Description

Produces a variety of plots for multiple tables analysis

## Usage

```

## S3 method for class 'multipletables'
plot(x,type=NULL,select=NULL,file=NULL, xlim=NULL,ylim=NULL,
      xlabel=NULL,mar=NULL,xlog=TRUE,
      addline=NULL,xlab=NULL,ylab=NULL,ciShow=TRUE,...)

```

## Arguments

x	an object inheriting from class multipletables.
type	a character string specifying the type of plots to produce. Options are sidebyside, overlap, and forest. See details
select	a numeric value or vector specifying which studies to be plotted. By default (when NULL), all of the studies will be plotted.
xlab	a character string specifying the x-axis label in the plot. Default is the name of the measure of association
ylab	a character string specifying the x-axis label in the plot. Default is "Density"
file	a character string specifying the filename as which the plots are saved. By default (when NULL), the plots are displayed on screen. See details.
xlim, ylim	a numeric vectors of length 2 specifying the lower and upper limits of the axes. By default (when NULL), xlim and ylim are computed. For forest plots, if the lower bound of any measure is smaller than xlim[1] or the upper bound of any measure is larger than xlim[2], arrows will be used at the limits to denote the bounds exceed the specified ranges.

<code>xlabel</code>	a numeric vector specifying at which tick-marks are to be drawn. By default (when NULL), tickmark locations are computed.
<code>addline</code>	a numeric value specifying the x-value for a vertical reference line at <code>x=addline</code> . Default is NULL
<code>xlog</code>	a logical value indicating whether a logarithmic scale should be used for x-axis. Default is TRUE for measures OR and RR and FALSE for measure RD.
<code>mar</code>	A numerical vector of 4 values which control the space (in the number of lines) between the axes and the border of the graph of the form <code>c(bottom, left, top, right)</code> the default values are NULL.
<code>ciShow</code>	a logical value; if TRUE (default), the true credible intervals numbers will display at the right hand side of the forest plot.
<code>...</code>	Other arguments can be passed to plot function

### Details

If `type="sidebyside"`, the posterior distributions of all study-specific measure are displayed side by side in 4-panel plots with study names.

If `type="overlap"`, the posterior distributions of all study-specific measure are displayed in one graph. To clarity, it is advisable to specify a few studies by `select` argument.

If `type="forest"`, a forest plot of all study-specific and overall measure with 95% credible/confidence intervals are plotted.

If `file=NULL`, the plots will be displayed on screen. Or else, the plots will be saved as `"/mmeta/codefile.pdf"`, where `"/"` denotes current working directory.

### Author(s)

Xiao Su <Xiao.Su@uth.tmc.edu>

### References

Luo, S., Chen, Y., Su, X., Chu, H., (2014). `mmeta`: An R Package for Multivariate Meta-Analysis. *Journal of Statistical Software*, 56(11), 1-26.

Chen, Y., Luo, S., (2011a). A Few Remarks on "Statistical Distribution of the Difference of Two Proportions" by Nadarajah and Kotz, *Statistics in Medicine* 2007; 26(18):3518-3523" . *Statistics in Medicine*, 30(15), 1913-1915.

Chen, Y., Chu, H., Luo, S., Nie, L., and Chen, S. (2014a). Bayesian analysis on meta-analysis of case-control studies accounting for within-study correlation. *Statistical Methods in Medical Research*, doi: 10.1177/0962280211430889. In press.

Chen, Y., Luo, S., Chu, H., Su, X., and Nie, L. (2014b). An empirical Bayes method for multivariate meta-analysis with an application in clinical trials. *Communication in Statistics: Theory and Methods*. In press.

Chen, Y., Luo, S., Chu, H., Wei, P. (2013). Bayesian inference on risk differences: an application to multivariate meta-analysis of adverse events in clinical trials. *Statistics in Biopharmaceutical Research*, 5(2), 142-155.



**See Also**

[multipletables summary.multipletables](#)

**Examples**

```
#library(mmeta)
# Analyze the dataset colorectal to conduct exact inference of the odds ratios
#data(colorectal)
#multiple.OR <- multipletables(data=colorectal, measure="OR", model="Sarmanov", method="exact")
# Generate the forest plot with 95% CIs of study-specific odds ratios
#and 95% CI of overall odds ratio
#plot(multiple.OR, type="forest", addline=1)
# Plot the posterior density functions of some target studies in an overlaying manner
#plot(multiple.OR, type="overlap", select=c(4,14,16,20))
# Plot the posterior density functions of some target studies in a
#side-by-side manner
#plot(multiple.OR, type="sidebyside", select=c(4,14,16,20), ylim=c(0,2.7), xlim=c(0.5,1.5))

# Analyze the dataset withdrawal to conduct inference of the relative risks
#data(withdrawal)
#multiple.RR <- multipletables(data=withdrawal, measure="RR",model="Sarmanov")
#plot(multiple.RR, type="forest", addline=1)
#plot(multiple.RR, type="overlap", select=c(3,8,14,16))
#plot(multiple.RR, type="sidebyside", select=c(3,8,14,16), ylim=c(0,1.2),
#xlim=c(0.4,3))

# Analyze the dataset withdrawal to conduct inference of the risk differences
#data(withdrawal)
#multiple.RD <- multipletables(data=withdrawal, measure="RD", model="Sarmanov")
#summary(multiple.RD)
#plot(multiple.RD, type="forest", addline=0)
#plot(multiple.RD, type="overlap", select=c(3,8,14,16))
#plot(multiple.RD, type="sidebyside", select=c(3,8,14,16))
#plot(multiple.RD, type="sidebyside", select=c(3,8,14,16),
#    ylim=c(0,6), xlim=c(-0.2,0.4))
```

---

plot.singletable

*Plot Method for singletable objects*

---

**Description**

Produces various plots for single table analysis.

**Usage**

```
## S3 method for class 'singletable'
plot(x, type=type, file=NULL, select=c(1,2)
, xlab=NULL, ylab=NULL, addline=NULL, xlim=NULL, ylim=NULL, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>singletable</code> .
<code>type</code>	a character string specifying the type of plots to produce. Options are <code>sidebyside</code> and <code>overlap</code> . See details
<code>file</code>	a character string specifying the filename as which the plots are saved. Default is <code>NULL</code> to view on screen. See details.
<code>select</code>	a numeric value or vector specifying which distribution should be plotted. <code>select=1</code> is posterior distribution. <code>select=2</code> is prior distribution. <code>select=c(1,2)</code> is both. Default is <code>c(1,2)</code> . This argument is only used when <code>type="sidebyside"</code> .
<code>xlab</code>	a character string specifying the x-axis label in the plot. Default is the name of the measure of association
<code>ylab</code>	a character string specifying the y-axis label in the plot. Default is "Density"
<code>addline</code>	a numeric value specifying the x-value for a vertical reference line at <code>x=addline</code> . Default is <code>NULL</code>
<code>xlim, ylim</code>	a numeric vectors of length 2 specifying the lower and upper limits of the axes
<code>...</code>	Other arguments can be passed to plot function

**Details**

If `type="sidebyside"`, the posterior distribution of measure and the prior distribution are drawn side by side in two plots. If `type="overlap"`, the posterior distribution of measure and the prior distribution are overlaid in one plot.

If `file=NULL`, the plots will be displayed on screen. Or else, the plots will be saved as `"/mmeta/codefile.pdf"`, where `"/"` denotes current working directory.

**References**

- Luo, S., Chen, Y., Su, X., Chu, H., (2014). `mmeta`: An R Package for Multivariate Meta-Analysis. *Journal of Statistical Software*, 56(11), 1-26.
- Chen, Y., Luo, S., (2011a). A Few Remarks on "Statistical Distribution of the Difference of Two Proportions" by Nadarajah and Kotz, *Statistics in Medicine* 2007; 26(18):3518-3523" . *Statistics in Medicine*, 30(15), 1913-1915.
- Chen, Y., Chu, H., Luo, S., Nie, L., and Chen, S. (2014a). Bayesian analysis on meta-analysis of case-control studies accounting for within-study correlation. *Statistical Methods in Medical Research*, doi: 10.1177/0962280211430889. In press.
- Chen, Y., Luo, S., Chu, H., Su, X., and Nie, L. (2014b). An empirical Bayes method for multivariate meta-analysis with an application in clinical trials. *Communication in Statistics: Theory and Methods*. In press.
- Chen, Y., Luo, S., Chu, H., Wei, P. (2013). Bayesian inference on risk differences: an application to multivariate meta-analysis of adverse events in clinical trials. *Statistics in Biopharmaceutical Research*, 5(2), 142-155.

**See Also**

[singletable](#)

**Examples**

```

# Inference under Jeffreys prior distribution
#single.OR.Jeffreys <- singletable(a1=0.5, b1=0.5, a2=0.5,
#                                b2=0.5, y1=40, n1=96, y2=49, n2=109,
#                                model="Independent",
#                                measure="OR", method="exact")
#summary(single.OR.Jeffreys)

# Inference under Laplace prior distribution
#single.OR.Laplace <- singletable(a1=1, b1=1, a2=1, b2=1,
#                                y1=40, n1=96, y2=49, n2=109,
#                                model="Independent", measure="OR",
#                                method="exact")
# Inference under Sarmanov prior distribution with positive correlation
#single.OR.Sar1 <- singletable(a1=0.5, b1=0.5, a2=0.5, b2=0.5,
#                              rho=0.5, y1=40, n1=96, y2=49, n2=109,
#                              model="Sarmanov",
#                              measure="OR", method="exact")
# Inference under Sarmanov prior distribution with negative correlation
#single.OR.Sar2 <- singletable(a1=0.5, b1=0.5, a2=0.5, b2=0.5,
#                              rho=-0.5, y1=40, n1=96, y2=49, n2=109,
#                              model="Sarmanov",
#                              measure="OR", method="exact")
# generate a 2X2 panel plot
#par(mfrow=c(2,2))
#plot(single.OR.Jeffreys, type="overlap", xlim=c(0.5, 2),
#      # main="Jefferys Prior")
#plot(single.OR.Laplace, type="overlap", xlim=c(0.5, 2),
#      # main="Laplace Prior")
#plot(single.OR.Sar1, type="overlap", xlim=c(0.5, 2),
#      # main=expression(paste("Sarmanov Prior ",rho," = 0.5")))
#plot(single.OR.Sar2, type="overlap", xlim=c(0.5, 2),
#      # main=expression(paste("Sarmanov Prior ",rho," = -0.5")))

```

---

singletable

*Exact posterior inference based on a single 2x2 table*


---

**Description**

This function conducts exact posterior inference based on a single 2x2 table.

**Usage**

```

singletable(y1=y1,n1=n1,y2=y2,n2=n2,measure=measure,model="Sarmanov",
            method="exact",a1=0.5,b1=0.5,a2=0.5,b2=0.5,rho=0,alpha=0.05,
            nsam=10000)

```

**Arguments**

y1	an integer indicating the number of events in group 1
n1	an integer indicating the total number of subjects in group 1
y2	an integer indicating the number of events in group 2
n2	an integer indicating the total number of subjects in group 2
measure	a character string specifying a measure. Options are OR, RR, and RD. OR is odds ratio, RR is relative risk, and RD is risk difference.
model	a character string specifying the model. Options are independent and Sarmanov. Independent is independent beta-binomial model. Sarmanov is Sarmanov beta-binomial model.
method	a character string specifying the method. Options are exact and sampling. exact (default) is a method based on Monte Carlo sampling. exact is exact method.
a1	a numeric value specifying the first hyperparameter of the beta prior for group 1. Default value set to 0.5
b1	a numeric value specifying the second hyperparameter of the beta prior for group 1. Default value set to 0.5
a2	a numeric value specifying the first hyperparameter of the beta prior for group 2. Default value set to 0.5
b2	a numeric value specifying the second hyperparameter of the beta prior for group 2. Default value set to 0.5
rho	a numeric value specifying correlation coefficient for Sarmanov bivariate prior distribution. Default value set to 0. It is subject to constraints. See Details.
alpha	a numeric value specifying the significant level. Default value sets to 0.05.
nsam	a numeric value specifying the number of samples if method is "sampling". Default value sets to 10000

**Details**

There are two kinds of study design, i.e., prospective study or clinical trial, and retrospective or case-control study. In a prospective study or clinical trial, data is a data frame that contains y1, n1, y2, n2, studynames. y1 is the number of subjects experienced a certain event in the unexposed group. n1 is the number of subjects in the unexposed group. y2 is the number of subjects experienced a certain event in the exposed group. n2 is the number of subjects in the exposed group. In this study, OR is odds ratio of event comparing exposed group with unexposed group. RR is relative risk of event comparing exposed group with unexposed group. RD is risk difference of event comparing exposed group with unexposed group.

For case-control study, y1 is the number of subjects with exposure in the control group. n1 is the number of subjects in the control group. y2 is the number of subjects with exposure in the case group. n2 is the number of subjects in the case group. In this study, OR is odds ratio of event comparing case group with control group. RR is relative risk of event comparing case group with control group. RD is risk difference of event comparing case group with control group.

When model="Sarmanov", rho is subject to constraints. See Chen et al (2011) for details.

**Value**

An object is returned, inheriting from class `singletable`. Objects of this class have methods for the generic functions `summary` and `plot`. The following components must be included in a legitimate `singletable` object.

<code>measure</code>	the value of <code>measure</code> argument.
<code>model</code>	the value of <code>model</code> argument.
<code>method</code>	the value of <code>method</code> argument.
<code>dataset</code>	a numeric vector of input data with components: <code>y1</code> , <code>n1</code> , <code>y2</code> , <code>n2</code>
<code>parameter</code>	a numeric vector of the hyperparameters: <code>a1</code> , <code>b1</code> , <code>a2</code> , <code>b2</code> , and <code>rho</code> .
<code>alpha</code>	the value of <code>alpha</code> argument.
<code>sample</code>	a list of samples for the posterior and prior distributions
<code>density</code>	a list of the density of the posterior and prior distributions
<code>studynames</code>	a character vector specifying the study names.

**References**

Luo, S., Chen, Y., Su, X., Chu, H., (2014). `mmeta`: An R Package for Multivariate Meta-Analysis. *Journal of Statistical Software*, 56(11), 1-26.

Chen, Y., Luo, S., (2011a). A Few Remarks on "Statistical Distribution of the Difference of Two Proportions" by Nadarajah and Kotz, *Statistics in Medicine* 2007; 26(18):3518-3523". *Statistics in Medicine*, 30(15), 1913-1915.

Chen, Y., Chu, H., Luo, S., Nie, L., and Chen, S. (2014a). Bayesian analysis on meta-analysis of case-control studies accounting for within-study correlation. *Statistical Methods in Medical Research*, doi: 10.1177/0962280211430889. In press.

Chen, Y., Luo, S., Chu, H., Su, X., and Nie, L. (2014b). An empirical Bayes method for multivariate meta-analysis with an application in clinical trials. *Communication in Statistics: Theory and Methods*. In press.

Chen, Y., Luo, S., Chu, H., Wei, P. (2013). Bayesian inference on risk differences: an application to multivariate meta-analysis of adverse events in clinical trials. *Statistics in Biopharmaceutical Research*, 5(2), 142-155.

**See Also**

[multipletables](#) [plot.singletable](#) [summary.singletable](#)

**Examples**

```
# Inference under Jeffreys prior distribution
#single.OR.Jeffreys <- singletable(a1=0.5, b1=0.5, a2=0.5,
#                                b2=0.5, y1=40, n1=96, y2=49, n2=109,
#                                model="Independent",
#                                measure="OR", method="exact")
#summary(single.OR.Jeffreys)

# Inference under Laplace prior distribution
```

```

#single.OR.Laplace <- singletable(a1=1, b1=1, a2=1, b2=1,
#                               y1=40, n1=96, y2=49, n2=109,
#                               model="Independent", measure="OR",
#                               method="exact")
#summary(single.OR.Laplace)

# Inference under Sarmanov prior distribution with positive correlation
#single.OR.Sar1 <- singletable(a1=0.5, b1=0.5, a2=0.5, b2=0.5,
#                              rho=0.5, y1=40, n1=96, y2=49, n2=109,
#                              model="Sarmanov",
#                              measure="OR", method="exact")
#summary(single.OR.Sar1)

# Inference under Sarmanov prior distribution with negative correlation
#single.OR.Sar2 <- singletable(a1=0.5, b1=0.5, a2=0.5, b2=0.5,
#                              rho=-0.5, y1=40, n1=96, y2=49, n2=109,
#                              model="Sarmanov",
#                              measure="OR", method="exact")
#summary(single.OR.Sar2)

# generate a 2X2 panel plot
#par(mfrow=c(2,2))
#plot(single.OR.Jeffreys, type="overlap", xlim=c(0.5, 2),
#      main="Jefferys Prior",file="singleOR_Jef")
#plot(single.OR.Laplace, type="overlap", xlim=c(0.5, 2),
#      main="Laplace Prior",file="singleOR_La")
#plot(single.OR.Sar1, type="overlap", xlim=c(0.5, 2),
#      main=expression(paste("Sarmanov Prior ",rho," = 0.5")),file="singleOR_Sar1")
#plot(single.OR.Sar2, type="overlap", xlim=c(0.5, 2),
#      main=expression(paste("Sarmanov Prior ",rho," = -0.5")),file="singleOR_Sar2")

```

---

summary.multipletables

*Summary a specific study of objects multipletables*

---

## Description

Summary a model of class multipletables fitted by multipletables.

## Usage

```
## S3 method for class 'multipletables'
summary(object,...)
```

## Arguments

object            an object inheriting from class multipletables.  
...                additional arguments; currently none is used.

**Value**

A list with the following components:

model	the value of model argument.
measure	the value of measure argument.
cov.matrix	the estimated covariance matrix of the estimated parameters in the transformed scales
hessian	the estimated hessian matrix of the estimated parameters in the transformed scales
overall	a list of two components that contain the overall measure (e.g., overall OR) and its 95% equal-tail credible interval.
studynames	a character string indicating all the study names
chi2	the chi-square test statistics of the likelihood ratio test
pvalue	the p-value of the likelihood ratio test
alpha	the value of alpha argument.
MLE	a numeric vector of the estimated hyperparameters in the following order: a1, b1, a2, b2, rho.
studyspecific	a Numeric matrix with columns being the posterior means, the lower bound, and the upper bound of the credible/confidence intervals of study-specific and overall measure.

**References**

- Luo, S., Chen, Y., Su, X., Chu, H., (2014). mmeta: An R Package for Multivariate Meta-Analysis. *Journal of Statistical Software*, 56(11), 1-26.
- Chen, Y., Luo, S., (2011a). A Few Remarks on "Statistical Distribution of the Difference of Two Proportions" by Nadarajah and Kotz, *Statistics in Medicine* 2007; 26(18):3518-3523" . *Statistics in Medicine*, 30(15), 1913-1915.
- Chen, Y., Chu, H., Luo, S., Nie, L., and Chen, S. (2014a). Bayesian analysis on meta-analysis of case-control studies accounting for within-study correlation. *Statistical Methods in Medical Research*, doi: 10.1177/0962280211430889. In press.
- Chen, Y., Luo, S., Chu, H., Su, X., and Nie, L. (2014b). An empirical Bayes method for multivariate meta-analysis with an application in clinical trials. *Communication in Statistics: Theory and Methods*. In press.
- Chen, Y., Luo, S., Chu, H., Wei, P. (2013). Bayesian inference on risk differences: an application to multivariate meta-analysis of adverse events in clinical trials. *Statistics in Biopharmaceutical Research*, 5(2), 142-155.

**See Also**

[multipletables](#) [plot.multipletables](#)

**Examples**

```

#library(mmeta)

# Analyze the dataset colorectal to conduct exact inference of the odds ratios
#data(colorectal)
#multiple.OR <- multiplatables(data=colorectal, measure="OR", model="Sarmanov", method="exact")
# Generate the forest plot with 95% CIs of study-specific odds ratios
#and 95% CI of overall odds ratio
#plot(multiple.OR, type="forest", addline=1)
# Plot the posterior density functions of some target studies in an overlaying manner
#plot(multiple.OR, type="overlap", select=c(4,14,16,20))
# Plot the posterior density functions of some target studies in a
#side-by-side manner
#plot(multiple.OR, type="sidebyside", select=c(4,14,16,20), ylim=c(0,2.7), xlim=c(0.5,1.5))

# Analyze the dataset withdrawal to conduct inference of the relative risks
#data(withdrawal)
#multiple.RR <- multiplatables(data=withdrawal, measure="RR", model="Sarmanov")
#plot(multiple.RR, type="forest", addline=1)
#plot(multiple.RR, type="overlap", select=c(3,8,14,16))
#plot(multiple.RR, type="sidebyside", select=c(3,8,14,16), ylim=c(0,1.2),
#xlim=c(0.4,3))

# Analyze the dataset withdrawal to conduct inference of the risk differences
#data(withdrawal)
#multiple.RD <- multiplatables(data=withdrawal, measure="RD",
#                               model="Sarmanov")
#summary(multiple.RD)
#plot(multiple.RD, type="forest", addline=0)
#plot(multiple.RD, type="overlap", select=c(3,8,14,16))
#plot(multiple.RD, type="sidebyside", select=c(3,8,14,16))
#plot(multiple.RD, type="sidebyside", select=c(3,8,14,16),
#     ylim=c(0,6), xlim=c(-0.2,0.4))

```

---

summary.singletable    *Summarize the objects singletable*

---

**Description**

Summary a model of class singletable fitted by singletable.

**Usage**

```

## S3 method for class 'singletable'
summary(object,...)

```





```
# Inference under Sarmanov prior distribution with negative correlation
#single.OR.Sar2 <- singletable(a1=0.5, b1=0.5, a2=0.5, b2=0.5,
#                             rho=-0.5, y1=40, n1=96, y2=49, n2=109,
#                             model="Sarmanov",
#                             measure="OR", method="exact")
# generate a 2X2 panel plot
#par(mfrow=c(2,2))
#plot(single.OR.Jeffreys, type="overlap", xlim=c(0.5, 2),
#      # main="Jefferys Prior")
#plot(single.OR.Laplace, type="overlap", xlim=c(0.5, 2),
#      # main="Laplace Prior")
#plot(single.OR.Sar1, type="overlap", xlim=c(0.5, 2),
#      # main=expression(paste("Sarmanov Prior ",rho," = 0.5")))
#plot(single.OR.Sar2, type="overlap", xlim=c(0.5, 2),
#      # main=expression(paste("Sarmanov Prior ",rho," = -0.5")))
```

---

withdrawal

*Studies on the association of withdrawal from study due to adverse events and tricyclic treatment*

---

### Description

Results from 16 clinical trials investigating the association of withdrawal from study due to adverse events and tricyclic treatment

### Format

The data frame contains the following columns:

**y1** number of subjects withdrew due to adverse events in the placebo group

**n1** number of subjects in the placebo group

**y2** number of subjects withdrew due to adverse events in the tricyclic treatment group

**n2** number of subjects in the tricyclic treatment group

**studynames** The study names indicating the last name of the first author and the year of each study

### Note

The dataset `withdrawal` is used to conduct exact posterior inference of relative risks and risk difference for multiple 2X2 tables.

### References

Jackson, J. L., Shimeall, W., Sessums, L., DeZee, K. J., Becher, D., Diemer, M., Berbano, E., O'Malley, P. G. (2010) Tricyclic antidepressants and headaches: systematic review and meta-analysis. *BMJ*, 341, C5222-c5234.

### See Also

[multipletables](#), [summary.multipletables](#), [plot.multipletables](#),

**Examples**

```
library(mmeta)  
data(withdrawal)  
summary(withdrawal)
```

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