Package: NMADTA (via r-universe)

May 15, 2026

Type Package

Title Network Meta-Analysis of Multiple Diagnostic Tests

Version 0.1.3

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Depends R (>= 4.0.0)

Imports rjags (>= 4-6), coda, ggplot2, ks, reshape2, MCMCpack, MASS, plotrix, graphics, stats, grDevices, Rdpack

SystemRequirements JAGS 4.x.y (http://mcmc-jags.sourceforge.net)

Description Provides statistical methods for network meta-analysis of diagnostic tests to simultaneously compare multiple tests within a missing data framework, including: - Bayesian hierarchical model for network meta-analysis of multiple diagnostic tests (Ma, Lian, Chu, Ibrahim, and Chen (2018) <doi:10.1093/biostatistics/kxx025>) - Bayesian Hierarchical Summary Receiver Operating Characteristic Model for Network Meta-Analysis of Diagnostic Tests (Lian, Hodges, and Chu (2019) <doi:10.1080/01621459.2018.1476239>).

License GPL (>= 2)

RdMacros Rdpack

Encoding UTF-8

RoxygenNote 7.3.3

Suggests testthat

NeedsCompilation no

LazyData true

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Config/pak/sysreqs jags libicu-dev

Repository https://xxing8jh.r-universe.dev

Date/Publication 2026-04-15 21:10:25 UTC

RemoteUrl https://github.com/cran/NMADTA

RemoteRef HEAD

RemoteSha 3a26d065d548e0bf246dd3fef78d12c30c07bd28

Contents

`dat.kang` *Study-level results on the multiple diagnostic tests for colorectal cancer detection*

Description

`dat.kang` provides an example dataset for hierarchical network meta-analysis of diagnostic test accuracy under the missing not at random (MNAR) assumption. The dataset is extracted from (Kang et al. 2013) and contains study-level results from multiple diagnostic tests for colorectal cancer detection. Each record corresponds to a study arm with test outcomes and missingness indicators.

Usage

```
data(dat.kang)
```

Format

A data frame with 48 observations and 8 variables:

sid Study identifier (integer)

delta0 Missing indicator for test 0 (1 = observed, 0 = missing)

delta1 Missing indicator for test 1 (1 = observed, 0 = missing)

delta2 Missing indicator for test 2 (1 = observed, 0 = missing)

T0 Test 0 result (1 = positive, 0 = negative, 999 = not applicable)

T1 Test 1 result (1 = positive, 0 = negative, 999 = not applicable)

T2 Test 2 result (1 = positive, 0 = negative, 999 = not applicable)

n Sample size for the corresponding cell

Source

Kang J, Brant R, Ghali WA (2013). "Statistical Methods for the Meta-Analysis of Diagnostic Tests Must Take into Account the Use of Surrogate Standards." *Journal of Clinical Epidemiology*, **66**(5), 566–574. doi:10.1016/j.jclinepi.2012.12.008.

Examples

```
data(dat.kang)
head(dat.kang)
```

`nmadt.hierarchical` *Hierarchical Model for Network Meta-Analysis of Diagnostic Accuracy Studies*

Description

`nmadt.hierarchical` performs meta-analysis using the hierarchical model (Ma et al. 2018) and outputs CIs for accuracy measurements.

Usage

```
nmadt.hierarchical(
  nstu,
  K,
  data,
  testname,
  directory = NULL,
  diag = 5,
  off_diag = 0.05,
  digits = 4,
  mu_alpha = 0,
  mu_beta = 0,
  mu_eta = -0,
  preci_alpha = 0.1,
  preci_beta = 0.1,
  preci_eta = 0.1,
  n.adapt = 5000,
  n.iter = 50000,
  n.chains = 3,
  n.burnin = floor(n.iter/2),
  n.thin = max(1, floor((n.iter - n.burnin)/50000)),
  conv.diag = FALSE,
  trace = NULL,
  dic = FALSE,
  mcmc.samples = FALSE
)
```

Arguments

nstu	an integer indicating the number of studies included in the dataset.
K	an integer indicating the number of candiate test in the dataset.
data	a list conating the input dataset to be used for meta-analysis.
testname	a string vector of the names of the candidate tests in the dataset in the same order as presetned in the dataset.
directory	a string specifying the designated directory to save trace plots or potential scale reduction factors calculated in the function. The default is NULL.
diag	A number specifying the diagonal entries of the scale matrix R in the Wishart prior for the precision matrix Σ^{-1}. Larger values of diag typically imply stronger prior shrinkage, favoring smaller between-study variability in prevalence, sensitivity, and specificity. The default is 5.
off_diag	A number specifying the off-diagonal entries of the scale matrix R in the Wishart prior for Σ^{-1}, controlling the strength of prior dependence among random effects (e.g., correlations between sensitivity and specificity and their association with prevalence). The default is 0.05. If strong correlations are expected, users may increase off_diag; if substantially larger heterogeneity is anticipated, users may decrease diag. We recommend sensitivity analyses alongside standard MCMC diagnostics.
digits	A positive integer specifying the number of digits to the right of the decimal point to keep in the printed results; the default is digits = 4.
mu_alpha	a number indicating the mean of the normal distribution that the prior of the fixed effect for sensitivity follows. The default is 0.
mu_beta	a number indicating the mean of the normal distribution that the prior of the fixed effect for specificity follows. The default is 0.
mu_eta	a number indicating the mean of the normal distribution that the prior of the fixed effect for prevalence follows. The default is 0.
preci_alpha	a number indicating the precision of the normal distribution that the prior of the fixed effect for sensitivity follows. The default is 0.1.
preci_beta	a number indicating the precision of the normal distribution that the prior of the fixed effect for specificity follows. The default is 0.1.
preci_eta	a number indicating the precision of the normal distribution that the prior of the fixed effect for prevalence follows. The default is 0.1.
n.adapt	a positive integer indicating the number of iterations for adaptation. The default is 5,000.
n.iter	a postive integer indicating the number of iterations in each MCMC chain. The default is 50,000.
n.chains	a postive interger indicating the number of MCMC chains. The default is 3.
n.burnin	a positive integer indicating the number of burn-in iterations at the beginning of each chain without saving any of the posterior samples. The default is floor(n.iter/2).
n.thin	the thinning rate for MCMC chains, which is used to save memory and computation time when n.iter is large. For example, the algorithm saves only one sample in every nth iteration, where n is given by n.thin.

conv.diag	a logical value specifying whether to compute potential scale reduction factors proposed for convergence diagnostics. The default is FALSE.
trace	a string vector containing a subset of different quantities which can be chosen from prevalence("prev"), sensitivity ("Se"), specificity ("Sp"), positive and negative predictive values ("ppv" and "npv" repectively), positive likelihood ("LRpos"), and negative likelihood ("LRneg").
dic	a logical value indicating whether the function will output the deviance information criterion (DIC) statistic. The default is false.
mcmc.samples	a logical value indicating whether the coda samples generated in the meta-analysis. The default is FALSE.

Value

A list with the raw output for graphing the results, the effect size estimates, which lists the posterior mean, standard deviation, median, and a 95% equal tail credible interval for the median.

Note

This example uses a small number of MCMC iterations (n.iter = 500) for demonstration. For real-world analyses, longer chains (e.g., n.iter = 50000) are recommended to achieve convergence and stable posterior summaries.

References

Ma X, Lian Q, Chu H, Ibrahim JG, Chen Y (2018). "A Bayesian hierarchical model for network meta-analysis of multiple diagnostic tests." *Biostatistics*, **19**(1), 87–102. ISSN 14684357, doi:10.1093/biostatistics/kxx025.

Examples

```
data(dat.kang)
set.seed(9)
kang.out <- nmadt.hierarchical(nstu = 12, K = 2, data = dat.kang,
                        directory = tempdir(), testname = c("D-dimer", "Ultrasonography"),
                          diag = 5, off_diag = 0.05, digits = 4, mu_alpha = 0, mu_beta = 0,
                          mu_eta = 0, preci_alpha = 0.1, preci_beta = 0.1, preci_eta = 0.1,
                             n.adapt = 1000, n.iter = 500, n.chains = 3, conv.diag = TRUE,
                                trace = "prev", dic = TRUE, mcmc.samples = FALSE)
```

---

nmadt.hierarchical.MNAR

Hierarchical Model Network Meta-Analysis of Diagnostic Accuracy Studies Under MNAR Assumptions

---

Description

`nmadt.hierarchical.MNAR` performs meta-analysis using the hierarchical model (Ma et al. 2018) based on the missing not at random(MNAR) assumption.

Usage

```
nmadt.hierarchical.MNAR(
  nstu,
  K,
  data,
  testname,
  directory = NULL,
  diag = 5,
  off_diag = 0.05,
  digits = 4,
  mu_alpha = 0,
  mu_beta = 0,
  mu_eta = -0,
  preci_alpha = 0.1,
  preci_beta = 0.1,
  preci_eta = 0.1,
  gamma1,
  gamma0,
  mu_gamma = 0,
  preci_gamma = 1,
  n.burnin = floor(n.iter/2),
  n.thin = max(1, floor((n.iter - n.burnin)/1e+05)),
  n.adapt = 5000,
  n.iter = 50000,
  n.chains = 3,
  conv.diag = FALSE,
  trace = NULL,
  dic = FALSE,
  mcmc.samples = FALSE
)
```

Arguments

`nstu`	an integer indicating the number of studies included in the dataset.
`K`	an integer indicating the number of candidate test in the dataset.
`data`	a list containing the input dataset to be used for meta-analysis.
`testname`	a string vector of the names of the candidate tests in the dataset in the same order as presetned in the dataset.
`directory`	a string specifying the designated directory to save trace plots or potential scale reduction factors calculated in the function. The default is NULL.
`diag`	A number specifying the diagonal entries of the scale matrix R in the Wishart prior for the precision matrix Σ^{-1}. Larger values of `diag` typically imply stronger

prior shrinkage, favoring smaller between-study variability in prevalence, sensitivity, and specificity. The default is 5.

`off_diag` A number specifying the off-diagonal entries of the scale matrix R in the Wishart prior for Σ^{-1}, controlling the strength of prior dependence among random effects (e.g., correlations between sensitivity and specificity and their association with prevalence). The default is `0.05`. If strong correlations are expected, users may increase `off_diag`; if substantially larger heterogeneity is anticipated, users may decrease `diag`. We recommend sensitivity analyses alongside standard MCMC diagnostics.

`digits` A positive integer specifying the number of digits to the right of the decimal point to keep in the printed results; the default is `digits = 4`.

`mu_alpha` a number indicating the mean of the normal distribution that the prior of the fixed effect for sensitivity follows. The default is 0.

`mu_beta` a number indicating the mean of the normal distribution that the prior of the fixed effect for specificity follows. The default is 0.

`mu_eta` a number indicating the mean of the normal distribution that the prior of the fixed effect for prevalence follows. The default is 0.

`preci_alpha` a number indicating the precision of the normal distribution that the prior of the fixed effect for sensitivity follows. The default is 0.1.

`preci_beta` a number indicating the precision of the normal distribution that the prior of the fixed effect for specificity follows. The default is 0.1.

`preci_eta` a number indicating the precision of the normal distribution that the prior of the fixed effect for prevalence follows. The default is 0.1.

`gamma1` A numeric vector (length `K`) for coefficients on $\text{logit}(\text{Se}_{ik})$ in the MNAR missingness model. Recommended to treat as sensitivity-analysis parameters. See `gamma0` for suggested grids and interpretation.

`gamma0` A numeric vector (length `K`) for coefficients on $\text{logit}(\text{Sp}_{ik})$ in the MNAR missingness model. Recommended to treat as sensitivity-analysis parameters. $\gamma_{0k} = 0$ corresponds to MAR with respect to accuracy; negative values (e.g., `c(0, -0.5, -1, -2)`) represent the common assumption that tests with poorer accuracy are more likely to be missing.

`mu_gamma` a number specifying mean of intercept in the MNAR model. The default is 0.

`preci_gamma` a number specifying precision of intercept in the MNAR model. The default is 1.

`n.burnin` a positive integer indicating the number of burn-in iterations at the beginning of each chain without saving any of the posterior samples. The default is `floor(n.iter/2)`.

`n.thin` the thinning rate for MCMC chains, which is used to save memory and computation time when `n.iter` is large. For example, the algorithm saves only one sample in every nth iteration, where n is given by `n.thin`.

`n.adapt` a positive integer indicating the number of iterations for adaptation. The default is 5,000.

`n.iter` a positive integer indicating the number of iterations in each MCMC chain. The default is 50,000.

n.chains	a positive integer indicating the number of MCMC chains. The default is 3.
conv.diag	a logical value specifying whether to compute potential scale reduction factors proposed for convergence diagnostics. The default is FALSE.
trace	a string vector containing a subset of different quantities which can be chosen from prevalence("prev"), sensitivity ("Se"), specificity ("Sp"), positive and negative predictive values ("ppv" and "npv" repectively), positive likelihood ("LRpos"), and negative likelihood ("LRneg").
dic	a logical value indicating whether the function will output the deviance information criterion (DIC) statistic. The default is false.
mcmc.samples	a logical value indicating whether the coda samples generated in the meta-analysis. The default is FALSE.

Value

A list with the raw output for graphing the results, the effect size estimates, which lists the posterior mean, standard deviation, median, and a 95% equal tail credible interval for the median.

Note

This example uses a small number of MCMC iterations (n.iter = 1000) for demonstration. For real-world analyses, longer chains (e.g., n.iter = 50000) are recommended to achieve convergence and stable posterior summaries.

References

Ma X, Lian Q, Chu H, Ibrahim JG, Chen Y (2018). "A Bayesian hierarchical model for network meta-analysis of multiple diagnostic tests." *Biostatistics*, **19**(1), 87–102. ISSN 14684357, doi:10.1093/biostatistics/kxx025.

Examples

```
data(dat.kang)
set.seed(9)
kang.out <- nmadt.hierarchical.MNAR(nstu = 12, K = 2, data = dat.kang,
                                    directory = tempdir(),
                                    testname = c("D-dimer", "Ultrasonography"),
                                    n.adapt = 1000, n.iter = 1000, n.chains = 2,
                                    gamma1=c(-0.5,-0.5), gamma0=c(-0.5,-0.5))
```

---

nmadt.hsroc *HSROC Model for Network Meta-Analysis of Diagnostic Accuracy Studies*

Description

nmadt.hsroc performs network meta-analysis of diagnostic tests using the HSROC (hierarchical summary receiver operating characteristic) model (Lian et al. 2019) and outputs estimations of accuracy measurements.

Usage

```
nmadt.hsroc(
  nstu,
  K,
  data,
  testname,
  directory = NULL,
  eta = 0,
  xi_preci = 1.25,
  digits = 4,
  n.adapt = 5000,
  n.iter = 50000,
  n.chains = 3,
  n.burnin = floor(n.iter/2),
  n.thin = max(1, floor((n.iter - n.burnin)/1e+05)),
  conv.diag = FALSE,
  trace = NULL,
  dic = FALSE,
  mcmc.samples = FALSE
)
```

Arguments

`nstu`	an integer indicating the number of studies included in the dataset.
`K`	an integer indicating the number of candiate test in the dataset.
`data`	a list conating the input dataset to be used for meta-analysis.
`testname`	a string vector of the names of the candidate tests in the dataset in the same order as presetned in the dataset.
`directory`	a string specifying the designated directory to save trace plots or potential scale reduction factors calculated in the function. The default is NULL.
`eta`	a number indicating the mean of log(S) and log(P) which determines the covariance matrices of the cutoff values and accuracy values respectively. The default is 0.
`xi_preci`	a number indicating the precision of log(S) and log(P) which determines the covariance matrices of the cutoff values and accuracy values respectively. The default is 1.25.
`digits`	a positive integer he number of digits to the right of the decimal point to keep for the results; digits=4 by default.
`n.adapt`	a positive integer indicating the number of iterations for adaptation. The default is 5,000.
`n.iter`	a postive integer indicating the number of iterations in each MCMC chain. The default is 50,000.
`n.chains`	a postive interger indicating the number of MCMC chains. The default is 3.
`n.burnin`	a positive integer indicating the number of burn-in iterations at the beginning of each chain without saving any of the posterior samples. The default is `floor(n.iter/2)`.

n.thin	the thinning rate for MCMC chains, which is used to save memory and computation time when n.iter is large. For example, the algorithm saves only one sample in every nth iteration, where n is given by n.thin.
conv.diag	a logical value specifying whether to compute potential scale reduction factors proposed for convergence diagnostics. The default is FALSE.
trace	a string vector containing a subset of different quantities which can be chosen from prevalence("prev"), sensitivity ("Se"), specificity ("Sp"), positive and negative predictive values ("ppv" and "npv" repectively), positive likelihood ("LRpos"), and negative likelihood ("LRneg").
dic	a logical value indicating whether the function will output the deviance information criterion (DIC) statistic. The default is false.
mcmc.samples	a logical value indicating whether the coda samples generated in the meta-analysis. The default is FALSE.

Value

A list with the raw output for graphing the results, the effect size estimates, which lists the posterior mean, standard deviation, median, and a 95% equal tail credible interval for the median.

References

Lian Q, Hodges JS, Chu H (2019). "A Bayesian Hierarchical Summary Receiver Operating Characteristic Model for Network Meta-Analysis of Diagnostic Tests." *Journal of the American Statistical Association*, **114**(527), 949-961. doi:10.1080/01621459.2018.1476239.

Examples

```
data(dat.kang)
set.seed(9)
kang.out.hsroc <- nmadt.hsroc(nstu=12, K=2, data=dat.kang, testname=c("D-dimer","Ultrasonography"))
```

---

nmadt.hsroc.MNAR *HSROC Model for Network Meta-Analysis of Diagnostic Accuracy Studies Under MNAR Assumptions*

Description

nmadt.hsroc.MNAR performs network meta-analysis of diagnostic tests using the HSROC (hierarchical summary receiver operating characteristic) model (Lian et al. 2019) based on the MNAR assumption.

Usage

```
nmadt.hsroc.MNAR(
  nstu,
  K,
  data,
  testname,
  directory = NULL,
  eta = 0,
  xi_preci = 1.25,
  digits = 4,
  gamma1,
  gamma0,
  mu_gamma = 0,
  preci_gamma = 1,
  n.adapt = 10000,
  n.iter = 50000,
  n.chains = 3,
  n.burnin = floor(n.iter/2),
  n.thin = max(1, floor((n.iter - n.burnin)/1e+05)),
  conv.diag = FALSE,
  trace = NULL,
  dic = FALSE,
  mcmc.samples = FALSE
)
```

Arguments

nstu	an integer indicating the number of studies included in the dataset.
K	an integer indicating the number of candidate test in the dataset.
data	a list containing the input dataset to be used for meta-analysis.
testname	a string vector of the names of the candidate tests in the dataset in the same order as presetned in the dataset.
directory	a string specifying the designated directory to save trace plots or potential scale reduction factors calculated in the function. The default is NULL.
eta	a number indicating the mean of log(S) and log(P) which determines the covariance matrices of the cutoff values and accuracy values respectively. The default is 0.
xi_preci	a number indicating the precision of log(S) and log(P) which determines the covariance matrices of the cutoff values and accuracy values respectively. The default is 1.25.
digits	a positive integer he number of digits to the right of the decimal point to keep for the results; digits=4 by default.
gamma1	A numeric vector (length K) for coefficients on logit(Se_{ik}) in the MNAR missingness model. Recommended to treat as sensitivity-analysis parameters. See gamma0 for suggested grids and interpretation.

gamma0	A numeric vector (length K) for coefficients on logit(Sp_{ik}) in the MNAR missingness model. Recommended to treat as sensitivity-analysis parameters. $\gamma_{0k} = 0$ corresponds to MAR with respect to accuracy; negative values (e.g., c(0, -0.5, -1, -2)) represent the common assumption that tests with poorer accuracy are more likely to be missing.
mu_gamma	a number specifying mean of intercept in the MNAR model. The default is 0.
preci_gamma	a number specifying precision of intercept in the MNAR model. The default is 1.
n.adapt	a positive integer indicating the number of iterations for adaptation. The default is 5,000.
n.iter	a positive integer indicating the number of iterations in each MCMC chain. The default is 50,000.
n.chains	a positive integer indicating the number of MCMC chains. The default is 3.
n.burnin	a positive integer indicating the number of burn-in iterations at the beginning of each chain without saving any of the posterior samples. The default is floor(n.iter/2).
n.thin	the thinning rate for MCMC chains, which is used to save memory and computation time when n.iter is large. For example, the algorithm saves only one sample in every nth iteration, where n is given by n.thin.
conv.diag	a logical value specifying whether to compute potential scale reduction factors proposed for convergence diagnostics. The default is FALSE.
trace	a string vector containing a subset of different quantities which can be chosen from prevalence("prev"), sensitivity ("Se"), specificity ("Sp"), positive and negative predictive values ("ppv" and "npv" repectively), positive likelihood ("LRpos"), and negative likelihood ("LRneg").
dic	a logical value indicating whether the function will output the deviance information criterion (DIC) statistic. The default is false.
mcmc.samples	a logical value indicating whether the coda samples generated in the meta-analysis. The default is FALSE.

Value

A list with the raw output for graphing the results, the effect size estimates, which lists the posterior mean, standard deviation, median, and a 95% equal tail credible interval for the median.

References

Lian Q, Hodges JS, Chu H (2019). "A Bayesian Hierarchical Summary Receiver Operating Characteristic Model for Network Meta-Analysis of Diagnostic Tests." *Journal of the American Statistical Association*, **114**(527), 949-961. doi:10.1080/01621459.2018.1476239.

Examples

```
data(dat.kang)
set.seed(9)
kangMNAR.out.hsroc <- nmadt.hsroc.MNAR(nstu=12, K=2, data=dat.kang,
testname=c("D-dimer","Ultrasonography"),gamma1=c(-0.5,-0.5), gamma0=c(-0.5,-0.5))
```

`plot.nmadt` *Plot method for 'nmadt' objects*

Description

This method automatically generates diagnostic meta-analysis plots based on the fitted 'nmadt' object and the specified plot 'type'.

Usage

```
## S3 method for class 'nmadt'
plot(x, type = c("sroc", "density", "forest", "contour"), ...)
```

Arguments

`x`	An object of class 'nmadt', typically produced by one of the model-fitting functions: • `nmadt.hierarchical()` — hierarchical model under MAR assumption; • `nmadt.hsroc()` — HSROC model under MAR assumption; • `nmadt.hierarchical.MNAR()` — hierarchical model allowing for MNAR (missing not at random) mechanism; • `nmadt.hsroc.MNAR()` — HSROC model allowing for MNAR mechanism. These functions all return an object of class 'nmadt' suitable for plotting.
`type`	Character string specifying the type of plot to generate. One of `"sroc"`, `"density"`, `"forest"`, or `"contour"`. Defaults to `"sroc"` if not specified.
`...`	Additional arguments passed to the underlying plotting functions (e.g., graphical parameters such as `cex.axis`, `cex.lab`, etc.).

Details

The available plot types are:

"sroc" (default) Summary Receiver Operating Characteristic (SROC) curve. Visualizes the trade-off between sensitivity and specificity across studies, along with the hierarchical model fit.

"density" Posterior density plots for study- and test-level sensitivity and specificity parameters. Useful for checking convergence and posterior uncertainty.

"forest" Forest plot summarizing point estimates and uncertainty intervals for sensitivity and specificity of each test across studies. Helpful for visualizing study heterogeneity.

"contour" Contour-enhanced plots showing joint posterior density of sensitivity and specificity for each test or study. Useful for visual comparison of test performance.

If `type` is not specified, the function defaults to `"sroc"`. For example, both `plot(x)` and `plot(x, type = "sroc")` will produce the SROC plot.

Value

Invisibly returns the input ‘nmadt‘ object x. The function is primarily called for its side effect of generating plots rather than returning a value.

Examples

```
data(dat.kang)
set.seed(9)
kang.out <- nmadt.hierarchical(nstu=12, K=2, data=dat.kang,
            testname=c("D-dimer","Ultrasonography"))
plot(kang.out, type = "sroc")
plot(kang.out, type = "forest")
plot(kang.out, type = "contour")
plot(kang.out, type = "density")
```

---

print.nmadt *Print method for ‘nmadt‘ objects*

Description

Print method for ‘nmadt‘ objects

Usage

```
## S3 method for class 'nmadt'
print(x, ...)
```

Arguments

x	An object of class ‘nmadt‘
...	Not used. Included for S3 method compatibility.

Examples

```
data(dat.kang)
set.seed(9)
kang.out <- nmadt.hierarchical(nstu=12, K=2, data=dat.kang,
            testname=c("D-dimer","Ultrasonography"))
print(kang.out)
```

summary.nmadt *Summary method for 'nmadt' objects*

Description

Provides a concise summary of posterior results from network meta-analysis of diagnostic tests fitted using the NMADTA framework. Displays median estimates and 95 sensitivity, specificity, predictive values, likelihood ratios, and prevalence.

Usage

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

Arguments

object	An object of class nmadt, typically created by nmadt.hierarchical() or nmadt.hsroc().
...	Additional arguments (currently not used).

Details

The function extracts and prints key posterior summaries from the fitted model, including medians and 95

The output is formatted for human readability, with each section clearly labeled.

Value

The function returns the input object (invisibly) after printing the summary.

Examples

```
data(dat.kang)
set.seed(9)
kang.out <- nmadt.hierarchical(nstu=12, K=2, data=dat.kang,
            testname=c("D-dimer","Ultrasonography"))
summary(kang.out)
```

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