Package 'NMADiagT'

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Type Package

Title Network Meta-Analysis of Multiple Diagnostic Tests

Version 0.1.2

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Description Implements HSROC (hierarchical summary receiver operating characteristic) model developed by Ma, Lian, Chu, Ibrahim, and Chen (2018) <doi:10.1093/biostatistics/kxx025> and hierarchical model developed by Lian, Hodges, and Chu (2019) <doi:10.1080/01621459.2018.1476239> for performing meta-analysis for 1-5 diagnostic tests to simultaneously compare multiple tests within a missing data framework. This package evaluates the accuracy of multiple diagnostic tests and also gives graphical representation of the results.

Depends R (>= 2.14.0), rjags (>= 4-6)

Imports coda, ggplot2, ks, reshape2, MCMCpack, MASS,plotrix, graphics, stats, grDevices, imguR, Rdpack

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R topics documented:

`hierarchical.plot` *Plotting Results from* `nmadt.hierarchical` *and* `nmadt.hierarchical.MNAR`

Description

`hierarchical.plot` plots the results from `nmadt.hierarchical` and `nmadt.hierarchical.MNAR`.Graphics representation includes density plots, forest plots, SROC curves, and contour plots of the results.

Usage

```
hierarchical.plot(nstu, K, data, testname, output, directory,
  typeofplot = c("density", "forest", "sroc", "contour"), n.chains = 3)
```

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.
`output`	a list object obtained by function `nmadt.hierarchical` and `nmadt.hierarchical.MNAR`.
`directory`	a string specifying the designated directory to save the plots.
`typeofplot`	a string vector containing the types of plot to be generated including "density", "forest","sroc", and "contour".
`n.chains`	a number indicating number of MCMC chains generated using `nmadt.hierarchical` and `nmadt.hierarchical.MNAR`. The default is 3.

Examples

```
kangdata<-read.csv(file=system.file("extdata","kangdata.csv",package="NMADiagT"),
header=TRUE, sep=",")
set.seed(9)
kang.out <- nmadt.hierarchical(nstu=12, K=2, data=kangdata, testname=c("D-dimer","Ultrasonography"))
hierarchical.plot(nstu=12, K=2, data=kangdata, directory = tempdir(),
testname=c("D-dimer","Ultrasonography"),output=kang.out)
```

hsroc.plot *Plotting Results from* nmadt.hsroc *and* nmadt.hsroc.MNAR

Description

hsroc.plot plots the results from nmadt.hsroc and nmadt.hsroc.MNAR.Graphics representation includes density plots, forest plots, SROC curves, and contour plots of the results.

Usage

```
hsroc.plot(nstu, K, data, testname, output, directory,
  typeofplot = c("density", "forest", "sroc", "contour"), n.chains = 3)
```

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.
output	a list object obtained by function nmadt.hsroc or nmadt.hsroc.MNAR.
directory	a string specifying the designated directory to save the plots.
typeofplot	a string vector containing the types of plot to be generated including "density", "forest","sroc", and "contour".
n.chains	a number indicating number of MCMC chains generated using nmadt.hsroc or nmadt.hsroc.MNAR. The default is 3.

Examples

```
kangdata<-read.csv(file=system.file("extdata","kangdata.csv",package="NMADiagT"),
header=TRUE, sep=",")
set.seed(9)
kang.out.hsroc <- nmadt.hsroc(nstu=12, K=2, data=kangdata, testname=c("D-dimer","Ultrasonography"))
hsroc.plot(nstu=12, K=2, data=kangdata, directory = tempdir(),
testname=c("D-dimer","Ultrasonography"),output=kang.out.hsroc)
```

`nmadt.hierarchical` *Network Meta-Analysis Using the Hierarchical Model*

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 indicating the value of diagonal entries of the scale matrix R of the precision matrix Σ. The default is 5.
`off_diag`	a number indicating the value of off-diagonal entries of the scale matrix R of the precision matrix Σ. The default is 0.05.
`digits`	a positive integer he number of digits to the right of the decimal point to keep for the results; digits=4 by default.
`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.

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

```
kangdata<-read.csv(file=system.file("extdata","kangdata.csv",package="NMADiagT"),
header=TRUE, sep=",")
set.seed(9)
kang.out <- nmadt.hierarchical(nstu=12, K=2, data=kangdata, testname=c("D-dimer","Ultrasonography"))
```

`nmadt.hierarchical.MNAR` *Network Meta-Analysis Using the Hierarchical Model 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 indimessageing 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 indicating the value of diagonal entries of the scale matrix R of the precision matrix Σ. The default is 5.
`off_diag`	a number indicating the value of off-diagonal entries of the scale matrix R of the precision matrix Σ. The default is 0.05.
`digits`	a positive integer he number of digits to the right of the decimal point to keep for the results; digits=4 by default.
`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 vector indicating coefficients of study-specific sensitivity in the MNAR model.

`gamma0` a vector indicating coefficients of study-specific specificity in the MNAR model.

`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 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.

`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

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

```
kangdata<-read.csv(file=system.file("extdata","kangdata.csv",package="NMADiagT"),
header=TRUE, sep=",")
set.seed(9)
kangMNAR.out <- nmadt.hierarchical.MNAR(nstu=12, K=2, data=kangdata, testname=c("D-dimer",
"Ultrasonography"),gamma1=c(-0.5,-0.5), gamma0=c(-0.5,-0.5))
```

`nmadt.hsroc` *Network Meta-Analysis Using the hierarchical model*

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

```
kangdata<-read.csv(file=system.file("extdata","kangdata.csv",package="NMADiagT"),
header=TRUE, sep=",")
set.seed(9)
kang.out.hsroc <- nmadt.hsroc(nstu=12, K=2, data=kangdata, testname=c("D-dimer","Ultrasonography"))
```

---

nmadt.hsroc.MNAR *Network Meta-Analysis Using the hierarchical model*

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 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.
`gamma1`	a vector indicating coefficients of study-specific sensitivity in the MNAR model.
`gamma0`	a vector indicating coefficients of study-specific specificity in the MNAR model.
`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 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

```
kangdata<-read.csv(file=system.file("extdata","kangdata.csv",package="NMADiagT"),
header=TRUE, sep=",")
set.seed(9)
kangMNAR.out.hsroc <- nmadt.hsroc.MNAR(nstu=12, K=2, data=kangdata,
testname=c("D-dimer","Ultrasonography"),gamma1=c(-0.5,-0.5), gamma0=c(-0.5,-0.5))
```

Index