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Description Performs arm-based network meta-analysis for datasets with binary, continuous, and count outcomes using the Bayesian methods of Zhang et al (2014) <doi:10.1177/1740774513498322> and Lin et al (2017) <doi:10.18637/jss.v080.i05>.

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R topics documented:

pcnetmeta-package 2
absolute.plot 3
contrast.plot 4
diabetes 5
dietaryfat 5
nma.ab.bin 6
nma.ab.cont 10
nma.ab.followup 14
nma.ab.py 18
nma.networkplot 22
parkinson 23
rank.prob 24
smoke 25

Index **26**

`pcnetmeta-package` *Patient-Centered Network Meta-Analysis*

Description

Provides functions to perform arm-based network meta-analysis for datasets with binary, continuous, and count outcomes.

Details

Currently, much effort in network meta-analysis has been devoted to contrast-based methods, which focus on modeling the relative treatment effects, such as log odds ratio. However, in some situations, patient-centered treatment-specific parameters, such as absolute risk, are preferred. For example, when the outcome is binary, consider two scenarios comparing treatments A and B according to one-year survival rates: (i) $\pi_A = 0.8$ vs $\pi_B = 0.5$ and (ii) $\pi_A = 0.004$ vs $\pi_B = 0.001$. Both scenarios yield an odds ratio 4.0, but patients would prefer treatment A in scenario (i) more strongly than in scenario (ii). The contrast-based network meta-analysis requires external data sources or separate modeling to estimate treatment-specific parameters.

Alternatively, arm-based network meta-analysis focuses on estimating treatment-specific parameters, and relative effects can be subsequently obtained. The arm-based models for binary outcomes are discussed in Salanti et al (2008) and Zhang et al (2014).

This package provides user-friendly functions for arm-based network meta-analysis. Function `nma.ab.bin` uses the model in Zhang et al (2014) for binary outcomes; it provides estimates for absolute risk (AR), risk ratio (RR), risk difference (RD), odds ratio (OR), log RR, and log OR. This package also handles continuous outcomes and count data.

Parameter estimation in arm-based Bayesian hierarchical models are performed through JAGS. Note that this package does not include a copy of JAGS library, so users must install JAGS separately. Please refer to the JAGS home page at `http://mcmc-jags.sourceforge.net/` for instructions on downloading and installing JAGS.

Author(s)

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References

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`absolute.plot` *Plotting Treatment-Specific 95% Credible Intervals*

Description

`absolute.plot` generates a plot of 95% credible intervals (CIs) for the treatment-specific effect sizes.

Usage

```
absolute.plot(nma.obj, alphabetic = TRUE, digits = 2, width = 5, height,
              network.name)
```

Arguments

`nma.obj`	a list object obtained by function `nma.ab.bin`, `nma.ab.cont`, `nma.ab.py`, or `nma.ab.followup`.
`alphabetic`	a logical value indicating whether to sort the CIs according to treatment names alphabetically. The default is `TRUE`. If `FALSE`, the CIs are plotted in the order of treatment IDs specified in `nma.obj`.
`digits`	an integer indicating the number of decimal places to be used for the point estimates and 95% CIs. The default is 2.
`width`	a positive number indicating the plot width. The default is 5.
`height`	a positive number indicating the plot height. The default is the treatment number minus 1.
`network.name`	a character string indicating the network name to be used for the produced .pdf file name.

Examples

```
data(smoke)
# increase n.iter to reach convergence
# increase n.adapt to enhance efficiency
set.seed(1234)
nma.out <- nma.ab.bin(s.id, t.id, r, n, data = smoke,
  trtname = c("NC", "SH", "IC", "GC"), param= "AR",
  model = "het_cor", n.adapt = 400, n.iter = 100, n.chains = 1)
absolute.plot(nma.out)
absolute.plot(nma.out, alphabetic = FALSE)
```

`contrast.plot` *Contrast Plot of Relative Effect Sizes*

Description

`contrast.plot` generates contrast plot, which shows 95% credible intervals (CIs) for relative effect sizes.

Usage

```
contrast.plot(nma.obj, effect.size, reference, digits = 2, width = 5, height,
              network.name)
```

Arguments

`nma.obj`	a list object obtained by function `nma.ab.bin`, `nma.ab.cont`, `nma.ab.py`, or `nma.ab.followup`.
`effect.size`	a character string indicating the relative effect size to be shown in the contrast plot. If `nma.obj` is obtained from `nma.ab.bin`, this argument can be `"OR"` (default), `"LOR"`, `"RR"`, `"LRR"`, or `"RD"`. If `nma.obj` is obtained from `nma.ab.cont`, this argument should be `"diff"` (default). If `nma.obj` is obtained from `nma.ab.py` or `nma.ab.followup`, this argument can be `"ratio"` (default) or `"logratio"`. Note that the specified effect sizes (or its logarithm/exponential) must have been estimated in `nma.obj`.
`reference`	a character string indicating the reference treatment name to be compared against.
`digits`	an integer indicating the number of decimal places to be used for the point estimates and 95% CIs. The default is 2.
`width`	a positive number indicating the plot width. The default is 5.
`height`	a positive number indicating the plot height. The default is the treatment number minus 1.
`network.name`	a character string indicating the network name to be used for the produced .pdf file name.

Value

A contrast plot for relative effect sizes is saved as a .pdf file in users' current working directory.

Examples

```
data(smoke)
# increase n.iter to reach convergence
# increase n.adapt to enhance efficiency
set.seed(1234)
nma.out <- nma.ab.bin(s.id, t.id, r, n, data = smoke,
  trtname = c("NC", "SH", "IC", "GC"), param= "LOR",
  model = "het_cor", n.adapt = 400, n.iter = 100, n.chains = 1)
contrast.plot(nma.out)
```

diabetes *Network Meta-Ananlysis on Diabetes*

Description

An example of network meta-analysis for binary outcomes with follow-up times reported.

Usage

```
data("diabetes")
```

Format

A data frame containing 22 studies which compare 6 treatments. The outcome is binary; mean follow-up time in each study is collected.

`s.id` a numeric vector indicating study IDs.

`folup` a numeric vector indicating follow-up time (in years) for each study.

`t.id` a numeric vector indicating treatment IDs.

`r` a numeric vector indicating the total mortality in each treatment group in each study.

`n` a numeric vector indicating the total number of participants in each treatment group in each study.

Details

This network meta-analysis is studied by Elliott and Meyer (2007) to assess the effects of anti-hypertensive agents on incident diabetes. Treatment IDs represent 1) diuretic; 2) placebo; 3) β-blocker; 4) CCB; 5) ACE inhibitor; and 6) ARB.

Source

Elliott WJ and Meyer PM (2007). "Incident diabetes in clinical trials of antihypertensive drugs: a network meta-analysis." *Lancet* **369**(9557), 201–7.

dietaryfat *Network Meta-Ananlysis on Dietary Fat*

Description

An example of network meta-analysis for binary outcomes with exposure times in person-years reported.

Usage

```
data("dietaryfat")
```

Format

A data frame containing 10 studies which compare 2 treatments. The total number of person-years at risk are reported for each treatment group in each study.

`s.id` a numeric vector indicating study IDs.

`t.id` a numeric vector indicating treatment IDs.

`py` a numeric vector indicating the total person-years in each treatment group in each study.

`r` a numeric vector indicating the total mortality in each treatment group in each study.

`n` a numeric vector indicating the total number of participants in each treatment group in each study.

Details

This network meta-analysis is collected by Hooper et al (2000) to assess the effects of change in dietary fats on cardiovascular mortality. Treatment 1 is a control diet and treatment 2 is a reduced fat diet. The original study 2 compares three treatments, which include treatment 1 and 2, and another diet. Here, we treat the two different types of diet as the same treatment, but keep the treatment arms separate.

Source

Hooper L, Summerbell CD, Higgins JPT, Thompson RL, Clements G, Capps N, Davey Smith G, Riemersma R, and Ebrahim S (2000). "Reduced or modified dietary fat for preventing cardiovascular disease." *The Cochrane Database of Systematic Reviews*.

`nma.ab.bin` *Arm-Based Network Meta-Analysis for Binary Outcomes*

Description

`nma.ab.bin` performs arm-based network meta-analysis proposed by Zhang et al (2014). It estimates absolute risk (AR), risk difference (RD), odds ratio (OR), risk ratio (RR), log odds ratio (LOR), and log risk ratio (LRR).

Usage

```
nma.ab.bin(s.id, t.id, event.n, total.n, data, trtname,
           param = c("AR", "LOR", "LRR", "RD", "rank.prob"),
           model = "het_cor", prior.type, a = 0.001, b = 0.001, c = 10,
           higher.better = FALSE, digits = 4, n.adapt = 5000,
           n.iter = 100000, n.burnin = floor(n.iter/2), n.chains = 3,
           n.thin = max(1, floor((n.iter - n.burnin)/100000)),
           conv.diag = FALSE, trace = NULL, dic = FALSE, postdens = FALSE,
           mcmc.samples = FALSE)
```

Arguments

s.id	a numeric or character vector indicating study ID, or the corresponding column name in the argument data.
t.id	a numeric or character vector indicating treatment ID, or the corresponding column name in the argument data.
event.n	a numeric vector of non-negative integers, indicating event number for a certain treatment in the corresponding study, or the corresponding column name in the argument data.
total.n	a numeric vector of positive integers, indicating total number of participants for a certain treatment in the corresponding study, or the corresponding column name in the argument data.
data	an optional data frame containing the dataset for network meta-analysis. If data is specified, the previous arguments, s.id, t.id, event.n, and total.n, should be specified as the corresponding column names in data; otherwise, the previous arguments use environment variables.
trtname	a vector of character strings indicating the treatment names for the corresponding treatment IDs according their order in t.id. If not specified, t.id is used as treatment names.
param	a vector of character strings indicating the effect sizes to be estimated. The default includes "AR" (absolute risk), "LOR" (log odds ratio), "LRR" (log risk ratio), "RD" (risk difference), "rank.prob" (treatment rank probability). "AR" is automatically added into param even if it is not specified. In addition to the defaults, "OR" (odds ratio) and "RR" (risk ratio) can be added into param.
model	a character string indicating which Bayesian hierarchical model to be applied in the arm-based network meta-analysis. This argument can be set as "hom_eqcor", "het_eqcor", or "het_cor" (default). See "Details" for the models.
prior.type	prior distribution of variances/covariances of random effects. If model is "hom_eqcor" or "het_eqcor", it can be set as "unif" (uniform prior for standard deviations, the default) or "invgamma" (inverse gamma prior for variances). If model is "het_cor", prior.type can be "invwishart" (the default) or "chol". Specifying "invwishart" yields an inverse-Wishart prior for the variance-covariance matrix of random effects; by specifying "chol", non-informative priors are assigned to variance and correlation components using the separation strategy by Cholesky decomposition. See "Details".
a, b	positive numbers, specifying the shape and scale parameters of inverse gamma priors for variance(s) of random effects if using prior.type as "invgamma" for model "hom_eqcor" or "het_eqcor". The defaults for both parameters are 0.001.
c	positive number, specifying the upper bound of uniform prior for standard deviations of random effects if using prior.type as "unif" for model "hom_eqcor" or "het_eqcor". The default is 10.
higher.better	an optional logical value which needs to be specified when estimating the treatment rank probabilities (i.e., "rank.prob" is included in the argument param). TRUE indicates higher event rate implying better treatment, and vice versa. The default is FALSE.

digits	a positive integer specifying the digits after the decimal point for the effect size estimates. The default is 4.
n.adapt	the number of iterations for adaptation in Markov chain Monte Carlo (MCMC) algorithm. The default is 5,000. If a warning "adaptation incomplete" appears, users may increase n.adapt. This argument and the following n.iter, n.burnin, n.chains, n.thin are passed to the functions in R package **rjags**.
n.iter	the total number of iterations in each MCMC chain. The default is 100,000.
n.burnin	the number of iterations for burn-in period. The default is n.iter/2.
n.chains	the number of MCMC chains. The default is 3.
n.thin	a positive integer indicating thinning rate. The default is the thinning rate which yields no more than 100,000 iterations remaining in each chain.
conv.diag	a logical value indicating whether to perform MCMC convergence diagnostic. The default is FALSE. If TRUE, n.chains must be greater than 1, and a .txt file, which contains the point estimates of the potential scale reduction factor and their upper confidence limits (see Gelman and Rubin 1992), will be written in users' current working directory.
trace	a vector of character strings of effect sizes. The character strings should be selected from those specified in param (except "rank.prob"), and trace plots of the specified effect sizes will be saved in users' current working directory. The default is not drawing trace plots (NULL).
dic	a logical value indicating whether the deviance information criterion (DIC) to be calculated. The default is FALSE.
postdens	a logical value indicating whether to draw the posterior density plots for treatment-specific absolue risks (ARs). If TRUE, a .pdf file containing the density plot will be saved in users' current working directory. The default is FALSE.
mcmc.samples	a logical value indicating whether to save MCMC posterior samples in the output object. The default is FALSE.

Details

Suppose that a network meta-analysis collects I studies on K treatments, where each study investigates a subset of the K treatments. Label the studies from $i = 1$ to I and the treatments from $k = 1$ to K. Let T_i be the subset of the K treatments that is compared in the ith study. Also, in the ith study, let n_{ik} be the number of participants allocated to treatment group k ($k \in T_i$), and y_{ik} be the number of events. The arm-based model is constructed as (Zhang et al 2014):

$$y_{ik} \sim Bin(n_{ik}, p_{ik}) \qquad k \in T_i$$

$$\Phi^{-1}(p_{ik}) = \mu_k + \nu_{ik}$$

$$(\nu_{i1}, \nu_{i2}, \ldots, \nu_{iK})^T \sim N(\mathbf{0}, \mathbf{\Sigma}_K),$$

where $\Phi(\cdot)$ is the standard normal cumulative distribution function, and $\mathbf{\Sigma}_K$ is a $K \times K$ positive definite covariance matrix. The μ_k's are treatment-specific fixed effects, and the random effects ν_{ik} are correlated within each study with the covariance matrix $\mathbf{\Sigma}_K$.

An unstructured covariance matrix $\mathbf{\Sigma}_K$ in the above model corresponds to model = "het_cor". The inverse-Wishart prior can be assigned to $\mathbf{\Sigma}_K$. Alternatively, using the separation strategy

by Cholesky decomposition (`prior.type = "chol"`), uniform priors $U(0, c)$ are assigned to the standard deviations in $\mathbf{\Sigma}_K$ and non-informative priors are assigned to the correlation components (Barnard et al, 2000; Lu and Ades, 2009; Wei and Higgins, 2013). Denote σ_k as the standard deviation of ν_{ik} and $\mathbf{D} = diag(\sigma_1, \ldots, \sigma_K)$, then the correlation matrix $\mathbf{R}_K = \mathbf{D}^{-1}\mathbf{\Sigma}_K\mathbf{D}^{-1}$. If we assume that all of the off-diagonal elements in $\mathbf{R}_K$ are equal, say to ρ, then this model corresponds to `model = "het_eqcor"`. If we further assume the homogeneity of variances of the random effects, that is, $\sigma_k = \sigma$ for $k = 1, 2, \ldots, K$, then the model is `"hom_eqcor"`. In addition, for the models `"hom_eqcor"` and `"het_eqcor"`, setting `prior.type` as `"invgamma"` implies using inverse-gamma priors with shape and scale parameters a, b for σ_k^2 or σ^2, and `"unif"` implies uniform priors $U(0, c)$ for σ_k or σ.

Value

`nma.ab.bin` returns a list with estimates of effect sizes specified in `param`. If the argument `dic = TRUE`, the deviance information criterion (DIC) statistic will be returned in the output list. In addition, if `conv.diag = TRUE`, a .txt file containing the point estimates of the potential scale reduction factor and their upper confidence limits by Gelman and Rubin (1992) will be saved in users' current working directory. If `postdens = TRUE`, the posterior densities of treatment-specific absolute risks will be saved as a .pdf file. If `trace` is specified, the trace plots are saved as .png files.

Note

If there exists a treatment that has no event in all studies, this function may give an error. To avoid this, users may set the zero event as a small positive number (say 0.5) in all studies.

Note that the earlier versions (< 4.0.0) of JAGS does not guarantee exact reproducibility of the results. Therefore, we recommend users install the latest version (>= 4.0.0) of JAGS so that exact reproducibility can be ensured by specifying certain seeds.

References

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See Also

nma.ab.cont, nma.ab.py, nma.ab.followup

Examples

```
data(smoke)

# For the smoke cessation data,
# higher event rate indicates better treatment

# use the model = "het_cor"
#set.seed(1234)
#het.cor.out <- nma.ab.bin(s.id, t.id, r, n, data = smoke,
#  trtname = c("NC", "SH", "IC", "GC"), param = c("AR", "OR", "RR", "LOR",
#  "LRR", "RD", "rank.prob"), model = "het_cor", higher.better = TRUE,
#  n.iter = 200000, n.thin = 1, conv.diag = TRUE, dic = TRUE,
#  trace = c("AR", "LOR"), postdens = TRUE)

# use the model = "hom_eqcor"
# increase n.iter to reach convergence
# increase n.adapt to enhance efficiency
set.seed(1234)
hom.eqcor.out <- nma.ab.bin(s.id, t.id, r, n, data = smoke,
  param = c("AR", "LRR"), model = "hom_eqcor", prior.type = "unif", c = 10,
  higher.better = TRUE, n.adapt = 400, n.iter = 100, n.chains = 1)
```

---

nma.ab.cont *Arm-Based Network Meta-Analysis for Continuous Outcomes*

Description

nma.ab.cont performs arm-based network meta-analysis for continuous outcomes. It estimates treatment-specific effects and effect differences.

Usage

```
nma.ab.cont(s.id, t.id, mean, sd, total.n, data, trtname,
            param = c("mu", "diff", "rank.prob"),model = "het_cor",
            prior.type, a = 0.001, b = 0.001, c = 10,
            higher.better = FALSE, digits = 4, n.adapt = 5000,
            n.iter = 100000, n.burnin = floor(n.iter/2), n.chains = 3,
            n.thin = max(1, floor((n.iter - n.burnin)/100000)),
            conv.diag = FALSE, trace = NULL, dic = FALSE, postdens = FALSE,
            mcmc.samples = FALSE)
```

Arguments

s.id	a numeric or character vector indicating study ID, or the corresponding column name in the argument data.
t.id	a numeric or character vector indicating treatment ID, or the corresponding column name in the argument data.
mean	a numeric vector indicating the sample mean of the continuous outcomes for a certain treatment group in the corresponding study, or the corresponding column name in the argument data.
sd	a numeric vector indicating the sample standard deviation of the continuous outcomes for a certain treatment group in the corresponding study, or the corresponding column name in the argument data.
total.n	a numeric vector of positive integers, indicating total number of participants for a certain treatment in the corresponding study, or the corresponding column name in the argument data.
data	an optional data frame containing the dataset for network meta-analysis. If data is specified, the previous arguments, s.id, t.id, mean, sd, and total.n, should be specified as the corresponding column names in data; otherwise, the previous arguments use environment variables.
trtname	a vector of character strings indicating the treatment names for the corresponding treatment IDs according their order in t.id. If not specified, t.id is used as treatment names.
param	a vector of character strings indicating the effect sizes to be estimated. The default includes treatment-specific effects ("mu"), effect differences ("diff"), and treatment rank probabilities ("rank.prob"). "mu" is automatically added into param even if it is not specified.
model	a character string indicating which Bayesian hierarchical model to be applied in the arm-based network meta-analysis. This argument can be set as "hom_eqcor", "het_eqcor", or "het_cor" (default). See "Details" for the models.
prior.type	prior distribution of variances/covariances of random effects. If model is "hom_eqcor" or "het_eqcor", it can be set as "unif" (uniform prior for standard deviations, the default) or "invgamma" (inverse gamma prior for variances). If model is "het_cor", prior.type can be "invwishart" (the default) or "chol". Specifying "invwishart" yields an inverse-Wishart prior for the variance-covariance matrix of random effects; by specifying "chol", non-informative priors are assigned to variance and correlation components using the separation strategy by Cholesky decomposition. See "Details".
a, b	positive numbers, specifying the shape and scale parameters of inverse gamma priors for variance(s) of random effects if using prior.type as "invgamma" for model "hom_eqcor" or "het_eqcor". The defaults for both parameters are 0.001.
c	positive number, specifying the upper bound of uniform prior for standard deviations of random effects if using prior.type as "unif" for model "hom_eqcor" or "het_eqcor". The default is 10.

`higher.better` an optional logical value which needs to be specified when estimating the treatment rank probabilities (i.e., `"rank.prob"` is included in the argument `param`). `TRUE` indicates higher sample mean of the continuous outcomes implying better treatment, and vice versa. The default is `FALSE`.

`digits` a positive integer specifying the digits after the decimal point for the effect sizes estimates. The default is 4.

`n.adapt` the number of iterations for adaptation in Markov chain Monte Carlo (MCMC) algorithm. The default is 5,000. If a warning "adaptation incomplete" appears, users may increase `n.adapt`. This argument and the following `n.iter`, `n.burnin`, `n.chains`, `n.thin` are passed to the functions in R package **rjags**.

`n.iter` the total number of iterations in each MCMC chain. The default is 100,000.

`n.burnin` the number of iterations for burn-in period. The default is `n.iter/2`.

`n.chains` the number of MCMC chains. The default is 3.

`n.thin` a positive integer indicating thinning rate. The default is the thinning rate which yields no more than 100,000 iterations remaining in each chain.

`conv.diag` a logical value indicating whether to perform MCMC convergence diagnostic. The default is `FALSE`. If `TRUE`, `n.chains` must be greater than 1, and a .txt file, which contains the point estimates of the potential scale reduction factor and their upper confidence limits (see Gelman and Rubin 1992), will be written in users' current working directory.

`trace` a vector of character strings of effect sizes. The character strings should be selected from those specified in `param` (except `"rank.prob"`), and trace plots of the specified effect sizes will be saved in users' current working directory. The default is not drawing trace plots (`NULL`).

`dic` a logical value indicating whether the deviance information criterion (DIC) to be calculated. The default is `FALSE`.

`postdens` a logical value indicating whether to draw the posterior density plots for treatment-specific effects. If `TRUE`, a .pdf file containing the density plot will be saved in users' current working directory. The default is `FALSE`.

`mcmc.samples` a logical value indicating whether to save MCMC posterior samples in the output object. The default is `FALSE`.

Details

Suppose that a network meta-analysis collects I studies on K treatments, where each study investigates a subset of the K treatments with continuous outcomes. Label the studies from $i = 1$ to I and the treatments from $k = 1$ to K. Let T_i be the subset of the K treatments that is compared in the ith study. Also, in the ith study, let n_{ik} be the number of participants allocated to treatment group k ($k \in T_i$), and $\bar{y}_{ik}$ and s^2_{ik} be the sample mean and standard deviation of the continuous outcomes. The arm-based model is constructed as:

$$\bar{y}_{ik} \sim N(\theta_{ik}, s^2_{ik}/n_{ik}) \qquad k \in T_i$$

$$\theta_{ik} = \mu_k + \nu_{ik}$$

$$(\nu_{i1}, \nu_{i2}, \ldots, \nu_{iK})^T \sim N(\mathbf{0}, \mathbf{\Sigma}_K),$$

where $\mathbf{\Sigma}_K$ is a $K \times K$ positive definite correlation matrix. The μ_k's are treatment-specific fixed effects, and the random effects ν_{ik} are correlated within each study with the covariance matrix $\mathbf{\Sigma}_K$.

An unstructured covariance matrix $\mathbf{\Sigma}_K$ in the above model corresponds to `model = "het_cor"`. The inverse-Wishart prior can be assigned to $\mathbf{\Sigma}_K$. Alternatively, using the separation strategy by Cholesky decomposition (`prior.type = "chol"`), uniform priors $U(0, c)$ are assigned to the standard deviations in $\mathbf{\Sigma}_K$ and non-informative priors are assigned to the correlation components (Barnard et al, 2000; Lu and Ades, 2009; Wei and Higgins, 2013). Denote σ_k as the standard deviation of ν_{ik} and $\mathbf{D} = diag(\sigma_1, \ldots, \sigma_K)$, then the correlation matrix $\mathbf{R}_K = \mathbf{D}^{-1}\mathbf{\Sigma}_K\mathbf{D}^{-1}$. If we assume that all of the off-diagonal elements in $\mathbf{R}_K$ are equal, say to ρ, then this model corresponds to `model = "het_eqcor"`. If we further assume the homogeneity of variances of the random effects, that is, $\sigma_k = \sigma$ for $k = 1, 2, \ldots, K$, then the model is `"hom_eqcor"`. In addition, for the models `"hom_eqcor"` and `"het_eqcor"`, setting `prior.type` as `"invgamma"` implies using inverse-gamma priors with shape and scale parameters a, b for σ_k^2 or σ^2, and `"unif"` implies uniform priors $U(0, c)$ for σ_k or σ.

Value

`nma.ab.cont` returns a list with estimates of effect sizes specified in `param`. If the argument `dic = TRUE`, the deviance information criterion (DIC) statistic will be returned in the output list. In addition, if `conv.diag = TRUE`, a .txt file containing the point estimates of the potential scale reduction factor and their upper confidence limits by Gelman and Rubin (1992) will be saved in users' current working directory. If `postdens = TRUE`, the posterior densities of treatment-specific absolute risks will be saved as a .pdf file. If `trace` is specified, the trace plots are saved as .png files.

Note

Note that the earlier versions (< 4.0.0) of JAGS does not guarantee exact reproducibility of the results. Therefore, we recommend users install the latest version (>= 4.0.0) of JAGS so that exact reproducibility can be ensured by specifying certain seeds.

References

Barnard J, McCulloch R, and Meng XL (2000). "Modeling covariance matrices in terms of standard deviations and correlations, with application to shrinkage." *Stat Sin* **10**(4), 1281–11.

Dias S, Sutton AJ, Ades AE, and Welton NJ (2013). "Evidence synthesis for decision making 2: A generalized linear modeling framework for pairwise and network meta-analysis of randomized controlled trials." *Med Decis Making* **33**(5), 607–17.

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Lin L, Zhang J, Hodges JS, and Chu H (2017). "pcnetmeta: An R package for arm-based network meta-analysis." *J Stat Softw*, **80**(5), 1–25.

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Lu G and Ades AE (2009). "Modeling between-trial variance structure in mixed treatment comparisons." *Biostatistics*, **10**(4), 792–805.

Spiegelhalter DJ, Best NG, Carlin BP, and van der Linde A (2002). "Bayesian measures of model complexity and fit." *J R Stat Soc Series B Stat Methodol* **64**(4), 583–639.

Wei Y and Higgins JPT (2013). "Bayesian multivariate meta-analysis with multiple outcomes." *Stat Med* **32**(17), 2911–34.

Zhang J, Carlin BP, Neaton JD, Soon GG, Nie L, Kane R, Virnig BA, and Chu H (2014). "Network meta-analysis of randomized clinical trials: Reporting the proper summaries." *Clin Trials* **11**(2), 246–62.

See Also

nma.ab.bin, nma.ab.py, nma.ab.followup

Examples

```
data(parkinson)
# increase n.iter to reach convergence of MCMC
# increase n.adapt to enhance efficiency
set.seed(1234)
cont.out <- nma.ab.cont(s.id, t.id, mean, sd, n, data = parkinson,
  param = c("mu", "diff"), model = "hom_eqcor", prior.type = "unif",
  n.adapt = 200, n.iter = 100, n.chains = 1)
```

---

nma.ab.followup *Arm-Based Network Meta-Analysis for Binary Outcomes with Follow-Up Times Reported*

Description

nma.ab.followup performs arm-based network meta-analysis for binary outcomes and the follow-up time of each study is collected. It estimates treatment-specific rate, rate ratio between treatments, and their logarithms.

Usage

```
nma.ab.followup(s.id, t.id, event.n, total.n, followup, data, trtname,
                param = c("lograte", "logratio", "rank.prob"),
                model = "het_cor", prior.type, a = 0.001, b = 0.001,
                c = 10, higher.better = FALSE, digits = 4, n.adapt = 5000,
                n.iter = 100000, n.burnin = floor(n.iter/2), n.chains = 3,
                n.thin = max(1, floor((n.iter - n.burnin)/100000)),
                conv.diag = FALSE, trace = NULL, dic = FALSE,
                postdens = FALSE, mcmc.samples = FALSE)
```

Arguments

s.id	a numeric or character vector indicating study ID, or the corresponding column name in the argument data.
t.id	a numeric or character vector indicating treatment ID, or the corresponding column name in the argument data.

`event.n` a numeric vector of non-negative integers, indicating number of events in each study's treatment group, or the corresponding column name in the argument `data`.

`total.n` a numeric vector of non-negative integers, indicating total number of participants in each study's treatment group, or the corresponding column name in the argument `data`.

`followup` a numeric vector of positive numbers, indicating follow-up times for different studies, or the corresponding column name in the argument `data`.

`data` an optional data frame containing the dataset for network meta-analysis. If `data` is specified, the previous arguments, `s.id`, `t.id`, `event.n`, `total.n`, and `followup`, should be specified as the corresponding column names in `data`; otherwise, the previous arguments use environment variables.

`trtname` a vector of character strings indicating the treatment names for the corresponding treatment IDs according their order in `t.id`. If not specified, `t.id` is used as treatment names.

`param` a vector of character strings indicating the effect sizes to be estimated. The default includes log treatment-specific rate (`"lograte"`), log rate ratio (`"logratio"`), and treatment rank probability (`"rank.prob"`). `"lograte"` is automatically added into `param` even if it is not specified. In addition to the defaults, treatment-specific rate (`"rate"`) and rate ratio (`"ratio"`) can be added into the argument `param`.

`model` a character string indicating which Bayesian hierarchical model to be applied in the arm-based network meta-analysis. This argument can be set as `"hom_eqcor"`, `"het_eqcor"`, or `"het_cor"` (default). See "Details" for the models.

`prior.type` prior distribution of variances/covariances of random effects. If `model` is `"hom_eqcor"` or `"het_eqcor"`, it can be set as `"unif"` (uniform prior for standard deviations, the default) or `"invgamma"` (inverse gamma prior for variances). If `model` is `"het_cor"`, `prior.type` can be `"invwishart"` (the default) or `"chol"`. Specifying `"invwishart"` yields an inverse-Wishart prior for the variance-covariance matrix of random effects; by specifying `"chol"`, non-informative priors are assigned to variance and correlation components using the separation strategy by Cholesky decomposition. See "Details".

`a, b` positive numbers, specifying the shape and scale parameters of inverse gamma priors for variance(s) of random effects if using `prior.type` as `"invgamma"` for model `"hom_eqcor"` or `"het_eqcor"`. The defaults for both parameters are 0.001.

`c` positive number, specifying the upper bound of uniform prior for standard deviations of random effects if using `prior.type` as `"unif"` for model `"hom_eqcor"` or `"het_eqcor"`. The default is 10.

`higher.better` an optional logical value which needs to be specified when estimating the treatment rank probabilities (i.e., "rank.prob" is included in argument `param`). `TRUE` indicates higher treatment-specific rate implying better treatment, and vice versa. The default is `FALSE`.

`digits` a positive integer specifying the digits after the decimal point for the effect size estimates. The default is 4.

n.adapt	the number of iterations for adaptation in Markov chain Monte Carlo (MCMC) algorithm. The default is 5,000. If a warning "adaptation incomplete" appears, users may increase n.adapt. This argument and the following n.iter, n.burnin, n.chains, n.thin are passed to the functions in R package **rjags**.
n.iter	the total number of iterations in each MCMC chain. The default is 100,000.
n.burnin	the number of iterations for burn-in period. The default is n.iter/2.
n.chains	the number of MCMC chains. The default is 3.
n.thin	a positive integer indicating thinning rate. The default is the thinning rate which yields no more than 100,000 iterations remaining in each chain.
conv.diag	a logical value indicating whether to perform MCMC convergence diagnostic. The default is FALSE. If TRUE, n.chains must be greater than 1, and a .txt file, which contains the point estimates of the potential scale reduction factor and their upper confidence limits (see Gelman and Rubin 1992), will be written in users' current working directory.
trace	a vector of character strings of effect sizes. The character strings should be selected from those specified in param (except "rank.prob"), and trace plots of the specified effect sizes will be saved in users' current working directory. The default is not drawing trace plots (NULL).
dic	a logical value indicating whether the deviance information criterion (DIC) to be calculated. The default is FALSE.
postdens	a logical value indicating whether to draw the posterior density plots for treatment-specific rates. If TRUE, a .pdf file containing the density plot will be saved in users' current working directory. The default is FALSE.
mcmc.samples	a logical value indicating whether to save MCMC posterior samples in the output object. The default is FALSE.

Details

Suppose that a network meta-analysis collects I studies on K treatments, where each study investigates a subset of the K treatments. The outcome is binary, and the follow-up time for each study is reported. Label the studies from $i = 1$ to I and the treatments from $k = 1$ to K. Let T_i be the subset of the K treatments that is compared in the ith study. Also, in the ith study, let y_{ik} and n_{ik} be the number of events and the total number of participants in treatment group k. Denote f_i as the follow-up time of the ith study. The arm-based network meta-analysis model for these settings is constructed as:

$$y_{ik} \sim Bin(n_{ik}, p_{ik}) \qquad k \in T_i$$
$$cloglog(p_{ik}) = \log(f_i) + \log(\lambda_{ik})$$
$$\log(\lambda_{ik}) = \mu_k + \nu_{ik}$$
$$(\nu_{i1}, \nu_{i2}, \ldots, \nu_{iK})^T \sim N(\mathbf{0}, \mathbf{\Sigma}_K),$$

where $cloglot(t) = \log(-\log(1-t))$ is the complementary log-log link function, and $\mathbf{\Sigma}_K$ is a $K \times K$ positive definite covariance matrix. The μ_k's are treatment-specific fixed effects, and the random effects ν_{ik} are correlated within each study with the covariance matrix $\mathbf{\Sigma}_K$.

An unstructured covariance matrix $\mathbf{\Sigma}_K$ in the above model corresponds to model = "het_cor". The inverse-Wishart prior can be assigned to $\mathbf{\Sigma}_K$. Alternatively, using the separation strategy

by Cholesky decomposition (`prior.type = "chol"`), uniform priors $U(0, c)$ are assigned to the standard deviations in $\mathbf{\Sigma}_K$ and non-informative priors are assigned to the correlation components (Barnard et al, 2000; Lu and Ades, 2009; Wei and Higgins, 2013). Denote σ_k as the standard deviation of ν_{ik} and $\mathbf{D} = diag(\sigma_1, \ldots, \sigma_K)$, then the correlation matrix $\mathbf{R}_K = \mathbf{D}^{-1}\mathbf{\Sigma}_K\mathbf{D}^{-1}$. If we assume that all of the off-diagonal elements in $\mathbf{R}_K$ are equal, say to ρ, then this model corresponds to `model = "het_eqcor"`. If we further assume the homogeneity of variances of the random effects, that is, $\sigma_k = \sigma$ for $k = 1, 2, \ldots, K$, then the model is `"hom_eqcor"`. In addition, for the models `"hom_eqcor"` and `"het_eqcor"`, setting `prior.type` as `"invgamma"` implies using inverse-gamma priors with shape and scale parameters a, b for σ_k^2 or σ^2, and `"unif"` implies uniform priors $U(0, c)$ for σ_k or σ.

Value

`nma.ab.followup` returns a list with estimates of effect sizes specified in `param`. If the argument `dic = TRUE`, the deviance information criterion (DIC) statistic will be returned in the output list. In addition, if `conv.diag = TRUE`, a .txt file containing the point estimates of the potential scale reduction factor and their upper confidence limits by Gelman and Rubin (1992) will be saved in users' current working directory. If `postdens = TRUE`, the posterior densities of treatment-specific absolute risks will be saved as a .pdf file. If `trace` is specified, the trace plots are saved as .png files.

Note

Note that the earlier versions (< 4.0.0) of JAGS does not guarantee exact reproducibility of the results. Therefore, we recommend users install the latest version (>= 4.0.0) of JAGS so that exact reproducibility can be ensured by specifying certain seeds.

References

Barnard J, McCulloch R, and Meng XL (2000). "Modeling covariance matrices in terms of standard deviations and correlations, with application to shrinkage." *Stat Sin* **10**(4), 1281–11.

Dias S, Sutton AJ, Ades AE, and Welton NJ (2013). "Evidence synthesis for decision making 2: A generalized linear modeling framework for pairwise and network meta-analysis of randomized controlled trials." *Med Decis Making* **33**(5), 607–17.

Gelman A and Rubin DB (1992). "Inference from iterative simulation using multiple sequences." *Stat Sci* **7**(4), 457–72.

Lin L, Zhang J, Hodges JS, and Chu H (2017). "pcnetmeta: An R package for arm-based network meta-analysis." *J Stat Softw*, **80**(5), 1–25.

Lu G and Ades AE (2004). "Combination of direct and indirect evidence in mixed treatment comparisons." *Stat Med* **23**(20), 3105–24.

Lu G and Ades AE (2009). "Modeling between-trial variance structure in mixed treatment comparisons." *Biostatistics*, **10**(4), 792–805.

Spiegelhalter DJ, Best NG, Carlin BP, and van der Linde A (2002). "Bayesian measures of model complexity and fit." *J R Stat Soc Series B Stat Methodol* **64**(4), 583–639.

Wei Y and Higgins JPT (2013). "Bayesian multivariate meta-analysis with multiple outcomes." *Stat Med* **32**(17), 2911–34.

Zhang J, Carlin BP, Neaton JD, Soon GG, Nie L, Kane R, Virnig BA, and Chu H (2014). "Network meta-analysis of randomized clinical trials: Reporting the proper summaries." *Clin Trials* **11**(2), 246–62.

See Also

nma.ab.bin, nma.ab.cont, nma.ab.py

Examples

```
#data(diabetes)
# increase n.iter to reach convergence of MCMC
# increase n.adapt to enhance efficiency
#set.seed(1234)
#followup.out <- nma.ab.followup(s.id, t.id, r, n, folup, data = diabetes,
#  model = "het_cor", n.adapt = 500, n.iter = 100, n.chains = 1)
```

---

nma.ab.py *Arm-Based Network Meta-Analysis for Count Datasets with Exposure Time in Person-Years Reported*

Description

nma.ab.py performs arm-based network meta-analysis for count datasets with exposure time in person-years reported. It estimates treatment-specific rate, rate ratio between treatments, and their logarithms.

Usage

```
nma.ab.py(s.id, t.id, event.n, py, data, trtname,
          param = c("lograte", "logratio", "rank.prob"), model = "het_cor",
          prior.type, a = 0.001, b = 0.001, c = 10, higher.better = FALSE,
          digits = 4, n.adapt = 5000, n.iter = 100000,
          n.burnin = floor(n.iter/2), n.chains = 3,
          n.thin = max(1, floor((n.iter - n.burnin)/100000)),
          conv.diag = FALSE, trace = NULL, dic = FALSE, postdens = FALSE,
          mcmc.samples = FALSE)
```

Arguments

s.id	a numeric or character vector indicating study ID, or the corresponding column name in the argument data.
t.id	a numeric or character vector indicating treatment ID, or the corresponding column name in the argument data.

`event.n` a numeric vector of non-negative integers, indicating number of events in each study's treatment group, or the corresponding column name in the argument `data`.

`py` a numeric vector of non-negative numbers, indicating exposure time in person-years in each study's treatment group, or the corresponding column name in the argument `data`.

`data` an optional data frame containing the dataset for network meta-analysis. If `data` is specified, the previous arguments, `s.id`, `t.id`, `event.n`, and `py`, should be specified as the corresponding column names in `data`; otherwise, the previous arguments use environment variables.

`trtname` a vector of character strings indicating the treatment names for the corresponding treatment IDs according their order in `t.id`. If not specified, `t.id` is used as treatment names.

`param` a vector of character strings indicating the effect sizes to be estimated. The default includes log treatment-specific rate (`"lograte"`), log rate ratio (`"logratio"`), and treatment rank probability (`"rank.prob"`). `"lograte"` is automatically added into `param` even if it is not specified. In addition to the defaults, treatment-specific rate (`"rate"`) and rate ratio (`"ratio"`) can be added into the argument `param`.

`model` a character string indicating which Bayesian hierarchical model to be applied in the arm-based network meta-analysis. This argument can be set as `"hom_eqcor"`, `"het_eqcor"`, or `"het_cor"` (default). See "Details" for the models.

`prior.type` prior distribution of variances/covariances of random effects. If `model` is `"hom_eqcor"` or `"het_eqcor"`, it can be set as `"unif"` (uniform prior for standard deviations, the default) or `"invgamma"` (inverse gamma prior for variances). If `model` is `"het_cor"`, `prior.type` can be `"invwishart"` (the default) or `"chol"`. Specifying `"invwishart"` yields an inverse-Wishart prior for the variance-covariance matrix of random effects; by specifying `"chol"`, non-informative priors are assigned to variance and correlation components using the separation strategy by Cholesky decomposition. See "Details".

`a, b` positive numbers, specifying the shape and scale parameters of inverse gamma priors for variance(s) of random effects if using `prior.type` as `"invgamma"` for model `"hom_eqcor"` or `"het_eqcor"`. The defaults for both parameters are 0.001.

`c` positive number, specifying the upper bound of uniform prior for standard deviations of random effects if using `prior.type` as `"unif"` for model `"hom_eqcor"` or `"het_eqcor"`. The default is 10.

`higher.better` an optional logical value which needs to be specified when estimating the treatment rank probabilities (i.e., "rank.prob" is included in argument `param`). `TRUE` indicates higher treatment-specific rate implying better treatment, and vice versa. The default is `FALSE`.

`digits` a positive integer specifying the digits after the decimal point of the effect sizes estimates. The default is 4.

`n.adapt` the number of iterations for adaptation in Markov chain Monte Carlo (MCMC) algorithm. The default is 5,000. If a warning "adaptation incomplete" appears, users may increase `n.adapt`. This argument and the following `n.iter`, `n.burnin`, `n.chains`, `n.thin` are passed to the functions in R package **rjags**.

n.iter	the total number of iterations in each MCMC chain. The default is 100,000.
n.burnin	the number of iterations for burn-in period. The default is n.iter/2.
n.chains	the number of MCMC chains. The default is 3.
n.thin	a positive integer indicating thinning rate. The default is the thinning rate which yields no more than 100,000 iterations remaining in each chain.
conv.diag	a logical value indicating whether to perform MCMC convergence diagnostic. The default is FALSE. If TRUE, n.chains must be greater than 1, and a .txt file, which contains the point estimates of the potential scale reduction factor and their upper confidence limits (see Gelman and Rubin 1992), will be written in users' current working directory.
trace	a vector of character strings of effect sizes. The character strings should be selected from those specified in param (except "rank.prob"), and trace plots of the specified effect sizes will be saved in users' current working directory. The default is not drawing trace plots (NULL).
dic	a logical value indicating whether the deviance information criterion (DIC) to be calculated. The default is FALSE.
postdens	a logical value indicating whether to draw the posterior density plots for treatment-specific rates. If TRUE, a .pdf file containing the density plot will be saved in users' current working directory. The default is FALSE.
mcmc.samples	a logical value indicating whether to save MCMC posterior samples in the output object. The default is FALSE.

Details

Suppose that a network meta-analysis collects I studies on K treatments, where each study investigates a subset of the K treatments. The exposure time in person-years and the count of events in each treatment group are reported. Label the studies from $i = 1$ to I and the treatments from $k = 1$ to K. Let T_i be the subset of the K treatments that is compared in the ith study. Also, in the ith study, let y_{ik} be the number of events in treatment group k, and E_{ik} be the corresponding exposure time in person-years. The arm-based network meta-analysis model for these settings is constructed as:

$$y_{ik} \sim Pois(E_{ik}\lambda_{ik}) \qquad k \in T_i$$

$$\log(\lambda_{ik}) = \mu_k + \nu_{ik}$$

$$(\nu_{i1}, \nu_{i2}, \ldots, \nu_{iK})^T \sim N(\mathbf{0}, \mathbf{\Sigma}_K),$$

where $\mathbf{\Sigma}_K$ is a $K \times K$ positive definite correlation matrix. The μ_k's are treatment-specific fixed effects, and the random effects ν_{ik} are correlated within each study with the covariance matrix $\mathbf{\Sigma}_K$.

An unstructured covariance matrix $\mathbf{\Sigma}_K$ in the above model corresponds to model = "het_cor". The inverse-Wishart prior can be assigned to $\mathbf{\Sigma}_K$. Alternatively, using the separation strategy by Cholesky decomposition (prior.type = "chol"), uniform priors $U(0, c)$ are assigned to the standard deviations in $\mathbf{\Sigma}_K$ and non-informative priors are assigned to the correlation components (Barnard et al, 2000; Lu and Ades, 2009; Wei and Higgins, 2013). Denote σ_k as the standard deviation of ν_{ik} and $\mathbf{D} = diag(\sigma_1, \ldots, \sigma_K)$, then the correlation matrix $\mathbf{R}_K = \mathbf{D}^{-1}\mathbf{\Sigma}_K\mathbf{D}^{-1}$. If we assume that all of the off-diagonal elements in $\mathbf{R}_K$ are equal, say to ρ, then this model corresponds to model = "het_eqcor". If we further assume the homogeneity of variances of the random effects,

that is, $\sigma_k = \sigma$ for $k = 1, 2, \ldots, K$, then the model is `"hom_eqcor"`. In addition, for the models `"hom_eqcor"` and `"het_eqcor"`, setting `prior.type` as `"invgamma"` implies using inverse-gamma priors with shape and scale parameters a, b for σ_k^2 or σ^2, and `"unif"` implies uniform priors $U(0, c)$ for σ_k or σ.

Value

`nma.ab.py` returns a list with estimates of effect sizes specified in `param`. If the argument `dic = TRUE`, the deviance information criterion (DIC) statistic will be returned in the output list. In addition, if `conv.diag = TRUE`, a .txt file containing the point estimates of the potential scale reduction factor and their upper confidence limits by Gelman and Rubin (1992) will be saved in users' current working directory. If `postdens = TRUE`, the posterior densities of treatment-specific absolute risks will be saved as a .pdf file. If `trace` is specified, the trace plots are saved as .png files.

Note

Note that the earlier versions (< 4.0.0) of JAGS does not guarantee exact reproducibility of the results. Therefore, we recommend users install the latest version (>= 4.0.0) of JAGS so that exact reproducibility can be ensured by specifying certain seeds.

References

Barnard J, McCulloch R, and Meng XL (2000). "Modeling covariance matrices in terms of standard deviations and correlations, with application to shrinkage." *Stat Sin* **10**(4), 1281–11.

Dias S, Sutton AJ, Ades AE, and Welton NJ (2013). "Evidence synthesis for decision making 2: A generalized linear modeling framework for pairwise and network meta-analysis of randomized controlled trials." *Med Decis Making* **33**(5), 607–17.

Gelman A and Rubin DB (1992). "Inference from iterative simulation using multiple sequences." *Stat Sci* **7**(4), 457–72.

Lin L, Zhang J, Hodges JS, and Chu H (2017). "pcnetmeta: An R package for arm-based network meta-analysis." *J Stat Softw*, **80**(5), 1–25.

Lu G and Ades AE (2004). "Combination of direct and indirect evidence in mixed treatment comparisons." *Stat Med* **23**(20), 3105–24.

Lu G and Ades AE (2009). "Modeling between-trial variance structure in mixed treatment comparisons." *Biostatistics*, **10**(4), 792–805.

Spiegelhalter DJ, Best NG, Carlin BP, and van der Linde A (2002). "Bayesian measures of model complexity and fit." *J R Stat Soc Series B Stat Methodol* **64**(4), 583–639.

Wei Y and Higgins JPT (2013). "Bayesian multivariate meta-analysis with multiple outcomes." *Stat Med* **32**(17), 2911–34.

Zhang J, Carlin BP, Neaton JD, Soon GG, Nie L, Kane R, Virnig BA, and Chu H (2014). "Network meta-analysis of randomized clinical trials: Reporting the proper summaries." *Clin Trials* **11**(2), 246–62.

See Also

`nma.ab.bin`, `nma.ab.cont`, `nma.ab.followup`

Examples

```
#data(dietaryfat)
# increase n.iter to reach convergence of MCMC
# increase n.adapt to enhance efficiency
#set.seed(1234)
#py.out <- nma.ab.py(s.id, t.id, r, py, data = dietaryfat, model = "het_cor",
#  n.adapt = 300, n.iter = 100, n.chains = 1)
```

`nma.networkplot` *Plotting the Network*

Description

`nma.networkplot` plots a visual network presenting treatment comparisons.

Usage

```
nma.networkplot(s.id, t.id, data, title = "", trtname, alphabetic = TRUE,
                weight.edge = TRUE, adjust.thick = 5,
                weight.node = TRUE, adjust.node.size = 10,
                node.col = "orange", edge.col = "black", text.cex = 1,
                adjust.figsizex = 1.1, adjust.figsizey = 1.1)
```

Arguments

`s.id`	a numeric or character vector indicating study ID, or the corresponding column name in the argument `data`.
`t.id`	a numeric or character vector indicating treatment ID, or the corresponding column name in the argument `data`.
`data`	an optional data frame containing the dataset for network meta-analysis. If `data` is specified, the previous arguments, `s.id` and `t.id`, should be specified as the corresponding column names in `data`; otherwise, the previous arguments use environment variables.
`title`	a character string indicating plot title.
`trtname`	a vector of character strings indicating the treatment names for the corresponding treatment IDs according their order in `t.id`. If not specified, `t.id` is used as treatment names.
`alphabetic`	a logical value indicating whether to sort treatment nodes alphabetically in the network plot. The default is `TRUE`. If `FALSE`, treatment nodes are sorted by the treatment IDs specified in `t.id`.
`weight.edge`	a logical value indicating whether to draw the edges proportionally to the number of direct treatment comparisons. The default is `TRUE`.
`adjust.thick`	a positive integer indicating the maximum thickness of the edge when `weight` is `TRUE`. The default is 5.

`weight.node` a logical value indicating whether node size is proportional to the number of direct treatment comparisons which include that node. The default is `TRUE`.

`adjust.node.size` a positive number to adjust the node sizes when `weight.node` is `TRUE`. The default is 10.

`node.col` a character string indicating the color of treatment nodes. The default is `"orange"`.

`edge.col` a character string indicating the color of edges between treatments nodes. The default is `"black"`.

`text.cex` a positive integer indicating the sizes of treatment names placed around/on the corresponding nodes. The default is 1.

`adjust.figsizex` a positive number used to adjust the plot width. The default is 1.1.

`adjust.figsizey` a positive number used to adjust the plot height. The default is 1.1.

Value

A network plot is generated. Each node represents a treatment, and the edges indicate the direct comparisons between the two treatments in various studies.

References

Lin L, Zhang J, Hodges JS, and Chu H (2017). "pcnetmeta: An R package for arm-based network meta-analysis." *J Stat Softw*, **80**(5), 1–25.

Examples

```
data(smoke)
nma.networkplot(s.id, t.id, data = smoke, title = "Smoke Cessation",
  trtname = c("NC", "SH", "IC", "GC"))
# NC: No contact; SH: Self-help
# IC: individual counselling; GC: group counselling

data(diabetes)
nma.networkplot(s.id, t.id, data = diabetes, title = "Diabetes",
  trtname = c("Diuretic", "Placebo", "b-blocker", "CCB", "ACE inhibitor",
  "ARB"))
```

---

parkinson *Network Meta-Ananlysis on Parkinson's Disease*

Description

An example of network meta-analysis for continuous outcomes.

Usage

```
data("parkinson")
```

Format

A data frame containing 7 studies which compare 5 treatments.

`s.id` a numeric vector indicating study IDs.

`t.id` a numeric vector indicating treatment IDs.

`mean` a numeric vector indicating the mean of continuous outcomes in each treatment group in each study.

`sd` a numeric vector indicating the standard deviance of continuous outcomes in each treatment group in each study.

`n` a numeric vector indicating the total number of participants in each treatment group in each study.

Details

The continuous outcome measures the off-time reduction in patients given dopamine agonists as adjunct therapy in Parkinson's disease. Treatment 1 is placebo and Treatments 2 to 5 are active drugs.

Source

Dias S, Sutton AJ, Ades AE, and Welton NJ (2013). "Evidence synthesis for decision making 2: A generalized linear modeling framework for pairwise and network meta-analysis of randomized controlled trials." *Med Decis Making* **33**(5), 607–17.

`rank.prob` *Plotting Treatment Rank Probabilities*

Description

`rank.prob` generates a plot for treatment rank probabilities.

Usage

```
rank.prob(nma.obj, cex.axis = 1, cex.lab = 1)
```

Arguments

`nma.obj`	a list object obtained by function `nma.ab.bin`, `nma.ab.cont`, `nma.ab.py`, or `nma.ab.followup`.
`cex.axis`	a numeric value specifying the size of the tick label numbers/text.
`cex.lab`	a numeric value specifying the size of the axis label text.

Details

A plot is generated. Each vertical bar represents probabilities of being different ranks for a specific treatment. A darker area indicates the probability of being a higher rank. The black area indicates the probability of being the best treatment.

Examples

```
data(smoke)
# increase n.iter to reach convergence
# increase n.adapt to enhance efficiency
set.seed(1234)
nma.out <- nma.ab.bin(s.id, t.id, r, n, data = smoke,
  trtname = c("NC", "SH", "IC", "GC"), param= "rank.prob", model = "het_cor",
  higher.better = TRUE, n.adapt = 400, n.iter = 100, n.chains = 1)
rank.prob(nma.out)
```

---

smoke *Network Meta-Analysis on Smoking Cessation Data*

Description

An example of network meta-analysis for binary outcomes.

Usage

```
data("smoke")
```

Format

A data frame containing 24 studies on smoking cessation, comparing four treatments.

`s.id` a numeric vector indicating study IDs.

`t.id` a numeric vector indicating treatment IDs.

`r` a numeric vector indicating event number for a certain treatment in the corresponding study.

`n` a numeric vector indicating the total number of participants for a certain treatment in the corresponding study.

Details

Treatment IDs stand for 1) no contact; 2) self-help; 3) individual counselling; and 4) group counselling.

Source

Hasselblad V (1998) "Meta-analysis of multitreatment studies." *Med Decis Making* **18**(1), 37–43.

Lu G and Ades AE (2006) "Assessing evidence inconsistency in mixed treatment comparisons." *J Am Stat Assoc* **101**(474), 447–59.

Index

∗Topic **datasets**
diabetes, 5
dietaryfat, 5
parkinson, 23
smoke, 25

absolute.plot, 3

contrast.plot, 4

diabetes, 5
dietaryfat, 5

nma.ab.bin, *2–4*, 6, *14*, *18*, *21*, *24*
nma.ab.cont, *3, 4*, *10*, 10, *18*, *21*, *24*
nma.ab.followup, *3, 4*, *10*, *14*, 14, *21*, *24*
nma.ab.py, *3, 4*, *10*, *14*, *18*, 18, *24*
nma.networkplot, 22

parkinson, 23
pcnetmeta *(*pcnetmeta-package*)*, 2
pcnetmeta-package, 2

rank.prob, 24

smoke, 25