

Package ‘RaCE.NMA’

August 5, 2026

Title Rank-Clustered Estimation for Network Meta-Analysis

Version 1.2.0

Description An implementation of the RaCE-NMA (Rank-Clustered Estimation for Network Meta-Analysis) model for post-hoc clustering of treatments or interventions by rank in network meta-analysis data. Functions for model estimation, assessment, and displaying results are provided. For more details, see Pearce and Zhou (2025) <[doi:10.1017/rsm.2025.10049](https://doi.org/10.1017/rsm.2025.10049)>.

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.3

LazyData TRUE

Imports utils, magrittr, dplyr, invgamma, mvtnorm, coda, reshape2, ggplot2, parallel

Suggests knitr, rmarkdown, devtools, cowplot, gridExtra, testthat (>= 3.0.0)

VignetteBuilder knitr

URL <https://pearce790.github.io/RaCE.NMA/>,
<https://github.com/pearce790/RaCE.NMA>

BugReports <https://github.com/pearce790/RaCE.NMA/issues>

Config/testthat/edition 3

NeedsCompilation no

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Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2026-08-05 09:10:02 UTC

Contents

calculate_Rhat	2
calculate_SUCRA_MNBT	3
clusterplot_ranks	3
cumulativeprobplot_ranks	4
fit_raceNMA	5
forestplot_muhat	6
mcmc_raceNMA	7
toy_data	9
traceplot_K	9
traceplot_mu	10
wang_posterior	10
Index	11

calculate_Rhat	<i>Calculate Gelman Diagnostics for Fitted RaCE NMA Models</i>
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Description

This function applies MCMC outputs from the mcmc_raceNMA function to the gelman.diag function in the coda package.

Usage

```
calculate_Rhat(mcmc, names = NULL, level = 0.95, multivariate = FALSE)
```

Arguments

mcmc	MCMC draws from the RaCE NMA model, in the form of the model output of the mcmc_raceNMA function.
names	A vector of intervention names (optional)
level	The level parameter from the gelman.diag function in the coda package. Defaults to 0.95.
multivariate	The multivariate parameter from the gelman.diag function in the coda package. Defaults to FALSE.

Value

Gelman diagnostics for the inputted MCMC chains, in the format of the output of the gelman.diag function in the coda package.

Examples

```
mcmc <- mcmc_raceNMA(mu_hat=c(0,0,1,1), s=c(.1,.1,.1,.1), seed=1)
calculate_Rhat(mcmc,names=paste0("Treatment ",1:4))
```

calculate_SUCRA_MNBT	<i>Calculate SUCRA and MNBT based on MCMC draws in NMA or RaCE-NMA models</i>
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Description

This function creates a results table of SUCRA and Median Number of Better Treatments (MNBT) based on MCMC draws from a standard NMA model or a fitted RaCE-NMA model.

Usage

```
calculate_SUCRA_MNBT(data = NULL, mcmc = NULL, level = 0.5, names = NULL)
```

Arguments

data	A NxJ matrix of data, where N is the number of observations and J the number of treatments. This feature is designed to display results from a standard NMA study.
mcmc	MCMC draws from the RaCE NMA model, in the form of the model output of the mcmc_raceNMA function.
level	The level level for the interval estimate of MNBT. Defaults to 0.50.
names	A vector of intervention names (optional)

Value

A table containing SUCRA and MNBT values for each treatment, ordered by descending SUCRA values.

Examples

```
mcmc <- mcmc_raceNMA(mu_hat=c(0,0,1,1), s=c(.1,.1,.1,.1), seed=1)
calculate_SUCRA_MNBT(mcmc=mcmc)
```

clusterplot_ranks	<i>Create a posterior clustering matrix for the interventions based on RaCE NMA models</i>
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Description

This function creates a posterior clustering matrix for the interventions in the form of a ggplot.

Usage

```
clusterplot_ranks(data = NULL, mcmc = NULL, names = NULL, label_ranks = NULL)
```

Arguments

data	A NxJ matrix of data, where N is the number of observations and J the number of treatments. This feature is designed to display results from a standard NMA study.
mcmc	MCMC draws from the RaCE NMA model, in the form of the model output of the mcmc_raceNMA function.
names	A vector of intervention names (optional)
label_ranks	A vector containing rank levels for which posterior rank probabilities should be displayed within the clustering matrix. Only non-zero probabilities are displayed. Defaults to NULL, indicating no probabilities are displayed as text.

Value

A ggplot of a posterior clustering matrix for the interventions.

Examples

```
data("toy_data")
mcmc <- mcmc_raceNMA(posterior=toy_data,iter=500,nu_iter=2,chains=1)
clusterplot_ranks(mcmc=mcmc,names=paste0("Treatment ",1:10),label_ranks=1:3)
```

cumulativeprobplot_ranks

Create a cumulative ranking plot in RaCE NMA models

Description

This function creates a cumulative ranking plot in the form of a ggplot.

Usage

```
cumulativeprobplot_ranks(data = NULL, mcmc = NULL, names = NULL)
```

Arguments

data	A NxJ matrix of data, where N is the number of observations and J the number of treatments. This feature is designed to display results from a standard NMA study.
mcmc	MCMC draws from the RaCE NMA model, in the form of the model output of the mcmc_raceNMA function.
names	A vector of intervention names (optional)

Value

A ggplot of a cumulative ranking plot.

Examples

```
mcmc <- mcmc_raceNMA(mu_hat=c(0,0,1,1), s=c(.1,.1,.1,.1), seed=1)
cumulativeproplot_ranks(mcmc=mcmc,names=paste0("Treatment ",1:4))
```

fit_raceNMA

Fit a Bayesian Rank-Clustered Estimation model for Network Meta-Analysis (RaCE-NMA). Recommended for internal use only; use mcmc_raceNMA instead.

Description

This function fits a Bayesian RaCE-NMA model to data from a previous network meta-analysis.

Usage

```
fit_raceNMA(
  posterior = NULL,
  mu_hat = NULL,
  cov = NULL,
  s = NULL,
  mu0 = NULL,
  sigma0 = NULL,
  tau,
  nu0,
  iter,
  nu_iter
)
```

Arguments

posterior	A matrix of posterior draws of relative intervention effects based on a previous NMA. The (i,j) is the ith draw of the effect of intervention j.
mu_hat	A vector of estimated average relative intervention effects based on a previous NMA. The jth entry is the effect of intervention j. Ignored if posterior is supplied.
cov	A variance covariance matrix of relative intervention effects based on a previous NMA. The (i,j) entry is the covariane between intervention i and j's effects. Ignored if posterior is supplied.
s	A vector of the estimated standard deviations of each intervention. The jth entry is the standard deviation of intervention j. Ignored if posterior is supplied.
mu0	The hyperparameter mu0. If NULL, set to mean(mu_hat).
sigma0	The hyperparameter sigma_0. If NULL, set to sqrt(10*var(mu_hat)) which aims to be minimally informative.
tau	The standard deviation of the Metropolis Hastings proposal distribution. If NULL, set to min(lmu_hat_i-mu_hat_jl).

<code>nu0</code>	A numeric vector for the initialization of worth parameters, μ , in the MCMC algorithm. Default to NULL, indicating random initialization.
<code>iter</code>	A numeric indicating the total number of outer MCMC iterations (i.e., the number of times the partition is updated in the Gibbs sampler).
<code>nu_iter</code>	A numeric indicating the number of times each worth parameter is drawn per update of the parameter partition. There will be a total of <code>iterxnu_iter</code> samples from the posterior.

Value

A list of 4 elements: μ , a `(iterxnu_iter)xJ` matrix of approximate posterior draws of the intervention-specific worth parameters, μ ; ν a `(iterxnu_iter)xJ` matrix of the unique parameter values corresponding to the j th partition cluster in posterior draw i , g a `(iterxnu_iter)xJ` matrix indicating the cluster membership of object j in posterior draw i , and K a vector of the number of non-empty partition clusters in each posterior draw.

Examples

```
fit_raceNMA(mu_hat=c(0,0,1,1), s=c(.1,.1,.1,.1), mu0=0.5, sigma0=5, tau=0.5,
            nu0 = NULL, iter = 5000, nu_iter = 2)
```

<code>forestplot_muhat</code>	<i>Create posterior forest plots for relative treatment effect estimates from a standard or RaCE NMA study</i>
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Description

This function creates posterior forest plots for relative treatment effect estimates from a standard or RaCE NMA study.

Usage

```
forestplot_muhat(
  data = NULL,
  mcmc = NULL,
  names = NULL,
  level = 0.95,
  order_by_average = TRUE
)
```

Arguments

<code>data</code>	A $N \times J$ matrix of data to display as a forest plot, where N is the number of observations and J the number of treatments. This feature is designed for use to display a forest plot of results from a standard NMA study.
<code>mcmc</code>	MCMC draws from the RaCE NMA model, in the form of the model output of the <code>mcmc_raceNMA</code> function.

names A vector of intervention names (optional)

level A numeric indicating the desired credible level to be displayed, as a proportion.
Defaults to 0.95.

order_by_average A boolean indicating if plot should order treatments by their average treatment effect.

Value

A ggplot of posterior forest plots for the mu parameter.

Examples

```
data("toy_data")
forestplot_muhat(data=toy_data,names=paste0("Treatment ",1:4))
```

mcmc_raceNMA	<i>Fit a Bayesian Rank-Clustered Estimation model for Network Meta-Analysis (RaCE-NMA) using multiple MCMC chains</i>
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Description

This function fits a Bayesian RaCE-NMA model to data from a previous network meta-analysis. The function has input parameters to permit drawing multiple MCMC chains, as well as chain thinning and burn-in. Chains are independent and may be drawn in parallel across multiple CPU cores via the cores argument.

Usage

```
mcmc_raceNMA(
  posterior = NULL,
  mu_hat = NULL,
  cov = NULL,
  s = NULL,
  mu0 = NULL,
  sigma0 = NULL,
  tau = NULL,
  nu0 = NULL,
  iter = 4000,
  nu_iter = 5,
  chains = 2,
  burn_prop = 0.5,
  thin = 1,
  seed = NULL,
  cores = 1,
  verbose = TRUE
)
```

Arguments

posterior	A matrix of posterior draws of relative intervention effects based on a previous NMA. The (i,j) is the ith draw of the effect of intervention j.
mu_hat	A vector of estimated average relative intervention effects based on a previous NMA. The jth entry is the effect of intervention j. Ignored if posterior is supplied.
cov	A variance covariance matrix of relative intervention effects based on a previous NMA. The (i,j) entry is the covariance between intervention i and j's effects. Ignored if posterior is supplied.
s	A vector of the estimated standard deviations of each intervention. The jth entry is the standard deviation of intervention j. Ignored if posterior is supplied.
mu0	The hyperparameter mu0. If NULL, set to mean(mu_hat).
sigma0	The hyperparameter sigma_0. If NULL, set to sqrt(10*var(mu_hat)) which aims to be minimally informative.
tau	The standard deviation of the Metropolis Hastings proposal distribution. If NULL, set to min(mu_hat_i-mu_hat_j).
nu0	A numeric vector for the initialization of worth parameters, mu, in the MCMC algorithm. Default to NULL, indicating random initialization.
iter	A numeric indicating the total number of outer MCMC iterations (i.e., the number of times the partition is updated in the Gibbs sampler).
nu_iter	A numeric indicating the number of times each worth parameter is drawn per update of the parameter partition. There will be a total of iterxnu_iter samples from the posterior.
chains	A numeric indicating the total number of independent MCMC chains to be run.
burn_prop	A numeric between 0 and 1 indicating the proportion of MCMC samples in each chain to be removed as burn-in.
thin	A numeric indicating that only every thin-th sample should be retained, to save computational memory.
seed	A numeric indicating the random seed used to generate the per-chain random number streams.
cores	A numeric indicating how many CPU cores to use when drawing chains. The default, 1, draws chains sequentially. Values above 1 draw chains in parallel; cores is silently capped at chains. Results do not depend on cores.
verbose	A boolean indicating if the function should print progress updates as the MCMC chains run. Default to TRUE.

Details

Each chain is assigned its own L'Ecuyer-CMRG random number stream, derived deterministically from seed. Chain i therefore produces the same draws whether it was run sequentially or on a parallel worker, so cores affects only run time.

Value

A (chainsxiter/thin)x(3J+3) matrix of posterior draws, one row per posterior sample of mu, nu, and g, with additional columns indicating the MCMC chain index, iteration index, and number of non-empty partition clusters K of each posterior sample.

Examples

```
mcmc <- mcmc_raceNMA(mu_hat=c(0,0,1,1), s=c(.1,.1,.1,.1), seed=1)
head(mcmc)
```

toy_data	<i>Toy data of posterior relative treatment effects</i>
----------	---

Description

The dataset includes relative treatment effects for 4 treatments across 10k posterior draws, as studied in Simulation Study 2 of Pearce and Zhou (2026).

Usage

```
toy_data
```

Format

data.frame in which the (i,j) entry is the relative treatment effect of treatment j in posterior draw i.

traceplot_K	<i>Create trace plots for the K parameter in RaCE NMA models</i>
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Description

This function creates trace plots for the K parameter in the form of a ggplot.

Usage

```
traceplot_K(mcmc)
```

Arguments

mcmc	MCMC draws from the RaCE NMA model, in the form of the model output of the mcmc_raceNMA function.
------	---

Value

A ggplot of trace plots for the K parameter.

Examples

```
mcmc <- mcmc_raceNMA(mu_hat=c(0,0,1,1), s=c(.1,.1,.1,.1), seed=1)
traceplot_K(mcmc)
```

traceplot_mu

Create trace plots for the mu parameter in RaCE NMA models

Description

This function creates trace plots for the mu parameter in the form of a ggplot.

Usage

```
traceplot_mu(mcmc, names = NULL)
```

Arguments

mcmc	MCMC draws from the RaCE NMA model, in the form of the model output of the mcmc_RCMVN function.
names	A vector of intervention names (optional)

Value

A ggplot of trace plots for the mu parameter.

Examples

```
mcmc <- mcmc_raceNMA(mu_hat=c(0,0,1,1), s=c(.1,.1,.1,.1), seed=1)
traceplot_mu(mcmc,names=paste0("Treatment ",1:4))
```

wang_posterior

Posterior relative treatment effects for non-baseline treatments based on Wang et. al (2022)

Description

The dataset includes relative treatment effects for 10 non-baseline treatments across 60k posterior draws based on an NMA study by Wang et. al (2022).

Usage

```
wang_posterior
```

Format

data.frame in which the (i,j) entry is the relative treatment effect of treatment j in posterior draw i.

Index

* datasets

toy_data, [9](#)

wang_posterior, [10](#)

calculate_Rhat, [2](#)

calculate_SUCRA_MNBT, [3](#)

clusterplot_ranks, [3](#)

cumulativeprobplot_ranks, [4](#)

fit_raceNMA, [5](#)

forestplot_muhat, [6](#)

mcmc_raceNMA, [7](#)

toy_data, [9](#)

traceplot_K, [9](#)

traceplot_mu, [10](#)

wang_posterior, [10](#)