Package ‘RaCE.NMA’

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Title Rank-Clustered Estimation for Network Meta-Analysis

Version 1.0.3

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>.

License GPL (>= 3)

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LazyData TRUE

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

Suggests knitr, rmarkdown, devtools, cowplot, gridExtra

VignetteBuilder knitr

URL `https://pearce790.github.io/RaCE.NMA/`,

`https://github.com/pearce790/RaCE.NMA/`

BugReports `https://github.com/pearce790/RaCE.NMA/issues`

NeedsCompilation no

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Contents

`calculate_Rhat` *Calculate Gelman Diagnostics for Fitted RaCE NMA Models*

Description

This function applies MCMC outputs from the mcmc_RCMVN package 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_RCMVN` 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` *Calculate SUCRA and MNBT based on MCMC draws in NMA or RaCE-NMA models*

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_RCMVN` 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` *Create a posterior clustering matrix for the interventions based on RaCE NMA models*

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_RCMVN` 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_RCMVN` 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)
cumulativeprobplot_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_RCMVN 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(|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.

Value

A list of 4 elements: `mu`, a (`iterxnu_iter`)x`J` matrix of approximate posterior draws of the intervention-specific worth parameters, mu; `nu` a (`iterxnu_iter`)x`J` matrix of the unique parameter values corresponding to the jth partition cluster in posterior draw i, `g` a a (`iterxnu_iter`)x`J` 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)
```

`forestplot_muhat` *Create posterior forest plots for relative treatment effect estimates from a standard or RaCE NMA study*

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

`data`	A NxJ 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.
`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)
`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` *Fit a Bayesian Rank-Clustered Estimation model for Network Meta-Analysis (RaCE-NMA) using multiple MCMC chains*

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.

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,
  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 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(|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 that should be set before running the first MCMC chain.
`verbose`	A boolean indicating if the function should print progress updates as the MCMC chains run. Default to `TRUE`.

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)
```

`sample_partition_correlation` *Partition sampling in Bayesian RaCE-NMA models (internal use only)*

Description

This function implements a reversible jump MCMC procedure for updating the parameter partition in Bayesian Rank-Clustered Estimation for Network Meta-Analysis models in the case when we assume correlation among treatment effects. For internal use only.

Usage

```
sample_partition_correlation(
  mu_hat,
  J,
  nu,
  g,
  K,
  mu0,
  sigma0,
  cov,
  tau = tau,
  b_g = 0.5,
  d_g = 0.5
)
```

Arguments

`mu_hat`	A vector of estimated average relative intervention effects based on a previous NMA. The jth entry is the effect of intervention j.
`J`	A numeric indicating the total number of interventions being compared.
`nu`	A vector indicating current values for nu in the Gibbs sampler.
`g`	A vector indicating current values for g in the Gibbs sampler.
`K`	A vector indicating current values for K in the Gibbs sampler.
`mu0`	The hyperparameter mu0, usually specified as the grand mean of the average intervention effects.
`sigma0`	The hyperparameter sigma_0, usually a large number as to be minimally informative.
`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.
`tau`	The standard deviation of the Metropolis Hastings proposal distribution.
`b_g`	The probability of "birth"ing a new partition cluster, if possible. Default is 0.5.
`d_g`	The probability of "death"ing an existing partition cluster, if possible. Default is 0.5.

Value

A list containing updated values for g, nu, and K.

Examples

```
sample_partition_correlation(mu_hat=c(1,1,1),J=3,nu=1,g=c(1,1,1),K=1,mu0=1,sigma0=1,tau=0.1)
```

`sample_partition_independence` *Partition sampling in Bayesian RaCE-NMA models (internal use only)*

Description

This function implements a reversible jump MCMC procedure for updating the parameter partition in Bayesian Rank-Clustered Estimation for Network Meta-Analysis models in the case when we assume independence between treatment effects. For internal use only.

Usage

```
sample_partition_independence(
  mu_hat,
  J,
  nu,
  g,
  K,
  mu0,
  sigma0,
  s,
  tau = tau,
  b_g = 0.5,
  d_g = 0.5
)
```

Arguments

`mu_hat`	A vector of estimated average relative intervention effects based on a previous NMA. The jth entry is the effect of intervention j.
`J`	A numeric indicating the total number of interventions being compared.
`nu`	A vector indicating current values for nu in the Gibbs sampler.
`g`	A vector indicating current values for g in the Gibbs sampler.
`K`	A vector indicating current values for K in the Gibbs sampler.
`mu0`	The hyperparameter mu0, usually specified as the grand mean of the average intervention effects.

`sigma0`	The hyperparameter sigma_0, usually a large number as to be minimally informative.
`s`	A vector of the estimated standard deviations of each intervention. The jth entry is the standard deviation of intervention j.
`tau`	The standard deviation of the Metropolis Hastings proposal distribution.
`b_g`	The probability of "birth"ing a new partition cluster, if possible. Default is 0.5.
`d_g`	The probability of "death"ing an existing partition cluster, if possible. Default is 0.5.

Value

A list containing updated values for g, nu, and K.

Examples

```
sample_partition_independence(mu_hat=c(1,1,1),J=3,nu=1,g=c(1,1,1),
K=1,mu0=1,sigma0=1,s=c(1,1,1),tau=0.1)
```

`toy_data` *Toy data of posterior relative treatment effects*

Description

The dataset includes relative treatment effects for 4 treatments across 10k posterior draws, as studied in Simulation Study 2 of Pearce and Zhou (2025).

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` *Create trace plots for the K parameter in RaCE NMA models*

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_RCMVN` 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.

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