

Package: metapack (via r-universe)

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Type Package

Title Bayesian Meta-Analysis and Network Meta-Analysis

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Description Contains functions performing Bayesian inference for meta-analytic and network meta-analytic models through Markov chain Monte Carlo algorithm. Currently, the package implements Hui Yao, Sungduk Kim, Ming-Hui Chen, Joseph G. Ibrahim, Arvind K. Shah, and Jianxin Lin (2015) <[doi:10.1080/01621459.2015.1006065](https://doi.org/10.1080/01621459.2015.1006065)> and Hao Li, Daeyoung Lim, Ming-Hui Chen, Joseph G. Ibrahim, Sungduk Kim, Arvind K. Shah, Jianxin Lin (2021) <[doi:10.1002/sim.8983](https://doi.org/10.1002/sim.8983)>. For maximal computational efficiency, the Markov chain Monte Carlo samplers for each model, written in C++, are fine-tuned. This software has been developed under the auspices of the National Institutes of Health and Merck & Co., Inc., Kenilworth, NJ, USA.

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LinkingTo Rcpp, RcppArmadillo, RcppProgress, BH

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL <https://events.stat.uconn.edu/metapack/>

BugReports <https://github.com/daeyounglim/metapack/issues>

Repository <https://daeyounglim.r-universe.dev>

RemoteUrl <https://github.com/daeyounglim/metapack>

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bayes_nmr

Fit Bayesian Network Meta-Regression Models

Description

This is a function that fits the model introduced in *Bayesian Network Meta-Regression Models Using Heavy-Tailed Multivariate Random Effects with Covariate-Dependent Variances*. The first seven arguments are required except ZCovariate. If not provided, ZCovariate will be assigned a vector of ones, `rep(1, length(Outcome))`. ZCovariate is the centerpiece of the modeling of variances and the heavy-tailed random effects distribution.

Usage

```

bayes_nmr(
  Outcome,
  SD,
  XCovariate,
  ZCovariate,
  Treat,
  Trial,
  Npt,
  prior = list(),
  mcmc = list(),
  control = list(),
  init = list(),
  Treat_order = NULL,
  Trial_order = NULL,
  scale_x = FALSE,
  verbose = FALSE
)

```

Arguments

Outcome	the aggregate mean of the responses for each arm of every study.
SD	the standard deviation of the responses for each arm of every study.
XCovariate	the aggregate covariates for the fixed effects.
ZCovariate	the aggregate covariates associated with the variance of the random effects.
Treat	the treatment identifiers for trial arm. This is equivalent to the arm labels in each study. The elements within will be coerced to consecutive integers
Trial	the study/trial identifiers. The elements within will be coerced to consecutive integers.
Npt	the number of observations/participants for a unique (k, t), or each arm of every trial.
prior	(Optional) a list of hyperparameters. The hyperparameters include df, c01, c02, a4, b4, a5, and b5. df indicates the degrees of freedom whose value is 20. The hyperparameters a* and b* will take effect only if sample_df=TRUE. See control.
mcmc	(Optional) a list of MCMC specification. ndiscard is the number of burn-in iterations. nskip configures the thinning of the MCMC. For instance, if nskip=5, bayes_nmr will save the posterior sample every 5 iterations. nkeep is the size of the posterior sample. The total number of iterations will be ndiscard + nskip * nkeep.
control	(Optional) a list of parameters for the Metropolis-Hastings algorithm . lambda, phi, and Rho are sampled through the localized Metropolis algorithm. *_stepsize with the asterisk replaced with one of the names above specifies the stepsize for determining the sample evaluation points in the localized Metropolis algorithm. sample_Rho can be set to FALSE to suppress the sampling of Rho. When

	sample_Rho is FALSE, Rho will be fixed using the value given by the <code>init</code> argument, which defaults to an equicorrelation matrix of $0.5\mathbf{I} + 0.5\mathbf{1}\mathbf{1}'$ where $\mathbf{1}$ is the vector of ones. When <code>sample_df</code> is TRUE, <code>df</code> will be sampled.
<code>init</code>	(Optional) a list of initial values for the parameters to be sampled: <code>theta</code> , <code>phi</code> , <code>sig2</code> , and <code>Rho</code> .
<code>Treat_order</code>	(Optional) a vector of unique treatments to be used for renumbering the <code>Treat</code> vector. The first element will be assigned treatment zero, potentially indicating placebo. If not provided, the numbering will default to an alphabetical/numerical order.
<code>Trial_order</code>	(Optional) a vector unique trials. The first element will be assigned trial zero. If not provided, the numbering will default to an alphabetical/numerical order.
<code>scale_x</code>	(Optional) a logical variable indicating whether <code>XCovariate</code> should be scaled/standardized. The effect of setting this to TRUE is not limited to merely standardizing <code>XCovariate</code> . The following generic functions will scale the posterior sample of <code>theta</code> back to its original unit: <code>plot</code> , <code>fitted</code> , <code>summary</code> , and <code>print</code> . That is <code>theta[j] <- theta[j] / sd(XCovariate[,j])</code> .
<code>verbose</code>	(Optional) a logical value indicating whether to print the progress bar during the MCMC sampling.

Value

`bayes_nmr` returns an object of class "bayesnmr". The functions `summary` or `print` are used to obtain and print a summary of the results. The generic accessor function `fitted` extracts the posterior mean, posterior standard deviation, and the interval estimates of the value returned by `bayes_nmr`.

An object of class `bayesnmr` is a list containing the following components:

- `Outcome` - the aggregate response used in the function call.
- `SD` - the standard deviation used in the function call.
- `Npt` - the number of participants for (k, t) used in the function call.
- `XCovariate` - the aggregate design matrix for fixed effects used in the function call. Depending on `scale_x`, this may differ from the matrix provided at function call.
- `ZCovariate` - the aggregate design matrix for random effects. `bayes_nmr` will assign `rep(1, length(Outcome))` if it was not provided at function call.
- `Trial` - the *renumbered* trial indicators. Depending on `Trial_order`, it may differ from the vector provided at function call.
- `Treat` - the *renumbered* treatment indicators. Depending on `Treat_order`, it may differ from the vector provided at function call.
- `TrtLabels` - the vector of treatment labels corresponding to the renumbered `Treat`. This is equivalent to `Treat_order` if it was given at function call.
- `TrialLabels` - the vector of trial labels corresponding to the renumbered `Trial`. This is equivalent to `Trial_order` if it was given at function call.
- `K` - the total number of trials.
- `nT` - the total number of treatments.
- `scale_x` - a Boolean indicating whether `XCovariate` has been scaled/standardized.

- `prior` - the list of hyperparameters used in the function call.
- `control` - the list of tuning parameters used for MCMC in the function call.
- `mcmc`time - the elapsed time for the MCMC algorithm in the function call. This does not include all the other preprocessing and post-processing outside of MCMC.
- `mcmc` - the list of MCMC specification used in the function call.
- `mcmc.draws` - the list containing the MCMC draws. The posterior sample will be accessible here.

Author(s)

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References

Li, H., Chen, M. H., Ibrahim, J. G., Kim, S., Shah, A. K., Lin, J., & Tershakovec, A. M. (2019). Bayesian inference for network meta-regression using multivariate random effects with applications to cholesterol lowering drugs. *Biostatistics*, **20**(3), 499-516.

Li, H., Lim, D., Chen, M. H., Ibrahim, J. G., Kim, S., Shah, A. K., & Lin, J. (2021). Bayesian network meta-regression hierarchical models using heavy-tailed multivariate random effects with covariate-dependent variances. *Statistics in Medicine*.

See Also

[bmeta_analyze](#) for using the [Formula](#) interface

Examples

```
library(metapack)
data(TNM)
groupInfo <- list(c("PBO"), c("R"))
nz <- length(groupInfo)
ns <- nrow(TNM)
XCovariate <- model.matrix(~ 0 + bldlc + bhdlc + btg + age +
  white + male + bmi + potencymed + potencyhigh + durat, data = TNM)
XCovariate <- scale(XCovariate, center = TRUE, scale = FALSE)
ZCovariate <- matrix(0, ns, nz)
for (j in 1:length(groupInfo)) {
  for (i in 1:ns) {
    if (TNM$treat[i] %in% groupInfo[[j]]) {
      ZCovariate[i, j] <- 1
    }
  }
}
addz <- scale(cbind(TNM$bldlc, TNM$btg), center=TRUE, scale=TRUE)
ZCovariate <- cbind(1, ZCovariate, addz)
theta_init <- c(0.05113, -1.38866, 1.09817, -0.85855, -1.12056, -1.14133,
  -0.22435, 3.63453, -2.09322, 1.07858, 0.80566, -40.76753,
  -45.07127, -28.27232, -44.14054, -28.13203, -19.19989,
  -47.21824, -51.31234, -48.46266, -47.71443)
set.seed(2797542)
```

```
fit <- bayes_nmr(TNM$ptg, TNM$sdgt, XCovariate, ZCovariate, TNM$treat,
  TNM$trial, TNM$n, prior = list(c01 = 1.0e05, c02 = 4, df = 3),
  mcmc = list(ndiscard = 1, nskip = 1, nkeep = 1),
  init = list(theta = theta_init),
  Treat_order = c("PBO", "S", "A", "L", "R", "P", "E", "SE",
    "AE", "LE", "PE"),
  scale_x = TRUE, verbose = FALSE)
```

 bayes_parobs

Fit Bayesian Inference for Meta-Regression

Description

This is a function for running the Markov chain Monte Carlo algorithm for the *Bayesian inference for multivariate meta-regression with a partially observed within-study sample covariance matrix* model. The first six arguments are required. `fmodel` can be one of 5 numbers: 1, 2, 3, 4, and 5. The first model, `fmodel = 1` denoted by M1, indicates that the Σ_{kt} are diagonal matrices with zero covariances. M2 indicates that Σ_{kt} are all equivalent but allowed to be full symmetric positive definite. M3 is where Σ_{kt} are allowed to differ across treatments, i.e., $\Sigma_{kt} = \Sigma_t$. M4 assumes that the correlation matrix, ρ , is identical for all trials/treatments, but the variances are allowed to vary. Finally, M5 assumes a hierarchical model where $(\Sigma_{kt}|\Sigma)$ follows an inverse-Wishart distribution with fixed degrees of freedom and scale matrix Σ . Σ then follows another inverse-Wishart distribution with fixed parameters.

Usage

```
bayes_parobs(
  Outcome,
  SD,
  XCovariate,
  WCovariate,
  Treat,
  Trial,
  Npt,
  fmodel = 1,
  prior = list(),
  mcmc = list(),
  control = list(),
  init = list(),
  Treat_order = NULL,
  Trial_order = NULL,
  group = NULL,
  group_order = NULL,
  scale_x = FALSE,
  verbose = FALSE
)
```

Arguments

Outcome	the aggregate mean of the responses for each arm of every study.
SD	the standard deviation of the responses for each arm of every study.
XCovariate	the aggregate covariates for the fixed effects.
WCovariate	the aggregate covariates for the random effects.
Treat	the treatment identifiers. This is equivalent to the arm number of each study. The number of unique treatments must be equal across trials. The elements within will be coerced to consecutive integers.
Trial	the trial identifiers. This is equivalent to the arm labels in each study. The elements within will be coerced to consecutive integers.
Npt	the number of observations/participants for a unique (k, t), or each arm of every trial.
fmodel	<p>the model number. The possible values for fmodel are 1 to 5, each indicating a different prior specification for Σ_{kt}. It will default to M1, fmodel=1 if not specified at function call. See the following model descriptions. The objects enclosed in parentheses at the end of every bullet point are the hyperparameters associated with each model.</p> <ul style="list-style-type: none"> • fmodel=1 - $\Sigma_{kt} = \text{diag}(\sigma_{kt,11}^2, \dots, \sigma_{kt,JJ}^2)$ where $\sigma_{kt,jj}^2 \sim IG(a_0, b_0)$ and $IG(a, b)$ is the inverse-gamma distribution. This specification is useful if the user does not care about the correlation recovery. (c0, dj0, a0, b0, Omega0) • fmodel=2 - $\Sigma_{kt} = \Sigma$ for every combination of (k, t) and $\Sigma^{-1} \sim Wish_{s_0}(\Sigma_0)$. This specification assumes that the user has prior knowledge that the correlation structure does not change across the arms included. (c0, dj0, s0, Omega0, Sigma0) • fmodel=3 - $\Sigma_{kt} = \Sigma_t$ and $\Sigma_t^{-1} \sim Wish_{s_0}(\Sigma_0)$. This is a relaxed version of fmodel=2, allowing the correlation structure to differ across trials but forcing it to stay identical within a trial. (c0, dj0, s0, Omega0, Sigma0) • fmodel=4 - $\Sigma_{kt} = \delta_{kt}\rho\delta_{kt}$ where $\delta_{kt} = \text{diag}(\Sigma_{kt,11}^{1/2}, \dots, \Sigma_{kt,JJ}^{1/2})$, and ρ is the correlation matrix. This specification allows the variances to vary across arms but requires that the correlations be the same. This is due to the lack of correlation information in the data, which would in turn lead to the nonidentifiability of the correlations if they were allowed to vary. However, this still is an ambitious model which permits maximal degrees of freedom in terms of variance and correlation estimation. (c0, dj0, a0, b0, Omega0) • fmodel=5 - The fifth model is hierarchical and thus may require more data than the others: $(\Sigma_{kt}^{-1} \Sigma) \sim Wish_{\nu_0}((\nu_0 - J - 1)^{-1}\Sigma^{-1})$ and $\Sigma \sim Wish_{d_0}(\Sigma_0)$. Σ_{kt} encodes the within-treatment-arm variation while Σ captures the between-treatment-arm variation. The hierarchical structure allows the "borrowing of strength" across treatment arms. (c0, dj0, d0, nu0, Sigma0, Omega0)
prior	(Optional) a list of hyperparameters. Despite theta in every model, each fmodel, along with the group argument, requires a different set of hyperparameters. See fmodel for the model specifications.

mcmc	(Optional) a list for MCMC specification. <code>ndiscard</code> is the number of burn-in iterations. <code>nskip</code> configures the thinning of the MCMC. For instance, if <code>nskip=5</code> , <code>bayes_parobs</code> will save the posterior sample every 5 iterations. <code>nkeep</code> is the size of the posterior sample. The total number of iterations will be <code>ndiscard + nskip * nkeep</code> .
control	(Optional) a list of tuning parameters for the Metropolis-Hastings algorithm . <code>Rho</code> , <code>R</code> , and <code>delta</code> are sampled through either localized Metropolis algorithm or delayed rejection robust adaptive Metropolis algorithm. <code>*_stepsize</code> with the asterisk replaced with one of the names above specifies the stepsize for determining the sample evaluation points in the localized Metropolis algorithm. <code>sample_Rho</code> can be set to <code>FALSE</code> to suppress the sampling of <code>Rho</code> for <code>fmodel=4</code> . When <code>sample_Rho</code> is <code>FALSE</code> , ρ will be fixed using the value given by the <code>init</code> argument, which defaults to $0.5I + 0.5111'$ where 1 is the vector of ones.
init	(Optional) a list of initial values for the parameters to be sampled: <code>theta</code> , <code>gamR</code> , <code>Omega</code> , and <code>Rho</code> . The initial value for <code>Rho</code> will be effective only if <code>fmodel=4</code> .
Treat_order	(Optional) a vector of unique treatments to be used for renumbering the <code>Treat</code> vector. The first element will be assigned treatment zero, potentially indicating placebo. If not provided, the numbering will default to an alphabetical/numerical order.
Trial_order	(Optional) a vector of unique trials. The first element will be assigned zero. If not provided, the numbering will default to an alphabetical/numerical order.
group	(Optional) a vector containing binary variables for u_{kt} . If not provided, <code>bayes_parobs</code> will assume that there is no grouping and set $u_{kt} = 0$ for all (k, t) .
group_order	(Optional) a vector of unique group labels. The first element will be assigned zero. If not provided, the numbering will default to an alphabetical/numerical order. <code>group_order</code> will take effect only if <code>group</code> is provided by the user.
scale_x	(Optional) a logical variable indicating whether <code>XCovariate</code> should be scaled/standardized. The effect of setting this to <code>TRUE</code> is not limited to merely standardizing <code>XCovariate</code> . The following generic functions will scale the posterior sample of <code>theta</code> back to its original unit: <code>plot</code> , <code>fitted</code> , <code>summary</code> , and <code>print</code> .
verbose	(Optional) a logical variable indicating whether to print the progress bar during the MCMC sampling.

Value

`bayes_parobs` returns an object of class "bayesparobs". The functions `summary` or `print` are used to obtain and print a summary of the results. The generic accessor function `fitted` extracts the posterior mean, posterior standard deviation, and the interval estimates of the value returned by `bayes_parobs`.

An object of class `bayesparobs` is a list containing the following components:

- `Outcome` - the aggregate response used in the function call.
- `SD` - the standard deviation used in the function call.
- `Npt` - the number of participants for (k, t) used in the function call.
- `XCovariate` - the aggregate design matrix for fixed effects used in the function call. Depending on `scale_x`, this may differ from the matrix provided at function call.

- WCovariate - the aggregate design matrix for random effects.
- Treat - the *renumbered* treatment indicators. Depending on Treat_order, it may differ from the vector provided at function call.
- Trial - the *renumbered* trial indicators. Depending on Trial_order, it may differ from the vector provided at function call.
- group - the *renumbered* grouping indicators in the function call. Depending on group_order, it may differ from the vector provided at function call. If group was missing at function call, bayes_parobs will assign NULL for group.
- TrtLabels - the vector of treatment labels corresponding to the renumbered Treat. This is equivalent to Treat_order if it was given at function call.
- TrialLabels - the vector of trial labels corresponding to the renumbered Trial. This is equivalent to Trial_order if it was given at function call.
- GroupLabels - the vector of group labels corresponding to the renumbered group. This is equivalent to group_order if it was given at function call. If group was missing at function call, bayes_parobs will assign NULL for GroupLabels.
- K - the total number of trials.
- T - the total number of treatments.
- fmodel - the model number as described [here](#).
- scale_x - a Boolean indicating whether XCovariate has been scaled/standardized.
- prior - the list of hyperparameters used in the function call.
- control - the list of tuning parameters used for MCMC in the function call.
- mcmctime - the elapsed time for the MCMC algorithm in the function call. This does not include all the other preprocessing and post-processing outside of MCMC.
- mcmc - the list of MCMC specification used in the function call.
- mcmc.draws - the list containing the MCMC draws. The posterior sample will be accessible here.

Author(s)

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References

Yao, H., Kim, S., Chen, M. H., Ibrahim, J. G., Shah, A. K., & Lin, J. (2015). Bayesian inference for multivariate meta-regression with a partially observed within-study sample covariance matrix. *Journal of the American Statistical Association*, **110**(510), 528-544.

See Also

[bmeta_analyze](#) for using the [Formula](#) interface

Examples

```

library(metapack)
data("cholesterol")
Outcome <- model.matrix(~ 0 + pldlc + phdlc + ptg, data = cholesterol)
SD <- model.matrix(~ 0 + sdldl + sdhdl + sdtg, data = cholesterol)
Trial <- cholesterol$trial
Treat <- cholesterol$treat
Npt <- cholesterol$n
XCovariate <- model.matrix(~ 0 + bldlc + bhdlc + btg + age + durat +
  white + male + dm, data = cholesterol)
WCovariate <- model.matrix(~ treat, data = cholesterol)

fmodel <- 1
set.seed(2797542)
fit <- bayes_parobs(Outcome, SD, XCovariate, WCovariate, Treat, Trial,
  Npt, fmodel, mcmc = list(ndiscard = 1, nskip = 1, nkeep = 1),
  scale_x = TRUE, group = cholesterol$onstat, verbose = FALSE)

```

bmeta_analyze	<i>bmeta_analyze supersedes the previous two functions: bayes_parobs, bayes_nmr</i>
---------------	---

Description

All other worker functions are superseded by this function, so that users can forget about the implementation details and focus on modeling. Meta-analytic data can be either aggregate or individual participant data (IPD). Aggregate data implies that the response consists of estimated effect sizes and their corresponding standard errors, whereas IPD is raw data. Data sets to be used for metapack should be formatted as follows:

Outcome	SD	DesignM1	DesignM2	Trial indicator (k)	Treatment indicator (t)	n
y_{13}	S_{13}	x_{13}	w_{13}	1	3	1000
y_{10}	S_{10}	x_{10}	w_{10}	1	0	545
y_{20}	S_{20}	x_{20}	w_{20}	2	0	1200

The first treatment indicator is intentionally selected to be 3, a number greater than 1, to indicate that this data format works for both meta-regression and network meta-regression. Meta-regression refers to when trials included have 2 treatments (i.e., $t = 0, 1$ for all k), and the treatments are compared head to head. On the other hand, network meta-regression includes more than two treatments, where each trial can have a different set of treatments, allowing indirect comparison between treatments that are not compared head to head as long as *consistency* holds (see [Higgins et al. \(2012\)](#) for consistency).

bmeta_analyze() and bmeta_analyse() are synonyms.

Usage

```

bmeta_analyze(
  formula,
  data,
  prior = list(),
  mcmc = list(),
  control = list(),
  init = list()
)

bmeta_analyse(
  formula,
  data,
  prior = list(),
  mcmc = list(),
  control = list(),
  init = list()
)

```

Arguments

- | | |
|---------|---|
| formula | an object of class Formula : a symbolic description of the meta-analytic model to fit. For aggregate models, the vector of arm sample sizes must be provided using the function <code>ns()</code> . For example, <code>y1 + y2 sd1 + sd2 ~ x1 + x2 + ns(n)</code> —an incomplete formula only for illustration purposes. If no <code>ns()</code> is found, individual participant data (IPD) model is assumed. |
| data | a data frame, list, or environment (or an object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>bmeta_analyze</code> is called. |
| prior | <p>an optional object that contains the hyperparameter values for the model. To see the complete list of hyperparameters for a specific model, refer to the corresponding worker function's help page, e.g., <code>help(bayes_parobs)</code> or <code>help(bayes_nmr)</code>. For meta-analysis, model is required in the prior argument, which is passed to <code>fmodel</code> as an integer. If the response is univariate, <code>NoRecovery</code> is the only valid option.</p> <ul style="list-style-type: none"> • <code>model="NoRecovery"</code> - $\Sigma_{tk} = \text{diag}(\sigma_{tk,11}^2, \dots, \sigma_{tk,JJ}^2)$ where $\sigma_{tk,jj}^2 \sim IG(a_0, b_0)$ and $IG(a, b)$ is the inverse-gamma distribution. This specification is useful if the user does not care about the correlation recovery. (<code>c0</code>, <code>dj0</code>, <code>a0</code>, <code>b0</code>, <code>Omega0</code>) • <code>model="EquiCovariance"</code> - $\Sigma_{tk} = \Sigma$ for every combination of (t, k) and $\Sigma^{-1} \sim Wish_{s_0}(\Sigma_0)$. This specification assumes that the user has prior knowledge that the correlation structure does not change across the arms included. (<code>c0</code>, <code>dj0</code>, <code>s0</code>, <code>Omega0</code>, <code>Sigma0</code>) • <code>model="EquiWithinTreat"</code> - $\Sigma_{tk} = \Sigma_t$ and $\Sigma_t^{-1} \sim Wish_{s_0}(\Sigma_0)$. This is a relaxed version of <code>model=2</code>, allowing the correlation structure to differ |

across trials but forcing it to stay identical within a trial. ($c\theta$, $dj\theta$, $s\theta$, $\Omega\theta$, $\Sigma\theta$)

- `model="EquiCorrelation"` - $\Sigma_{tk} = \delta_{tk}\rho\delta_{tk}$ where $\delta_{tk} = \text{diag}(\Sigma_{tk,11}^{1/2}, \dots, \Sigma_{tk,JJ}^{1/2})$, and ρ is the correlation matrix. This specification allows the variances to vary across arms but requires that the correlations be the same. This is due to the lack of correlation information in the data, which would in turn lead to the nonidentifiability of the correlations if they were allowed to vary. However, this still is an ambitious model which permits maximal degrees of freedom in terms of variance and correlation estimation. ($c\theta$, $dj\theta$, $a\theta$, $b\theta$, $\Omega\theta$)
- `model="Hierarchical"` - The fifth model is hierarchical and thus may require more data than the others: $(\Sigma_{tk}^{-1} | \Sigma) \sim \text{Wish}_{\nu_0}((\nu_0 - J - 1)^{-1}\Sigma^{-1})$ and $\Sigma \sim \text{Wish}_{d_0}(\Sigma_0)$. Σ_{tk} encodes the within-treatment-arm variation while Σ captures the between-treatment-arm variation. The hierarchical structure allows the "borrowing of strength" across treatment arms. ($c\theta$, $dj\theta$, $d\theta$, $\nu\theta$, $\Sigma\theta$, $\Omega\theta$)

For network meta-analysis,

- `df` - the degrees of freedom of the multivariate t-distribution for the random effects. Any positive value can be assigned; if `df=Inf`, multivariate normal random effects will be assumed.
- `c01` - the variance of the fixed-effect coefficients' prior distribution, a multivariate normal distribution, i.e., $\theta \sim N(0, c_1I)$.
- `c02` - the variance of the random-effects' variance-related coefficients' prior distribution, a multivariate normal distribution, i.e., $\phi \sim N(0, c_2I)$.
- `a4`, `b4`, `a5`, `b5` - the hyperparameters related to when the degrees of freedom for the random effects are treated as unknown/random. `df` is then considered to follow $Ga(\nu_a, \nu_a/\nu_b)$, $\nu_a \sim Ga(a_4, b_4)$, and $\nu_b \sim IG(a_5, b_5)$. All gamma and inverse-gamma distributions are rate-parameterized.

<code>mcmc</code>	an optional object containing MCMC specification. <code>ndiscard</code> is the number of burn-in iterations. <code>nskip</code> configures the thinning of the MCMC. For instance, if <code>nskip=5</code> , parameters will be saved every 5 iterations. <code>nkeep</code> is the size of the posterior sample. The total number of iterations will be <code>ndiscard + nskip * nkeep</code> .
<code>control</code>	an optional object that contains the control tuning parameters for the Metropolis-Hastings algorithm. Similar to <code>prior</code> , the complete list of control parameters for a specific model is given in the corresponding worker function's help page (see bayes_parobs or bayes_nmr). These are the lists of available tuning parameters in <code>control</code> for meta-analysis and network meta-analysis. Keep in mind that <code>model</code> will render some irrelevant tuning parameters ineffective. <ul style="list-style-type: none"> • Meta-analysis - <code>model</code> (string), <code>sample_Rho</code> (logical), <code>Rho_stepsize</code> (double), <code>R_stepsize</code> (double), <code>delta_stepsize</code> (double), <code>sample_Rho</code> (logical) • Network meta-analysis - <code>sample_df</code> (logical), <code>sample_Rho</code> (logical), <code>lambda_stepsize</code> (double), <code>phi_stepsize</code> (double), <code>Rho_stepsize</code> (double)
<code>init</code>	(Optional) a list of initial values for the parameters to be sampled. The following is the list of available parameters for meta-analysis and network meta-analysis.

- Meta-analysis - theta (vector), gamR (matrix), Omega (matrix), Rho (matrix)
- Network meta-analysis - theta (vector), phi (vector), sig2 (vector), Rho (matrix)

The dimensions of the initial values must be conformable for matrix operations. If dimensions don't agree, bmeta_analyze will tell you the correct dimension.

Details

bmeta_analyze currently subsumes two worker functions: bayes_parobs and bayes_nmr. bmeta_analyze offers a formula interface. All formulas are parsed using [Formula](#). Formulas for bmeta_analyze are constrained to have a strict structure: one or two LHS, and two or three RHS. That is, lhs_1 ~ rhs_1 | rhs2 | rhs3 or lhs_1 | lhs_2 ~ rhs_1 | rhs2 | rhs3 (see Examples for more). The tilde (~) separates the LHS's and RHS's, each side further separated into parts by vertical bars (|). The meaning of each part is syntactically determined by its location inside the formula, like an English sentence. Therefore, all parts **must** come in the exact order as prescribed for bmeta_analyze to correctly configure your model.

- The first LHS, the responses, is required for all models.
- The second LHS is only required for aggregate models, corresponding to the standard deviations of the responses.
- The first RHS corresponds to fixed-effects covariates.
- The second RHS corresponds to the variables in either the random-effects matrix ($w'_{tk} * \gamma_k$) for multivariate meta-analysis or modeling the variances ($\log \tau_{tk} = z'_{tk} * \phi$) for univariate network meta-analysis.
- The third RHS corresponds to the treatment and trial indicators, and optionally the grouping variable if it exists. The order must be treat + trial + group, or treat + trial if no grouping exists. Variables here must be supplied in the exact order described; otherwise, model will not be correctly identified.

Internally, bmeta_analyze looks for three things: multivariate/univariate, meta-analysis/network meta-analysis, and [aggregate/IPD](#).

- multivariate/univariate: the dimension of the response is explicit in the formula, and determines univariate versus multivariate.
- meta-analysis/network meta-analysis: the number of levels (nlevels) of treatments determines this. If treat is not already a factor variable, it is coerced to one.
- aggregate/IPD: bmeta_analyze looks for ns() in the first RHS. Aggregate models **must** provide the arm sample sizes using the function ns() (e.g., if n is the sample sizes, y1 + y2 | sd1 + sd2 ~ x1 + x2 + ns(n)). If there is no ns(), IPD is assumed. Currently, IPD models are a work in progress and not supported yet.

Currently, only univariate/multivariate + meta-analysis and univariate + network meta-analysis are allowed. More models will be added in the future.

Value

bmeta_analyze returns a classed object of bsynthesis for *Bayesian synthesis*

Author(s)

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References

Yao, H., Kim, S., Chen, M. H., Ibrahim, J. G., Shah, A. K., & Lin, J. (2015). Bayesian inference for multivariate meta-regression with a partially observed within-study sample covariance matrix. *Journal of the American Statistical Association*, **110(510)**, 528-544.

Li, H., Chen, M. H., Ibrahim, J. G., Kim, S., Shah, A. K., Lin, J., & Tershakovec, A. M. (2019). Bayesian inference for network meta-regression using multivariate random effects with applications to cholesterol lowering drugs. *Biostatistics*, **20(3)**, 499-516.

Li, H., Lim, D., Chen, M. H., Ibrahim, J. G., Kim, S., Shah, A. K., & Lin, J. (2021). Bayesian network meta-regression hierarchical models using heavy-tailed multivariate random effects with covariate-dependent variances. *Statistics in Medicine*.

See Also

[bayes_parobs](#) for multivariate meta-analysis, and [bayes_nmr](#) for univariate network meta-analysis.

Examples

```
set.seed(2797542)
data("cholesterol")
f_1 <- 'pldlc + phdlc + ptg | sdldl + sdhdl + sdtg ~ 0 + bldlc + bhdhc + btg +
  age + durat + white + male + dm + ns(n) | treat | treat + trial + onstat'
out_1 <- bmeta_analyze(as.formula(f_1), data = cholesterol,
  prior = list(model="NoRecovery"),
  mcmc = list(ndiscard = 3, nskip = 1, nkeep = 1),
  control=list(scale_x = TRUE, verbose=FALSE))
```

```
set.seed(2797542)
data("TNM")
TNM$group <- factor(match(TNM$treat, c("PBO", "R"), nomatch = 0))
f_2 <- 'ptg | sdtg ~
  0 + bldlc + bhdhc + btg + age + white + male + bmi +
  potencymed + potencyhigh + durat + ns(n) |
  scale(bldlc) + scale(btg) + group | treat + trial'
out_2 <- bmeta_analyze(as.formula(f_2), data = TNM,
  mcmc = list(ndiscard = 1, nskip = 1, nkeep = 1),
  control=list(scale_x = TRUE, verbose=FALSE))
```

cholesterol

26 double-blind, randomized, active, or placebo-controlled clinical trials on patients with primary hypercholesterolemia sponsored by Merck & Co., Inc., Kenilworth, NJ, USA.

Description

A data set containing clinical trial on hypercholesterolemia including 26 trials and 2 treatment arms each, and other attributes of the participants

Usage

```
data(cholesterol)
```

Format

A data frame with 52 rows and 19 variables

study study identifier

trial trial identifier

treat treatment indicator for Statin or Statin+Ezetimibe

n the number of participants in the study arms corresponding to the trial and treatment

pldlc aggregate percentage change in LDL-C

phdlc aggregate percentage change from baseline in HDL-C

ptg aggregate percentage change from baseline in triglycerides (TG)

sddl sample standard deviation of percentage change in LDL-C

sdhdl sample standard deviation of percentage change in HDL-C

sdtg sample standard deviation of percentage change in triglycerides (TG)

onstat whether the participants were on Statin prior to the trial

bdlc baseline LDL-C

bhdlc baseline HDL-C

btg baseline triglycerides (TG)

age age in years

white the proportion of white participants

male the proportion of male participants

dm the proportion of participants with diabetes mellitus

durat duration in weeks

Examples

```
data(cholesterol)
```

coef.bsynthesis	<i>get the posterior mean of fixed-effect coefficients</i>
-----------------	--

Description

get the posterior mean of fixed-effect coefficients

Usage

```
## S3 method for class 'bsynthesis'
coef(object, ...)
```

Arguments

object	a class of bsynthesize
...	other arguments

Value

Coefficients extracted from the model object object

fitted.bayesnmr	<i>get fitted values</i>
-----------------	--------------------------

Description

get fitted values

Usage

```
## S3 method for class 'bayesnmr'
fitted(object, level = 0.95, HPD = TRUE, ...)
```

Arguments

object	the output model from fitting a meta analysis/regression model
level	credible level for interval estimation; set to 0.95 by default
HPD	a logical argument indicating whether HPD intervals should be computed; if FALSE, equal-tail credible intervals are computed
...	additional arguments for fitted

Value

a list of fitted values

fitted.bayesparobs *get fitted values*

Description

get fitted values

Usage

```
## S3 method for class 'bayesparobs'
fitted(object, level = 0.95, HPD = TRUE, ...)
```

Arguments

object	the output model from fitting a meta analysis/regression model
level	credible level for interval estimation; set to 0.95 by default
HPD	a logical argument indicating whether HPD intervals should be computed; if FALSE, equal-tail credible intervals are computed
...	additional arguments for fitted

Value

a list of fitted values

hpd *get the highest posterior density (HPD) interval*

Description

get the highest posterior density (HPD) interval

Usage

```
hpd(object, parm, level = 0.95, HPD = TRUE)
```

Arguments

object	the output model from fitting a (network) meta analysis/regression model
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the probability which the HPD interval will cover
HPD	a logical value indicating whether HPD or equal-tailed credible interval should be computed; by default, TRUE

Details

A $100(1 - \alpha)\%$ HPD interval for θ is given by

$$R(\pi_\alpha) = \theta : \pi(\theta|D) \geq \pi_\alpha,$$

where π_α is the largest constant that satisfies $P(\theta \in R(\pi_\alpha)) \geq 1 - \alpha$. `hpd` computes the HPD interval from an MCMC sample by letting $\theta_{(j)}$ be the j th smallest of the MCMC sample, θ_i and denoting

$$R_j(n) = (\theta_{(j)}, \theta_{(j+[(1-\alpha)n])}),$$

for $j = 1, 2, \dots, n - [(1 - \alpha)n]$. Once θ_i 's are sorted, the appropriate j is chosen so that

$$\theta_{(j+[(1-\alpha)n])} - \theta_{(j)} = \min_{1 \leq j \leq n - [(1-\alpha)n]} (\theta_{(j+[(1-\alpha)n])} - \theta_{(j)}).$$

Value

dataframe containing HPD intervals for the parameters

References

Chen, M. H., & Shao, Q. M. (1999). Monte Carlo estimation of Bayesian credible and HPD intervals. *Journal of Computational and Graphical Statistics*, **8(1)**, 69-92.

hpd.bayesnmr

get the highest posterior density (HPD) interval

Description

get the highest posterior density (HPD) interval

Usage

```
## S3 method for class 'bayesnmr'
hpd(object, parm, level = 0.95, HPD = TRUE)
```

Arguments

<code>object</code>	the output model from fitting a (network) meta analysis/regression model
<code>parm</code>	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
<code>level</code>	the probability which the HPD interval will cover
<code>HPD</code>	a logical value indicating whether HPD or equal-tailed credible interval should be computed; by default, TRUE

Value

dataframe containing HPD intervals for the parameters

hpd.bayesparobs	<i>get the highest posterior density (HPD) interval or equal-tailed credible interval</i>
-----------------	---

Description

get the highest posterior density (HPD) interval or equal-tailed credible interval

Usage

```
## S3 method for class 'bayesparobs'
hpd(object, parm, level = 0.95, HPD = TRUE)
```

Arguments

object	the output model from fitting a (network) meta analysis/regression model
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the probability which the HPD interval will cover
HPD	a logical value indicating whether HPD or equal-tailed credible interval should be computed; by default, TRUE

Value

dataframe containing HPD intervals for the parameters

metapack	<i>metapack: a package for Bayesian meta-analysis and network meta-analysis</i>
----------	---

Description

The metapack package provides one category of functions: bayes.parobs and bayes.nmr

Multivariate Meta-Regression function

The bayes.parobs function fits the multivariate meta-regression model with partially observed sample covariance matrix to the given data.

Network Meta-Regression function

The bayes.nmr function fits the network meta-regression model with heavy-tailed random effects distribution to the given data.

model_comp	<i>compute the model comparison measures: DIC, LPML, or Pearson's residuals</i>
------------	---

Description

model_comp is a generic function that computes the model comparison measures (DIC and LPML) or the Pearson's residuals. Note that the Pearson's residuals are not available for bayes.nmr when df is either random or fixed but smaller than 2 since the variance of the random effects is not finite.

Usage

```
model_comp(object, type = "lpml", verbose = FALSE, ncores = NULL)
```

Arguments

object	the output model from fitting a meta analysis/regression model
type	the type of model comparison measure to compute; DIC or LPML
verbose	FALSE by default; If TRUE, then progress bar will appear
ncores	the number of CPU cores to use for parallel processing. It must not exceed the number of existing cores. If unspecified, it will default to 2 cores or the number of existing cores, whichever is smaller.

Value

dataframe containing the compute the model comparison measures

model_comp.bayesnmr	<i>get compute the model comparison measures</i>
---------------------	--

Description

get compute the model comparison measures

Usage

```
## S3 method for class 'bayesnmr'
model_comp(object, type = "lpml", verbose = FALSE, ncores = NULL)
```

Arguments

object	the output model from fitting a meta analysis/regression model
type	the type of model comparison measures; DIC or LPML
verbose	FALSE by default; If TRUE, then progress bar will appear
ncores	the number of CPU cores to use for parallel processing. It must not exceed the number of existing cores. If unspecified, it will default to 2 cores or the number of existing cores, whichever is smaller.

Value

dataframe containing the compute the model comparison measures

model_comp.bayesparobs

compute the model comparison measures

Description

compute the model comparison measures

Usage

```
## S3 method for class 'bayesparobs'
model_comp(object, type = "lpml", verbose = FALSE, ncores = NULL)
```

Arguments

object	the output model from fitting a meta analysis/regression model
type	the type of model comparison measures; DIC or LPML
verbose	FALSE by default; If TRUE, then progress bar will appear
ncores	the number of CPU cores to use for parallel processing. It must not exceed the number of existing cores. If unspecified, it will default to 2 cores or the number of existing cores, whichever is smaller.

Value

dataframe containing the compute the model comparison measures

ns *helper function encoding trial sample sizes in formulas*

Description

helper function encoding trial sample sizes in formulas

Usage

```
ns(x)
```

Arguments

x	the name of the variable containing trial sample sizes
---	--

plot.bayesnmr *get goodness of fit*

Description

get goodness of fit

Usage

```
## S3 method for class 'bayesnmr'  
plot(x, ...)
```

Arguments

x the output model from fitting a meta analysis/regression model
... additional parameters for plot

Value

No return value

plot.bayesparobs *get goodness of fit*

Description

get goodness of fit

Usage

```
## S3 method for class 'bayesparobs'  
plot(x, ...)
```

Arguments

x the output model from fitting a meta analysis/regression model
... additional parameters for plot

Value

No return value

plot.sucra	<i>plot the surface under the cumulative ranking curve (SUCRA)</i>
------------	--

Description

plot the surface under the cumulative ranking curve (SUCRA)

Usage

```
## S3 method for class 'sucra'
plot(x, legend.position = "none", ...)
```

Arguments

x	the output model from fitting a network meta analysis/regression model
legend.position	the position of the legend that will be passed onto ggplot
...	additional arguments for plot

Value

No return value

print.bayesnmr	<i>Print results</i>
----------------	----------------------

Description

Print results

Usage

```
## S3 method for class 'bayesnmr'
print(x, level = 0.95, HPD = TRUE, ...)
```

Arguments

x	the output model from fitting a network meta analysis/regression model
level	credible level for interval estimation; set to 0.95 by default
HPD	a logical argument indicating whether HPD intervals should be computed; if FALSE, equal-tail credible intervals are computed
...	additional arguments for print

Value

No return value; print a summary of the output

```
print.bayesparobs      Print results
```

Description

Print results

Usage

```
## S3 method for class 'bayesparobs'
print(x, level = 0.95, HPD = TRUE, ...)
```

Arguments

x	the output model from fitting a meta analysis/regression model
level	credible level for interval estimation; set to 0.95 by default
HPD	a logical argument indicating whether HPD intervals should be computed; if FALSE, equal-tail credible intervals are computed
...	additional arguments for print

Value

No return value; print a summary of the output

```
sucra      get surface under the cumulative ranking curve (SUCRA)
```

Description

get surface under the cumulative ranking curve (SUCRA)

Usage

```
sucra(object)
```

Arguments

object	the output model from fitting a network meta analysis/regression model
--------	--

Value

a list containing SUCRA and the discrete rank probability matrix of size T by T

sucra.bayesnmr *get surface under the cumulative ranking curve (SUCRA)*

Description

get surface under the cumulative ranking curve (SUCRA)

Usage

```
## S3 method for class 'bayesnmr'
sucra(object)
```

Arguments

object the output model from fitting a network meta analysis/regression model

Value

a list containing SUCRA and the discrete rank probability matrix of size T by T

summary.bayesnmr *'summary' method for class "'bayesnmr'"*

Description

'summary' method for class "'bayesnmr'"

Usage

```
## S3 method for class 'bayesnmr'
summary(object, level = 0.95, HPD = TRUE, ...)
```

Arguments

object the output model from fitting a network meta analysis/regression model
level credible level for interval estimation; set to 0.95 by default
HPD a logical argument indicating whether HPD intervals should be computed; if FALSE, equal-tail credible intervals are computed
... additional arguments for print

Value

does not return anything; print a summary of the output

```
summary.bayesparobs    summary method for class "bayesparobs"
```

Description

summary method for class "bayesparobs"

Usage

```
## S3 method for class 'bayesparobs'
summary(object, level = 0.95, HPD = TRUE, ...)
```

Arguments

<code>object</code>	the output model from fitting a meta analysis/regression model
<code>level</code>	credible level for interval estimation; set to 0.95 by default
<code>HPD</code>	a logical argument indicating whether HPD intervals should be computed; if FALSE, equal-tail credible intervals are computed
<code>...</code>	additional arguments for summary

Value

print summary for the model fit

TNM	<i>Triglycerides Network Meta (TNM) data</i>
-----	--

Description

A systemically reviewed network meta data set on tryglyceride (TG) lowering drugs

Usage

```
data(TNM)
```

Format

A data frame with 73 rows and 15 variables

trial trial identifier

treat treatment indicator for placebo (PBO), simvastatin (S), atorvastatin (A), lovastatin (L), rosuvastatin (R), pravastatin (P), ezetimibe (E), simvastatin+ezetimibe (SE), atorvastatin+ezetimibe (AE), lovastatin+ezetimibe (LE), or pravastatin+ezetimibe (PE)

n the number of participants in the study corresponding to the trial and treatment

ptg percentage change from baseline in triglycerides (TG)
sdtg sample standard deviation of percentage change in triglycerides (TG)
ldlc baseline LDL-C
hdlc baseline HDL-C
btg baseline triglycerides (TG)
age age in years
white the proportion of white participants
male the proportion of male participants
bmi body fat index
potencymed the proportion of medium statin potency
potencyhigh the proportion of high statin potency
durat duration in weeks

Examples

```
data(TNM)
```

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