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| crosnma.model {crosnma} | R Documentation |

Create JAGS model to cross-synthesis in NMA and NMR for dichotomous outcomes

**Description**

This function create JAGS model and data; jags code is created from the internal function crosnma.code.

**Usage**

crosnma.model(

prt.data,

std.data,

trt,

study,

outcome,

n,

design,

reference,

trt.effect = "random",

covariate = NULL,

reg0.effect = "independent",

regb.effect = "random",

regw.effect = "random",

split.regcoef = T,

method.bias = NULL,

bias = NULL,

bias.type = NULL,

bias.covariate = NULL,

bias.effect = "common",

prior = list(tau.trt = NULL, tau.reg0 = NULL, tau.regb = NULL, tau.regw = NULL,

tau.gamma = NULL, pi.high.rct = NULL, pi.low.rct = NULL, pi.high.nrs = NULL,

pi.low.nrs = NULL),

run.nrs = list(var.infl = 1, mean.shift = 0, n.adapt = 500, n.iter = 10000, n.burnin

= 4000, thin = 1, n.chains = 2)

)

**Arguments**

|  |  |
| --- | --- |
| prt.data | An object of class data.frame containing the individual participant dataset. Each row contains the data of a single participant. The data frame needs to have the following columns: trt, study, outcome, design. Additional columns might be required for certain analysis. The columns don't have to take certain names. |
| std.data | An object of class data.frame containing the study-level dataset. Each row represents the information of study arm. The data frame needs to have the following columns: trt, study, outcome, n and design. Additional columns might be required for certain analysis. The columns don't have to take certain names. |
| trt | A vector of length 2 with the names of the treatment variable (as character) in prt.data and std.data, respectively. |
| study | A vector of length 2 with the names of the study variable (as character) in prt.data and std.data, respectively. |
| outcome | A vector of length 2 with the names of the outcome variable (as character) in prt.data and std.data, respectively. |
| n | A character of the name of the number of participants variable in std.data. |
| design | A vector of length 2 with the names of the design variable (as character) in prt.data and std.data, respectively. |
| reference | A character indicating the name of the reference treatment. This option must be specified otherwise the 'placebo' is set as a reference. |
| trt.effect | A character for the relationship within the study-specific treatment effects. Options are 'random' or 'common'. |
| covariate | An optional list indicating the name of the covariates in prt.data and std.data,respectively, to conduct network meta regression The covariates can be either numeric or dichotomous variables. The user can provide up to 3 covaraites. The covariate needs to be provided for both prt.data and std.data, respectively. The default option is covariate=NULL where no covariate adjustment is applied (network meta-analysis). |
| reg0.effect | An optional character (when covariate is not NULL) indicating the relationship across studies for prognostic effects expressed by the regression coefficient, (*β\_{1,j}*), in a study *j*. Options are 'independent' or 'random'. We recommend using 'independent' (default). |
| regb.effect | An optional character (when covariate is not NULL) indicating the relationship across studies between-study regression coefficient. This parameter quantify the treatment-mean covariate interaction. Options are 'random' or 'common'. Default is 'random'. |
| regw.effect | An optional character (when covariate is not NULL) indicating the relationship across studies for the within-study regression coefficient. This parameter models the treatment-covariate interaction effect at the individual level. Options are 'random' or 'common'. Default is 'random'. |
| split.regcoef | A logical (when covariate is not NULL). If TRUE the within- and between-study coefficients will be splitted in the analysis of prt.data. The default is TRUE. When the split.regcoef = FALSE, only one regression coefficient will be estimated under either random effect model (regb.effect='random' or regw.effect='random') or common-effect model, otherwise. |
| method.bias | An optional character for defining the method to combine randomised clinical trials (RCT) and non-randomised studies (NRS) (required when design has nrs in addition to rct). Options are 'naive' for naive synthesize, 'prior' for using NRS estimates as a prior information and RCTs in the likelihood or 'adjust1' and 'adjust2' to allow a bias adjustment following either Dias or Verde approaches, respectively. |
| bias | An optional vector of length 2 (required when method.bias='adjust1' or 'adjust2') indicating the name of the variable (as character) that includes the risk of bias adjustment in prt.data and std.data, respectively. The entries of this variable should be a character with entries either low, high or unclear. These values need to be repeated for the participants that belong to the same study. |
| bias.type | An optional charachter of the effect of bias in the treatment effect (required when method.bias='adjust1' or 'adjust2'). Three options are possible: 'add' for additive bias effect,'mult' for multiplicative bias effect and'both' for both an additive and a multiplicative term. |
| bias.covariate | An optional vector of two characters (required when method.bias='adjust1' or 'adjust2'). It has the variable name of the variable that will be used in estimating the probability of bias. |
| bias.effect | An optional character indicating the relationship for the bias coefficients across studies. Options are 'random' or 'common'. It is required when method.bias='adjust1' or 'adjust2'. |
| prior | An optional list to control the prior for various parameters in JAGS model. Those are the heterogeneity parameters for: the treatment effects (when 'random' is assigned to trt.effect): tau.reg0 for the effect of progonostic covariates, tau.regb and tau.regw for within- and between-study covariate effect, respectively, and tau.gamma for bias effect. Currently only the uniform distribution is supported, e.g. 'dunif(0,3)'. When the method.bias='adjust1' or 'adjust2', the user may provide priors to control the bias probability. There are 4 possible bias probabilities: RCT with low/high bias (pi.low.rct, pi.high.rct), NRS with low/high bias (pi.low.nrs, pi.high.nrs). Each prior should be given a beta distribution with the two parameters as this for example 'dbeta(3,1)'. |
| run.nrs | An optional list is needed when the NRS used as a prior (method.bias='prior'). The list consists of the follwoing (we assign a default for each element of the list): (var.infl) controls the inflation of the varaince of NRS estimates and its values range between 0 (the least confidence in NRS) and 1 (full confidence in NRS, default value). (mean.shift) is the bias shift to be added/subtracted from the estimated NRS parameters (0 is the default). Either (var.infl) or (mean.shift) should be provided but not both. and other arguments to control the MCMC chains (default value is in the parentheses): the number of adaptions n.adapt (500), number of iterations n.iter(10000), number of burn in n.burnin (4000), number of thinning thin (1) and number of chains n.chains (2), see [jags.model](http://127.0.0.1:31985/help/library/crosnma/help/jags.model)arguments from rjags package. |

**Value**

crosnma.model returns an object of class crosnmaModel which is a list containing the following components:

jagsmodel A long character string containing JAGS code that will be run in [jags](http://127.0.0.1:31985/help/library/crosnma/help/jags).

data The data used in the JAGS code.

trt.key A Table of the treatments and its mapped integer number (used in JAGS model).

trt.effect A character for the relationship within the study-specific treatment effects.

method.bias A character for defining the method to combine randomised clinical trials (RCT) and non-randomised studies (NRS).

covariate A list of the the names of the covariate variable in prt.data and std.data.

split.regcoef A logical. If TRUE the within- and between-study coefficients will be splitted in the analysis of prt.data.

regb.effect An optional character indicating the relationship across studies for the between-study regression coefficient.

regw.effect A character indicating the relationship across studies for the within-study regression coefficient.

bias.effect A character indicating the relationship for the bias coefficients across studies.

bias.type A charachter indicating the effect of bias on the treatment effect; additive ('add') or multiplicative ('mult') or both ('both').

**See Also**

[crosnma.run](http://127.0.0.1:31985/help/library/crosnma/help/crosnma.run), [jags.model](http://127.0.0.1:31985/help/library/crosnma/help/jags.model)

**Examples**

# An example from participant-level data and study-level data.

# data

data(prt.data)

data(std.data)

#=========================#

# Create a jags model #

#=========================#

# We conduct a network meta-analysis assuming a random effect model.

# The data comes from randomised-controlled trials and non-randomised studies. They will be combined naively.

# The data has 2 different formats: individual participant data (prt.data) and study-level data (std.data).

mod <- crosnma.model(prt.data=prt.data,

std.data=std.data,

trt=c('trt','trt'),

study=c('study','study'),

outcome=c('outcome','outcome'),

n='n',

design=c('design','design'),

reference='A',

trt.effect='random',

covariate = NULL,

method.bias='naive'

)

#=========================#

# Fit jags model #

#=========================#

fit <- crosnma.run(model=mod,

n.adapt = 20,

n.iter=50,

thin=1,

n.chains=3)

#=========================#

# Display the output #

#=========================#

summary(fit)

plot(fit)

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| crosnma.run {crosnma} | R Documentation |

Run NMA or NMR model to cross-synthesis in NMA and NMR for dichotomous outcomes

**Description**

Takes jags model from an object produced by crosnma.model and runs model using jags.

**Usage**

crosnma.run(

model,

n.adapt = 1000,

n.burnin = floor(n.iter/2),

n.iter,

thin = 1,

n.chains = 2,

quiet = TRUE

)

**Arguments**

|  |  |
| --- | --- |
| model | A crosnmaModel object produced by running crosnma.model. |
| n.adapt | Number of adaptations for the mcmc chains. |
| n.burnin | Number of burnin iterations for the mcmc chains. |
| n.iter | Number of iterations for the mcmc chains. |
| thin | Number of thinning for the mcmc chains. Default is 1. |
| n.chains | Number of mcmc chains. Default is 2. |
| quiet | A logical. If TRUE, the warning message will not be displayed See [jags.model](http://127.0.0.1:31985/help/library/crosnma/help/jags.model) for more info. |

**Value**

crosnma.run returns an object of class crosrun which is a list containing the following components:

samples The MCMC samples produced by running the BUGS model.

model The crosnmaModel object obtained from crosnma.model which was used to run jags.

trt.key A Table of the treatments and its mapped integer number (used in JAGS model).

**See Also**

[crosnma.model](http://127.0.0.1:31985/help/library/crosnma/help/crosnma.model),[jags.model](http://127.0.0.1:31985/help/library/crosnma/help/jags.model)

**Examples**

# An example from participant-level data and study-level data.

# data

data(prt.data)

data(std.data)

#=========================#

# Create a jags model #

#=========================#

# We conduct a network meta-analysis assuming a random effect model.

# The data comes from randomised-controlled trials and non-randomised studies. They will be combined naively.

# The data has 2 different formats: individual participant data (prt.data) and study-level data (std.data).

mod <- crosnma.model(prt.data=prt.data,

std.data=std.data,

trt=c('trt','trt'),

study=c('study','study'),

outcome=c('outcome','outcome'),

n='n',

design=c('design','design'),

reference='A',

trt.effect='random',

covariate = NULL,

method.bias='naive'

)

#=========================#

# Fit jags model #

#=========================#

fit <- crosnma.run(model=mod,

n.adapt = 20,

n.iter=50,

thin=1,

n.chains=3)

#=========================#

# Display the output #

#=========================#

summary(fit)

plot(fit)

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| summary.crosnma {crosnma} | R Documentation |

Generic summary function for crosnma.run object

**Description**

Generic summary function for crosnma.run object

**Usage**

## S3 method for class 'crosnma'

summary(x, digits = 3, quantiles = c(0.025, 0.5, 0.975), expo = TRUE, ...)

**Arguments**

|  |  |
| --- | --- |
| x | The object generated by the crosnma.run function. |
| digits | The number of significant digits printed. The default value is 3. |
| quantiles | A numeric vector of probabilities. The default value is c(0.025, 0.5, 0.975). |
| expo | A logical indicating whether to expontiate the parameters of relative treatment effect and covariate effect |
| ... | ... |