Package ‘BayesSenMC’

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Title Different Models of Posterior Distributions of Adjusted Odds Ratio

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URL https://github.com/formidify/BayesSenMC

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Description Generates different posterior distributions of adjusted odds ratio under different priors of sensitivity and specificity, and plots the models for comparison. It also provides estimations for the specifications of the models using diagnostics of exposure status with a non-linear mixed effects model. It implements the methods that are first proposed in <doi:10.1016/j.annepidem.2006.04.001> and <doi:10.1177/0272989X09353452>.

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The 'BayesSenMC' package.

Description

This package generates different posterior distributions of adjusted odds ratio under different priors of sensitivity and specificity, and plots the models for comparison. It also provides estimations for the specifications of the models using diagnostics of exposure status with a non-linear mixed effects model.

References


Meta-analysis data on Bipolar Disorder diagnosis accuracy

Description

Records the true positive, true negative, false positive and false negative of each diagnosis accuracy study. Also includes the type of screening instruments (Bipolar Spectrum diagnostic scale / HCL-21 / Mood disorder questionnaire), the cut-off value for diagnostics, and the percentage of bipolar cases that were of bipolar disorder type II or not specified.

Usage

data(bd_meta)
correctedOR

Format
An object of class tbl_df (inherits from tbl, data.frame) with 55 rows and 8 columns.

Source

References

Examples
data(bd_meta)

correctedOR  Model with constant nondifferential misclassification

description
Generate a stanfit object corresponding to a posterior distribution of corrected odds ratio given nondifferential misclassification with Se and Sp (i.e., both are constant and at least one of Se or Sp is lower than 1).

Usage
correctedOR(
a,  # number of studies
N1,  # number of true positives
C,   # number of false positives
N0,  # number of true negatives
prior_list = NULL,  # prior hyperparameter list
se = NULL,  # sensitivity
sp = NULL,  # specificity
logitpi0_prior = c(0, 10),  # prior hyperparameter list
lor_prior = c(0, 2),  # prior hyperparameter list
chains = 2,  # number of chains
traceplot = FALSE,  # whether to generate traceplot
inc_warmup = FALSE,  # whether to include warmup
window = NULL,  # window
refresh = 0,  # refresh
seed = NA,  # seed
...  # additional arguments
)

Arguments

- `a` number of exposed subjects in the case group.
- `N1` number of total subjects in the case group.
- `c` number of exposed subjects in the control group.
- `N0` number of total subjects in the control group.
- `prior_list` list of priors. Can be replaced by the function call to `paramEst`, or a list of prior parameters (se, sp). If `prior_list` is specified, the values for the function parameters se and sp will be disregarded.
- `se` sensitivity. Do not have to specify this if `prior_list` is given - this will be disregarded.
- `sp` specificity. Do not have to specify this if `prior_list` is given - this will be disregarded.
- `logitpi0_prior` mean and sd of the prior normal distribution of logit(pi0). Default to `c(0, 10)`.
- `lor_prior` mean and sd of the prior normal distribution of corrected log odds ratio. Default to `c(0, 2)`.
- `chains` number of Markov Chains. Default to 2.
- `traceplot` Logical, defaulting to `FALSE`. If `TRUE` it will draw the `traceplot` corresponding to one or more Markov chains.
- `inc_warmup` Only evaluated when `traceplot = TRUE`. TRUE or FALSE, indicating whether or not to include the warmup sample in the `traceplot`; defaults to `FALSE`.
- `window` Only evaluated when `traceplot = TRUE`. A vector of length 2. Iterations between `window[1]` and `window[2]` will be shown in the plot. The default shows all iterations if `inc_warmup` is `TRUE` and all iterations from the sampling period only if `inc_warmup` is `FALSE`. If `inc_warmup` is `FALSE` the iterations specified in `window` do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional `iter` argument.
- `refresh` an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus `refresh <= 0`. If on, `refresh = max(iter/10, 1)` is generally recommended.
- `seed` the seed for random number generation. See `stan` for more details.
- `...` optional parameters passed to `stan`.

Value

It returns a stanfit object of this model, which inherits stanfit class methods. See `rstan` for more details.

Examples

```r
# Case-control study data of Bipolar Disorder with rheumatoid arthritis (Farhi et al. 2016)
# Data from 

mod <- nlmeNDiff(bd_meta, lower = 0) # see \code{nlmeNDiff()}) for detailed example.
prior_list <- paramEst(mod)
correctedOR(a = 66, N1 = 11782, c = 243, N0 = 57973, prior_list = prior_list,
chains = 3, iter = 10000)
```
crudeOR

Model without misclassification

Description

Generate a stanfit object corresponding to a posterior distribution of uncorrected odds ratio given no misclassification.

Usage

```
crudeOR(
a,  
N1,  
c,  
N0,  
logitpi0_prior = c(0, 10),  
lor_prior = c(0, 2),  
chains = 2,  
traceplot = FALSE,  
inc_warmup = FALSE,  
window = NULL,  
refresh = 0,  
seed = NA,  
...
)
```

Arguments

- **a**: number of exposed subjects in the case group.
- **N1**: number of total subjects in the case group.
- **c**: number of exposed subjects in the control group.
- **N0**: number of total subjects in the control group.
- **logitpi0_prior**: mean and sd of the prior normal distribution of \( \text{logit}(\pi^0) \). Default to \(c(0, 10)\).
- **lor_prior**: mean and sd of the prior normal distribution of corrected log odds ratio. Default to \(c(0, 2)\).
- **chains**: number of Markov Chains. Default to 2.
- **traceplot**: Logical, defaulting to FALSE. If TRUE it will draw the traceplot corresponding to one or more Markov chains.
- **inc_warmup**: Only evaluated when traceplot = TRUE. TRUE or FALSE, indicating whether or not to include the warmup sample in the traceplot; defaults to FALSE.
- **window**: Only evaluated when traceplot = TRUE. A vector of length 2. Iterations between \text{window}[1] and \text{window}[2] will be shown in the plot. The default shows all iterations if inc_warmup is TRUE and all iterations from the sampling period only if inc_warmup is FALSE. If inc_warmup is FALSE the iterations specified in window do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional iter argument.
refresh an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus refresh \leq 0. If on, refresh = max(iter/10, 1) is generally recommended.

seed the seed for random number generation. See stan for more details.

Value

It returns a stanfit object of this model, which inherits stanfit class methods. See rstan for more details.

Examples

# Case-control study data of Bipolar Disorder with rheumatoid arthritis (Farhi et al. 2016)
# Data from \url{https://www.sciencedirect.com/science/article/pii/S0165032715303864#bib13}

# 3 MCMC chains with 10000 iterations each
crudeOR(a = 66, N1 = 11782, c = 243, N0 = 57973, chains = 3, iter = 10000)

diffOR  Model with differential misclassification

Description

Generate a stanfit object corresponding to a posterior distribution of corrected odds ratio given a four-variate differential misclassification.

Usage

diffOR(
a, N1, c, N0, mu, s.lg.se0, s.lg.se1, s.lg.sp0, s.lg.sp1, corr.sesp0, corr.sesp1, corr.group = 0, z = NULL, logitpi0_prior = c(0, 10), lor_prior = c(0, 2), chains = 2, traceplot = FALSE,
Arguments

- **a**: number of exposed subjects in the case group.
- **N1**: number of total subjects in the case group.
- **c**: number of exposed subjects in the control group.
- **N0**: number of total subjects in the control group.
- **mu**: vector of length 4; multivariate normal distribution of \( z \sim (\mu, \varz) \), where each \( \mu \) corresponds to the logit mean of \( Se_0, Se_1, Sp_0 \) and \( Sp_1 \) (0 for controls, 1 for cases group).
- **s.lg.se0**: standard deviation of logit \( Se \) in the control group.
- **s.lg.se1**: standard deviation of logit \( Se \) in the case group.
- **s.lg.sp0**: standard deviation of logit \( Sp \) in the control group.
- **s.lg.sp1**: standard deviation of logit \( Sp \) in the case group.
- **corr.sesp0**: correlation between \( Se_0 \) and \( Sp_0 \).
- **corr.sesp1**: correlation between \( Se_1 \) and \( Sp_1 \).
- **corr.group**: correlation between \( Se_0 \) and \( Se_1 \), \( Sp_0 \) and \( Sp_1 \). Default to 0.
- **z**: vector of length 4; used as an initial value for \( z \sim (\mu, \varz) \). Default to \( \mu \).
- **logitpi0_prior**: mean and sd of the prior normal distribution of logit \( \pi_0 \). Default to \( c(0, 10) \).
- **lor_prior**: mean and sd of the prior normal distribution of corrected log odds ratio. Default to \( c(0, 10) \).
- **chains**: number of Markov Chains. Default to 2.
- **traceplot**: Logical, defaulting to FALSE. If TRUE it will draw the traceplot corresponding to one or more Markov chains.
- **inc_warmup**: Only evaluated when traceplot = TRUE. TRUE or FALSE, indicating whether or not to include the warmup sample in the traceplot; defaults to FALSE.
- **window**: Only evaluated when traceplot = TRUE. A vector of length 2. Iterations between \( window[1] \) and \( window[2] \) will be shown in the plot. The default shows all iterations if inc_warmup is TRUE and all iterations from the sampling period only if inc_warmup is FALSE. If inc_warmup is FALSE the iterations specified in window do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional iter argument.
- **refresh**: an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus refresh <= 0. If on, refresh = max(iter/10, 1) is generally recommended.
- **seed**: the seed for random number generation. See stan for more details.
- **...**: optional parameters passed to stan.
Value

It returns a stanfit object of this model, which inherits stanfit class methods. See rstan for more details.

Examples

# Case-control study data of Bipolar Disorder with rheumatoid arthritis (Farhi et al. 2016)
# Data from https://www.sciencedirect.com/science/article/pii/S0165032715303864#bib13

diffOR(a = 66, N1 = 11782, c = 243, N0 = 57973, mu = c(1.069, 1.069, 1.126, 1.126),
s.lg.se0 = 0.712, s.lg.se1 = 0.712, s.lg.sp0 = 0.893, s.lg.sp1 = 0.893, corr.sesp0 = -0.377,
corr.sesp1 = -0.377, corr.group = 0, chains = 3, iter = 10000)

fixedCorrOR

Model with nondifferential, correlated misclassification

Description

Generate a stanfit object corresponding to a posterior distribution of corrected odds ratio given nondifferential misclassification that extends from the logit model but allows there to be a fixed correlation between sensitivity and specificity.

Usage

fixedCorrOR(
  a,
  N1,
  c,
  N0,
  prior_list = NULL,
  m.lg.se = NULL,
  m.lg.sp = NULL,
  s.lg.se = NULL,
  s.lg.sp = NULL,
  lg.se = NULL,
  lg.sp = NULL,
  rho = NULL,
  logitpi0_prior = c(0, 10),
  lor_prior = c(0, 2),
  chains = 2,
  traceplot = FALSE,
  inc_warmup = FALSE,
  window = NULL,
  refresh = 0,
  seed = NA,
  ...
)
Model Arguments

- **a**: number of exposed subjects in the case group.
- **N1**: number of total subjects in the case group.
- **c**: number of exposed subjects in the control group.
- **N0**: number of total subjects in the control group.
- **prior_list**: list of priors. Can be replaced by the function call to `paramEst`, or a list of prior parameters (`m.lg.se`, `s.lg.se`, `m.lg.sp`, `s.lg.sp`, `rho`). If `prior_list` is specified, the values for the corresponding function parameters will be disregarded.
- **m.lg.se**: normal distribution of logit Se with (mean = m.lg.se, sd = s.lg.se). Do not have to specify this if `prior_list` is given - it will be disregarded.
- **m.lg.sp**: conditional normal distribution of logit Sp given Se with (m.lg.sp, s.lg.sp). Do not have to specify this if `prior_list` is given - it will be disregarded.
- **s.lg.se**: standard deviation of logit Se. Do not have to specify this if `prior_list` is given - it will be disregarded.
- **s.lg.sp**: standard deviation of logit Sp. Do not have to specify this if `prior_list` is given - it will be disregarded.
- **lg.se**: used as an initial value for logit Se. Default to `m.lg.se`.
- **lg.sp**: used as an initial value for logit Sp. Default to `m.lg.sp`.
- **rho**: correlation between Se and Sp. Do not have to specify this if `prior_list` is given - it will be disregarded.
- **logitpi0_prior**: mean and sd of the prior normal distribution of logit(pi0). Default to `c(0, 10)`.
- **lor_prior**: mean and sd of the prior normal distribution of corrected log odds ratio. Default to `c(0, 2)`.
- **chains**: number of Markov Chains. Default to 2.
- **traceplot**: Logical, defaulting to FALSE. If TRUE it will draw the `traceplot` corresponding to one or more Markov chains.
- **inc_warmup**: Only evaluated when `traceplot = TRUE`. TRUE or FALSE, indicating whether or not to include the warmup sample in the traceplot; defaults to FALSE.
- **window**: Only evaluated when `traceplot = TRUE`. A vector of length 2. Iterations between `window[1]` and `window[2]` will be shown in the plot. The default shows all iterations if `inc_warmup` is TRUE and all iterations from the sampling period only if `inc_warmup` is FALSE. If `inc_warmup` is FALSE the iterations specified in `window` do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional `iter` argument.
- **refresh**: an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus refresh <= 0. If on, refresh = max(iter/10, 1) is generally recommended.
- **seed**: the seed for random number generation. See `stan` for more details.
- **...**: optional parameters passed to `stan`.
logitOR

Value

It returns a stanfit object of this model, which inherits stanfit class methods. See rstan for more details.

Examples

# Case-control study data of Bipolar Disorder with rheumatoid arthritis (Farhi et al. 2016)
# Data from \url{https://www.sciencedirect.com/science/article/pii/S0165032715303864#bib13}

mod <- nlmeNDiff(bd_meta, lower = 0) # see \code{nlmeNDiff()} for detailed example.
prior_list <- paramEst(mod)
fixedCorrOR(a = 66, N1 = 11782, c = 243, N0 = 57973, prior_list = prior_list,
 chains = 3, iter = 10000)

---

logitOR Model with nondifferential, logit normal-distributed misclassification

Description

Generate a stanfit object corresponding to a posterior distribution of corrected odds ratio given nondifferential misclassification under a logit-transformed scaled bivariate normal distribution.

Usage

logitOR(
  a,
  N1,
  c,
  N0,
  prior_list = NULL,
  m.lg.se = NULL,
  m.lg.sp = NULL,
  s.lg.se = NULL,
  s.lg.sp = NULL,
  lg.se = NULL,
  lg.sp = NULL,
  logitpi0_prior = c(0, 10),
  lor_prior = c(0, 2),
  chains = 2,
  traceplot = FALSE,
  inc_warmup = FALSE,
  window = NULL,
  refresh = 0,
  seed = NA,
  ...
)
logitOR

Arguments

- **a**
  number of exposed subjects in the case group.

- **N1**
  number of total subjects in the case group.

- **c**
  number of exposed subjects in the control group.

- **N0**
  number of total subjects in the control group.

- **prior_list**
  list of priors. Can be replaced by the function call to `paramEst`, or a list of prior parameters (`m.lg.se`, `s.lg.se`, `m.lg.sp`, `s.lg.sp`). If `prior_list` is specified, the values for the corresponding function parameters will be disregarded.

- **m.lg.se**
  normal distribution of logit Se with (mean = `m.lg.se`, sd = `s.lg.se`). Do not have to specify this if `prior_list` is given - it will be disregarded.

- **m.lg.sp**
  normal distribution of logit Sp with (`m.lg.sp`, `s.lg.sp`). Do not have to specify this if `prior_list` is given - it will be disregarded.

- **s.lg.se**
  standard deviation of logit Se. Do not have to specify this if `prior_list` is given - it will be disregarded.

- **s.lg.sp**
  standard deviation of logit Sp. Do not have to specify this if `prior_list` is given - it will be disregarded.

- **lg.se**
  used as an initial value for logit Se. Default to `m.lg.se`.

- **lg.sp**
  used as an initial value for logit Sp. Default to `m.lg.sp`.

- **logitpi0_prior**
  mean and sd of the prior normal distribution of logit(pi0). Default to `c(0,10)`.

- **lor_prior**
  mean and sd of the prior normal distribution of corrected log odds ratio. Default to `c(0,2)`.

- **chains**
  number of Markov Chains. Default to 2.

- **traceplot**
  Logical, defaulting to `FALSE`. If `TRUE` it will draw the traceplot corresponding to one or more Markov chains.

- **inc_warmup**
  Only evaluated when `traceplot = TRUE`. `TRUE` or `FALSE`, indicating whether or not to include the warmup sample in the traceplot; defaults to `FALSE`.

- **window**
  Only evaluated when `traceplot = TRUE`. A vector of length 2. Iterations between `window[1]` and `window[2]` will be shown in the plot. The default shows all iterations if `inc_warmup` is `TRUE` and all iterations from the sampling period only if `inc_warmup` is `FALSE`. If `inc_warmup` is `FALSE` the iterations specified in `window` do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional `iter` argument.

- **refresh**
  an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus `refresh <= 0`. If on, `refresh = max(iter/10, 1)` is generally recommended.

- **seed**
  the seed for random number generation. See `stan` for more details.

- **...**
  optional parameters passed to `stan`.

Value

It returns a stanfit object of this model, which inherits stanfit class methods. See rstan for more details.
Examples

# Case-control study data of Bipolar Disorder with rheumatoid arthritis (Farhi et al. 2016)
# Data from \url{https://www.sciencedirect.com/science/article/pii/S0165032715303864#bib13}

mod <- nlmeNDiff(bd_meta, lower = 0) # see \code{nlmeNDiff()} for detailed example.
prior_list <- paramEst(mod)
logitOR(a = 66, N1 = 11782, c = 243, N0 = 57973, prior_list = prior_list,
       chains = 3, iter = 10000)

nlmeNDiff  
\textit{Non-differential Generalized Linear Mixed Effects Model}

Description

Fit a bivariate generalized linear mixed-effects model (GLMM) for non-differential sensitivity and specificity using the \code{glmer} function in \code{lme4}. Lower and upper bounds for Se and Sp can be specified according to the assumptions of the study.

Usage

\code{nlmeNDiff(data, lower = 0.5, upper = 1, id = FALSE, ...)}

Arguments

data a data frame containing the 2 by 2 data of the diagnostics table of exposure status for every study in a meta-analysis. It contains at least 4 columns in the data named as following: \code{n11} indicates the true positives, \code{n01} the false positives, \code{n00} the true negatives and \code{n10} the false negatives. Each column is a vector of same length, which is the number of meta-analysis study results used in the model.

lower an optional argument specifying the lower bound assumption of Se and Sp. Default to 0.5 (or the lowest Se/Sp of all studies, whichever is lower), which provides the mild assumption that Se and Sp are better than chance.

upper an optional argument specifying the upper bound assumption of Se and Sp. Default to 1.

id a \code{TRUE} of \code{FALSE} argument indicating if the supplied data has a \code{sid} column that gives same studies the same subject ID. Default to \code{FALSE}, which assumes that all studies have different IDs.

Value

It returns an object of class \code{merMod}. Besides generic class methods, \code{paramEst()} is implemented in \code{BayesSenMC} to get the parameter estimates used in the Bayesian misclassification model functions.
paramEst

Examples

```r
data(bd_meta)
mod <- nlmeNDiff(bd_meta, lower = 0)
```

---

**Description**

Get parameter estimates of the GLMM model to plug into modeling functions in BayesSenMC for Bayesian inference of adjusted odds ratio.

**Usage**

```r
paramEst(model, lower = 0.5, upper = 1)
```

**Arguments**

- `model`: a GLMM model built with the `nlmeNDiff()` function.
- `lower`: an optional argument matching the lower bound assumption of Se and Sp of the input model. Default to 0.5 as in `nlmeNDiff()`.
- `upper`: an optional argument matching the upper bound assumption of Se and Sp. Default to 1 as in `nlmeNDiff()`.

**Value**

It returns a list of parameter estimates which can be input into the Bayesian model functions in BayesSenMC. `(m.lg.se, s.lg.se)` and `(m.lg.sp, s.lg.sp)` are the logit prior distributions for Se and Sp. `se` and `sp` are the corresponding mean values given the logit prior means. `rho` is the correlation estimate between Se and Sp. `m.fisher` is the Fisher’s mean of the correlation assume a Fisher’s distribution.

**Examples**

```r
data(bd_meta)
mod <- nlmeNDiff(bd_meta, lower = 0)  # see `code(nlmeNDiff())` for detailed example.
prior_list <- paramEst(mod)
```
plotOR

Plot Model

Description
Plot the posterior distribution of adjusted odds ratio given the stanfit object. It also plots the
density lines of crude/uncorrected odds ratio and corrected odds ratio with constant misclassification,
assuming log-normality is true. If both Se and Sp are set to 1 (i.e., no misclassification), then only
the density line of crude OR will be plotted.

Usage
plotOR(
  model,
  a,
  N1,
  c,
  N0,
  se = 1,
  sp = 1,
  x.min = 0,
  x.max = NULL,
  y.max = NULL,
  binwidth = 0.25,
  fill = "gray",
  ...
)

Arguments
model  A stanfit object.
a  number of exposed subjects in the case group. Along with N1, c, N0, se and sp,
they are used to plot probability density with no misclassification and constant
misclassification as a comparison.
N1  number of total subjects in the case group.
c  number of exposed subjects in the control group.
N0  number of total subjects in the control group.
se  sensitivity. Default to 1. If no other values are specified for either se or sp, then
only the density curve of corrected model will be drawn.
sp  specificity. Default to 1.
x.min  shows only samples with corrected odds ratio larger or equal to x.min. Default
to 0.
x.max  shows only samples with corrected odds ratio smaller or equal to x.max. Default
to the largest OR in the posterior samples.
randCorrOR

### Description

Generate a stanfit object corresponding to a posterior distribution of corrected odds ratio given nondifferential misclassification that extends from the logit model but allows a random correlation between Sensitivity and Specificity.

### Usage

```r
randCorrOR(
  a,
  N1,
  c,
  N0,
  prior_list = NULL,
  m.lg.se = NULL,
  m.lg.sp = NULL,
  s.lg.se = NULL,
  s.lg.sp = NULL,
  lg.se = NULL,
  ...)
```

### Examples

```r
# Case-control study data of Bipolar Disorder with rheumatoid arthritis (Farhi et al. 2016)
# Data from \url{https://www.sciencedirect.com/science/article/pii/S0165032715303864#bib13}

library(ggplot2)
my.mod <- randCorrOR(a = 66, N1 = 11782, c = 243, N0 = 57973, m.lg.se = 1.069,
m.lg.sp = 1.126, s.lg.se = 0.893, s.lg.sp = 0.712, m.z = -0.399, s.z = 0.139,
seed = 0)

my.plot <- plotOR(my.mod, a = 66, N1 = 11782, c = 243, N0 = 57973, se = 0.744,
sp = 0.755, x.max = 3, y.max = 5, binwidth = 0.1) + ggtitle("Model with random correlation")

# the user can also directly extract the data from a stanfit object using the following
my.data <- as.data.frame(my.mod)
```
lg.sp = NULL,
m.z = NULL,
s.z = NULL,
z = NULL,
logitpi0_prior = c(0, 10),
lor_prior = c(0, 2),
chains = 2,
traceplot = FALSE,
inc_warmup = FALSE,
window = NULL,
refresh = 0,
seed = NA,
...}

Arguments

- **a**: number of exposed subjects in the case group.
- **N1**: number of total subjects in the case group.
- **c**: number of exposed subjects in the control group.
- **N0**: number of total subjects in the control group.
- **prior_list**: list of priors. Can be replaced by the function call to `paramEst`, or a list of prior parameters (`m.lg.se`, `s.lg.se`, `m.lg.sp`, `s.lg.sp`, `m.z`, `s.z`). If `prior_list` is specified, the values for the corresponding function parameters will be disregarded.
- **m.lg.se**: normal distribution of logit Se with (mean = m.lg.se, sd = s.lg.se). Do not have to specify this if `prior_list` is given - it will be disregarded.
- **m.lg.sp**: conditional normal distribution of logit Sp given Se with (m.lg.sp, s.lg.sp). Do not have to specify this if `prior_list` is given - it will be disregarded.
- **s.lg.se**: standard deviation of logit Se. Do not have to specify this if `prior_list` is given - it will be disregarded.
- **s.lg.sp**: standard deviation of logit Sp. Do not have to specify this if `prior_list` is given - it will be disregarded.
- **lg.se**: used as an initial value for logit Se. Default to m.lg.se. Do not have to specify this if `prior_list` is given - it will be disregarded. Default to m.lg.se.
- **lg.sp**: used as an initial value for logit Sp. Default to m.lg.sp. Do not have to specify this if `prior_list` is given - it will be disregarded. Default to m.lg.sp.
- **m.z**: normal distribution of Z with (mean = m.z, sd = s.z). Do not have to specify this if `prior_list` is given - it will be disregarded.
- **s.z**: normal distribution of Z with (mean = m.z, sd = s.z). Do not have to specify this if `prior_list` is given - it will be disregarded.
- **z**: used as an initial value of Fisher's Z transformed of rho, where correlation rho = \((\exp(2z)-1)/(1+\exp(2z)))\). Do not have to specify this if `prior_list` is given - it will be disregarded. Default to m.z.
- **logitpi0_prior**: mean and sd of the prior normal distribution of `logit(pi0)`. Default to c(0, 10).
lor_prior: mean and sd of the prior normal distribution of corrected log odds ratio. Default to $c(0, 2)$.

chains: number of Markov Chains. Default to 2.

traceplot: Logical, defaulting to FALSE. If TRUE it will draw the traceplot corresponding to one or more Markov chains.

inc_warmup: Only evaluated when traceplot = TRUE. TRUE or FALSE, indicating whether or not to include the warmup sample in the traceplot; defaults to FALSE.

window: Only evaluated when traceplot = TRUE. A vector of length 2. Iterations between window[1] and window[2] will be shown in the plot. The default shows all iterations if inc_warmup is TRUE and all iterations from the sampling period only if inc_warmup is FALSE. If inc_warmup is FALSE the iterations specified in window do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional iter argument.

refresh: an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus refresh <= 0. If on, refresh = max(iter/10, 1) is generally recommended.

seed: the seed for random number generation. See stan for more details.

Value

It returns a stanfit object of this model, which inherits stanfit class methods. See rstan for more details.

Examples

# Case-control study data of Bipolar Disorder with rheumatoid arthritis (Farhi et al. 2016)
# Data from \url{https://www.sciencedirect.com/science/article/pii/S0165032715303864#bib13}

mod <- nlmeNDiff(bd_meta, lower = 0) # see \code{nlmeNDiff()} for detailed example.
prior_list <- paramEst(mod)
randCorrOR(a = 66, N1 = 11782, c = 243, N0 = 57973, prior_list = prior_list, chains = 3, iter = 10000)
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