Package ‘BayesSenMC’

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Title Different Models of Posterior Distributions of Adjusted Odds Ratio

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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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BayesSenMC-package  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


bd_meta  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)
Corrected OR

Format

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

Source


References


Examples

data(bd_meta)

<table>
<thead>
<tr>
<th>correctedOR</th>
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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,
  N1,
  c,
  N0,
  prior_list = NULL,
  se = NULL,
  sp = NULL,
  logitpi0_prior = c(0, 10),
  lor_prior = c(0, 2),
  chains = 2,
  traceplot = FALSE,
  inc_warmup = FALSE,
  window = NULL,
  refresh = 0,
  seed = 0,
  ...
)
Arguments

\begin{itemize}
\item \texttt{a} \hspace{0.7em} number of exposed subjects in the case group.
\item \texttt{N1} \hspace{0.7em} number of total subjects in the case group.
\item \texttt{c} \hspace{0.7em} number of exposed subjects in the control group.
\item \texttt{N0} \hspace{0.7em} number of total subjects in the control group.
\item \texttt{prior\_list} \hspace{0.7em} list of priors. Can be replaced by the function call to \texttt{paramEst}, or a list of prior parameters (\texttt{se}, \texttt{sp}). If \texttt{prior\_list} is specified, the values for the function parameters \texttt{se} and \texttt{sp} will be disregarded.
\item \texttt{se} \hspace{0.7em} sensitivity. Do not have to specify this if \texttt{prior\_list} is given - this will be disregarded.
\item \texttt{sp} \hspace{0.7em} specificity. Do not have to specify this if \texttt{prior\_list} is given - this will be disregarded.
\item \texttt{logitpi0\_prior} \hspace{0.7em} mean and sd of the prior normal distribution of \texttt{logit(pi0)}. Default to \texttt{c(0,10)}.
\item \texttt{lor\_prior} \hspace{0.7em} mean and sd of the prior normal distribution of corrected log odds ratio. Default to \texttt{c(0,2)}.
\item \texttt{chains} \hspace{0.7em} number of Markov Chains. Default to 2.
\item \texttt{traceplot} \hspace{0.7em} Logical, defaulting to \texttt{FALSE}. If \texttt{TRUE} it will draw the \texttt{traceplot} corresponding to one or more Markov chains.
\item \texttt{inc\_warmup} \hspace{0.7em} Only evaluated when \texttt{traceplot = TRUE}. \texttt{TRUE} or \texttt{FALSE}, indicating whether or not to include the warmup sample in the traceplot; defaults to \texttt{FALSE}.
\item \texttt{window} \hspace{0.7em} Only evaluated when \texttt{traceplot = TRUE}. A vector of length 2. Iterations between \texttt{window[1]} and \texttt{window[2]} will be shown in the plot. The default shows all iterations if \texttt{inc\_warmup} is \texttt{TRUE} and all iterations from the sampling period only if \texttt{inc\_warmup} is \texttt{FALSE}. If \texttt{inc\_warmup} is \texttt{FALSE} the iterations specified in \texttt{window} do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional \texttt{iter} argument.
\item \texttt{refresh} \hspace{0.7em} an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus \texttt{refresh <= 0}. If on, \texttt{refresh = max(iter/10, 1)} is generally recommended.
\item \texttt{seed} \hspace{0.7em} the seed for random number generation. Default to 0. See \texttt{stan} for more details.
\item \ldots \hspace{0.7em} optional parameters passed to \texttt{stan}.
\end{itemize}

Value

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

Examples

\begin{verbatim}
# 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 <- nlmexpdiff(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)
\end{verbatim}
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 = 0,
    ...
)

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 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 \( \leq 0 \). If on, refresh = max(iter/10, 1) is generally recommended.

seed the seed for random number generation. Default to 0. 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

\[
\text{crudeOR}(a = 66, N1 = 11782, c = 243, N0 = 57973, \text{chains} = 3, \text{iter} = 10000)
\]

---

diffOR \hspace{1cm} \\textit{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,
```

\begin{verbatim}
diffOR =
    inc_warmup = FALSE,
    window = NULL,
    refresh = 0,
    seed = 0,
    ...
)

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, 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. Default to 0. See \texttt{stan} for more details.
...
optional parameters passed to stan.
\end{verbatim}
fixedCorrOR

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}

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 = 0,
  ...
)
**fixedCorrOR**

**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. Default to 0. 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 = 0,
  ...
)

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).
- `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. Default to 0. 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

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 \pkg{lme4}. Lower and upper bounds for Se and Sp can be specified according to the assumptions of the study.

Usage

\f[ \text{nlmeNDiff}(\text{data, lower = 0.5, upper = 1, id = FALSE, \ldots}) \]

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: \texttt{n11} indicates the true positives, \texttt{n01} the false positives, \texttt{n00} the true negatives and \texttt{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 \TRUE or \FALSE argument indicating if the supplied data has a \texttt{sid} column that gives same studies the same subject ID. Default to \FALSE, which assumes that all studies have different IDs.

...
  optional parameters passed to \code{glmer}.

Value

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

Examples

data(bd_meta)

mod <- nlmeNDiff(bd_meta, lower = 0)

data(bd_meta)

mod <- nlmeNDiff(bd_meta, lower = 0)

---

paramEst

Parameter estimates of the GLMM model

Description

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

Usage

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)
```
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

```r
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**

*y.max* shows only samples or density line within the range of (0, *y.max*).

**binwidth** default to 0.25

**fill** default to "gray"

... optional additional arguments passed to geom_histogram

**Value**

It returns a *ggplot* that can be further customized using the ggplot2 package.

**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)
```

---

**randCorrOR**

*Model with nondifferential, randomly 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 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,)
```
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 = 0,
...
)

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 = \(\frac{\exp(2z)-1}{1+\exp(2z)}\). 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).
loCrior

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. Default to 0. 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{n1meNDiff()} 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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