

# Package ‘BayesSenMC’

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**Title** Different Models of Posterior Distributions of Adjusted Odds Ratio

**Version** 0.1.5

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**URL** <https://github.com/formidify/BayesSenMC>

**BugReports** <https://github.com/formidify/BayesSenMC/issues>

**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>.

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**Biarch** true

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**SystemRequirements** GNU make

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BayesSenMC-package	<i>The 'BayesSenMC' package.</i>
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### 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

Stan Development Team (2020). RStan: the R interface to Stan. R package version 2.21.2. <https://mc-stan.org>

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bd_meta	<i>Meta-analysis data on Bipolar Disorder diagnosis accuracy</i>
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### 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)
```

**Format**

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

**Source**

<https://www.sciencedirect.com/science/article/pii/S0165032714006466>

**References**

Carvalho et al. (2015) "Screening for bipolar spectrum disorders: A comprehensive meta-analysis of accuracy studies". *Journal of Affective Disorders* 172: 337 - 346. ([ScienceDirect](#))

**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,  
  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**

<code>a</code>	number of exposed subjects in the case group.
<code>N1</code>	number of total subjects in the case group.
<code>c</code>	number of exposed subjects in the control group.
<code>N0</code>	number of total subjects in the control group.
<code>prior_list</code>	list of priors. Can be replaced by the function call to <code>paramEst</code> , or a list of prior parameters ( <code>se</code> , <code>sp</code> ). If <code>prior_list</code> is specified, the values for the function parameters <code>se</code> and <code>sp</code> will be disregarded.
<code>se</code>	sensitivity. Do not have to specify this if <code>prior_list</code> is given - this will be disregarded.
<code>sp</code>	specificity. Do not have to specify this if <code>prior_list</code> is given - this will be disregarded.
<code>logitpi0_prior</code>	mean and sd of the prior normal distribution of $\text{logit}(\pi_0)$ . Default to <code>c(0, 10)</code> .
<code>lor_prior</code>	mean and sd of the prior normal distribution of corrected log odds ratio. Default to <code>c(0, 2)</code> .
<code>chains</code>	number of Markov Chains. Default to 2.
<code>traceplot</code>	Logical, defaulting to FALSE. If TRUE it will draw the <a href="#">traceplot</a> corresponding to one or more Markov chains.
<code>inc_warmup</code>	Only evaluated when <code>traceplot = TRUE</code> . TRUE or FALSE, indicating whether or not to include the warmup sample in the traceplot; defaults to FALSE.
<code>window</code>	Only evaluated when <code>traceplot = TRUE</code> . A vector of length 2. Iterations between <code>window[1]</code> and <code>window[2]</code> will be shown in the plot. The default shows all iterations if <code>inc_warmup</code> is TRUE and all iterations from the sampling period only if <code>inc_warmup</code> is FALSE. If <code>inc_warmup</code> is FALSE the iterations specified in <code>window</code> do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional <code>iter</code> argument.
<code>refresh</code>	an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus <code>refresh &lt;= 0</code> . If on, <code>refresh = max(iter/10, 1)</code> is generally recommended.
<code>seed</code>	the seed for random number generation. Default to 0. See <a href="#">stan</a> for more details.
<code>...</code>	optional parameters passed to <a href="#">stan</a> .

**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)
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 = 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 $\text{logit}(\pi_0)$ . 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 <a href="#">traceplot</a> corresponding to one or more Markov chains.
inc_warmup	Only evaluated when <code>traceplot = TRUE</code> . TRUE or FALSE, indicating whether or not to include the warmup sample in the traceplot; defaults to FALSE.
window	Only evaluated when <code>traceplot = TRUE</code> . A vector of length 2. Iterations between <code>window[1]</code> and <code>window[2]</code> will be shown in the plot. The default shows all iterations if <code>inc_warmup</code> is TRUE and all iterations from the sampling period only if <code>inc_warmup</code> is FALSE. If <code>inc_warmup</code> is FALSE the iterations specified in <code>window</code> do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional <code>iter</code> 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 =  $\max(\text{iter}/10, 1)$  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}

# 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,
```

```

    inc_warmup = FALSE,
    window = NULL,
    refresh = 0,
    seed = 0,
    ...
)

```

## Arguments

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

**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,
  ...
)
```



**Arguments**

<code>a</code>	number of exposed subjects in the case group.
<code>N1</code>	number of total subjects in the case group.
<code>c</code>	number of exposed subjects in the control group.
<code>N0</code>	number of total subjects in the control group.
<code>prior_list</code>	list of priors. Can be replaced by the function call to <code>paramEst</code> , or a list of prior parameters ( <code>m.lg.se</code> , <code>s.lg.se</code> , <code>m.lg.sp</code> , <code>s.lg.sp</code> , <code>rho</code> ). If <code>prior_list</code> is specified, the values for the corresponding function parameters will be disregarded.
<code>m.lg.se</code>	normal distribution of logit $Se$ with (mean = <code>m.lg.se</code> , sd = <code>s.lg.se</code> ). Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>m.lg.sp</code>	conditional normal distribution of logit $Sp$ given $Se$ with ( <code>m.lg.sp</code> , <code>s.lg.sp</code> ). Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>s.lg.se</code>	standard deviation of logit $Se$ . Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>s.lg.sp</code>	standard deviation of logit $Sp$ . Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>lg.se</code>	used as an initial value for logit $Se$ . Default to <code>m.lg.se</code>
<code>lg.sp</code>	used as an initial value for logit $Sp$ . Default to <code>m.lg.sp</code>
<code>rho</code>	correlation between $Se$ and $Sp$ . Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>logitpi0_prior</code>	mean and sd of the prior normal distribution of $\logit(\pi_0)$ . Default to <code>c(0, 10)</code> .
<code>lor_prior</code>	mean and sd of the prior normal distribution of corrected log odds ratio. Default to <code>c(0, 2)</code> .
<code>chains</code>	number of Markov Chains. Default to 2.
<code>traceplot</code>	Logical, defaulting to FALSE. If TRUE it will draw the <a href="#">traceplot</a> corresponding to one or more Markov chains.
<code>inc_warmup</code>	Only evaluated when <code>traceplot = TRUE</code> . TRUE or FALSE, indicating whether or not to include the warmup sample in the traceplot; defaults to FALSE.
<code>window</code>	Only evaluated when <code>traceplot = TRUE</code> . A vector of length 2. Iterations between <code>window[1]</code> and <code>window[2]</code> will be shown in the plot. The default shows all iterations if <code>inc_warmup</code> is TRUE and all iterations from the sampling period only if <code>inc_warmup</code> is FALSE. If <code>inc_warmup</code> is FALSE the iterations specified in <code>window</code> do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional <code>iter</code> argument.
<code>refresh</code>	an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus <code>refresh &lt;= 0</code> . If on, <code>refresh = max(iter/10, 1)</code> is generally recommended.
<code>seed</code>	the seed for random number generation. Default to 0. See <a href="#">stan</a> for more details.
<code>...</code>	optional parameters passed to <a href="#">stan</a> .

**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,
  ...
)
```

**Arguments**

<code>a</code>	number of exposed subjects in the case group.
<code>N1</code>	number of total subjects in the case group.
<code>c</code>	number of exposed subjects in the control group.
<code>N0</code>	number of total subjects in the control group.
<code>prior_list</code>	list of priors. Can be replaced by the function call to <code>paramEst</code> , or a list of prior parameters ( <code>m.lg.se</code> , <code>s.lg.se</code> , <code>m.lg.sp</code> , <code>s.lg.sp</code> ). If <code>prior_list</code> is specified, the values for the corresponding function parameters will be disregarded.
<code>m.lg.se</code>	normal distribution of logit $\text{Se}$ with (mean = <code>m.lg.se</code> , sd = <code>s.lg.se</code> ). Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>m.lg.sp</code>	normal distribution of logit $\text{Sp}$ with ( <code>m.lg.sp</code> , <code>s.lg.sp</code> ). Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>s.lg.se</code>	standard deviation of logit $\text{Se}$ . Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>s.lg.sp</code>	standard deviation of logit $\text{Sp}$ . Do not have to specify this if <code>prior_list</code> is given - it will be disregarded.
<code>lg.se</code>	used as an initial value for logit $\text{Se}$ . Default to <code>m.lg.se</code>
<code>lg.sp</code>	used as an initial value for logit $\text{Sp}$ . Default to <code>m.lg.sp</code>
<code>logitpi0_prior</code>	mean and sd of the prior normal distribution of $\text{logit}(\pi_0)$ . Default to <code>c(0, 10)</code> .
<code>lor_prior</code>	mean and sd of the prior normal distribution of corrected log odds ratio. Default to <code>c(0, 2)</code> .
<code>chains</code>	number of Markov Chains. Default to 2.
<code>traceplot</code>	Logical, defaulting to FALSE. If TRUE it will draw the <a href="#">traceplot</a> corresponding to one or more Markov chains.
<code>inc_warmup</code>	Only evaluated when <code>traceplot = TRUE</code> . TRUE or FALSE, indicating whether or not to include the warmup sample in the traceplot; defaults to FALSE.
<code>window</code>	Only evaluated when <code>traceplot = TRUE</code> . A vector of length 2. Iterations between <code>window[1]</code> and <code>window[2]</code> will be shown in the plot. The default shows all iterations if <code>inc_warmup</code> is TRUE and all iterations from the sampling period only if <code>inc_warmup</code> is FALSE. If <code>inc_warmup</code> is FALSE the iterations specified in <code>window</code> do not include iterations from the warmup period. The default number of iterations is 2000 unless otherwise specified in the optional <code>iter</code> argument.
<code>refresh</code>	an integer value used to control how often the progress of sampling is reported. By default, the progress indicator is turned off, thus <code>refresh &lt;= 0</code> . If on, <code>refresh = max(iter/10, 1)</code> is generally recommended.
<code>seed</code>	the seed for random number generation. Default to 0. See <a href="#">stan</a> for more details.
<code>...</code>	optional parameters passed to <a href="#">stan</a> .

**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 `glmer` function in `lme4`. Lower and upper bounds for Se and Sp can be specified according to the assumptions of the study.

## Usage

```
nlmeNDiff(data, lower = 0.5, upper = 1, id = FALSE, ...)
```

## Arguments

<code>data</code>	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</code> indicates the true positives, <code>n01</code> the false positives, <code>n00</code> the true negatives and <code>n10</code> the false negatives. Each column is a vector of same length, which is the number of meta-analysis study results used in the model.
<code>lower</code>	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.
<code>upper</code>	an optional argument specifying the upper bound assumption of Se and Sp. Default to 1.
<code>id</code>	a TRUE or FALSE argument indicating if the supplied data has a <code>sid</code> column that gives same studies the same subject ID. Default to FALSE, which assumes that all studies have different IDs.
<code>...</code>	optional parameters passed to <a href="#">glmer</a> .

## Value

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

**Examples**

```
data(bd_meta)

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

---

paramEst	<i>Parameter estimates of the GLMM model</i>
----------	--

---

**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**

```
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.

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**

```
# 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**

```
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 = $(\exp(2z)-1)/(1+\exp(2z))$ . 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 <a href="#">traceplot</a> 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 = $\max(\text{iter}/10, 1)$ is generally recommended.
seed	the seed for random number generation. Default to 0. See <a href="#">stan</a> for more details.
...	optional parameters passed to <a href="#">stan</a> .

### 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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