Package 'BayesSenMC'

May 3, 2019

Title Different Models of Posterior Distributions of Adjusted Odds
Ratio

Version 0.1.1

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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 nonlinear mixed effects model. It implements the methods that are first proposed by Chu et al. (2006) <doi:10.1016/j.annepidem.2006.04.001> and Chu et al. (2010) <doi:10.1177/0272989X0935345

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Encoding UTF-8

LazyData true

Imports dplyr, ggplot2, rstan (>= 2.16.2), lme4,

Depends Rcpp (>= 0.12.19)

Suggests gridExtra

RoxygenNote 6.1.1

NeedsCompilation no

Repository CRAN

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R topics documented:

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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)
```

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)
iplotCurves(phe, times)
```

---

correctedOR   *Model without misclassification*

Description

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

Usage

```
correctedOR(a, N1, c, N0, name = "Corrected Model", chains = 2,
  traceplot = FALSE, inc_warmup = FALSE, window = NULL,
  refresh = 0, seed = NA, ...)
```

Arguments

a	# of exposed subjects in the case group.
N1	# of total subjects in the case group.
c	# of exposed subjects in the control group.
N0	# of total subjects in the control group.
name	a string of the name of the model. Default to "Corrected Model".
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 here 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

correctedOR(a = 66, N1 = 11782, c = 243, N0 = 57973, chains = 3,
iter = 10000, seed = 0)
correctedOR(a = 66, N1 = 11782, c = 243, N0 = 57973, traceplot = TRUE)
```

---

crudeOR   *Model with constant nondifferential misclassification*

Description

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

Usage

```
crudeOR(a, N1, c, N0, se, sp, name = "Constant Misclassification Model",
  chains = 2, traceplot = FALSE, inc_warmup = FALSE, window = NULL,
  refresh = 0, seed = NA, ...)
```

Arguments

a	# of exposed subjects in the case group.
N1	# of total subjects in the case group.
c	# of exposed subjects in the control group.
N0	# of total subjects in the control group.
se	sensitivity
sp	specificity
name	a string of the name of the model. Default to "Constant Misclassification Model".
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 here 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}\

crudeOR(a = 66, N1 = 11782, c = 243, N0 = 57973, se = 0.744, sp = 0.755, chains = 3,
iter = 10000, seed = 0)
crudeOR(a = 66, N1 = 11782, c = 243, N0 = 57973, se = 0.744, sp = 0.755, traceplot = TRUE)
```

---

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,
  name = "Model with differential classification", chains = 2,
  traceplot = FALSE, inc_warmup = FALSE, window = NULL,
  refresh = 0, seed = 0, ...)
```

Arguments

a	# of exposed subjects in the case group.
N1	# of total subjects in the case group.
c	# of exposed subjects in the control group.
N0	# of total subjects in the control group.
mu	vector of length 4; multivariate normal distribution of $z \sim (mu, varz)$, where each μ 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.
name	a string of the name of the model. Default to "Model with differential misclassification".
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 here 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, chains = 3, mu = c(1.069, 1.069, 1.126, 1.126),
  s.lg.se0 = 0.893, s.lg.se1 = 0.893, s.lg.sp0 = 0.712, s.lg.sp1 = 0.712, corr.sesp0 = -0.377,
  corr.sesp1 = -0.377, corr.group = 0, iter = 10000, seed = 0)
diffOR(a = 66, N1 = 11782, c = 243, N0 = 57973, , mu = c(1.069, 1.069, 1.126, 1.126),
  s.lg.se0 = 0.893, s.lg.se1 = 0.893, s.lg.sp0 = 0.712, s.lg.sp1 = 0.712, corr.sesp0 = -0.377,
  corr.sesp1 = -0.377, corr.group = 0, traceplot = TRUE)
```

---

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 sentivity and specificity.

Usage

```
fixedCorrOR(a, N1, c, N0, m.lg.se, m.lg.sp, s.lg.se, s.lg.sp,
  lg.se = NULL, lg.sp = NULL, rho,
  name = "Logit Model with Fixed Correlation", chains = 2,
  traceplot = FALSE, inc_warmup = FALSE, window = NULL,
  refresh = 0, seed = NA, ...)
```

Arguments

a	# of exposed subjects in the case group.
N1	# of total subjects in the case group.
c	# of exposed subjects in the control group.
N0	# of total subjects in the control group.
m.lg.se	normal distribution of logit Se with (mean = m.lg.se, sd = s.lg.se).
m.lg.sp	conditional normal distribution of logit Sp given Se with (m.lg.sp, s.lg.sp).
s.lg.se	standard deviation of logit Se
s.lg.sp	standard deviation of logit Sp
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
name	a string of the name of the model. Default to "Logit Model with Fixed Correlation".
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 here 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}

fixedCorrOR(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, rho = -0.379, chains = 3, iter = 10000, seed = 0)
fixedCorrOR(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, lg.se = 2.197, lg.sp = 0.744, rho = -0.379,
  traceplot = TRUE)
```

---

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, m.lg.se, m.lg.sp, s.lg.se, s.lg.sp, lg.se = NULL,
  lg.sp = NULL, name = "Logit Normal Misclassification Model",
  chains = 2, traceplot = FALSE, inc_warmup = FALSE, window = NULL,
  refresh = 0, seed = NA, ...)
```

Arguments

a	# of exposed subjects in the case group.
N1	# of total subjects in the case group.
c	# of exposed subjects in the control group.
N0	# of total subjects in the control group.
m.lg.se	normal distribution of logit Se with (mean = m.lg.se, sd = s.lg.se).
m.lg.sp	normal distribution of logit Sp with (m.lg.sp, s.lg.sp).

s.lg.se	standard deviation of logit Se
s.lg.sp	standard deviation of logit Sp
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
name	a string of the name of the model. Default to "Logit Normal Misclassification Model".
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 here 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}

logitOR(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, chains = 3, iter = 10000, seed = 0)
logitOR(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, lg.se = 2.197, lg.sp = 2.197, traceplot = TRUE)
```

---

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

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: `n11` indicates the true positives, `n01` the false positives,
                  `n00` the true negatives and `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. De-
                  fault to 0.5 (or the lowest Se/Sp of all studies, whichever is lower), which pro-
                  vides the mild assumption that Se and Sp are better than chance.

upper   an optional argument specifying the upper bound assumption of Se and Sp. De-
                  fault to 1.

id   a TRUE of FALSE argument indicating if the supplied data has a `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 glmer.

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 *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 `nlme_nondiff()` function.

lower   an optional argument matching the lower bound assumption of Se and Sp of the
            input `model`. Default to 0.5 as in `nlme_nondiff()`.

upper   an optional argument matching the upper bound assumption of Se and Sp. De-
            fault to 1 as in `nlme_nondiff()`.

Value

It returns a list of parameter estimates which can be input into the Bayesian model functions in
`BayesSenMC`. (`mean_logSe`,`var_logSe`) and (`mean_logSp`,`var_logSp`) are the logit prior distri-
butions 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. `fisher_mean` is the Fisher's mean of the correlation
assume a Fisher's distribution.

Examples

```
data(bd_meta)

mod <- nlmeNDiff(bd_meta, lower = 0) # see nlme_nondiff() for detailed example.
pList <- 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 corrected odds ratio given no or constant misclassification, assuming log-normality is true.

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`	# 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`	# of total subjects in the case group.
`c`	# of exposed subjects in the control group.
`N0`	# 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")
```

---

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, m.lg.se, m.lg.sp, s.lg.se, s.lg.sp,
  lg.se = NULL, lg.sp = NULL, m.z, s.z, z = NULL,
  name = "Logit Model with Random Correlation", chains = 2,
  traceplot = FALSE, inc_warmup = FALSE, window = NULL,
  refresh = 0, seed = NA, ...)
```

Arguments

a	# of exposed subjects in the case group.
N1	# of total subjects in the case group.
c	# of exposed subjects in the control group.
N0	# of total subjects in the control group.
m.lg.se	normal distribution of logit Se with (mean = m.lg.se, sd = s.lg.se).
m.lg.sp	conditional normal distribution of logit Sp given Se with (m.lg.sp, s.lg.sp).
s.lg.se	standard deviation of logit Se
s.lg.sp	standard deviation of logit Sp
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
m.z	normal distribution of Z with (mean = m.z, sd = s.z).
s.z	normal distribution of Z with (mean = m.z, sd = s.z).
z	used as an initial value of Fisher's Z transformed of rho, where correlation rho = (exp(2*z)-1)/(1+exp(2*z))).
name	a string of the name of the model. Default to "Logit Model with Random Correlation".
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 here 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}

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, chains = 3,
  iter = 10000, seed = 0)
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, lg.se = 2.197, lg.sp = 0.744, m.z = -0.399,
  s.z = 0.139, traceplot = TRUE)
```

---

smoke_meta   *Meta-analysis data on self-reported smoking diagnosis accuracy*

Description

Records the true positive, true negative, false positive and false negative of each diagnosis accuracy study. Also includes the type of questionnaire for reporting (self (SAQ) or interviewer-administered (IAQ)), and the type of diagnosis (by carbon monoxide (CO) / carboxyhemoglobin (COHb) /thio-cyanate (SCN) /cotinine (COT)). And the type of subjects (G = general population; S = students), and design of the study (O = observational; I = intervention).

Usage

```
data(smoke_meta)
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 51 rows and 10 columns.

Source

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1614767/

References

Patrick, D L et al. Patrick, D L et al. "The validity of self-reported smoking: a review and meta-analysis". American journal of public health vol. 84,7 (1994): 1086-93. (PMC)

Examples

```
data(smoke_meta)
```

Index