Package ‘MetaStan’

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Title Bayesian Meta-Analysis via ‘Stan’
Description Performs Bayesian meta-analysis, meta-regression and model-based meta-analysis using ‘Stan’. Includes binomial-normal hierarchical models and option to use weakly informative priors for the heterogeneity parameter and the treatment effect parameter which are described in Guenhan, Roever, and Friede (2020) <doi:10.1002/jrsm.1370>.
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MetaStan-package

Description

Fitting Bayesian meta-analysis models via Rstan.

Details

To fit meta-analysis models using frequentist methods, there are many R packages available including ‘metafor’. On the other hand, Bayesian estimation methods such as Markov chain Monte Carlo (MCMC) are very attractive for meta-analysis, especially because they can be used to fit more complicated models. These include binomial-normal hierarchical models and beta-binomial models which are based on the exact distributional assumptions unlike (commonly used) normal-normal hierarchical model. Another advantage of Bayesian methods to be able to use informative prior distributions for example to regularize heterogeneity estimates in case of low number of studies. Thus, we developed ‘MetaStan’ which uses Stan (a modern MCMC engine) to fit several pairwise meta-analysis models including binomial-normal hierarchical model and beta-binomial model. This package is also the accompanying package of Guenhan et al (2020). Another important functionality of the package is the model-based meta-analysis models.
Author(s)

Burak Kuersad Guenhan <burak.gunhan@med.uni-goettingen.de>

References


compare_MBMAs

Compare MBMA fits using LOO-IC

Description

Takes a vector of MBMA Stan fits and give the model comparison results based on LOO-IC criteria. This is useful to compare different dose-response models. The function depends on loo_compare function from loo package.

Usage

compare_MBMA(model_list, digits = 2, ...)

Arguments

model_list A vector of MBMA_stan object.
digits An integer indicating the number of decimal places.
... Further arguments passed to or from other methods.

References


See Also

loo::loo_compare
### convert_data_arm

Convert contrast-based dataset to arm-based dataset (deprecated)

#### Description

convert_data_arm creates a dataframe to fit a meta-analysis model using meta_Stan function.

#### Usage

```r
classic_data_arm(nt, nc, pt, pc, pub, data = NULL)
```

#### Arguments

- `nt`: Number of subjects in treatment arm
- `nc`: Number of subjects in control arm
- `pt`: Number of events in treatment arm
- `pc`: Number of events in treatment arm
- `pub`: The corresponding publication
- `data`: Optional data frame containing the variables given to the arguments above.

#### Value

A dataframe object

#### Examples

```r
## Create arm-based dataset
data('dat.Crins2014', package = "MetaStan")
dat_converted <- convert_data_arm(exp.total, cont.total,  
                                   exp.AR.events, cont.AR.events,  
                                   publication, data = dat.Crins2014)
```

---

### create_MetaStan_dat

Prepare model-based meta-analysis dataset for Stan.

#### Description

create_METAStan_dat converts datasets in the one-study-per-row format to one-arm-per-row format,
create_MetaStan_dat

Usage

create_MetaStan_dat(
  dat = NULL,
  armVars = c(dose = "d", responders = "r", sampleSize = "n"),
  nArmsVar = "nd"
)

Arguments

dat Data in one-study-per-row format.
armVars Vector of per-arm variables The name of each component will be the column
  name in the resulting dataset.
nArmsVar Variable holding the number of arms for each study.

Details

The resulting data.frame can be used as data argument in MBMA_stan.

Value

A data frame with the generated columns.

Author(s)

Burak Kuersad Guenhan, <burak.gunhan@med.uni-goettingen.de> and Gert van Valkenhoef

See Also

gemtc::mtc.data.studyrow and nmaINLA::create_INLA_dat

Examples

## Not run:
data('dat.Eletriptan')
## Create the dataset suitable for MBMA_stan
EletriptanDat <- create_MetaStan_dat(dat = dat.Eletriptan,
  armVars = c(dose = "d",
              responders = "r",
              sampleSize = "n"),
  nArmsVar = "nd")

## Check that the data are correct
print(EletriptanDat)

## End(Not run)
**dat.Boucher2016**

*Trials investigating effectiveness of the BCG vaccine against TB*

**Description**

A dataset containing the results from 13 trials examining the efficacy of Bacillus Calmette-Guerin (BCG) vaccine against tuberculosis (TB).

**Usage**

`dat.Berkey1995`

**Format**

A data frame with following columns

<table>
<thead>
<tr>
<th>Trial</th>
<th>Trial number</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>r1</code></td>
<td>number of TB events in treatment arm</td>
</tr>
<tr>
<td><code>n1</code></td>
<td>number of subjects in treatment arm</td>
</tr>
<tr>
<td><code>r2</code></td>
<td>number of TB events in control arm</td>
</tr>
<tr>
<td><code>n2</code></td>
<td>number of subjects in control arm</td>
</tr>
<tr>
<td><strong>Latitude</strong></td>
<td>absolute latitude of the study location</td>
</tr>
<tr>
<td><strong>publication</strong></td>
<td>author and date</td>
</tr>
</tbody>
</table>

**Source**


---

**dat.Boucher2016**

*Paresthesia rates with Topiramate in migraine prophylaxis trials*

**Description**

Numbers of patients and events (paresthesia rates) in experimental and control groups of 6 studies. It is in one-study-per-row format.

**Usage**

`dat.Boucher2016`
Format

A data frame with following columns:

- **d1**  dose (mg) in the first arm (placebo)
- **r1**  number of events in the first arm (placebo)
- **n1**  number of patients in the first arm (placebo)
- **d2**  dose (mg) in the second arm
- **r2**  number of events in the second arm
- **n2**  number of patients in the second arm
- **d3**  dose (mg) in the third arm
- **r3**  number of events in the third arm
- **n3**  number of patients in the third arm
- **d4**  dose (mg) in the fourth arm
- **r4**  number of events in the fourth arm
- **n4**  number of patients in the fourth arm
- **nd**  number of treatment arms

Source


---

**dat.Boucher2016.pairwise**

*PARESTHESIA RATES WITH TOPIRAMATE IN MIGRAINE PROPHYLAXIS TRIALS*

---

Description

Numbers of patients and events (paresthesia rates) in experimental and control groups of 6 studies. It is in one-study-per-row format. Only the arm with 200 mg is included.

Usage

`dat.Boucher2016.pairwise`

Format

A data frame with following columns:

- **study**  Study ID
- **duration**  Duration of the study
- **r1**  number of events in the first arm (placebo)
- **n1**  number of patients in the first arm (placebo)
- **r2**  number of events in the second arm
- **n2**  number of patients in the second arm
Source


---

**dat.Crins2014**

**Pediatric liver transplant example data**

**Description**

Numbers of cases and events (PTLDs or deaths) in experimental and control groups of six studies.

**Usage**

dat.Crins2014

**Format**

A data frame with following columns

- **publication** publication identifier (first author and publication year)
- **year** publication year
- **randomized** randomization status (y/n)
- **control.type** type of control group ("concurrent" or "historical")
- **comparison** type of comparison ("IL-2RA only", "delayed CNI", or "no/low steroids")
- **followup** follow-up time in months
- **exp.AR.events** number of AR events in experimental group
- **exp.PTLD.events** number of PTLD events in experimental group
- **exp.deaths** number of deaths in experimental group
- **exp.total** number of patients in experimental group
- **exp.SRR.events** number of SRR events in experimental group
- **cont.AR.events** number of AR events in control group
- **cont.SRR.events** number of SRR events in control group
- **cont.PTLD.events** number of PTLD events in control group
- **cont.deaths** number of deaths in control group
- **cont.total** number of patients in control group
- **r2** number of AR events in experimental group
- **n1** number of patients in control group
- **n2** number of patients in experimental group
- **r1** number of AR events in control group

**Source**

Description

Numbers of patients and events (headache free at 2 hours) in experimental and control groups of 12 studies. It is in one-study-per-row format.

Usage

dat.Eletriptan

Format

A data frame with following columns

ID trial ID
d1 dose (mg) in the first arm (placebo)
r1 number of events in the first arm (placebo)
n1 number of patients in the first arm (placebo)
d2 dose (mg) in the second arm
r2 number of events in the second arm
n2 number of patients in the second arm
d3 dose (mg) in the third arm
r3 number of events in the third arm
n3 number of patients in the third arm
d4 dose (mg) in the fourth arm
r4 number of events in the fourth arm
n4 number of patients in the fourth arm
nd number of treatment arms

Source

forest_plot

Description

Takes a meta_stan object which is obtained by function meta_stan and plot a forestplot, showing individual estimates along with their 95 percent credible intervals, resulting effect estimate and prediction interval.

Usage

forest_plot(
  x = NULL,
  labels = NULL,
  digits = 2,
  boxsize = 0.3,
  heterogeneity = TRUE,
  col,
  ...
)

Arguments

- **x**: A meta_stan object.
- **labels**: Optional vector with labels for the studies (publication author/year).
- **digits**: A numerical value specifying the number of significant digits to be shown. Default is 2.
- **boxsize**: A numerical value specifying the box size. Default is 0.3.
- **heterogeneity**: A logical value to include heterogeneity estimates (DEFAULT = TRUE)
- **col**: A function specifying the colors. See forestplot::fpColors for details.
- **...**: Further arguments passed to or from other methods.

Value

The return value is invisible NULL.

Author(s)

Christian Roever and Burak Kuersad Guenhan

Source

This function is based foresplot function from foresplot R package.

See Also

forestplot::foresplot
Examples

```r
# Not run:
data('dat.Crins2014', package = "MetaStan")
dat_long <- create_MetaStan_dat(dat = dat.Crins2014,
               armVars = c(responders = "r", sampleSize = "n"))
bnhm.Crins <- meta_stan(data = dat_long, likelihood = "binomial",
                        mu_prior = c(0, 10), theta_prior = c(0, 100),
                        tau_prior = 0.5)
forest_plot(bnhm.Crins, xlab = "log-OR", labels = dat.Crins2014$publication)
```

## End(Not run)

---

### MBMA_stan

**Fitting a model-based meta-analysis model using Stan**

**Description**

‘MBMA_stan‘ fits a model-based meta-analysis model using Stan.

**Usage**

```r
MBMA_stan(
  data = NULL,
  likelihood = NULL,
  dose_response = "emax",
  mu_prior = c(0, 10),
  Emax_prior = c(0, 100),
  alpha_prior = c(0, 100),
  tau_prior = 0.5,
  tau_prior_dist = "half-normal",
  ED50_prior = c(-2.5, 1.8),
  ED50_prior_dist = "functional",
  gamma_prior = c(1, 2),
  Pred_doses,
  re = TRUE,
  ncp = TRUE,
  chains = 4,
  iter = 2000,
  warmup = 1000,
  adapt_delta = 0.95,
  ...
)
```

**Arguments**

- `data` An object of ‘create_MBMA_dat‘.
likelihood A string specifying the likelihood of distributions defining the statistical model. Options include "normal", "binomial", and "Poisson".

dose_response A string specifying the function defining the dose-response model. Options include "linear", "log-linear", "emax", and "sigmoidal".

mu_prior A numerical vector specifying the parameter of the normal prior density for baseline risks, first value is parameter for mean, second is for variance. Default is c(0, 10).

Emax_prior A numerical vector specifying the parameter of the normal prior density for Emax parameter, first value is parameter for mean, second is for standard deviation. Default is c(0, 10). Needed for emax and sigmoidal models.

alpha_prior A numerical vector specifying the parameter of the normal prior density for the alpha parameter, first value is parameter for mean, second is for variance. Default is c(0, 10). Needed for linear and linear log-dose models.

tau_prior A numerical value specifying the standard dev. of the prior density for heterogeneity stdev. Default is 0.5.

tau_prior_dist A string specifying the prior density for the heterogeneity standard deviation, option is 'half-normal' for half-normal prior, 'uniform' for uniform prior, 'half-cauchy' for half-cauchy prior.

ED50_prior A numerical vector specifying the parameter of the normal prior density for ED50 parameter, first value is parameter for mean, second is for standard deviation. Default is c(0, 10). Needed for emax and sigmoidal models.

ED50_prior_dist A string specifying the prior density for the ED50 parameter, ‘functional’ is for a functional uniform prior, ‘half-normal’ for uniform prior, ‘half-cauchy’ for half-cauchy prior.

gamma_prior A numerical vector specifying the parameter of the normal prior density for gamma parameter, first value is parameter for mean, second is for standard deviation. Default is c(1, 2). Needed for sigmoidal model.

Pred_doses A numerical vector specifying the doses which prediction will be made.

re A string specifying whether random-effects are included to the model. When ‘FALSE’, the model corresponds to a fixed-effects model. The default is ‘TRUE’.

ncp A string specifying whether to use a non-centered parametrization. The default is ‘TRUE’.

chains A positive integer specifying the number of Markov chains. The default is 4.

iter A positive integer specifying the number of iterations for each chain (including warmup). The default is 2000.

warmup A positive integer specifying the number of warmup (aka burnin) iterations per chain. The default is 1000.

adapt_delta A numerical value specifying the target average proposal acceptance probability for adaptation. See Stan manual for details. Default is 0.95. In general you should not need to change adapt_delta unless you see a warning message about divergent transitions, in which case you can increase adapt_delta from the default to a value closer to 1 (e.g. from 0.95 to 0.99, or from 0.99 to 0.999, etc).

... Further arguments passed to or from other methods.
meta_stan

Value

An object of class 'stanfit' returned by 'rstan::sampling'.

References


Examples

```r
## Not run:
## Load the dataset
data('dat.Eletriptan', package = "MetaStan")
datMBMA = create_MetaStan_dat(dat = dat.Eletriptan,
   armVars = c(dose = "d",
               responders = "r",
               sampleSize = "n"),
   nArmsVar = "nd")
MBMA.Emax <- MBMA_stan(data = datMBMA,
   likelihood = "binomial",
   dose_response = "emmax",
   Pred_doses = seq(0, 80, length.out = 11),
   mu_prior = c(0, 100),
   Emax_prior = c(0, 100),
   tau_prior_dist = "half-normal",
   tau_prior = 0.5)
plot(MBMA.Emax) + ggplot2::xlab("Doses (mg)") + ggplot2::ylab("response probabilities")

## End(Not run)
```

Description

'`meta_stan`' fits a meta-analysis model using Stan.
Usage

```r
meta_stan(
  data = NULL,
  likelihood = NULL,
  mu_prior = c(0, 10),
  theta_prior = NULL,
  tau_prior = 0.5,
  tau_prior_dist = "half-normal",
  beta_prior = c(0, 100),
  delta = NULL,
  param = "Smith",
  re = TRUE,
  ncp = TRUE,
  interval.type = "shortest",
  mreg = FALSE,
  cov = NULL,
  chains = 4,
  iter = 2000,
  warmup = 1000,
  adapt_delta = 0.95,
  ...
)
```

Arguments

- **data**: Data frame created by `create_MetaStan_dat`
- **likelihood**: A string specifying the likelihood function defining the statistical model. Options include 'normal', 'binomial', and 'Poisson'.
- **mu_prior**: A numerical vector specifying the parameter of the normal prior density for baseline risks, first value is parameter for mean, second is for variance. Default is c(0, 10).
- **theta_prior**: A numerical vector specifying the parameter of the normal prior density for treatment effect estimate, first value is parameter for mean, second is for variance. Default is NULL.
- **tau_prior**: A numerical value specifying the standard dev. of the prior density for heterogeneity stdev. Default is 0.5.
- **tau_prior_dist**: A string specifying the prior density for the heterogeneity standard deviation, option is 'half-normal' for half-normal prior, 'uniform' for uniform prior, 'half-cauchy' for half-cauchy prior.
- **beta_prior**: A numerical vector specifying the parameter of the normal prior density for beta coefficients in a meta-regression model, first value is parameter for mean, second is for variance. Default is c(0, 100).
- **delta**: A numerical value specifying the upper bound of the a priori interval for treatment effect on odds ratio scale. This is used to calculate a normal weakly informative prior. For theta. Thus when this argument is specified, 'theta' should be left empty. Default is NULL.
param  Paramterizaion used. The default is the ‘Smith’ model suggested by Smith et al (1995). The alternative is ‘Higgins’ is the common meta-analysis model (Simmonds and Higgins, 2014).

re  A string specifying whether random-effects are included to the model. When ‘FALSE’, the model corresponds to a fixed-effects model. The default is ‘TRUE’.

ncp  A string specifying whether to use a non-centered parametrization. The default is ‘TRUE’.

interval.type  A string specifying the type of interval estimate. Options include shortest credible interval ‘shortest’ (default) and qui-tailed credible interval ‘central’.

mreg  A string specifying whether to fit a meta-regression model. The default is ‘FALSE’.

cov  A numeric vector or matrix specifying trial-level covariates (in each row). This is needed when ‘mreg = TRUE’.

chains  A positive integer specifying the number of Markov chains. The default is 4.

iter  A positive integer specifying the number of iterations for each chain (including warmup). The default is 2000.

warmup  A positive integer specifying the number of warmup (aka burnin) iterations per chain. The default is 1000.

adapt_delta  A numerical value specifying the target average proposal acceptance probability for adaptation. See Stan manual for details. Default is 0.95. In general you should not need to change adapt_delta unless you see a warning message about divergent transitions, in which case you can increase adapt_delta from the default to a value closer to 1 (e.g. from 0.95 to 0.99, or from 0.99 to 0.999, etc).

...  Further arguments passed to or from other methods.

Value

an object of class ‘MetaStan’.

References


Examples

## Not run:

## TB dataset
plot.MBMA_stan

Plot a dose-response plot

Description

Takes a MBMA_stan object which is obtained by function MBMA_stan and plot a dose-response plot, showing observed event probabilities and the estimated dose-response function with pointwise 95

Usage

## S3 method for class 'MBMA_stan'
plot(x = MBMA.stan, ...)

Arguments

x  A MBMA_stan object.

...  Further arguments passed to ggplot.

Value

The return value is invisible NULL.
Author(s)
Christian Roever and Burak Kuersad Guenhan

Source
This function uses ggplot function from ggplot2 R package.

See Also
ggplot2::ggplot

Examples
## Not run:
data('[quotesingle.Var] Eletriptan', package = 'MetaStan')
datMBMA = create_MetaStan_dat(dat = dat.Eletriptan,
-armVars = c(dose = 'd',
    responders = 'r',
    sampleSize = 'n'),
-nArmsVar = 'nd')

MBMA.Emax <- MBMA_stan(data = datMBMA,
    likelihood = 'binomial',
    dose_response = 'emax',
    Pred_doses = seq(0, 80, length.out = 11),
    mu_prior = c(0, 100),
    Emax_prior = c(0, 100),
    tau_prior_dist = 'half-normal',
    tau_prior = 0.5)
plot(MBMA.Emax) + ggplot2::xlab("Doses (mg)") + ggplot2::ylab("response probabilities")

## End(Not run)
print.meta_stan

Arguments

x       A MBMA_stan object.
digits  An integer indicating the number of decimal places.
...     Further arguments passed to or from other methods.

Value

The return value is invisible NULL

print.meta_stan   Print meta_stan object

Description

Takes an meta_stan object which is obtained by function meta_stan and print the model and data information such as model type used in the model.

Usage

## S3 method for class 'meta_stan'
print(x, digits = 2, ...)

Arguments

x       A meta_stan object.
digits  An integer indicating the number of decimal places.
...     Further arguments passed to or from other methods.

Value

The return value is invisible NULL
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