Package ‘nmaINLA’

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Type Package
Title Network Meta-Analysis using Integrated Nested Laplace Approximations
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Date 2018-07-23
Description Performs network meta-analysis using integrated nested Laplace approximations (‘INLA’). Includes methods to assess the heterogeneity and inconsistency in the network. Contains more than ten different network meta-analysis data. 'INLA' package can be obtained from <http://www.r-inla.org>. We recommend the testing version.
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Anestheticdat

Data for the Anesthetic example in Greco et al. (2013)

Description

Greco et al. (2013) considered four anaesthetic agents used in cardiac surgery (called here 1, 2, 3 and 4) and investigated through NMA.

Usage

Anestheticdat

Format

An object of class data.frame with 30 rows and 10 columns.

Source

Certolizumabdat

Data for the Certolizumab NMA-network discussed in Dias et al. (2013)

Description

Data are available from a review of trials of certolizumab pegol (CZP) for the treatment of rheumatoid arthritis in patients who had failed on disease-modifying antirheumatic drugs, including methotrexate (MTX). 20 Twelve MTX controlled trials were identified, comparing 6 different treatments with placebo. The primary outcome is improving by at least 50 of Rheumatology scale (ACR50) at 6 months. A trial-specific covariate, the mean disease duration in years for patients, is also given.

Usage

Certolizumabdat

Format

An object of class data.frame with 12 rows and 9 columns.

Source


CooperStrokedat

Data for the stroke prevention NMA-network discussed in Cooper et al. (2009)

Description

The stroke prevention dataset describes a network comparing 17 treatments with 26 trials.

Usage

CooperStrokedat

Format

A data frame with 26 observations on the following 17 variables.

r1 Number of events (responses) in the baseline treatment (treatment 1).

r2 Number of events (responses) in the second study arm treatment (treatment 2).

r3 Number of events (responses) in the third study arm treatment (treatment 3).
create_INLA_dat

Description

create_INLA_dat prepares network meta-analysis datasets for INLA.

Usage

create_INLA_dat(dat = dat, armVars = c(treatment = "t", responders = "r", sampleSize = "n"), covariate = "cov", design = "des", nArmsVar = "na")

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.
covariate    Optional. Vector of study-specific covariate
design       Optional. Vector of study-specific design. We refer design for the set of treatments in each trial.
nArmsVar     Variable holding the number of arms for each study.

Source

create_INLA_dat_pair

Details

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

Value

A data frame with the generated columns.

Author(s)

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

See Also

gemtc::mtc.data.studyrow

Examples

data('Smokdat')
## Create the dataset suitable for INLA
SmokdatINLA <- create_INLA_dat(dat = Smokdat, armVars = c('treatment' = 't', 'responders' = 'r', 'sampleSize' = 'n'), nArmsVar = 'na')
## Check that the data are correct
print(SmokdatINLA)

create_INLA_dat_pair  Prepare pairwise meta-analysis dataset for INLA.

Description

create_INLA_dat_pair creates two dataframes, one to use in a contrast based and the other in an arm-based pairwise meta-analysis.

Usage

create_INLA_dat_pair(ntrt, nctrl, ptrt, pctrl, cov = NULL)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ntrt</td>
<td>Number of subjects in treatment arm</td>
</tr>
<tr>
<td>nctrl</td>
<td>Number of subjects in control arm</td>
</tr>
<tr>
<td>ptrt</td>
<td>Number of events in treatment arm</td>
</tr>
<tr>
<td>pctrl</td>
<td>Number of events in treatment arm</td>
</tr>
<tr>
<td>cov</td>
<td>Optional argument to include a covariate in the model</td>
</tr>
</tbody>
</table>
Details

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

Value

A list of two dataframe objects

Examples

data('TBdat')
## Create the dataset suitable for INLA
TBdatINLA <- create_INLA_dat_pair(TBdat$TRT, TBdat$CON, TBdat$TRTB, TBdat$CONTB)

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

---

Diabetesdat  

Data for the Diabetes example in Senn et al. (2013)

Description

Results from 26 trials examining the effectiveness of glucose-lowering agents in patients with type 2 diabetes.

Usage

Diabetesdat

Format

An object of class data.frame with 26 rows and 11 columns.

Source

Dietaryfatdat

Data for the Dietary fat example in Dias et al. (2011)

Description

In a Cochrane Review of randomised controlled trials to assess the effect of change in dietary fats on total and cardiovascular mortality, 104 data extracted was in the form of rates and given as the number of events per person-years observed.

Usage

Dietaryfatdat

Format

An object of class data.frame with 10 rows and 10 columns.

Source


Flourdat

Data for the Flour NMA example in Dias et al. (2010)

Description

The flour dataset describes a network comparing 6 treatments with 130 trials. There are 121 pairwise comparisons, 8 three-arm trials and 1 four-arm trial. The main outcome is caries increment, as measured by the change in decayed, missing, and filled tooth surfaces (DMFS) in the permanent dentition of children. Data that are available for study i include the mean caries increment in trial i arm k, y ik, the number of patients at risk in each trial arm, n ik, the time that individuals are at risk in arm k of study i, t i (measured as the trial follow-up time, which is the same for both arms) and the interventions being compared.

Usage

Flourdat

Format

An object of class data.frame with 130 rows and 20 columns.
### IncDiabetesdat

**Data for the Incident Diabetes example in Elliott et al. (2007)**

**Description**

An example of network meta-analysis for binary outcomes with follow-up times reported.

**Usage**

IncDiabetesdat

**Format**

An object of class `data.frame` with 22 rows and 12 columns.

**Details**

This network meta-analysis is studied by Elliott and Meyer (2007) to assess the effects of antihypertensive agents on incident diabetes. Treatment IDs represent 1) diuretic; 2) placebo; 3) beta-blocker; 4) CCB; 5) ACE inhibitor; and 6) ARB.

**Source**


### KussHeartdat

**Data for the ischemic heart disease sparse pairwise meta-analysis discussed in Kuss (2014)**

**Description**

Dataset for pairwise meta-analysis with many zero entries. Data is from a Cochrane review on postoperative stroke occurrence when comparing off-pump and on-pump coronary artery bypass grafting for ischemic heart disease. This data is used as an example in Kuss (2014).

**Usage**

KussHeartdat
meta_inla

Format

An object of class tbl_df (inherits from tbl.data.frame) with 60 rows and 4 columns.

Source


meta_inla

Fitting a pairwise meta-analysis model using INLA.

Description

meta_inla fits a pairwise meta-analysis model using INLA

Usage

meta_inla(datINLA, fixed.par = c(0, 1000), tau.prior = "uniform",
tau.par = c(0, 5), type = "FE", approach = "arm-level", mreg = FALSE,
verbose = FALSE, inla.strategy = "simplified.laplace",
improve.hyperpar.dz = 0.75, correct = FALSE, correct.factor = 10)

Arguments

datINLA An object of create_INLA_dat_pair
fixed.par A numerical vector specifying the parameter of the normal prior density for mean treatment effect, first value is parameter for mean, second is for variance.
tau.prior A string specifying the prior density for the heterogeneity standard deviation, options are 'uniform' for uniform prior and 'half-normal' for half-normal prior.
tau.par A numerical vector specifying the parameter of the prior density for heterogeneity stddev.
  * var.par = c(u, l): u is lower bound and l is upper bound when var.prior = 'uniform'
  * var.par = c(m, v): m is mean and v is variance when var.prior = 'uniform'
type A string indicating the type of the model, options are "FE", "RE".
approach A string indicating the approach of the model, options are "summary-level", "arm-level"
mreg Logical indicating whether covariate(s) should be incorporated to fit a meta-regression model, default FALSE
verbose Logical indicating whether the program should run in a verbose model, default FALSE.
inla.strategy A string specifying the strategy to use for the approximations of INLA; one of 'gaussian', 'simplified.laplace' (default) or 'laplace', see ?INLA::control.inla.
improve.hyperpar.dz
Step length in the standardized scale used in the construction of the grid, default
0.75, see INLA::inla.hyperpar.

correct
Logical Add correction for the Laplace approximation, default FALSE, see INLA::inla.hyperpar.
correct.factor
Numerical Factor used in adjusting the correction factor if correct=TRUE, de-
default 10, see INLA::inla.hyperpar.

Details
The following model types are supported

• FE, fixed-effect model
• RE, random effects model

Value
meta_inla returns a meta_inla object with components:

Examples

data('TBdat')
## Create the dataset suitable for INLA
TBdatINLA <- create_INLA_dat_pair(TBdat$TRT, TBdat$CON, TBdat$TRTBB, TBdat$CONB)

## Fitting a random-effects model using arm-level approach
## Not run:
if(requireNamespace('INLA', quietly = TRUE)){
  require('INLA', quietly = TRUE)
  fit.TB.RE.INLA <- meta_inla(TBdatINLA, type = 'RE', approach = 'arm-level',
    tau.prior = 'uniform', tau.par = c(0, 5))
}
## End(Not run)

nnmAINLA

nnmAINLA: Network meta-analysis using INLA

Description
An R package for performing network meta-analysis using INLA.
Details

Network meta-analysis is a generalization of pairwise meta-analysis to analyze networks of trials comparing two or more treatments simultaneously (Dias et al, 2011). Bayesian hierarchical models are commonly used for network meta-analysis (Dias et al, 2011). The default choice for performing inference within such models are Markov Chain Monte Carlo (MCMC), for example using BUGS-variants programs such as JAGS. A deterministic approach to do fully Bayesian inference for latent Gaussian models (LGMs) are integrated nested Laplace approximations (INLA) (Rue et al, 2009) which is a fast and accurate alternative to MCMC. INLA methodology is implemented as an R package INLA (<www.r-inla.org>). Sauter and Held (2015) has shown that INLA can be used for fitting many NMA models including fixed effect and consistency models, node-splitting models.

This package extends the INLA implementation of Sauter and Held (2015) to Jackson model (Jackson et al, 2014) and network meta-regression and extracts the features needed for NMA models from INLA R package and presents in an intuitive way (Guenhan et al, in preparation). Currently, contrast-based network meta-analysis using trial-arm level data for datasets with binary, continuous, and survival outcomes are supported. Note that the installation of R package ‘INLA’ is compulsory for successful usage. The ‘INLA’ package can be obtained from <http://www.r-inla.org>. We recommend the testing version, which can be downloaded by running: source("http://www.math.ntnu.no/inla/givemeINLA-testing.R"). Type vignette("nmaINLA") to how to use this package.

The development version of nmaINLA is available on GitHub <https://github.com/gunhanb/nmaINLA>.

Author(s)

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

Source


**Description**

*nma_inla* fits a network meta-analysis model using INLA.

**Usage**

```{r}
nma_inla(datINLA, likelihood = NULL, fixed.par = c(0, 1000),
  tau.prior = "uniform", tau.par = c(0, 5), kappa.prior = "uniform",
  kappa.par = c(0, 5), mreg = FALSE, type = "consistency",
  verbose = FALSE, inla.strategy = "simplified.laplace",
  improve.hyperpar.dz = 0.75, correct = FALSE, correct.factor = 10,
  improve.hyperpar = TRUE)
```

**Arguments**

- **datINLA** An object of `create_INLA_dat`
- **likelihood** The likelihood to be used.
- **fixed.par** A numerical vector specifying the parameter of the normal prior density for basic parameters, first value is parameter for mean, second is for variance.
- **tau.prior** A string specifying the prior density for the heterogeneity standard deviation, options are 'uniform' for uniform prior and 'half-normal' for half-normal prior.
- **tau.par** A numerical vector specifying the parameter of the prior density for heterogeneity stdev.
  - `var.par = c(u, l)`: `u` is lower bound and `l` is upper bound when `var.prior = 'uniform'`.
  - `var.par = c(m, v)`: `m` is mean and `v` is variance when `var.prior = 'half-normal'`.
- **kappa.prior** A string specifying the prior density for the inconsistency standard deviation, options are 'uniform' for uniform prior and 'half-normal' for half-normal prior.
- **kappa.par** A numerical vector specifying the parameter of the prior density for inconsistency stdev. The definition of the priors is the same as for `tau.par`.
- **mreg** Logical indicating whether covariate(s) should be incorporated to fit a network meta-regression model, default `FALSE`.
- **type** A string indicating the type of the model, options are "FE", "consistency" and "jackson".
- **verbose** Logical indicating whether the program should run in a verbose model, default `FALSE`.
- **inla.strategy** A string specifying the strategy to use for the approximations of INLA; one of 'gaussian', 'simplified.laplace' (default) or 'laplace', see `?INLA::control.inla`.
- **improve.hyperpar.dz** Step length in the standardized scale used in the construction of the grid, default 0.75, see `INLA::inla.hyperpar`. Not used if `mod = 'FE'`. 
correct Logical Add correction for the Laplace approximation, default FALSE, see INLA::inla.hyperpar. Not used if mod = 'FE'.
correct.factor Numerical Factor used in adjusting the correction factor if correct=TRUE, default 10, see INLA::inla.hyperpar. Not used if mod = 'FE'.
improve.hyperpar Improve the estimates of the posterior marginals for the hyperparameters of the model using the grid integration strategy, default TRUE. see INLA::inla.hyperpar.

Details

The following likelihood types are supported
  • normal: for continuous (mean difference) data.
    Required columns: [mean, std.err]
    Result: relative mean difference
  • binomial: for dichotomous data.
    Required columns: [responders, sampleSize]
    Result: log odds ratio
  • normal: for event-rate (survival) data.
    Required columns: [responders, exposure]
    Result: log hazard ratio

The following model types are supported
  • FE, ordinary fixed effect model, assuming homogeneity between trials (Dias et al., 2013)
  • consistency, ordinary consistency model, assuming consistency in the network. (Jackson et al., 2014)
  • jackson, the design-by-treatment interaction model with random inconsistency parameters. (Jackson et al., 2014)

Value

nma_inla returns a nma_inla object.

Examples

SmokdatINLA <- create_INLA_dat(dat = Smokdat, armVars = c('treatment' = 't', 'responders' = 'r', 'sampleSize' = 'n'), nArmsVar = 'na')
## Not run:
## Fitting a consistency model
if(requireNamespace('INLA', quietly = TRUE)){
  require('INLA', quietly = TRUE)
  fit.Smok.cons.INLA <- nma_inla(SmokdatINLA, likelihood = 'binomial', type = 'consistency', tau.prior = 'uniform', tau.par = c(0, 5))
}
## End(Not run)
Data for the Parkinson NMA-network discussed in Dias et al. (2013)

Description
Data are the mean off-time reduction in patients given dopamine Agonists as adjunct therapy in Parkinson’s disease. The data available are the mean, standard deviation and number of patients in each trial arm, for 7 studies of five different drugs: placebo, coded 1, and five active drugs coded 2 to 5.

Usage
Parkinsondat

Format
An object of class data.frame with 7 rows and 11 columns.

Source

Plot a network plot

Description
Takes a create_INLA_dat output and plots a network graph.

Usage
plot_nma(s.id = "study", t.id = "treatment", data, title = "", adjust.figsizex = 1.1, adjust.figsizey = 1.1)

Arguments
s.id Variable holding the study IDs for each study. The default is "study".
t.id Variable holding the treatments for each study. The default is "treatment".
data A create_INLA_dat object.
title A character string indicating plot title.
adjust.figsizex a positive number used to adjust the plot width. The default is 1.1.
adjust.figsizey a positive number used to adjust the plot height. The default is 1.1.
Author(s)

Lifeng Lin, Jing Zhang, and Haitao Chu

Source

This function is taken from nma.networkplot function from pcnetmeta R package.

See Also

pcnetmeta::nma.networkplot

print.nma_inla

Print nmainla object

Description

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

Usage

## S3 method for class 'nma_inla'
print(x, digits = 3, ...)

Arguments

x An nma_inla object.

digits An integer indicating the number of decimal places.

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

Details

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

Value

The return value is invisible NULL
**Smokdat**

*Data for the smoking cessation NMA-network discussed in Dias et al. (2010)*

---

**Description**

The smoking cessation dataset describes a network comparing 4 treatments with 24 trials. There are 22 pairwise comparisons and 2 three-arm trials.

**Usage**

Smokdat

**Format**

A data frame with 24 observations on the following 10 variables.

- **r1**: Number of events (responses) in the baseline treatment (treatment 1).
- **r2**: Number of events (responses) in the second study arm treatment (treatment 2).
- **r3**: Number of events (responses) in the third study arm treatment (treatment 3).
- **n1**: Total number of study participants in the baseline treatment (treatment 1).
- **n2**: Total number of study participants in the second study arm treatment (treatment 2).
- **n3**: Total number of study participants in the third study arm treatment (treatment 3).
- **t1**: Indicator variable identifying treatment 1.
- **t2**: Indicator variable identifying treatment 2.
- **t3**: Indicator variable identifying treatment 3.
- **na**: Indicator with number of arms in trial.
- **des**: Design, the set of treatments included in each study.

**Source**

Strokedat

Data for the Stroke NMA regression discussed in Batson et al. (2016)

Description

Dataset for network meta-regression of stroke prevention in Atrial Fibrillation. A total of 19 studies, and primary endpoint is reported ischaemic stroke. It includes 15 comparators which include fixed low dose warfarin with or without aspirin, aspirin monotherapy, aspirin plus clopidogrel, indobufen, idraparinux, triflusal and ximelagatran. Study level covariates are the proportion of patients with a previous stroke/TIA, proportion of males, mean age, and the duration of study.

Usage

Strokedat

Format

An object of class data.frame with 19 rows and 18 columns.

Source


TBdat

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

TBdat

Format

A data frame with following columns

<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trial</td>
<td>Trial number</td>
</tr>
<tr>
<td>TRTBB</td>
<td>number of TB events in treatment arm</td>
</tr>
<tr>
<td>TRT</td>
<td>number of subjects in treatment arm</td>
</tr>
<tr>
<td>CONTB</td>
<td>number of TB events in control arm</td>
</tr>
<tr>
<td>CON</td>
<td>number of subjects in control arm</td>
</tr>
<tr>
<td>Latitude</td>
<td>absolute latitude of the study location</td>
</tr>
</tbody>
</table>
Source


Thrombdat

Data for the thrombolytic NMA-network discussed in Dias et al. (2010)

Description

The thrombolytic dataset describes a network comparing 9 treatments with 50 trials. There are 22 pairwise comparisons and 2 thee-arm trials.

Usage

Thrombdat

Format

A data frame with 50 observations on the following 11 variables.

- r1 Number of events (responses) in the baseline treatment (treatment 1).
- r2 Number of events (responses) in the second study arm treatment (treatment 2).
- r3 Number of events (responses) in the third study arm treatment (treatment 3).
- n1 Total number of study participants in the baseline treatment (treatment 1).
- n2 Total number of study participants in the second study arm treatment (treatment 2).
- n3 Total number of study participants in the second study arm treatment (treatment 3).
- t1 Indicator variable identifying treatment 1.
- t2 Indicator variable identifying treatment 2.
- t3 Indicator variable identifying treatment 3.
- na Indicator with number of arms in trial.

Source

Woodsdat

Data for the Woods example in Woods et al. (2010)

Description

Count mortality statistics in randomised controlled trials of treatments for chronic obstructive pulmonary disease (Woods et al. (2010), Table 1)

Usage

Woodsdat

Format

An object of class data.frame with 3 rows and 14 columns.

Source

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