Package 'nmaINLA'

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Type Package

Title Network Meta-Analysis using Integrated Nested Laplace Approximations

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Description Performs network meta-analysis using integrated nested Laplace approximations ('INLA') which is described in Guenhan, Held, and Friede (2018) <doi:10.1002/jrsm.1285>. Includes methods to assess the heterogeneity and inconsistency in the network. Contains more than ten different network meta-analysis dataset. 'INLA' package can be obtained from <https://www.r-inla.org>.

License GPL (>= 2)

LazyData TRUE

Depends R (>= 2.10)

Additional_repositories https://inla.r-inla-download.org/R/stable/

RoxygenNote 7.1.1

Suggests INLA, knitr, testthat

VignetteBuilder knitr

URL https://github.com/gunhanb/nmaINLA

BugReports https://github.com/gunhanb/nmaINLA/issues

Encoding UTF-8

NeedsCompilation no

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Repository CRAN

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R topics documented:

`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

Greco, T., Landoni, G., Biondi-Zoccai, G., D'Ascenzo, F. and Zangrillo, A., 2013. A Bayesian network meta-analysis for binary outcome: how to do it. Statistical methods in medical research, p.0962280213500185.

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-specificc 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

Dias, S., Sutton, A.J., Welton, N.J. and Ades, A.E., 2013. Evidence synthesis for decision making 3 heterogeneity-subgroups, meta-regression, bias, and bias-adjustment. Medical Decision Making, 33(5), pp.618-640.

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).

`r4` Number of events (responses) in the third study arm treatment (treatment 4).

`r5` Number of events (responses) in the third study arm treatment (treatment 5).

`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).

`n4` Total number of study participants in the second study arm treatment (treatment 4).

`n5` Total number of study participants in the second study arm treatment (treatment 5).

`t1` Indicator variable identifying treatment 1.

`t2` Indicator variable identifying treatment 2.

`t3` Indicator variable identifying treatment 3.

`t4` Indicator variable identifying treatment 4.

`t5` Indicator variable identifying treatment 5.

`na` Indicator with number of arms in trial.

`cov` Covariate, study-specific covariates

`des` Design, the set of treatments included in each study

Source

Cooper, N.J., Sutton, A.J., Morris, D., Ades, A.E. and Welton, N.J., 2009. Addressing between-study heterogeneity and inconsistency in mixed treatment comparisons: Application to stroke prevention treatments in individuals with non-rheumatic atrial fibrillation. Statistics in medicine, 28(14), pp.1861-1881.

`create_INLA_dat` *Prepare network meta-analysis dataset for INLA.*

Description

`create_INLA_dat` converts datasets in the one-study-per-row format to one-arm-per-row format , then adds indicator (dummy) variables for the basic contrasts, heterogeneity random effects and design-specific inconsistency random effects and for correlated multi-arm trials.

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.

Details

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

Value

A data frame with the generated coloumns.

Author(s)

Burak Kuersad Guenhan, <burak.gunhan@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

ntrt	Number of subjects in treatment arm
nctrl	Number of subjects in control arm
ptrt	Number of events in treatment arm
pctrl	Number of events in treatment arm
cov	Optional argument to include a covariate in the model

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$TRTTB, TBdat$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

Senn, S., Gavini, F., Magrez, D., & Scheen, A. (2013). Issues in performing a network meta-analysis. Statistical Methods in Medical Research, 22, 169–189.

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

Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E. NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011; last updated September 2016; available from http://www.nicedsu.org.uk

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.

Source

Dias, S., Welton, N.J., Marinho, V.C.C., Salanti, G., Higgins, J.P.T. and Ades, A.E., 2010. Estimation and adjustment of bias in randomized evidence by using mixed treatment comparison meta-analysis. Journal of the Royal Statistical Society: Series A (Statistics in Society), 173(3), pp.613-629.

`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 an ti-hypertensive agents on incident diabetes. Treatment IDs represent 1) diuretic; 2) placebo; 3) beta-blocker; 4) CCB; 5) ACE inhibitor; and 6) ARB.

Source

Elliott WJ and Meyer PM (2007). "Incident diabetes in clinical trials of antihypertensive drugs: a network meta-analysis." Lancet 369(9557), 201-7.

`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
```

Format

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

Source

Kuss O. (2015), Statistical methods for meta-analyses including information from studies without any events–add nothing to nothing and succeed nevertheless, Statist. Med., 34; pages 1097-1116, doi: 10.1002/sim.6383

`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 heterogenety 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 = '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 specfying 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, 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$TRTTB, TBdat$CONTB)

## 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)
```

nmaINLA *nmaINLA: 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, 2018). 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: install.packages("INLA",repos=c(getOption("repos"), INLA="https://inla.r-inla-download.org/R/testing"), dep=TRUE).

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 <burakgunhan@gmail.com>

Source

Guenhan, B.K., Friede, T., Held, L. (2018) A design-by-treatment interaction model for network meta-analysis and meta-regression with integrated nested Laplace approximations. Res Syn Meth. 2018;1-14. https://doi.org/10.1002/jrsm.1285

Sauter, R. and Held, L. (2015). Network meta-analysis with integrated nested Laplace approximations. Biometrical Journal 57 1038–1050.

Jackson, D., Barrett, J. K., Rice, S., White, I. R. and Higgins, J. P. (2014). A design-by-treatment interaction model for network meta-analysis with random inconsistency effects. Statistics in Medicine 33 3639–3654.

Rue, H., Martino, S. and Chopin, N. (2009). Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations. Journal of the Royal Statistical Society: Series B (Statistical Methodology) 71 319–392.

Dias, S., Welton, N. J., Sutton, A. J. and Ades, A. (2011). NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework for Pairwise and Network Meta-analysis of Randomised Controlled Trials. Last updated September 2016.

Dias, S., Sutton, A. J., Welton, N. J. and Ades, A. E. (2013). Evidence synthesis for Decision Making 3: Heterogeneity–Subgroups, Meta-Regression, Bias, and Bias-Adjustment. Medical Decision Making 33 618–640.

`nma_inla` *Fitting a network meta-analysis model using INLA*

Description

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

Usage

```
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 heterogenety 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 specfying 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 coloumns: `[mean, std.err]`
  Result: relative mean difference
- `binomial`: for dichotomous data.
  Required coloumns: `[responders, sampleSize]`
  Result: log odds ratio
- `normal`: for event-rate (survival) data.
  Required coloumns: `[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)
```

Parkinsondat *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

Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E. NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011; last updated September 2016; available from http://www.nicedsu.org.uk

plot_nma *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 thee-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 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.

`des` Design, the set of treatments included in each study

Source

Dias, S., Welton, N. J., Caldwell, D. M. and Ades, A. E. (2010) Checking consistency in mixed treatment comparison meta-analysis, Statistics in Medicine, 29:932–944.

`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

Batson S, Sutton A, Abrams K (2016) Exploratory Network Meta Regression Analysis of Stroke Prevention in Atrial Fibrillation Fails to Identify Any Interactions with Treatment Effect. PLoS ONE 11

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 coloumns

Trial Trial number

TRTTB number of TB events in treatment arm

TRT number of subjects in treatment arm

CONTB number of TB events in control arm

CON number of subjects in control arm

Latitude absolute latitude of the study location

Source

Berkey, C.S., Hoaglin, D.C., Mosteller, F. and Colditz, G.A., 1995. A random-effects regression model for meta-analysis. Statistics in medicine, 14(4), pp.395-411

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

Dias, S., Welton, N. J., Caldwell, D. M. and Ades, A. E. (2010) Checking consistency in mixed treatment comparison meta-analysis, Statistics in Medicine, 29:932–944.

`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

Woods BS, Hawkins N, Scott DA (2010). Network meta-analysis on the log-hazard scale, combining count and hazard ratio statistics accounting for multi-arm trials: A tutorial. BMC Medical Research Methodology 10, 54.

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