# Package 'gemtc'

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**Title** GeMTC network meta-analysis

**Author** Gert van Valkenhoef, Joel Kuiper

**Maintainer** Gert van Valkenhoef <g.h.m.van.valkenhoef@rug.nl>

**Description** An R package for performing network meta-analyses (mixed treatment comparisons).

**Depends** coda (>= 0.13)

**Imports** igraph (>= 0.6.4), meta (>= 2.1), XML (>= 3.6)

**Suggests** rjags (>= 3-0), BRugs (>= 0.8), R2WinBUGS (>= 2.1), testthat (>= 0.8), Matrix

**URL** http://github.com/gertvv/gemtc

**License** GPL-3

**NeedsCompilation** yes

**Repository** CRAN

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## R topics documented:

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`gemtc-package` *GeMTC: Network meta-analysis in R*

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## Description

An R package for performing network meta-analyses (mixed treatment comparisons).

## Details

Network meta-analysis, or mixed treatment comparison (MTC) is a technique to meta-analyze networks of trials comparing two or more treatments at the same time [Dias et al. 2013]. Using a Bayesian hierarchical model, all direct and indirect comparisons are taken into account to arrive at a single consistent estimate of the effect of all included treatments based on all included studies.

This package allows the automated generation of network meta-analysis models [van Valkenhoef et al. 2012] that can be run using JAGS (using the rjags package), OpenBUGS (using the BRugs package) or WinBUGS (using the R2WinBUGS package). Note that there is a known issue with BUGS that prevents some models from running, though the remaining models appear to run correctly. It is highly recommended to use JAGS rather than BUGS.

This package is interoperable with GeMTC files that were created by the GeMTC GUI or exported from ADDIS. The source for GeMTC is available under the GPL-3 on Github.

See `http://drugis.org/gemtc` for more information.

## Author(s)

Gert van Valkenhoef

## References

S. Dias, N.J. Welton, D.M. Caldwell, and A.E. Ades (2010), *Checking consistency in mixed treatment comparison meta-analysis*, Statistics in Medicine 29(7-8, Sp. Iss. SI):932-944. [doi:10.1002/sim.3767]

S. Dias, A.J. Sutton, A.E. Ades, and N.J. Welton (2013a), *A Generalized Linear Modeling Framework for Pairwise and Network Meta-analysis of Randomized Controlled Trials*, Medical Decision Making 33(5):607-617. [doi:10.1177/0272989X12458724]

S. Dias, N.J. Welton, A.J. Sutton, D.M. Caldwell, G. Lu, and A.E. Ades (2013b), *Inconsistency in Networks of Evidence Based on Randomized Controlled Trials*, Medical Decision Making 33(5):641-656. [doi:10.1177/0272989X12455847]

R.M. Turner, J. Davey, M.J. Clarke, S.G. Thompson, J.P.T. Higgins (2012), *Predicting the extent of heterogeneity in meta-analysis, using empirical data from the Cochrane Database of Systematic Reviews*, International Journal of Epidemiology 41(3):818-827. [doi:10.1093/ije/dys041]

G. van Valkenhoef, G. Lu, B. de Brock, H. Hillege, A.E. Ades, and N.J. Welton (2012), *Automating network meta-analysis*, Research Synthesis Methods 3(4):285-299. [doi:10.1002/jrsm.1054]

G. van Valkenhoef, S. Dias, A.E. Ades, and N.J. Welton (2014a), *Automated generation of node-splitting models for the assessment of inconsistency in network meta-analysis*, draft manuscript.

G. van Valkenhoef et al. (2014b), *Modeling inconsistency as heterogeneity in network meta-analysis*, draft manuscript.

## See Also

mtc.network, mtc.model, mtc.run

## Examples

```
# Load the example network and generate a consistency model:
file <- system.file("extdata/luades-smoking.gemtc", package="gemtc")
network <- read.mtc.network(file)
model <- mtc.model(network, type="consistency")

# Load pre-generated samples instead of runing the model:
## Not run: results <- mtc.run(model, thin=10)
results <- dget(system.file("extdata/luades-smoking.samples.gz", package="gemtc"))

# Print a basic statistical summary of the results:
summary(results)
## Iterations = 5010:25000
## Thinning interval = 10
## Number of chains = 4
## Sample size per chain = 2000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##         Mean     SD Naive SE Time-series SE
## d.A.B 0.4965 0.4081 0.004563       0.004989
## d.A.C 0.8359 0.2433 0.002720       0.003147
## d.A.D 1.1088 0.4355 0.004869       0.005280
## sd.d  0.8465 0.1913 0.002139       0.002965
##
## 2. Quantiles for each variable:
##
##          2.5%    25%    50%    75% 97.5%
## d.A.B -0.2985 0.2312 0.4910 0.7530 1.341
## d.A.C  0.3878 0.6720 0.8273 0.9867 1.353
## d.A.D  0.2692 0.8197 1.0983 1.3824 2.006
## sd.d   0.5509 0.7119 0.8180 0.9542 1.283
```

---

# blobbogram *Plot a blobbogram (AKA forest plot)*

---

## Description

blobbogram is a flexible function for creating blobbograms (forest plots), making no specific assumptions about the data being plotted. It supports column and row grouping as well as pagination.

## Usage

```
blobbogram(data, id.label="Study", ci.label="Mean (95% CI)",
    left.label=NULL, right.label=NULL,
    log.scale=FALSE, xlim=NULL, styles=NULL,
    grouped=TRUE, group.labels=NULL,
    columns=NULL, column.labels=NULL,
    column.groups=NULL, column.group.labels=NULL,
    digits=2,
    ask=dev.interactive(orNone=TRUE))
```

## Arguments

| | |
|---|---|
| `data` | A data frame containing one row for each confidence interval to be visualized. The data format is described below. |
| `id.label` | Label to show above the row-id column. |
| `ci.label` | Label to show above the confidence intervals. |
| `left.label` | Label to show on the left-hand side of the no-difference line. |
| `right.label` | Label to show on the right-hand side of the no-difference line. |
| `log.scale` | If TRUE, the confidence intervals are given on a log scale, and axis labels will be `exp()` transformed. |
| `xlim` | The scale limits of the plot, if the confidence interval exceeds these limits an arrow will be shown at the limit. If unspecified, limits will be chosen that encompass all confidence intervals. |
| `styles` | A data frame describing the different row styles. By default, the styles "normal", "pooled" and "group" are defined. |
| `grouped` | If TRUE, and group.labels are specified, rows will be grouped according to the "group" column given in the data argument. |
| `group.labels` | Vector of group labels. |
| `columns` | Additional user-defined columns to be shown (names of columns given in the data argument). |
| `column.labels` | A vector of labels for the user-defined columns. |
| `column.groups` | Column groups, a numeric vector specifying the column group for each column. |
| `column.group.labels` | A vector of labels for the column groups. |
| `digits` | The number of (significant) digits to print. |
| `ask` | If TRUE, a prompt will be displayed before generating the next page of a multi-page plot. |

## Details

The `blobbogram` function creates a blobbogram (forest plot) from the given data (point estimates and confidence intervals) and meta-data (labels, column specifications, column groups, row groups, styles) using the `grid` package. If the plot would not fit the device's graphics region, the content is broken up into multiple plots generated in sequence (pagination).

The `data` argument is given as a data frame containing the following columns:

- id: identifier (label) for this row.
- group (optional): row group this row belongs to (indexes into the `group.labels` argument).
- pe: point estimate.
- ci.l: lower confidence interval limit.
- ci.u: upper confidence interval limit.
- style: the style to apply to this row (defined in the `styles` argument).

Additional user-defined columns can be specified using the `columns` and `column.labels` arguments.

The `styles` argument is given as a data frame containing the following columns:

- style: name of the style.
- weight: font weight.
- pe.style: symbol to draw for the point estimate ("circle" or "square", currently).

## Value

None.

## Note

This method should not be considered stable. We intend to generalize it further and possibly provide it in a separate package. The interface may change at any time.

## Author(s)

Gert van Valkenhoef, Joël Kuiper

## See Also

`meta::forest`, `grid::Grid`

## Examples

```
data <- read.table(textConnection('
id               group pe       ci.l ci.u style      value.A    value.B
"Study 1"  1         0.35 0.08 0.92 "normal" "2/46"     "7/46"
"Study 2"  1         0.43 0.15 1.14 "normal" "4/50"     "8/49"
"Study 3"  2         0.31 0.07 0.74 "normal" "2/97"     "10/100"
"Study 4"  2         0.86 0.34 2.90 "normal" "9/104"    "6/105"
"Study 5"  2         0.33 0.10 0.72 "normal" "4/74"     "14/74"
"Study 6"  2         0.47 0.23 0.91 "normal" "11/120" "22/129"
"Pooled"     NA      0.42 0.15 1.04 "pooled" NA             NA
'), header=TRUE)
data$pe <- log(data$pe)
data$ci.l <- log(data$ci.l)
data$ci.u <- log(data$ci.u)

blobbogram(data, group.labels=c('GROUP 1', 'GROUP 2'),
```

```
columns=c('value.A', 'value.B'), column.labels=c('r/n', 'r/n'),
column.groups=c(1, 2), grouped=TRUE,
column.group.labels=c('Intervention', 'Control'),
id.label="Trial", ci.label="Odds Ratio (95% CrI)", log.scale=TRUE)
```

---

`ll.call` *Call a likelihood/link-specific function*

---

## Description

GeMTC implements various likelihood/link combinations. Functionality specific to the likelihood/link is handled by methods with names ending in `.<likelihood>.<link>`. This convenience function calls such methods.

## Usage

```
ll.call(fnName, model, ...)
```

## Arguments

| | |
|---|---|
| `fnName` | The name of the function to call. See details for available functions. |
| `model` | An object of S3 class `mtc.model` describing a network meta-analysis model, or a list containing elements named 'likelihood' and 'link'. |
| `...` | Additional arguments to be passed to the function. |

## Details

The following methods currently need to be implemented to implement a likelihood/link:

- `mtc.arm.mle`: calculates a (corrected) maximum likelihood estimate for an arm-level effect. Used to generate starting values.
- `mtc.rel.mle`: calculates a (corrected) maximum likelihood estimate for a relative effect. Used to generate starting values.
- `mtc.code.likelihood`: generates JAGS/BUGS code implementing the likelihood.
- `scale.log`: returns TRUE if plots should use the log scale.
- `scale.name`: returns the user-facing name of the outcome metric.
- `scale.limit.inits`: returns an upper and lower bound for the initial values, because some initial values might trigger boundary conditions such as probability 0 or 1 for the binomial.
- `required.columns.ab`: returns the required columns for arm-based data.

## Value

The return value of the called function.

## Author(s)

Gert van Valkenhoef

## See Also

mtc.model

## Examples

```
# The "model" may be a stub.
model <- list(likelihood="poisson", link="log")

ll.call("scale.name", model)
# "Hazard Ratio"

ll.call("mtc.arm.mle", model, c('responders'=12, 'exposure'=80))
#      mean         sd
#-1.8562980  0.1118034
```

---

mtc.anohe *Analysis of heterogeneity (ANOHE)*

---

## Description

(EXPERIMENTAL) Generate an analysis of heterogeneity for the given network. Three types of model are estimated: unrelated study effects, unrelated mean effects, and consistency. Output of the summary function can passed to plot for a visual representation.

## Usage

```
mtc.anohe(network, ...)
```

## Arguments

| | |
|---|---|
| network | An object of S3 class mtc.network. |
| ... | Arguments to be passed to mtc.run or mtc.model. This can be used to set the likelihood/link or the number of iterations, for example. |

## Details

Analysis of heterogeneity is intended to be a unified set of statistics and a visual display that allows the simultaneous assessment of both heterogeneity and inconsistency in network meta-analysis [van Valkenhoef et al. 2014b (draft)].

mtc.anohe returns the MCMC results for all three types of model. To get appropriate summary statistics, call summary() on the results object. The summary can be plotted.

To control parameters of the MCMC estimation, see mtc.run. To specify the likelihood/link or to control other model parameters, see mtc.model. The ... arguments are first matched against mtc.run, and those that do not match are passed to mtc.model.

## Value

For `mtc.anohe`: an object of class `mtc.anohe`. This is a list with the following elements:

| | |
|---|---|
| `result.use` | The result for the USE model (see `mtc.run`). |
| `result.ume` | The result for the UME model (see `mtc.run`). |
| `result.cons` | The result for the consistency model (see `mtc.run`). |

For `summary`: an object of class `mtc.anohe.summary`. This is a list with the following elements:

| | |
|---|---|
| `cons.model` | Generated consistency model. |
| `studyEffects` | Study-level effect summaries (multi-arm trials downweighted). |
| `pairEffects` | Pair-wise pooled effect summaries (from the UME model). |
| `consEffects` | Consistency effect summaries. |
| `indEffects` | Indirect effect summaries (back-calculated). |
| `isquared.comp` | Per-comparison I-squared statistics. |
| `isquared.glob` | Global I-squared statistics. |

## Note

This method should not be considered stable. It is an experimental feature and heavily work in progress. The interface may change at any time.

## Author(s)

Gert van Valkenhoef, Joël Kuiper

## See Also

`mtc.model` `mtc.run`

---

# mtc.data.studyrow *Convert one-study-per-row datasets*

---

## Description

Converts datasets in the one-study-per-row format to one-arm-per-row format used by GeMTC

## Usage

```
mtc.data.studyrow(data,
  armVars=c('treatment'='t', 'responders'='r', 'sampleSize'='n'),
  nArmsVar='na',
  studyVars=c(),
  studyNames=1:nrow(data),
  treatmentNames=NA,
  patterns=c('%s..', '%s..%d.'))
```

## Arguments

| | |
|---|---|
| `data` | 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. The column name in the source dataset is derived from the value of each component. |
| `nArmsVar` | Variable holding the number of arms for each study. |
| `studyVars` | Vector of per-study variables. The name of each component will be the column name in the resulting dataset. The column name in the source dataset is derived from the value of each component. |
| `studyNames` | Vector of study names. |
| `treatmentNames` | Vector of treatment names. |
| `patterns` | Patterns to generate column names in the source dataset. The first is for per-study variables, the second for per-arm variables. |

## Details

Maps the one-study-per-row format that is widely used and convenient for BUGS models to the one-arm-per-row format used by GeMTC. As the primary purpose is to input datasets from BUGS models, the defaults work for the standard BUGS data table format. In most cases, it should be possible to just copy/paste the BUGS data table (without the final 'END') and `read.table` it into R, then apply `mtc.data.studyrow`. In many cases, the resulting table can be processed directly by `mtc.network`.

## Value

A data table with the requested columns.

## Author(s)

Gert van Valkenhoef

## See Also

`mtc.network`

## Examples

```
## Example taken from the NICE DSU TSD series in Evidence Synthesis, #2
## Dopamine agonists for the treatment of Parkinson's

# Read the bugs-formatted data
data.src <- read.table(textConnection('
t[,1] t[,2] t[,3] y[,1] y[,2] y[,3] se[,1] se[,2] se[,3] na[]
1 3 NA -1.22 -1.53 NA 0.504 0.439 NA 2
1 2 NA -0.7 -2.4 NA 0.282 0.258 NA 2
1 2 4 -0.3 -2.6 -1.2 0.505 0.510 0.478 3
3 4 NA -0.24 -0.59 NA 0.265 0.354 NA 2
3 4 NA -0.73 -0.18 NA 0.335 0.442 NA 2
```

```
4 5 NA -2.2 -2.5 NA 0.197 0.190 NA 2
4 5 NA -1.8 -2.1 NA 0.200 0.250 NA 2'), header=TRUE)

# Convert the data, setting treatment names
data <- mtc.data.studyrow(data.src,
  armVars=c('treatment'='t', 'mean'='y', 'std.err'='se'),
  treatmentNames=c('Placebo', 'DA1', 'DA2', 'DA3', 'DA4'))

# Check that the data are correct
print(data)

# Create a network
network <- mtc.network(data)
```

---

`mtc.hy.prior` *Set priors for the heterogeneity parameter*

---

## Description

These functions generate priors for the heterogeneity parameter in `mtc.model`. Priors can be set explicitly or, for outcomes on the log odds-ratio scale, based on empirical research.

## Usage

```
mtc.hy.prior(type, distr, ...)

mtc.hy.empirical.lor(outcome.type, comparison.type)
```

## Arguments

| | |
|---|---|
| `type` | Type of heterogeneity prior: 'std.dev', 'var', or 'prec' for standard deviation, variance, or precision respectively. |
| `distr` | Prior distribution name (BUGS/JAGS syntax). Typical ones would be 'dunif' (uniform), 'dgamma' (Gamma), or 'dlnorm' (log-normal). |
| `...` | Arguments to the `distr`. Can be numerical values or "om.scale" for the estimated outcome measure scale (see `mtc.model`) |
| `outcome.type` | The type of outcome to get an empirical prior for. Can be one of 'mortality' (all-cause mortality), 'semi-objective' (e.g. cause-specific mortality, major morbidity event, drop-outs), or 'subjective' (e.g. pain, mental health, dichotomous biomarkers). |
| `comparison.type` | The type of comparison to get an empirical prior for. Can be one of 'pharma-control' (pharmacological interventions versus control), 'pharma-pharma' (pharmacological versus pharmacological interventions) and 'non-pharma' (any other comparisons). |

### Details

The generated prior is a list, the structure of which may change without notice. It can be converted to BUGS compatible code using `as.character`.

Empirical priors for the log odds-ratio (LOR) are taken from [Turner et al. 2012].

### Value

A value to be passed to `mtc.model`.

### Author(s)

Gert van Valkenhoef

### See Also

`mtc.model`

### Examples

```
file <- system.file("extdata/luades-smoking.gemtc", package="gemtc")
network <- read.mtc.network(file)

# NOTE: the mtc.run commands below are for illustrative purposes, such a small
# number of iterations should obviously not be used in practice.

# set a uniform prior standard deviation
model1 <- mtc.model(network, hy.prior=mtc.hy.prior("std.dev", "dunif", 0, 2))
result <- mtc.run(model1, n.adapt=10, n.iter=10)

# set an empirical (log-normal) prior on the variance
model2 <- mtc.model(network, hy.prior=mtc.hy.empirical.lor("subjective", "non-pharma"))
result <- mtc.run(model2, n.adapt=10, n.iter=10)

# set a gamma prior on the precision
model3 <- mtc.model(network, hy.prior=mtc.hy.prior("prec", "dgamma", 0.01, 0.01))
result <- mtc.run(model3, n.adapt=10, n.iter=10)
```

---

## `mtc.model` *Generate network meta-analysis models*

---

### Description

The `mtc.model` function generates network meta-analysis models from an `mtc.network` object.

### Usage

```
mtc.model(network, type = "consistency", factor = 2.5, n.chain = 4,
  likelihood=NULL, link=NULL, linearModel="random",
  om.scale=NULL, hy.prior=mtc.hy.prior("std.dev", "dunif", 0, "om.scale"),
  ...)
```

## Arguments

| | |
|---|---|
| network | An object of S3 class mtc.network |
| type | A string literal indicating the type of model (either "consistency", "nodesplit", "ume", or "use"). |
| factor | Variance scaling factor for the starting values |
| n.chain | Number of chains in the model |
| likelihood | The likelihood to be used. If unspecified, a suitable likelihood will be inferred for the given data. |
| link | The link function to be used. If unspecified, a suitable link function will be inferred for the given data. |
| linearModel | The type of linear model to be generated. Can be "random" for a random effects model, or "fixed" for a fixed effect model. |
| om.scale | Outcome measure scale. Represents a "very large" difference on the analysis' outcome scale. This is used to set vague priors. For the log odds-ratio, values between 2 and 5 are considered reasonable. For continuous outcomes, this depends heavily on the specific outcome. If left unspecified, it is determined from the data. |
| hy.prior | Heterogeneity prior. See mtc.hy.prior. |
| ... | Additional arguments to be passed to the type-specific model generation function. |

## Details

The mtc.model function generates an object of S3 class mtc.model, which can be visualized by the generic plot function or summarized by the generic summary function.

These likelihood/links are supported:

- normal/identity: for continuous (mean difference) data.
  Required columns: [mean, std.err] or [mean, std.dev, sampleSize].
  Result: relative mean difference.
- binom/logit: for dichotomous data.
  Required columns [responders, sampleSize].
  Result: (log) odds ratio.
- binom/cloglog: for rate (survival) data - equal follow-up in each arm.
  Required columns [responders, sampleSize].
  Result: (log) hazard ratio.
- poisson/log: for rate (survival) data.
  Required columns [responders, exposure].
  Result: (log) hazard ratio.

The following model types are supported:

- consistency: ordinary consistency model. No additional parameters. [Dias et al. 2013a, van Valkenhoef et al. 2012]

- `nodesplit`: node-splitting model. Removes both arms used to estimate the direct evidence from the network of indirect evidence, rather than just one of those arms. This means that three-arm trials do not contribute any evidence in the network of indirect evidence. When relative effect data are present, these are transformed appropriately (using an assumption of normality) to enable this direct/indirect evidence split. Additional parameters: `t1` and `t2`, which indicate the comparison to be split. [Dias et al. 2010, van Valkenhoef et al. 2014a (draft)]
- `use`: unrelated study effects. Models the effects within each study as if the studies are independent. No additional parameters. [van Valkenhoef et al. 2014b (draft)]
- `ume`: unrelated mean effects. Models the effects within each comparison as if they are independent. Does not properly handle multi-arm trials, and warns when they are present in the network. No additional parameters. [Dias et al. 2013b, van Valkenhoef et al. 2014b (draft)]

## Value

An object of class `mtc.model`. The following elements are descriptive:

| | |
|---|---|
| `type` | The type of model |
| `network` | Network the model was generated from |
| `tree` | Spanning tree formed by the basic parameters |
| `var.scale` | The scaling factor used to over-disperse starting values |
| `likelihood` | The likelihood used |
| `link` | The link function used |
| `om.scale` | The scale for the variance parameters |

These elements determine the model run by JAGS/BUGS:

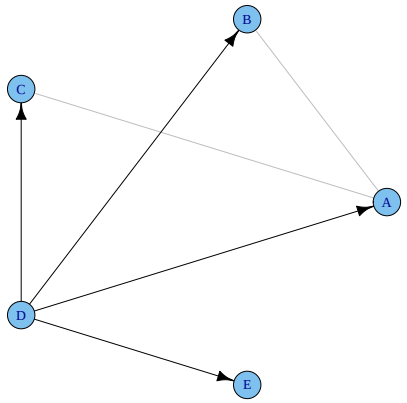
| | |
|---|---|
| `n.chain` | The number of chains |
| `code` | Model code in JAGS/BUGS syntax. Use `cat()` for proper formatting. |
| `data` | Data in JAGS/BUGS compatible format |
| `inits` | Initial values in JAGS/BUGS compatible format |
| `monitors` | The nodes of the JAGS/BUGS model to monitor |

These latter fields can be modified to alter the statistical model, but such changes may break the model or assumptions made elsewhere in the package.

## Visualization

Calling the generic plot method on an S3 `mtc.model` object will show a graph with the treatments as vertices and the comparisons as edges. The lines with solid arrows represent basic parameters, and the other lines represent comparisons that are not associated with any parameter but do have direct evidence from trials.

The example code will generate the following graph:




The default layout algorithm is `igraph::layout.circle`, other layout algorithms can be used by passing them as an optional argument called `layout` to `plot`. The `igraph::layout.fruchterman.reingold` algorithm also seems to produce nice results and may be better for large graphs. The default up-to version 0.1-2 was `igraph::layout.kamada.kawai` but could produce overlapping edges.

## Author(s)

Gert van Valkenhoef, Joël Kuiper

## See Also

`mtc.network`, `mtc.run`

## Examples

```
file <- system.file("extdata/parkinson.gemtc", package="gemtc")
network <- read.mtc.network(file)
model <- mtc.model(network)
plot(model)
summary(model)
```

---

`mtc.network` *Create an mtc.network*

---

## Description

Creates an object of class `mtc.network`

## Usage

```
mtc.network(data.ab, treatments, description, data.re, data)
read.mtc.network(file)
write.mtc.network(network, file)
```

## Arguments

| | |
|---|---|
| data.ab | Arm-level data. A data frame defining the arms of each study, containing the columns 'study' and 'treatment', where 'treatment' must refer to an existing treatment ID if treatments were specified. Further columns define the data per arm, and depend on the likelihood/link to be used. See mtc.model for supported likelihood/links and their data requirements. |
| data.re | Relative effect data. A data frame defining the arms of each study, containing the columns 'study' and 'treatment', where 'treatment' must refer to an existing treatment ID if treatments were specified. The column 'diff' specifies the mean difference between the current arm and the baseline arm; set 'diff=NA' for the baseline arm. The column 'std.err' specifies the standard error of the mean difference (for non-baseline arms). For trials with more than two arms, specify the standard error of the mean of the baseline arm in 'std.err', as this determines the covariance of the differences. |
| treatments | Optional. A data frame with columns 'id' and 'description' defining the treatments or a vector giving the treatment IDs. |
| description | Optional. Short description of the network. |
| data | Deprecated. Arm-level data; automatically assigned to data.ab if it is not specified. Present for compatibility with older versions. |
| network | An object of the S3 class mtc.network. |
| file | Path to the file to read (read.mtc.network) or write (write.mtc.network). For write.mtc.network, if file="", the output is printed to standard output. If it is file="\|cmd", the output is piped to the command given by cmd. See base::cat for further details. |

## Details

One-arm trials are automatically removed, which results in a warning.

read.mtc.network and write.mtc.network deal with the older GeMTC XML format. This format supports dichotomous data as responders/sampleSize and continuous data as mean/std.dev/sampleSize only. Relative effect data, or other forms of arm-based data, are not supported. In general, it may be more convenient to use dput and dget to read and write networks.

Also see mtc.data.studyrow for a convenient way to import data from the one-study-per-row format, which is very popular for BUGS code.

## Value

For mtc.network and read.mtc.network, an object of the class mtc.network which is a list containing:

| | |
|---|---|
| description | A short description of the network |

| | |
|---|---|
| `treatments` | A data frame describing the treatments |
| `data.ab` | A data frame containing the network data (arm-level) |
| `data.re` | A data frame containing the network data (relative effects) |

These are cleaned up and standardized versions of the arguments provided, or generated defaults for 'treatments' if the argument was omitted.

## Author(s)

Gert van Valkenhoef, Joël Kuiper

## See Also

`mtc.data.studyrow` `mtc.model`

## Examples

```
# Create a new network by specifying all information.
treatments <- read.table(textConnection('
  id  description
  A   "Treatment A"
  B   "Treatment B"
  C   "Treatment C"'), header=TRUE)
data <- read.table(textConnection('
  study  treatment  responders  sampleSize
  01     A          2           100
  01     B          5           100
  02     B          6           110
  02     C          1           110
  03     A          3           60
  03     C          4           80
  03     B          7           80'), header=TRUE)
network <- mtc.network(data, description="Example", treatments=treatments)
plot(network)

# Create a new network by specifying only the data.
data <- read.table(textConnection('
  study  treatment  mean   std.dev  sampleSize
  01     A          -1.12  0.6      15
  01     B          -1.55  0.5      16
  02     A          -0.8   0.7      33
  02     B          -1.1   0.5      31'), header=TRUE)
network <- mtc.network(data)

# Print the network
print(network)
## MTC dataset: Network
##   study treatment  mean std.dev sampleSize
## 1     1         A -1.12     0.6         15
## 2     1         B -1.55     0.5         16
## 3     2         A -0.80     0.7         33
## 4     2         B -1.10     0.5         31
```

```
# Read an example GeMTC XML file
file <- system.file("extdata/luades-smoking.gemtc", package="gemtc")
network <- read.mtc.network(file)

# Summarize the network (generate some interesting network properties)
summary(network)
## $Description
## [1] "MTC dataset: Smoking cessation rates"
##
## $`Studies per treatment`
##  A  B  C  D
## 19  6 19  6
##
## $`Number of n-arm studies`
## 2-arm 3-arm
##    22     2

# Write the network to a temporary file in the GeMTC XML format
tmp <- tempfile()
write.mtc.network(network, file=tmp)
```

---

`mtc.nodesplit` *Node-splitting analysis of inconsistency*

---

## Description

Generate and run an ensemble of node-splitting models, results of which can be jointly summarized and plotted.

## Usage

```
mtc.nodesplit(network, comparisons=mtc.nodesplit.comparisons(network), ...)
mtc.nodesplit.comparisons(network)
```

## Arguments

| | |
|---|---|
| `network` | An object of S3 class `mtc.network`. |
| `comparisons` | Data frame specifying the comparisons to be split. The frame has two columns: 't1' and 't2'. |
| `...` | Arguments to be passed to `mtc.run` or `mtc.model`. This can be used to set the likelihood/link or the number of iterations, for example. |

## Details

`mtc.nodesplit` returns the MCMC results for all relevant node-splitting models [van Valkenhoef et al. 2014a (draft)]. To get appropriate summary statistics, call `summary()` on the results object. The summary can be plotted. See `mtc.model` for details on how the node-splitting models are generated.

To control parameters of the MCMC estimation, see mtc.run. To specify the likelihood/link or to control other model parameters, see mtc.model. The ... arguments are first matched against mtc.run, and those that do not match are passed to mtc.model.

mtc.nodesplit.comparisons returns a data frame enumerating all comparisons that can reasonably be split (i.e. have independent indirect evidence).

## Value

For mtc.nodesplit: an object of class mtc.nodesplit. This is a list with the following elements:

| | |
|---|---|
| d.X.Y | For each comparison (t1=X, t2=Y), the MCMC results |
| consistency | The consistency model results |

For summary: an object of class mtc.nodesplit.summary. This is a list with the following elements:

| | |
|---|---|
| dir.effect | Summary of direct effects for each split comparison |
| ind.effect | Summary of indirect effects for each split comparison |
| cons.effect | Summary of consistency model effects for each split comparison |
| p.value | Inconsistency p-values for each split comparison |
| cons.model | The generated consistency model |

## Author(s)

Gert van Valkenhoef, Joël Kuiper

## See Also

mtc.model mtc.run

---

# mtc.run *Running an* mtc.model *using an MCMC sampler*

---

## Description

The function mtc.run is used to generate samples from a object of type mtc.model using a MCMC sampler. The resulting mtc.results object can be coerced to an mcmc.list for further analysis of the dataset using the coda package.

## Usage

```
mtc.run(model, sampler = NA, n.adapt = 5000, n.iter = 20000, thin = 1)
```

## Arguments

| | |
|---|---|
| model | An object of S3 class mtc.model describing a network meta-analysis model. |
| sampler | A string literal indicating which sampler to use. Allowed values are 'JAGS' or 'BUGS'. Alternatively, the specific package to be used can be specified: 'rjags', 'BRugs' or 'R2WinBUGS'. When unspecified it will try 'rjags', 'BRugs', and 'R2WinBUGS', in that order. |
| n.adapt | Amount of adaptation (or tuning) iterations. |
| n.iter | Amount of simulation iterations. |
| thin | Thinning factor. |

## Value

An object of class mtc.result. This is a list with the following elements:

| | |
|---|---|
| samples | The samples resulting from running the MCMC model, in mcmc.list format. |
| model | The mtc.model used to produce the samples. |
| sampler | The sampler (R package) used to produce the samples. |

The object can be coerced to an mcmc.list from the coda package by the generic S3 method as.mcmc.list.

## Analysis of the results

Convergence of the model can be assessed using methods from the coda package. For example the Brooks-Gelman-Rubin method (coda::gelman.diag, coda::gelman.plot). The summary also provides useful information, such as the MCMC error and the time series and densities given by plot should also be inspected.

The forest function can provide forest plots for mtc.result objects. This is especially useful in combination with the relative.effect function that can be used to calculate relative effects compared to any baseline for consistency models. The rank.probability function calculates rank probabilities for consistency models.

## Author(s)

Gert van Valkenhoef, Joël Kuiper

## See Also

mtc.model, relative.effect, rank.probability, coda::gelman.diag, coda::gelman.plot

## Examples

```
file <- system.file("extdata/luades-smoking.gemtc", package="gemtc")
network <- read.mtc.network(file)
model <- mtc.model(network)

## Not run: results <- mtc.run(model, thin=10)
results <- dget(system.file("extdata/luades-smoking.samples.gz", package="gemtc"))
```

```
# Convergence diagnostics
gelman.plot(results)

# Posterior summaries
summary(results)
## Iterations = 5010:25000
## Thinning interval = 10
## Number of chains = 4
## Sample size per chain = 2000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##         Mean     SD Naive SE Time-series SE
## d.A.B 0.4965 0.4081 0.004563       0.004989
## d.A.C 0.8359 0.2433 0.002720       0.003147
## d.A.D 1.1088 0.4355 0.004869       0.005280
## sd.d  0.8465 0.1913 0.002139       0.002965
##
## 2. Quantiles for each variable:
##
##          2.5%    25%    50%    75% 97.5%
## d.A.B -0.2985 0.2312 0.4910 0.7530 1.341
## d.A.C  0.3878 0.6720 0.8273 0.9867 1.353
## d.A.D  0.2692 0.8197 1.0983 1.3824 2.006
## sd.d   0.5509 0.7119 0.8180 0.9542 1.283

plot(results) # Shows time-series and density plots of the samples
forest(results) # Shows a forest plot
```

---

`rank.probability` *Calculating rank-probabilities*

---

## Description

Rank probabilities indicate the probability for each treatment to be best, second best, etc.

## Usage

```
rank.probability(result, preferredDirection=1)
```

## Arguments

| | |
|---|---|
| `result` | Object of S3 class `mtc.result` to be used in creation of the rank probability table |
| `preferredDirection` | Preferential direction of the outcome. Set 1 if higher values are preferred, -1 if lower values are preferred. |

### Details

For each MCMC iteration, the treatments are ranked by their effect relative to an arbitrary baseline. A frequency table is constructed from these rankings and normalized by the number of iterations to give the rank probabilities.

### Value

A matrix with the treatments as rows and the ranks as columns. The matrix is given class `mtc.rank.probability`, for which `print` and `plot` are overriden.

### Author(s)

Gert van Valkenhoef, Joël Kuiper

### See Also

`relative.effect`

### Examples

```
file <- system.file("extdata/luades-smoking.gemtc", package="gemtc")
network <- read.mtc.network(file)
model <- mtc.model(network)
# To save computation time we load the samples instead of running the model
## Not run: results <- mtc.run(model)
results <- dget(system.file("extdata/luades-smoking.samples.gz", package="gemtc"))

ranks <- rank.probability(results)
print(ranks)
## Rank probability; preferred direction = 1
##       [,1]     [,2]     [,3]     [,4]
## A 0.000000 0.003000 0.105125 0.891875
## B 0.057875 0.175875 0.661500 0.104750
## C 0.228250 0.600500 0.170875 0.000375
## D 0.713875 0.220625 0.062500 0.003000

plot(ranks) # plot a cumulative rank plot
plot(ranks, beside=TRUE) # plot a 'rankogram'
```

---

## `relative.effect` *Calculating relative effects*

---

### Description

Calculates the relative effects of pairs of treatments.

### Usage

```
relative.effect(result, t1, t2 = c(), preserve.extra = TRUE)
```

## Arguments

| | |
|---|---|
| result | An object of S3 class mtc.result to derive the relative effects from. |
| t1 | A list of baselines to calculate a relative effects against. Will be extended to match the length of t2. |
| t2 | A list of treatments to calculate the relative effects for. Will be extended to match the length of t1. If left empty and t1 is a single treatment, relative effects of all treatments except t1 will be calculated. |
| preserve.extra | Indicates whether to preserve extra parameters such as the sd.w and sd.d. |

## Value

Returns an mtc.results object containing the calculated relative effects.

## Author(s)

Gert van Valkenhoef, Joël Kuiper

## See Also

rank.probability

## Examples

```
file <- system.file("extdata/luades-smoking.gemtc", package="gemtc")
network <- read.mtc.network(file)
model <- mtc.model(network)
# To save computation time we load the samples instead of running the model
## Not run: results <- mtc.run(model)
results <- dget(system.file("extdata/luades-smoking.samples.gz", package="gemtc"))

# Creates a forest plot of the relative effects
forest(relative.effect(results, "A"))

summary(relative.effect(results, "B", c("A", "C", "D")))
## Iterations = 5010:25000
## Thinning interval = 10
## Number of chains = 4
## Sample size per chain = 2000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##          Mean     SD Naive SE Time-series SE
## d.B.A -0.4965 0.4081 0.004563       0.004989
## d.B.C  0.3394 0.4144 0.004634       0.004859
## d.B.D  0.6123 0.4789 0.005354       0.005297
## sd.d   0.8465 0.1913 0.002139       0.002965
##
## 2. Quantiles for each variable:
##
```

```
##          2.5%     25%     50%     75%  97.5%
## d.B.A -1.3407 -0.7530 -0.4910 -0.2312 0.2985
## d.B.C -0.4809  0.0744  0.3411  0.5977 1.1702
## d.B.D -0.3083  0.3005  0.6044  0.9152 1.5790
## sd.d   0.5509  0.7119  0.8180  0.9542 1.2827
```

# Index