Package ‘RcmdrPlugin.RMTCJags’

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Type Package
Title R MTC Jags ‘Rcmdr’ Plugin
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Imports Rcmdr (>= 2.0.0), runjags, rmeta, igraph, coda, rjags
Description Mixed Treatment Comparison is a methodology to compare directly and/or indirectly health strategies (drugs, treatments, devices). This package provides an ‘Rcmdr’ plugin to perform Mixed Treatment Comparison for binary outcome using BUGS code from Bristol University (Lu and Ades).
SystemRequirements jags (>= 3.0.0)
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R topics documented:

  RcmdrPlugin.RMTCJags-package .............................................. 2
database-structure ............................................................. 2

Index 4
RcmdrPlugin.RMTCJags-package

*RMTC Jags Rcmdr Plugin*

**Description**

Mixed Treatment Comparison is a methodology to compare directly and/or indirectly health strategies (drugs, treatments, devices). This package provides an Rcmdr plug-in to perform Mixed Treatment Comparison for binary outcome using BUGS code from Bristol University (Lu and Ades).

**Details**

- **Package:** RcmdrPlugin.RMTCJags
- **Type:** Package
- **Version:** 1.01-1
- **Date:** 2015-06-17
- **License:** GPL (>= 2)

**Author(s)**

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**See Also**

Rcmdr.

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**database-structure**

*How to format database for analysis?*

**Description**

Manual to build database for RcmdrPlugin.RMTCJags

**Details**

Fixed Effect Model (FE Model), Random Effect Model (RE Model) Ignoring multi-arm trials and Random Effect Model (RE Model) for 2- and 3-arms trials:

A database with six (6) variables:
- s -> Study index (Number)
- t -> Treatment index (Number)
database-structure

r -> Number of cases on the treatment
n -> Total population on the treatment
b -> Baseline treatment
m -> Arm index (Only needed on RE Model for 2- and 3-arms trials), where 1 is the baseline treatment and 2,...,n are for the other treatments

Each line on the database is a treatment of a trial (study), for example:

```
  s  t  r  n  b  m
  1  1  40 100 1  1
  1  3  15  90 1  2
  1  4  10  75 1  3
  ... ... ... ... ...
  4  2  50 200 2  1
  4  4  60 150 2  2
```

Random Effect Model (RE Model) for multi-arm trial:
A database with N*3 + 1 columns, where N is the highest number of arms from a trial collection.
t[1,...N,] -> Treatment index
r[1,...N,] -> Number of cases on the treatment
n[1,...N,] -> Total population on the treatment
na -> Number of arms on the study

Each line on the database is a trial. For example, if we collect 10 trials and after check them we have the biggest trial with 5 arms our database structure is:

```
t[1,...] t[2,...] t[3,...] t[4,...] t[5,...] r[1,...] r[2,...] r[3,...] r[4,...] r[5,...] n[1,...] n[2,...] n[3,...] n[4,...] n[5,...] na
1  2  3  4  5  20  30  10  5  14  100  90  80  110  50  5
1  3  4  5  NA  10  50  60 15  NA  150  200 340 165  1  4
2  4  5  NA NA  40  70  80 NA NA  70  190 500  1  1  3
... ... ... ... ... ... ... ... ... ... ... ... ...
3  4  NA NA NA  80  90 NA NA NA  250  580  1  1  1  2
```
Index

* package
  RcmdrPlugin.RMTCJags-package, 2
* read.data
  database-structure, 2

BestStrat
  (RcmdrPlugin.RMTCJags-package), 2

database-structure, 2

DensityPlots
  (RcmdrPlugin.RMTCJags-package), 2

ForestPlot
  (RcmdrPlugin.RMTCJags-package), 2

GelmanRubinPlot
  (RcmdrPlugin.RMTCJags-package), 2

Rcmdr, 2
RcmdrPlugin.RMTCJags
  (RcmdrPlugin.RMTCJags-package), 2
RcmdrPlugin.RMTCJags-package, 2
read.data(database-structure), 2
Relationship
  (RcmdrPlugin.RMTCJags-package), 2

SummaryModel
  (RcmdrPlugin.RMTCJags-package), 2