

# Package ‘RcmdrPlugin.RMTCJags’

May 10, 2016

**Type** Package

**Title** R MTC Jags 'Rcmdr' Plugin

**Version** 1.0-2

**Date** 2016-05-10

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**Depends** R (>= 3.0.0)

**Imports** Rcmdr (>= 2.0.0), runjags, rmeta, igrph, 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)

**Repository** CRAN

**License** GPL (>= 2)

**NeedsCompilation** no

**Date/Publication** 2016-05-10 19:05:02

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RcmdrPlugin.RMTCJags-package

*R MTC Jags Rcmdr Plugin*

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### 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?*

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### 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)

- 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

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