Package: RcmdrPlugin.RMTCJags (via r-universe)

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Type Package

Title R MTC Jags 'Rcmdr' Plugin

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Depends R (>= 3.0.0)

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)

License GPL (>= 2)

NeedsCompilation no

Config/pak/sysreqs jags

Repository https://cran.r-universe.dev

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`RcmdrPlugin.RMTCJags-package` *R MTC 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`.

`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)
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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