Package 'nmadb'

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Type Package

Title Network Meta-Analysis Database API

Version 1.2.0

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Description Set of functions for accessing database of network meta-analyses described in
Petropoulou M, et al. Bibliographic study showed improving statistical methodology of network
meta-analyses published between 1999 and 2015
<doi:10.1016/j.jclinepi.2016.11.002>. The database is hosted in a REDcap database at the
Institute of Social and Preventive Medicine (ISPM) in the University of Bern.

License GPL-3

LazyLoad Yes

Depends R (>= 3.3.1)

Imports devtools , RCurl , readxl , jsonlite

Suggests netmeta (>= 1.0-1) , V8

Encoding UTF-8

RoxygenNote 6.1.1

NeedsCompilation no

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R topics documented:

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getNMADB *NMA catalog*

Description

Petropoulou et al. compiled a database of network meta-analyses to serve as a source for empirical studies Petropoulou (2016). The database is hosted in a REDcap database at the Institute of Social and Preventive Medicine (ISPM) in the University of Bern. Function getNMADB downloads the list of networks included in Petropoulou (2016).

Usage

```
getNMADB()
```

Value

A data.frame with the network meta-analyses included in [1]. Several characterstics related to the publications (e.g. Journal.Name, Title) are included in the data.frame.

References

Petropoulou M, Nikolakopoulou A A, Veroniki A, Rios P, Vafaei A, Zarin W, Giannatsi M, Sullivan S, Tricco A C, Chaimani A, Egger M, Salanti G (2016) <doi:10.1016/j.jclinepi.2016.11.002>.

Examples

```
catalog = getNMADB()
## Not run:
  Networks that labeled Verified have outcome data
  that allow the analysis to be repeated.

## End(Not run)
nmalist = catalog[catalog$Verified=="True",]
nmalist
```

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readByID *Read NMA dataset*

Description

ReadByID downloads the dataset and main characteristics of the specified network meta-analysis. You can list all ids from the catalog by calling getNMADB.

Usage

```
readByID(recid)
```

Arguments

recid   Record id of network

Value

A list with the name (id), data (dataset), type (continuous, binary, rate, survival), effect (type of measure: RR OR RR RD ...), format (long, wide, iv).

- 'long' refers to data where each row represents a study treatment arm
- 'wide' refers to data where each row represents a study treatment comparison
- 'iv' refers to an 'inverse variance' format, where a comparison specific estimate of the treatment effect and its standard error are reported.

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runnetmeta   *Run* netmeta

Description

R package netmeta provides frequenstist methods for network meta-analysis based on Rücker (2012) and Rücker (2014). This function is used to run netmeta on a specified network included in the database of network meta-analyses, which can be downloaded using function getNMADB.

Usage

```
runnetmeta(recid, model = "random", measure = "notset")
```

Arguments

recid   ID of network in database

model   "fixed" or "random"; specifies if fixed or random effects network meta-analysis should be conducted.

measure   - "notset" (default) is the type of effect measure in the original publication
               - "OR" odds ratio for binary data
               - "RR" risk ratio for binary data
               - "RD" risk difference for binary data
               - "MD" mean difference for continuous data
               - "SMD" standardized mean difference for continuous data
               - "HR" hazard ratio for survival data
               - "IRR" incidence rate ratio for rate data

               If the measure entered is not compatible with network's type you get an error

Value

An object of class netmeta; for the descirption of the components included in the object, see the help file of netmeta.

References

Rücker G (2012) <doi:10.1002/jrsm.1058>.

Rücker G, Schwarzer G (2014) <doi:10.1002/sim.6236>.

See Also

netmeta ,getNMADB ,readByID

Examples

```
## Not run:
  Conduct random effects network meta-analysis
  in a random network with continuous outcome

## End(Not run)
cid <- 501427
netc <- readByID(cid)
## Not run: get type and effect
netc$type
netc$effect
## Not run: In order to run netmeta but get "SMD" summary effects instead
runnetmeta(recid=cid, measure="SMD")



## Not run: If we the following example choosing OR we get an error
runnetmeta(recid=cid, measure="OR")
## End(Not run)

## Not run: As before for a network with binary outcome
bid <- 481216
netb <- readByID(bid)
## Not run: get type and effect
netb$type
netb$effect
runnetmeta(recid=bid, measure="OR")

## Not run: Survival outcome
sid <- 479888
nets <- readByID(sid)
## Not run: get type and effect
nets$type
nets$effect
runnetmeta(recid=sid)

## Not run: Rate outcome
rid <- 479999
netr <- readByID(rid)
## Not run: get type and effect
netr$type
netr$effect
runnetmeta(recid=rid)
```

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