Package ‘nmadb’

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Type Package
Title Network Meta-Analysis Database API
Version 1.2.0
Date 2019-12-19
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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getNMADB

* 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 characteristics related to the publications (e.g. Journal.Name, Title) are included in the data.frame.

* References*


* Examples*

```r
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

* 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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**Description**

R package `netmeta` provides frequentist 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**

```r
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 description of the components included in the object, see the help file of `netmeta`. 

References


See Also

netmeta, getNMADB, readByID

Examples

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

## End(Not run)

# 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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