Package ‘nmadb’

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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 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
```

---

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)
runnetmeta

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

Value

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

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

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