Package: tracenma (via r-universe)

August 31, 2024

Type Package

Title Database for Developing Transitivity Methodology in Network Meta-Analysis

Version 0.1.0

Date 2024-03-27

Maintainer Loukia Spineli <`Spineli.Loukia@mh-hannover.de`>

Description Functions to access the database of 217 data-frames with aggregate study-level characteristics (that may act as effect modifiers) extracted from published systematic reviews with network meta-analysis. The database shall only be used for developing and appraising the methodology to assess the transitivity assumption quantitatively.

License GPL (>= 3)

URL `https://CRAN.R-project.org/package=tracenma`, `https://github.com/LoukiaSpin/tracenma`, `https://loukiaspin.github.io/tracenma/`

BugReports `https://github.com/LoukiaSpin/tracenma/issues`

Depends R (>= 4.0.0)

Suggests knitr, netmeta, nmadb, rmarkdown

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

Language en-US

LazyData true

RoxygenNote 7.3.1

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

RemoteUrl https://github.com/loukiaspin/tracenma

RemoteRef HEAD

RemoteSha 28f2e2f09395225d3b92060507989c6a2f8fea84

Contents

`tracenma-package` *tracenma: Database for Developing Transitivity Methodology in Network Meta-Analysis*

Description

A database with extracted study-level aggregate characteristics (that may act as effect modifiers) from 217 systematic reviews with network meta-analysis and a set of functions to facilitate access. The database is aimed at methodology development and appraisal to assess transitivity assumption quantitatively.

Details

R-package **tracenma** is built upon the R-package nmadb (version 1.2.0) by using the provided database to define the set of connected networks and extract available study-level aggregate clinical and methodological characteristics (that may act as effect modifiers) from the corresponding systematic reviews. The database of **tracenma** currently includes a subset of the systematic reviews available in nmadb; the included systematic reviews were published between 2004 and 2015 and had available data characteristics for extraction.

tracenma comprises functions to access the catalogue with the available systematic reviews with network meta-analysis and datasets with the extracted characteristics.

tracenma should only be used for the purpose of developing and appraising methodology to assess the transitivity assumption quantitatively. **tracenma** should **not be used** in the context of an empirical-like study, for instance, to map the characteristics reported in specific healthcare fields, as the content and completeness of the extracted characteristics in **tracenma** strongly depend on the reporting quality and completeness of the considered systematic reviews, as well as the knowledge of the involved authors regarding the investigated research field. The latter also requires that the authors of systematic reviews are familiar with the notion of effect modification. Therefore, the extracted characteristics may not comprise a complete set of the necessary effect modifiers for the various investigated research fields.

Furthermore, most of the included systematic reviews reported the characteristics inconsistently across the studies. To achieve a consistent format, we proceeded to transformations using 1) the statistical methods that Wan et al. (2014) developed and evaluated for quantitative characteristics and 2) subjective judgments for qualitative characteristics. Therefore, the accuracy of the extracted data may have been compromised to some extent.

Type `citation("tracenma")` on how to cite **tracenma**.

To report possible bugs and errors, send an email to Loukia Spineli (`<Spineli.Loukia@mh-hannove.de>`).

The development version of **tracenma** is available on GitHub under the GPL-3.0 License.

Author(s)

Loukia M. Spineli

References

Papakonstantinou T. nmadb: Network Meta-Analysis Database API. R package version 1.2.0. 2019. <https://CRAN.R-project.org/package=nmadb>.

Wan X, Wang W, Liu J, Tong T. Estimating the sample mean and standard deviation from the sample size, median, range and/or interquartile range. *BMC Med Res Methodol* 2014;**14**:1–13. doi:10.1186/1471-2288-14-135

`get.dataset` *Get the selected dataset*

Description

Retrieving a dataset with study-level aggregate clinical and methodological characteristics (that may act as effect modifiers) extracted from the selected systematic review of the database.

Usage

```
get.dataset(pmid, show.index = FALSE, show.type = FALSE)
```

Arguments

`pmid`	A scalar with the PMID number of the systematic review found in the database.
`show.index`	Logical to indicate whether to return a data-frame with the full name of the abbreviated characteristics. The default is `FALSE` (do not report).
`show.type`	Logical to indicate whether to return a data-frame with the type (Demographic, Clinical, Methodological) and subtype (Age, Ethnicity, Intervention, Outcome, Participant, Risk of bias, Sex, Study design, Study setting, Withdrawals) of the characteristics. The default is `FALSE` (do not report).

Details

The selected dataset refers to a connected network for a specific outcome studied in the corresponding systematic review. The R package nmadb was used to retrieve the corresponding dataset. Specifically, the function `readByID` was employed to download the dataset in the long format. Then, the function `pairwise` of the R package netmeta was implemented to convert the dataset into wide format with each row repeated as many times as the number of possible comparisons made in the corresponding study. The study names (or references) and treatment comparisons, as returned by `readByID`, were used to locate the studies in the corresponding report of the systematic review (and Appendix, if available) and extract the characteristics available in the relevant table(s). Each characteristic occupies one column in the dataset. Characteristics pertaining to intervention features occupied one column for the experimental and another for the control treatment in the corresponding comparison.

Value

`get.dataset` returns the following:

`Dataset`	A data-frame (tibble style) with rows referring to the studies and columns to the study-level aggregate characteristics as extracted from the report of the corresponding systematic review.
`Characteristics_index`	A data-frame (tibble style) with the rows referring to the extracted characteristics (abbreviated name) and columns to the their full name (if `show.index = TRUE`), their type and subtype (if `show.type = TRUE`).

Author(s)

Loukia M. Spineli

See Also

`pairwise`, `readByID`

Examples

```
get.dataset(pmid = 25626481)
```

`get.dataset.index` *Get the index of specific dataset(s)*

Description

Retrieving the characteristics of one of more systematic reviews found in the database using their PMID number or year of publication.

Usage

```
get.dataset.index(pmid, year = NULL, show.title = FALSE, show.comment = FALSE)
```

Arguments

`pmid`	A scalar or vector with the PMID number(s) of the systematic reviews found in the database.
`year`	A scalar to define the year of publication. `get.dataset.index` will return all systematic reviews found in the database under this year.
`show.title`	Logical to indicate whether to show the title of the selected systematic review(s). The default is `FALSE` (do not show).
`show.comment`	Logical to indicate whether to show the comment referring to extraction notes about the selected systematic review(s). The default is `FALSE` (do not show).

Details

When `year` is specified, the argument `pmid` should be NULL. Then, `get.dataset.index` returns all systematic reviews found in the database under this year.

Except for **PMID**, **Includes.ToC.where**, and **Source.ToC**, all other characteristics were retrieved from the R package nmadb using the function `getNMADB` and subsetting to those systematic reviews with available data (i.e., `Data.available == "True"` when using the function `getNMADB`). The database was reduced further during extraction, for instance, due to the reporting issues and data unavailability of the systematic review relating to the extraction process.

Value

`get.dataset.index` returns a vector (when `pmid` is scalar) or a data-frame (when `pmid` is a vector) with the following characteristics (column names):

`nmadb.ID`	The ID number as provided in the R package nmadb.
`PMID`	The PMID number.
`First.Author`	The name of the first author.
`Year`	The year of publication.
`Journal.Name`	The abbreviated name of the journal.
`Title`	The title of the systematic review.
`Outcome.Type`	The outcome type as suggested by Turner et al. (2012) and distinguished into objective, semi-objective and subjective.
`Intervention.Comparison.Type`	The treatment-comparator type as suggested by Turner et al. (2012) and distinguished into pharmacological versus placebo, pharmacological versus pharmacological, and non-pharmacological versus any.
`Includes.ToC.where`	Whether the extracted study-level aggregate characteristics were found in the main article, Appendix or both.
`Source.ToC`	The exact location in the systematic review where the extracted study-level aggregate characteristics were found, such as Table(s) in the main article, and/ or Appendix.
`Comment`	Notes related to the extraction for the selected systematic review(s).

Author(s)

Loukia M. Spineli

References

Turner RM, Davey J, Clarke MJ, Thompson SG, Higgins JP. Predicting the extent of heterogeneity in meta-analysis, using empirical data from the Cochrane Database of Systematic Reviews. *Int J Epidemiol* 2012;**41**(3):818–27. doi: 10.1093/ije/dys041.

See Also

`getNMADB`

Examples

```
# For one systematic review with PMID number 25626481.
get.dataset.index(pmid = 25626481)

# For two systematic reviews with PMID numbers 25626481 and 15147585,
# respectively.
get.dataset.index(pmid = c(25626481, 15147585))

# For systematic reviews published during 2010.
get.dataset.index(pmid = NULL, year = 2010)
```

`index` *Dataset catalogue*

Description

A database with 217 systematic reviews with network meta-analysis (NMA) published from 2004 to April 14, 2015. The collected systematic reviews were retrieved from the R package nmadb and pertain to those with available data in the R package nmadb.

Usage

```
data(index)
```

Format

A data-frame with 217 rows and 10 columns referring to the analysed systematic reviews with NMA and their characteristics, respectively.

Details

The characteristics of the systematic reviews comprise:

nmadb.ID	The ID number as provided in the R package nmadb.
PMID	The PMID number.
First.Author	The name of the first author.
Year	The year of publication.
Journal.Name	The abbreviated name of the journal.
Title	The title of the systematic review.
Outcome.Type	The outcome type as suggested by Turner et al. (2012) and distinguished into objective, se

Intervention.Comparison.Type	The treatment-comparator type as suggested by Turner et al. (2012) and distinguished into
Includes.ToC.where	Whether the extracted study-level aggregate characteristics were found in the main article,
Source.ToC	The exact location in the systematic review where the extracted study-level aggregate char
Comment	Notes related to the extraction for the selected systematic review(s).

Except for **PMID**, **Includes.ToC.where**, **Source.ToC**, and **Comment**, all other characteristics were retrieved from the R package nmadb using the function `getNMADB` and subsetting to those systematic reviews with available data (i.e., `Data.available == "True"` when using the function `getNMADB`). The database was reduced further during extraction, for instance, due to the limited reporting quality and data of the systematic review relating to the extraction process.

Source

Turner RM, Davey J, Clarke MJ, Thompson SG, Higgins JP. Predicting the extent of heterogeneity in meta-analysis, using empirical data from the Cochrane Database of Systematic Reviews. *Int J Epidemiol* 2012;**41**(3):818–27. doi: 10.1093/ije/dys041.

See Also

`getNMADB`

Index