

# Package ‘tracenma’

March 29, 2024

**Type** Package

**Title** Database for Developing Transitivity Methodology in Network  
Meta-Analysis

**Version** 0.1.0

**Date** 2024-03-27

**Maintainer** Loukia Spinelis <Spinelis.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** netmeta, nmadb, rmarkdown

**Config/testthat/edition** 3

**Encoding** UTF-8

**Language** en-US

**LazyData** true

**RoxygenNote** 7.3.1

**NeedsCompilation** no

**Author** Loukia Spinelis [aut, cre]

**Repository** CRAN

**Date/Publication** 2024-03-29 21:40:02 UTC

## R topics documented:

tracenma-package . . . . .	2
get.dataset . . . . .	3
get.dataset.index . . . . .	4
index . . . . .	6

<b>Index</b>	<b>8</b>
--------------	----------

---

tracenma-package	<i>tracenma: Database for Developing Transitivity Methodology in Network Meta-Analysis</i>
------------------	--

---

### 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 **nma** (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 **nma**; 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 or 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):

<code>nmadb.ID</code>	The ID number as provided in the R package <code>nmadb</code> .
<code>PMID</code>	The PMID number.
<code>First.Author</code>	The name of the first author.
<code>Year</code>	The year of publication.
<code>Journal.Name</code>	The abbreviated name of the journal.
<code>Title</code>	The title of the systematic review.
<code>Outcome.Type</code>	The outcome type as suggested by Turner et al. (2012) and distinguished into objective, semi-objective and subjective.
<code>Intervention.Comparison.Type</code>	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.
<code>Includes.ToC.where</code>	Whether the extracted study-level aggregate characteristics were found in the main article, Appendix or both.
<code>Source.ToC</code>	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.
<code>Comment</code>	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:

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

<b>Intervention.Comparison.Type</b>	The treatment-comparator type as suggested by Turner et al. (2012) and distinguished into
<b>Includes.ToC.where</b>	Whether the extracted study-level aggregate characteristics were found in the main article,
<b>Source.ToC</b>	The exact location in the systematic review where the extracted study-level aggregate char

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 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

\* **dataset**

index, [6](#)

\* **package**

tracenna-package, [2](#)

get.dataset, [3](#)

get.dataset.index, [4](#)

getNMADB, [5](#), [7](#)

index, [6](#)

pairwise, [3](#), [4](#)

readByID, [3](#), [4](#)

tracenna (tracenna-package), [2](#)

tracenna-package, [2](#)