Package: NMAforest (via r-universe)

May 11, 2026

Type Package

Title Forest Plots for Network Meta-Analysis with Proportion for Paths and Studies

Version 0.1.3

Description Provides customized forest plots for network meta-analysis incorporating direct, indirect, and NMA effects. Includes visualizations of evidence contributions through proportion bars based on the hat matrix and evidence flow decomposition.

Imports netmeta, meta, dplyr, magrittr, igraph, ggplot2, scales, grid, utils, tibble, stats, rlist

Suggests pcnetmeta

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

License GPL-2

Depends R (>= 3.5)

NeedsCompilation no

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

Date/Publication 2026-02-10 08:00:02 UTC

RemoteUrl https://github.com/cran/NMAforest

RemoteRef HEAD

RemoteSha bd9eea4a8c4bac6bd749c49e996dba00ddf3f357

Contents

`example_data` *Example Dataset for NMAPropForest*

Description

A small dataset used to demonstrate the usage of `NMAPropForest()`.

Usage

```
example_data
```

Format

A data frame:

study Study label

id Study id

t Treatment label

r Number of events (for binary outcomes)

n Sample size

rob Risk of bias

Source

Example dataset included with the NMAPropForest package

`NMAforest` *Generate Forest Plot with Proportion Contributions for Network Meta-analysis*

Description

This function extends the capabilities of network meta-analysis visualization by generating a forest plot that incorporates direct, indirect, and network meta-analysis (NMA) treatment effects, along with contribution proportions from individual studies and comparison paths. It builds on the statistical foundation provided by the 'netmeta' package and is particularly useful for evaluating the influence of study evidence in complex treatment networks.

Usage

```
NMAforest(
  data,
  sm,
  reference,
  model = "random",
  comparison,
  study = "study",
  treat = "t",
  event = "r",
  N = "n",
  mean = "y",
  sd = "sd",
  study_id = "study_id",
  study_path = TRUE
)
```

Arguments

`data`	A data frame in long format with required variables `study` (study identifier) and `t` (treatment label), plus outcome columns: for binary outcomes, `r` (events) and `N` (sample size); for continuous outcomes, `y` (mean), `sd` (standard deviation), and `N` (sample size). Column names are configurable via `study`, `treat`, `event`, `N`, `mean`, and `sd`.
`sm`	A Character string specifying the summary measure to use (e.g., "OR" for odds ratio, "RR" for risk ratio, "RD" for risk difference, "MD" for mean difference, "SMD" for standardized mean difference, etc.).
`reference`	Specify the reference treatment for comparisons.
`model`	Choose "random" or "fixed" effect model.
`comparison`	A vector of two treatments to compare.
`study`	Column name identifying the study label.
`treat`	Column name for treatment assignment.
`event`	Column name for event counts (for binary outcomes).
`N`	Column name for total sample size (for binary and continuous outcomes).
`mean`	Column name for mean values (for continuous outcomes).
`sd`	Column name for standard deviations (for continuous outcomes).
`study_id`	Column name used to uniquely identify each study arm (default = "study_id"). If the column is not present in the original dataset, the updated data frame will be returned with this column added.
`study_path`	Logical. TRUE to include study combination contributions, FALSE to exclude.

Details

This package includes an implementation of ‘comparisonStreams()‘ originally developed by Papakonstantinou et al. (2018) and released with the paper’s supplementary material.

Value

A list containing:

- **plot** A ggplot object of the forest plot.
- **output** A data frame summarizing the results for the specified treatment comparison, including study-level and overall estimates. Columns contain the effect sizes with their 95% confidence intervals, standard errors, study weights, and contribution proportions, along with labels indicating whether the row corresponds to a study, direct effect, indirect effect, or the overall NMA estimate.
- **updated_df** The input data frame after preprocessing, with a unique study identifier column (from the argument `study_id`) added when not already present. This guarantees consistent referencing of studies in both the analysis and the output.

References

Balduzzi, S., Rücker, G., Nikolakopoulou, A., Papakonstantinou, T., Salanti, G., Efthimiou, O., & Schwarzer, G. (2023). netmeta: An R Package for Network Meta-Analysis Using Frequentist Methods. *Journal of Statistical Software*, 106(2), 1–40. https://doi.org/10.18637/jss.v106.i02

Csardi, G., & Nepusz, T. (2006). The igraph software package for complex network research. *InterJournal*, Complex Systems, 1695. https://igraph.org

Csárdi, G., Nepusz, T., Traag, V., Horvát, Sz., Zanini, F., Noom, D., & Müller, K. (2025). *igraph: Network Analysis and Visualization in R*. https://doi.org/10.5281/zenodo.7682609

Wickham, H. (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. https://ggplot2.tidyverse.org

Papakonstantinou, T., Nikolakopoulou, A., Rücker, G., Chaimani, A., Schwarzer, G., Egger, M., & Salanti, G. (2018). Estimating the contribution of studies in network meta-analysis: paths, flows and streams. *F1000Research*, 7:610. https://doi.org/10.12688/f1000research.14527.3

flow_contribution GitHub repository: https://github.com/esm-ispm-unibe-ch/flow_contribution

Examples

```
# Example 1: Binary outcome data
data(example_data)

NMAforest(
  data = example_data,
  sm = "OR",
  reference = "x",
  model = "random",
  comparison = c("x", "y"),
  study = "study",
  treat = "t",
  event = "r",
  N = "n",
  study_id = "id",
  study_path = TRUE
)
```

```
# Example 2: Continuous outcome data
data("parkinson", package = "pcnetmeta")

NMAforest(
  data = parkinson,
  sm = "MD",
  reference = "1",
  model = "random",
  comparison = c("1", "3"),
  study = "s.id",
  treat = "t.id",
  mean = "mean",
  sd = "sd",
  N = "n",
  study_path = TRUE
)
```

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