Package 'NMAforest'

August 27, 2025

Type Package

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

Version 0.1.0

Description Provides customized forest plots for network meta-
analysis incorporating direct, indirect, and network meta-
analysis 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

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

License GPL-2

Depends R (>= 3.5)

NeedsCompilation no

Author Yanqi Zhang [aut, cre]

Maintainer Yanqi Zhang <zyq1998@iastate.edu>

Repository CRAN

Date/Publication 2025-08-27 16:30:22 UTC

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 = "OR",
  reference = "x",
  model = "random",
  comparison = c("x", "y"),
  study = "study",
  treat = "t",
  event = "r",
  N = "n",
  mean = "y",
  sd = "sd",
  id = "id",
  study_path = TRUE
)
```

Arguments

data	A data frame containing the input data.
sm	A Character string specifying the summary measure to use (e.g., "RR" for risk ratio, "OR" for odds ratio, "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 ID or 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 outcomes).
mean	Column name for mean values (for continuous outcomes).
sd	Column name for standard deviations (for continuous outcomes).
id	Column name used to uniquely identify each study arm (default = "id"). If the column is not present, one will be 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.

effects A data.frame with all effect sizes, confidence intervals, and weights.

proportions A data.frame with proportion values.

df_updated The input data frame with a unique id column added if not already present.

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

```
# Load example data from the package
data(example_data)
# Generate the forest plot and return effect estimates and proportion contributions
NMAforest(
  data = example_data,
  sm = "OR",
  reference = "x",
  model = "random",
  comparison = c("x", "y"),
  study = "study",
  treat = "t",
  event = "r",
  N = "n",
  id = "id",
  study_path = TRUE
)
```

Index