

Package ‘survNMA’

January 23, 2025

Type Package

Title Network Meta-Analysis Combining Survival and Count Outcomes

Version 1.1-1

Date 2025-01-23

Maintainer Hisashi Noma <noma@ism.ac.jp>

Description

Network meta-analysis for survival outcome data often involves several studies only involve dichotomized outcomes (e.g., the numbers of event and sample sizes of individual arms). To combine these different outcome data, Woods et al. (2010) proposed a Bayesian approach using complicated hierarchical models. Besides, frequentist approaches have been alternative standard methods for the statistical analyses of network meta-analysis, and the methodology has been well established. We proposed an easy-to-implement method for the network meta-analysis based on the frequentist framework in Noma and Maruo (2025). This package involves some convenient functions to implement the simple pooling method.

Depends R (>= 3.5.0)

Imports stats, netmeta

License GPL-3

Encoding UTF-8

LazyData true

R topics documented:

survNMA-package	1
calcHR	2
calcse	3
woods	4

Index	5
--------------	----------

survNMA-package	<i>The ‘survNMA’ package</i>
-----------------	------------------------------

Description

Network meta-analysis for survival outcome data often involves several studies only involve dichotomized outcomes (e.g., the numbers of event and sample sizes of individual arms). To combine these different outcome data, Woods et al. (2010) proposed a Bayesian approach using complicated hierarchical models. Besides, frequentist approaches have been alternative standard methods for the statistical analyses of network meta-analysis, and the methodology has been well established. We proposed an easy-to-implement method for the network meta-analysis based on the frequentist framework in Noma (2025). This package involves some convenient functions to implement the simple pooling method.

References

Noma, H. and Maruo, K. (2025). Network meta-analysis combining survival and count outcome data: A simple frequentist approach. Forthcoming.

calcHR	<i>Computation of log hazard ratio estimate and its standard error estimate from dichotomized data</i>
--------	--

Description

Log hazard ratio estimate and its standard error estimate are calculated from dichotomized data.

Usage

```
calcHR(d1, n1, d0, n0)
```

Arguments

d1	The number of events in arm 1.
n1	The number of sample size in arm 1.
d0	The number of events in arm 2.
n0	The number of sample size in arm 2.

Value

- TE: The log hazard ratio estimate.
- seTE: Standard error estimate for the log hazard ratio.

References

Noma, H. and Maruo, K. (2025). Network meta-analysis combining survival and count outcome data: A simple frequentist approach. Forthcoming.

Salika, T., Turner, R. M., Fisher, D., Tierney, J. F. and White, I. R. (2022). Implications of analysing time-to-event outcomes as binary in meta-analysis: empirical evidence from the Cochrane Database of Systematic Reviews. *BMC Medical Research Methodology* **22**, 73.

Examples

```
calcHR(1,229,1,227)
```

```
calcHR(4,374,7,361)
```

```
calcHR(3,372,7,361)
```

```
calcHR(2,358,7,361)
```

calcse	<i>Computation of standard error estimate of a contrast measure from a multi-arm trial</i>
--------	--

Description

In network meta-analysis, standard error estimates cannot often be obtained for some contrasts of arms in multi-arm trials. This function calculate the standard error estimate of a contrast measure (e.g., log hazard ratio) estimator from partially obtained summary data in multi-arm trials. Without loss of generality, we consider three arms 0, 1 and 2 in the corresponding trial, and suppose the standard error of the contrast measure comparing the arms 1 vs. 2 is not obtained; however, those comparing the arms 1 vs. 0 and 2 vs. 0 are obtained. We can calculate the standard error estimate comparing the arms 1 vs. 2 from the partially available data.

Usage

```
calcse(se1,se2,n1,n2,n0)
```

Arguments

se1	The standard error estimate of a contrast measure (e.g., log hazard ratio) estimator for arms 1 vs. 0.
se2	The standard error estimate of a contrast measure (e.g., log hazard ratio) estimator for arms 2 vs. 0.
n1	The sample size of arm 1.
n2	The sample size of arm 2.
n0	The sample size of arm 0.

Value

The standard error estimate of a contrast measure (e.g., log hazard ratio) estimator for arms 1 vs. 2.

References

- Noma, H. and Maruo, K. (2025). Network meta-analysis combining survival and count outcome data: A simple frequentist approach. Forthcoming.
- Salika, T., Turner, R. M., Fisher, D., Tierney, J. F. and White, I. R. (2022). Implications of analysing time-to-event outcomes as binary in meta-analysis: empirical evidence from the Cochrane Database of Systematic Reviews. *BMC Medical Research Methodology* **22**, 73.

woods

Transformed data to log hazard ratio statistics of Woods et al. (2010)

Description

A network meta-analysis dataset whose dichotomized outcome data was transformed by `calCHR`.

- `id`: ID variable of studies.
- `study`: Study name.
- `treat1`: Treatment 1.
- `treat2`: Treatment 2.
- `outcome`: Type of outcome (HR or count).
- `logHR`: Log hazard ratio estimate.
- `se_logHR`: Standard error estimate of the log hazard ratio estimator.

Usage

```
data(woods)
```

Format

A data frame for network meta-analysis with 5 trials.

References

Woods, B. S., Hawkins, N. and Scott, D. A. (2010). Network meta-analysis on the log-hazard scale, combining count and hazard ratio statistics accounting for multi-arm trials: A tutorial. *BMC Medical Research Methodology* **10**: 54.

Examples

```
library("netmeta")

netmeta(TE=logHR, seTE=se_logHR, treat1=treat1, treat2=treat2,
  studlab=study, data=woods, common=FALSE, ref="Placebo", sm="HR")
```

Index

* **datasets**

woods, [4](#)

calcHR, [2](#)

calcse, [3](#)

survNMA-package, [1](#)

woods, [4](#)