

Package ‘survNMA’

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Type Package

Title Network Meta-Analysis Combining Survival and Count Outcomes

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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) <[doi:10.1186/1471-2288-10-54](https://doi.org/10.1186/1471-2288-10-54)> 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) <[doi:10.1101/2025.01.23.25321051](https://doi.org/10.1101/2025.01.23.25321051)>. This package involves some convenient functions to implement the simple synthesis method.

URL <https://doi.org/10.1101/2025.01.23.25321051>

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Author Hisashi Noma [aut, cre] (<<https://orcid.org/0000-0002-2520-9949>>)

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survNMA-package	<i>The 'survNMA' package</i>
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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 synthesis method.

References

Noma, H. and Maruo, K. (2025). Network meta-analysis combining survival and count outcome data: A simple frequentist approach. medRxiv: 10.1101/2025.01.23.25321051.

calcHR	<i>Computation of log hazard ratio estimate and its standard error estimate from dichotomized data</i>
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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. medRxiv: 10.1101/2025.01.23.25321051.

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>
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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. medRxiv: 10.1101/2025.01.23.25321051.

Woods, B. S., Hawkins, N., 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

```
calcse(0.096, 0.092, 1521, 1534, 1524)
```

combine2

Merging two dataset for the analysis by "netmeta"

Description

Merging two dataset for the analysis by netmeta package (e.g., an output object by pairwiseHR for dichotomized outcome dataset and the survival outcome dataset). The output object can be straightforwardly applied to the netmeta function.

Usage

```
combine2(data1, data2)
```

Arguments

data1	Dataset 1.
data2	Dataset 2.

Value

- studlab: ID variable of studies.
- treat1: The treatment of arm 1.
- treat2: The treatment of arm 2.
- TE: The effect measure estimate.
- seTE: Standard error estimate for the effect measure estimator.

References

Noma, H. and Maruo, K. (2025). Network meta-analysis combining survival and count outcome data: A simple frequentist approach. medRxiv: 10.1101/2025.01.23.25321051.

Examples

```
data(woods1)
data(woods2)

woods3 <- pairwiseHR(treat, studlab=study, event=d, n, data=woods2)
combine2(woods1, woods3)
```

pairwiseHR	<i>Computation of log hazard ratio estimate and its standard error estimate from dichotomized dataset</i>
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Description

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

Usage

```
pairwiseHR(treat, studlab, event, n, data)
```

Arguments

treat	The treatments of individual arms.
studlab	ID variable of studies.
event	The number of events of individual arms.
n	The number of sample size of individual arms.
data	The dataset object.

Value

- studlab: ID variable of studies.
- treat1: The treatment of arm 1.
- treat2: The treatment of arm 2.
- TE: The log hazard ratio estimate.
- seTE: Standard error estimate for the log hazard ratio.
- n1: The sample size of arm 1.
- n2: The sample size of arm 2.

References

Noma, H. and Maruo, K. (2025). Network meta-analysis combining survival and count outcome data: A simple frequentist approach. medRxiv: 10.1101/2025.01.23.25321051.

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

```
data(woods2)
```

```
pairwiseHR(treat, studlab=study, event=d, n, data=woods2)
```

woods1

Hazard ratio statistics of two trials directly extracted in Woods et al. (2010)

Description

A network meta-analysis dataset summarized in hazard ratio statistics provided in Woods et al. (2010).

- studlab: ID variable of studies.
- treat1: Treatment 1.
- treat2: Treatment 2.
- TE: Log hazard ratio estimate.
- seTE: Standard error estimate of the log hazard ratio estimator.
- n1: Sample size 1.
- n2: Sample size 2.

Usage

```
data(woods1)
```

Format

A data frame for network meta-analysis with 2 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.

woods2

Dichotomized dataset of three trials provided in Woods et al. (2010)

Description

A network meta-analysis dataset reported as dichotomized data provided in Woods et al. (2010).

- study: ID variable of studies.
- treat: Treatment.
- d: The number of events.
- n: Sample size.

Usage

```
data(woods2)
```

Format

A data frame for network meta-analysis with 3 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.

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