

Package: metaSurvival (via r-universe)

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Type Package

Title Meta-analysis of a single survival curve using the multivariate methodology of DerSimonian and Laird

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Description This package contains functions to assess a summary survival curve from survival probabilities and number of at-risk patients collected at various points in time in various studies, and to test the between-strata heterogeneity.

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Encoding UTF-8

LazyData true

Imports mvtnorm, survival

RoxygenNote 7.1.1

Depends R (>= 2.10)

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL <https://github.com/shubhrampandey/metaSurvival>

BugReports <https://github.com/shubhrampandey/metaSurvival/issues>

Repository <https://shubhrampandey.r-universe.dev>

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exampleData

*The data extracted from a meta-analysis by Cabibbo et al.***Description**

Data were extracted from the studies included in the meta-analysis by Cabibbo et al. which aimed to assess the survival rate in untreated patients with hepatocellular carcinoma.

Usage

exampleData

Format

A data frame with with the 8 following variables (columns).

Study This numeric vector represents number of the study.

FirstAuthor This vector represents the name of the first author.

YearPub This numeric vector represents the publication year.

Time This numeric vector represents the times for which the survival rates are collected in years.

Survival This numeric vector represents the survival rates for each value of Time

NbRisk This numeric vector represents the number of at-risk patients for each value of Time

Location This factor indicates the location of the study (Asia, North Amercia or Europe)

Design This factor indicates if the study is monocentric ou multicentric. ...

Details

The survival probabilities were extracted from the published survival curves each month during the first six months and then by step of three months. The pictures of the curves were digitalized using the R package ReadImage and the probabilities were extracted using the package digitize proposed by Poisot. The numbers of at-risk patients for each interval of time were derived from the numbers of at-risk patients reported in the studies, and using the methods of Parmar or Williamson to account for censorship. Studies have different length of follow-up. For each study, survival probabilities and the numbers of at-risk patients were collected at all points in time before the end of follow-up.

Author(s)

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msurv	<i>Summary survival curve from aggregated survival data of a meta-analysis</i>
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Description

Estimation of the summary survival curve from the survival rates and the numbers of at-risk individuals extracted from studies of a meta-analysis.

Usage

```
msurv(  
  study,  
  time,  
  n.risk,  
  surv.rate,  
  confidence,  
  correctionFlag = TRUE,  
  correctionVal = c(0.25, 0.5)  
)
```

Arguments

study	A numeric vector with the numbering of the studies included in the meta-analysis. The numbering of a study is repeated for each survival probabilities extracted from this study.
time	A numeric vector with the time at which the survival probabilities are collected.
n.risk	A numeric vector with the number of at-risk patients in the study for each value of thr time.
surv.rate	A numeric vector with the survival rates collected per study for each value of time.
confidence	A text argument indicating the method to calculate the confidence interval of the summary survival probabilities: "Greenwood" or "MonteCarlo".
correctionFlag	A logical variable which takes into account if user wants the continuity correac-tion or not (By default TRUE).
correctionVal	A numeric vector for continuity correction, if you don't want to apply correction pass c(0,0).

Value

list

Author(s)

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Examples

```
attach(exampleData)
result <- msurv(study = Study,
               time = Time,
               n.risk = NbRisk,
               surv.rate = Survival,
               confidence = "Greenwood",
               correctionFlag = FALSE
               )
result
```

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