Package ‘msce’

July 23, 2025

Type Package

Title Hazard of Multi-Stage Clonal Expansion Models

Version 1.0.1

Date 2020-10-15

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Description Functions to calculate hazard and survival function of Multi-Stage Clonal Expansion Models used in cancer epidemiology. For the Two-Stage Clonal Expansion Model an exact solution is implemented assuming piecewise constant parameters. Numerical solutions are provided for its extensions.

License GPL (>= 2)

Imports Rcpp (>= 1.0.3), RcppParallel (>= 5.0.0)

LinkingTo Rcpp, RcppParallel

Encoding UTF-8

RoxygenNote 7.1.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation yes

Repository CRAN

Date/Publication 2020-10-29 15:10:02 UTC

Contents

`lungCancerRadon` *Exemplary person year table*

Description

Data set of fatal lung cancer in rats exposed to Radon at Pacific Northwest National Laboratory. For each rat, the age at start of Radon exposure, the age at end of exposure and the age at end of follow-up/death is provided in weeks. The Radon dose rate is given in WL (working level).

Usage

```
data(lungCancerRadon)
```

Format

Data frame with 5 variables.

Source

Pacific Northwest National Laboratory, see Heidenreich, W, Jacob P, Paretzke H., et al. (1999). Radiation research, 151 2, 209-17 DOI:10.2307/3579772.

Examples

```
data(lungCancerRadon)
lungCancerRadon[1000,]
```

`lungCancerSmoking` *Exemplary person year table*

Description

Fictitious data set providing the number of lung cancer cases and person years in some population stratified according to age, age of smoking start, age of smoking cessation, and average number of cigarettes per day during the active smoking period.

Usage

```
data(lungCancerSmoking)
```

Format

Data frame with 6 variables.

Source

Fictitious data set, only for illustration and test.

Examples

```
data(lungCancerSmoking)
lungCancerSmoking[1000,]
```

`msce` *msce: A package to compute hazard and survival function for Multi-Stage Clonal Expansion models*

Description

Functions `tsce` and `msce_numerical` are provided to compute hazard and survival function for the Two- and the more general Multi-Stage Clonal Expansion model. Models can be evaluated for time-dependent parameters. However, parameters are assumed to be constant within the time intervals specified by the user. To allow parameter fits on many strata or cohort members, the models are implemented with RcppParallel. For details, see the package vignette.

`msce_numerical` *Numerical solution of the Multi-Stage Clonal Expansion Model*

Description

This function aims to solve the general multi-stage model with piecewise constant parameters approximatively by integrating the characteristic equations with Euler's method. For sufficiently small time intervalls, this approximation often yields reasonable results. Small time intervals can either be provided explicitly with many columns in argument `t`. An alternative is the optional parameter `innerSteps`.

Usage

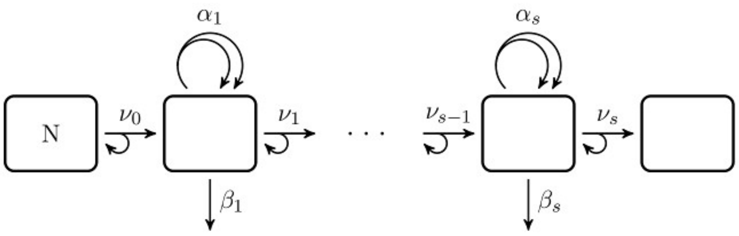
```
msce_numerical(t, parameterList, innerSteps = 1000L)
```

Arguments

`t`	Each element in a row of `t` defines the endpoint of a time interval. The first time interval starts at time `0`. The last element is the time point for which hazard and survival function are evaluated. Elements in a row have to be in monotonously increasing order. In order to achieve a different number of time intervals for different rows, rows may start with an arbitrary number of zeros (i.e. time intervals of length zero).
`parameterList`	List of Matrices. Each list member has to be named. Allowed names are `Nnu0`, `alphaX`, `gammaX`, and `nuX` where `X` can be any positive integer value. The number of stages is deduced from `nuX` with the highest `X`. Matrices `Nnu0` and successive `nuX` must be provided. Missing other matrices are assumed to be zero. For each matrix it has to hold that the number of columns must be equal to the ones in

	`t`. The number of rows can either equal to the number of rows in `t`, or only one row is provided, which then is applied to all rows of `t`. Values in matrices `Nnu0`, `alphaX`, `gammaX`, `nuX` correspond to parameters for each time interval, see the figure and explanations in the package vignette. Here, `Nnu0` is the product of N and ν_0 and γ_X is defined by $\alpha_X - \beta_X$.
`innerSteps`	Positive integer. To improve accuracy, each time interval is internally divided into `innerSteps` time intervals of equal length. Defaults to 1000. Note, however, that even in the limit of infinite innerSteps, there will always be a finite discrepancy to the exact result.

Details



Value

The output list contains all used arguments of the `parameterList` and vectors of the model results for hazard and logarithm of the survival function for each row of the input.

See Also

`tsce`

Examples

```
t <-matrix(data=c(10,20,65,10,20,70),nrow=2,byrow=TRUE)
Nnu0 <- matrix(c(0.3,0.7,1),nrow = 1)
nu1  <- matrix(1e-6,nrow=1,ncol=3)
alpha1<- matrix(1,nrow=1,ncol=3)
gamma1<- matrix(c(0.13,0.13,0.13, 0.15,0.15,0.15),nrow=2,byrow=TRUE)
pars = list(Nnu0=Nnu0, nu1=nu1,alpha1=alpha1,gamma1=gamma1)

msce_numerical(t,pars)
```

`tsce` *Exact solution of the Two-Stage Clonal Expansion Model*

Description

For piecewise constant parameters `tsce(t,parameterList)` returns the exact hazard and logarithm of the survival function of the Two-Stage Clonal Expansion Model. All arguments are matrices. Evaluation is performed separately for each row.

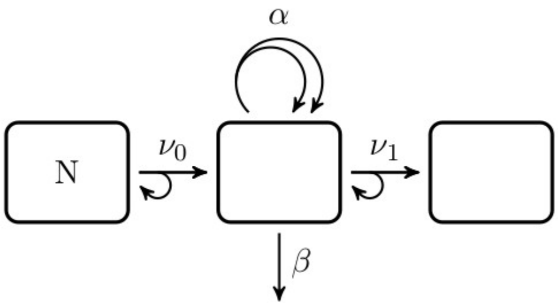
Usage

```
tsce(t, parameterList)
```

Arguments

`t`	Each element in a row of `t` defines the endpoint of a time interval. The first time interval starts at time `0`. The last element is the time point for which hazard and survival function are evaluated. Elements in a row have to be in monotonously increasing order. In order to achieve a different number of time intervals for different rows, rows may start with an arbitrary number of zeros (i.e. time intervals of length zero).
`parameterList`	List of Matrices. Each list member has to be named. Allowed names are `Nnu0`, `alpha`, `gamma`, and `nu1`. Matrices `Nnu0` and `nu1` must be provided. If `alpha` or `gamma` are missing, they are assumed to be zero. For each matrix it has to hold that the number of columns must be equal to the ones in `t`. The number of rows can either equal to the number of rows in `t`, or only one row is provided, which then is applied to all rows of `t`. Values in matrices `Nnu0`, `alpha`, `gamma`, `nu1` correspond to parameters for each time interval, see the figure and explanations in the package vignette. Here, `Nnu0` is the product of N and ν_0 and γ is defined by $\alpha - \beta$.

Details



See Also

`msce_numerical`

Examples

```
t <-matrix(data=c(10,20,65,10,20,70),nrow=2,byrow=TRUE)
Nnu0 <- matrix(c(0.3,0.7,1),nrow = 1)
alpha<- matrix(1,nrow=1,ncol=3)
gamma<- matrix(c(0.13,0.13,0.13, 0.15,0.15,0.15),nrow=2,byrow=TRUE)
nu1  <- matrix(1e-6,nrow=1,ncol=3)
pars = list(Nnu0=Nnu0, alpha=alpha,gamma=gamma,nu1=nu1)

tsce(t,pars)
```

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