Package ‘RPEXE.RPEXT’

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Title Reduced Piecewise Exponential Estimate/Test Software

Version 0.0.1

Author Gang Han [aut, cre],
        Yu Zhang [aut]

Maintainer Gang Han <hangang.true@gmail.com>

URL https://github.com/hangangtrue/RPEXE.RPEXT

BugReports https://github.com/hangangtrue/RPEXE.RPEXT/issues

Description This reduced piecewise exponential survival software implements the likelihood ratio test and backward elimination procedure in Han, Schell, and Kim (2012 <doi:10.1080/19466315.2012.698945>, 2014 <doi:10.1002/sim.5915>), and Han et al. (2016 <doi:10.1111/biom.12590>). Inputs to the program can be either times when events/censoring occur or the vectors of total time on test and the number of events. Outputs of the programs are times and the corresponding p-values in the backward elimination. Details about the model and implementation are given in Han et al. 2014. This program can run in R version 3.2.2 and above.

Depends R (>= 3.2.2)

License GPL-3

Imports stats, graphics

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1.9000

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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R topics documented:

bisection algorithm in Beta distribution

Description

Running bisection algorithm to search for \(a_2\), the minimizer of \((\log((a_2)^{dea_1}*(1-a_2)^{dea_2}-delta))^2\)

Usage

bisec(delta, dea1, dea2, upbd, lowbd)
**Arguments**

delta  
Test statistic in Han et al. (2012), \( \text{delta} = \left( \frac{ttot1}{ttot1+ttot2} \right)^{dea1} \left( \frac{ttot2}{ttot1+ttot2} \right)^{dea2}; \)

dea1  
first parameter in Beta distribution (number of events from the first arm)

dea2  
second parameter in Beta distribution (number of events from the second arm)

upbd  
upper bound of a2

lowbd  
lower bound of a2

**Value**

a2

**Examples**

bisec(-74.4824, 33, 98, 1, 0.252)

data2  
**RPEXE_fitting**

**Description**

A breast cancer clinical trial dataset in Adelson et al. (2016).

**Usage**

data(data2)

**Details**

- first column - times : time to event
- second column - censor : censoring status; 0=censored, 1=event.
- third column - group : labels the single agent arm and combination arm

**References**

Description
A dataset containing predictions for chemo-sensitivity and pathological response from Hatzis (2011)

Usage
data(df)

Details
- validate: Validation status
- drfs: Censoring status; 0=censored, 1=event.
- drfs.time: Time to event or censoring
- er.status: ER status, P=positive, N=negative
- chemo.pred: Prediction for chemo sensitivity from the ACES predictor, sensitive or insensitive
- pre.N: Prediction of nodal status
- pCR.RD: pathological complete response (pCR) or residual disease (RD)
- pre.grade: prediction of tumor grade
- pre.T: T stage prediction
- dlda30: DLDA30 prediction for the pathological response.

References

exact_pvalue
P-value for the two exponential comparison in Han et al.(2012)

Description
This function computes the exact p-value from the likelihood ratio test

Usage
exact_pvalue(ttot1,ttot2,dea1,dea2,mono)
Arguments

- **ttot1**: total time on test 1
- **ttot2**: total time on test 2
- **dea1**: number of death 1
- **dea2**: number of death 2
- **mono**: 0: 2-sided hypothesis: \( H_0: \lambda_1 \text{ is equal to } \lambda_2; \ H_1: \lambda_1 \text{ is not equal to } \lambda_2 \)  
  1: 1-sided hypothesis: \( H_0: \lambda_1 \text{ is greater than or equal to } \lambda_2; \ H_1: \lambda_1 \text{ is less than } \lambda_2 \)  
  2: 1-sided hypothesis: \( H_0: \lambda_1 \text{ is less than or equal to } \lambda_2; \ H_1: \lambda_1 \text{ is greater than } \lambda_2 \)

Value

- **a2**: Beta distribution quantile computed using bisec.R  
- **pval**: p-value

Examples

```r
exact_pvalue(1, 302.04, 2, 25, 1)
```

---

**gamllik**

*Log likelihood from the gamma distribution*

Description

A function computing the log likelihood from the gamma distribution under an order restriction reduction.

Usage

```r
gamllik(structtime, structttot, structdeaths, time_die, ttot, deaths)
```

Arguments

- **structtime**: change-point times to be used to compute the likelihood value
- **structttot**: total time on test (ttot) between each time point and the previous time point (or 0) corresponding to structtime
- **structdeaths**: number of deaths corresponding to structttot
- **time_die**: all event and censoring times from small to large
- **ttot**: total time on test corresponding to time_die
- **deaths**: the number of deaths corresponding to "ttot"

Value

log of the likelihood
Examples

```r
time_die <- c(0.05, 0.08, 0.38, 0.41, 0.64)
ttot <- c(9.2, 5.8, 52.1, 5.8, 40.0)
deaths <- c(1, 1, 1, 1, 1)
structtime <- c(0.05, 0.64)
structttot <- c(9.2, 40.0)
structdeaths <- c(1, 5)
gamllik(structtime, structttot, structdeaths, time_die, ttot, deaths)
```

---

### km

**Kaplan-Meier curve**

---

**Description**

This function plots the Kaplan-Meier curve without returning outputs.

**Usage**

```r
km(time, censor, plotcens)
```

**Arguments**

- `time`: a vector of event or censoring time
- `censor`: a vector indicating censoring: 0 = censored; 1 = uncensored
- `plotcens`: 0: don’t add censored data symbol to the output curve; 1: add censored data symbol to the output curve

**Value**

Kaplan-Meier curve only

**Examples**

```r
t1 <- c(2, 3, 4, 5, 5, 7, 10, 12, 15)
c1 <- c(0, 0, 1, 0, 0, 1, 0, 0)
km(t1, c1, 0)
```
kmvalue

Obtain values for Kaplan-Meier plotting

Description

Obtain values for Kaplan-Meier plotting

Usage

kmvalue(x)

Arguments

x

Nx2 data matrix, first column represents survival time of the i-th subject, second column represents censored flag (0 if not censored, 1 if censored)

Value

Values used for Kaplan-Meier plotting

Examples

t1 <- c(2,3,4,5,5,7,10,12,15)
c1 <- c(0,0,1,0,0,0,0,1,0)
x1<-cbind(t1,c1)
kmvalue(x1)

km_blacksolid

Kaplan-Meier curve

Description

This function plots the Kaplan-Meier curve without returning outputs

Usage

km_blacksolid(time, censor, plotcens)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>time</td>
<td>a vector of event or censoring time</td>
</tr>
<tr>
<td>censor</td>
<td>a vector indicating censoring: 0 = censored; 1 = uncensored</td>
</tr>
<tr>
<td>plotcens</td>
<td>0: don’t add censored data symbol to the output curve 1: add censored data symbol to the output curve</td>
</tr>
</tbody>
</table>
km_combine

Value

Kaplan-Meier curve only

Examples

t1 <- c(2, 3, 4, 5, 5, 7, 10, 12, 15)
c1 <- c(0, 0, 1, 0, 0, 1, 0, 0)
km_blacksolid(t1, c1, 0)

tR <- c(1, 3, 5, 4, 8, 10, 9, 11)
cR <- c(0, 0, 0, 1, 0, 0, 0)
x1 <- cbind(t1, c1)
x2 <- cbind(t2, c2)
km_combine(x1, x2)
km_combine(x1, x2, pos = 1)
**km_log**  

*Plot a Kaplan Meier curve in log scale*

**Description**

The function plots a Kaplan Meier curve in log scale

**Usage**

```r
km_log(time, censor, plotcens)
```

**Arguments**

- `time`: time of observed event
- `censor`: a vector indicating censored or not at the given times, 0 = censored; 1 = uncensored
- `plotcens`: 0: add censored data to the output curve  
  1: don’t add censored data to the output curve

**Value**

A Kaplan Meier curve in log scale

**Examples**

```r
t1 <- c(2, 3, 4, 5, 5, 7, 10, 12, 15)  
c1 <- c(0, 0, 1, 0, 0, 1, 0, 0)  
km_log(t1, c1, 0)
```

---

**km_red**  

*Plot a Kaplan Meier curve in red*

**Description**

The function plots a Kaplan Meier curve in red

**Usage**

```r
km_red(time, censor, plotcens)
```

**Arguments**

- `time`: time of observed event
- `censor`: a vector indicating censored or not at the given times, 0 = censored; 1 = uncensored
- `plotcens`: 0: add censored data to the output curve  
  1: don’t add censored data to the output curve
km_redsolid

Value

A red Kaplan Meier curve

Examples

t1 <- c(2, 3, 4, 5, 5, 7, 10, 12, 15)
c1 <- c(0, 0, 1, 0, 0, 1, 0, 0)
km_redsolid(t1, c1, 0)

km_redsolid  Plot a Kaplan Meier curve in red solid line

Description

The function plots a Kaplan Meier curve in red solid line

Usage

km_redsolid(time, censor, plotcens)

Arguments

time  time of observed event
censor  a vector indicating censored or not at the given times, 0 = censored; 1 = uncensored
plotcens  0: add censored data to the output curve
          1: don’t add censored data to the output curve

Value

A red solid Kaplan Meier curve

Examples

t1 <- c(2, 3, 4, 5, 5, 7, 10, 12, 15)
c1 <- c(0, 0, 1, 0, 0, 1, 0, 0)
km_redsolid(t1, c1, 0)
Description

A function that iterates to compute the p-values from the backward elimination procedure (Han et al. 2014)

Usage

```r
loopcuts(time, censor, cuttimes, mono)
```

Arguments

time: a sequence of time
censor: a vector indicating censored or not at the given times, 0 = censored; 1 = uncensored
cuttimes: unique, sorted, possible times to make the cuts, including 0 and the ending time
mono: 0: 2-sided hypothesis: H0: lam1 is equal to lam2; H1: lam1 is not equal to lam2
1: 1-sided hypothesis: H0: lam1 is greater than or equal to lam2; H1: lam1 is less than lam2
2: 1-sided hypothesis: H0: lam1 is less than or equal to lam2; H1: lam1 is greater than lam2

Value

the times in the backward elimination procedure and the corresponding p-values for each change-point in the iteration

Examples

```r
data(loopcuts_t_c)
data(loopcuts_cut)
time = loopcuts_t_c[, 1]
censor = loopcuts_t_c[, 2]
loopcuts(time, censor, loopcuts_cut, 1)
```
loopcuts_onestep  \textit{Change-point p-values at given time points}

\textbf{Description}

This function computes the p-values at the current time points in input "time"

\textbf{Usage}

\texttt{loopcuts_onestep(time, censor, cuttimes, mono)}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{time} \hspace{1cm} a sequence of time
  \item \texttt{censor} \hspace{1cm} a vector indicating censored or not at the given times, 0 = censored; 1 = uncensored
  \item \texttt{cuttimes} \hspace{1cm} unique, sorted, possible times to make the cuts, including 0 and the ending time
  \item \texttt{mono} \hspace{1cm} 0: 2-sided hypothesis: H0: lam1 is equal to lam2; H1: lam1 is not equal to lam2 1: 1-sided hypothesis: H0: lam1 is greater than or equal to lam2; H1: lam1 is less than lam2 2: 1-sided hypothesis: H0: lam1 is less than or equal to lam2; H1: lam1 is greater than lam2
\end{itemize}

\textbf{Value}

P-values at for all time points in "time"

\textbf{Examples}

\begin{verbatim}
data(loopcuts_t_c)
time = loopcuts_t_c[,1]
censor = loopcuts_t_c[,2]
loopcuts_onestep(time, censor, 28.03013699, 1)
\end{verbatim}

loopcuts_t_c  \textit{Example data for loopcut_times_censoring}

\textbf{Description}

Example data for loopcut_times_censoring

\textbf{Usage}

\texttt{data(loopcuts_t_c)}
loopcuts_umbrella

Description
A function that iterates to compute the p-values from the backward elimination procedure (Han et al. 2014) with umbrella alternative order restriction.

Usage
loopcuts_umbrella(time, censor, cuttimes, mono)

Arguments
- time: a sequence of time
- censor: a vector indicating censored or not at the given times, 0 = censored; 1 = uncensored
- cuttimes: unique, sorted, possible times to make the cuts, including 0 and the ending time
- mono: 0: 2-sided hypothesis: H0: lam1 is equal to lam2; H1: lam1 is not equal to lam2
  1: 1-sided hypothesis: H0: lam1 is greater than or equal to lam2; H1: lam1 is less than lam2
  2: 1-sided hypothesis: H0: lam1 is less than or equal to lam2; H1: lam1 is greater than lam2

Value
the times in the backward elimination procedure and the corresponding p-values for each change-point in the iteration

Examples
```
data(loopcuts_t_c)
data(loopcuts_umbrella_cuttimes_mono)
time = loopcuts_t_c[,1]
censor = loopcuts_t_c[,2]
cuttimes = loopcuts_umbrella_cuttimes_mono[,1]
mono = loopcuts_umbrella_cuttimes_mono[,2]
loopcuts_umbrella(time, censor, cuttimes, mono)
```
Example data for loopcut_umbrella

**Description**
Example data for loopcut_umbrella

**Usage**
```r
data(loopcuts_umbrella_cuttimes_mono)
```

Example data for loopcut_onestep

**Description**
Example data for loopcut_onestep

**Usage**
```r
data(loopcut_onestep_data)
```

PAVA order restriction under decreasing failure rate (DFR)

**Description**
This function imposes the PAVA DFR order restriction by eliminating change-points violating the restriction

**Usage**
```r
pava_dfr(time_die, ttot, deaths)
```

**Arguments**
- `time_die`: event times
- `ttot`: the total time on test (ttot) corresponding to the event times
- `deaths`: the number of deaths at each event time
**pava_dfrd**

**Value**

time2: the event times after PAVA
ttot2: the corresponding ttot
deaths2: the corresponding number of deaths

**Examples**

data(pava_dfrd)
t_d = pava_dfrd[,1]
t = pava_dfrd[,2]
d = pava_dfrd[,3]
pava_dfr(t_d, t, d)

**Description**

Example data for pava

**Usage**

data(pava_dfrd)

---

**pava_ifr**

**PAVA order restriction under increasing failure rate (IFR)**

**Description**

This function imposes the PAVA IFR order restriction by eliminating change-points violating the restriction

**Usage**

pava_ifr(time_die, ttot, deaths)

**Arguments**

time_die: event times
ttot: the total time on test (ttot) corresponding to the event times
deaths: the number of deaths at each event time

**Value**

time2: the event times after PAVA
ttot2: the corresponding ttot after PAVA
deaths2: the corresponding number of deaths after PAVA
Examples

```r
data(pava_dfrd)
t_d = pava_dfrd[,1]
t = pava_dfrd[,2]
d = pava_dfrd[,3]
pava_ifr(t_d, t, d)
```

---

**Description**

This function estimates the survival probability at `tx` when a piecewise exponential distribution is fitted to `(times, cens)` `cens = 0` for censored, `cens = 1` for uncensored. The change point is `tchange` and `lamest` is the estimated parameters.

**Usage**

```r
pexeest(times, cens, tchange, tx)
```

**Arguments**

- `times`: All the event/censoring times used to fit the model
- `cens`: Censoring status used to fit the model
- `tchange`: Change-points
- `tx`: Time points to estimate the survival probability

**Value**

`quan` survival probability `lamest` Lambda estimates for time periods divided by the change-points

**Examples**

```r
data(pexeest_times_censoring)
data(t100)
times = pexeest_times_censoring[,1]
cens = pexeest_times_censoring[,2]
pexeest(times, cens, 28.03014, t100)
```
Example data for pexeest_times_censoring

Description

Example data for pexeest_times_censoring

Usage

data(pexeest_times_censoring)

RPEXE.RPEXT  Reduced Piecewise Exponential Estimate/Test Software

Description

This reduced piecewise exponential survival software implements the likelihood ratio test and backward elimination procedure in Han, Schell, and Kim (2012, 2014), and Han et al. (2016). Inputs to the program can be either times when events/censoring occur or the vectors of total time on test and the number of events. Outputs of the programs are times and the corresponding p-values in the backward elimination. Details about the model and implementation are given in Han et al. 2014. This program can run in R version 3.2.2 and above.

References


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<th>Description</th>
<th>RPEXE main function</th>
</tr>
</thead>
<tbody>
<tr>
<td>This is the RPEXE main function taking inputs including time, censoring, change-point candidates, order restriction, critical value, and display position. This function produces the RPEXE estimate. The prediction of the survival probability will be made on 100 equally spaced time points within the range of the event times based on the piecewise exponential estimate determined by all the change-points.</td>
<td></td>
</tr>
</tbody>
</table>

| Usage | RPEXEv1_2(times,censoring,cuttimes=NULL, monotone=0, criticalp=-1, pos = 0) |

<table>
<thead>
<tr>
<th>Arguments</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>times</td>
<td>A sequence of times where the events occur</td>
</tr>
<tr>
<td>censoring</td>
<td>A sequence of dichotomous values indicating censored or not (0=censored and 1=not censored)</td>
</tr>
<tr>
<td>cuttimes</td>
<td>A vector of unique, sorted, possible times to make the cuts. When it’s set to NULL, it’s the Default value, which is sorted event times from small to large.</td>
</tr>
<tr>
<td>monotone</td>
<td>An input having indicating the monotonicity assumption – 0: no monotonic assumption (default) – 1: failure rate is decreasing over time – 2: failure rate is increasing over time – 3: monotonic failure rate – 4: failure rate is increasing and then decreasing – 5: failure rate is decreasing and then increasing – 6: failure rate is increasing and then decreasing with the peak removed first – 7: failure rate is decreasing and then increasing with the peak removed first</td>
</tr>
<tr>
<td>criticalp</td>
<td>The critical (naive) p-value cutoff where all p-values in the backward elimination that are lower than this will be regarded as being significant. For example, at type I error rate 0.05, the critical p-value was 0.004 in the real example of Han et al. (2014). Default == -1 (equivalent to NA).</td>
</tr>
<tr>
<td>pos</td>
<td>The position of the legend. Can be 0 or 1. The legend will be on the topright if set to 0. The legend will be on the bottomleft if set to 1. Default is 0.</td>
</tr>
</tbody>
</table>

| Value | times: event/censoring times taking out from the backward elimination p-values: p-values corresponding to "times" times_c: significant change-points pvalues_c: critical p-values that are smaller than the critical p-value trend: trend information struct: structure information for multiple order restrictions changeT: change-point time of trend for umbrella alternatives. |
Examples

t1 <- c(2,3,4,5,5,7,10,12,15)
c1 <- c(0,0,1,0,0,1,0,0)
RPEXEvl_2(t1, c1, monotone = 1, criticalp = 0.05, pos = 0)

---

**simple**

None Small Cell Lung cancer data

---

**Description**

A dataset non-small-cell lung cancer trial data from Simon et al. (2011)

**Usage**

data(simple)

**Details**

- first column - censor: censoring status; 0=censored, 1=event.
- second column - times: time to event

**References**


---

**t100**

Example data for pexeest_tx

---

**Description**

Example data for pexeest_tx

**Usage**

data(t100)
**totaltest**  
*total time on test*

**Description**

Function `totaltest` computes total-time-on-test.

**Usage**

```r
totaltest(time, censor)
```

**Arguments**

- `time`  
  event/censoring times

- `censor`  
  censoring status

**Value**

time_die time points where events occur (in ascending order)  
ttot total time on test corresponding to each time point in "time_die"  
deaths number of death corresponding to each time point in "time_die"

**Examples**

```r
t1 <- c(2,3,4,5,5,7,10,12,15)  
c1 <- c(0,0,1,0,0,1,0,0)  
totaltest(t1, c1)
```

---

**umbrella**  
*Umbrella alternative.*

**Description**

Using the umbrella alternative to merge certain entries to make the sequence of ttot/deaths to increase then decrease or to decrease then increase. Note that the pava function imposes non-decreasing or non-increasing order. This function directly uses function pava().

**Usage**

```r
umbrella(time_die, ttot, deaths, indi)
```

**Arguments**

- `time_die`  
  a sequence of times where deaths happened.

- `ttot`  
  the total time on test between each time point and the previous time point (or 0).

- `deaths`  
  the number of deaths at each time point.

- `indi`  
  an indicator indi == 0: monotonic failure rate (either decrease or increase)  
  indi == 1: denoting the failure rate increase then decrease  
  indi == 2: denoting the failure rate decrease then increase
Value

time2 == the merged time_die after the umbrella alternative order restriction; struct == a structure saves the partition information; label == a note about how the failure rate varies; indx == the position where the change point value is.

Examples

data(pava_dfrd)
t_d = pava_dfrd[,1]
t = pava_dfrd[,2]
d = pava_dfrd[,3]
umbrella(t_d, t, d, 2)
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