

Package: survELtest (via r-universe)

October 17, 2024

Title Comparing Multiple Survival Functions with Crossing Hazards

Version 2.0.1

Description Computing the one-sided/two-sided integrated/maximally selected EL statistics for simultaneous testing, the one-sided/two-sided EL tests for pointwise testing, and an initial test that precedes one-sided testing to exclude the possibility of crossings or alternative orderings among the survival functions.

Depends R (>= 3.5.0)

Imports Iso, nloptr, methods, plyr, survival, stats

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URL <https://github.com/news11/survELtest>

LazyData true

Encoding UTF-8

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Archs i386, x64

RoxygenNote 7.0.1

NeedsCompilation no

Repository <https://news11.r-universe.dev>

RemoteUrl <https://github.com/news11/surveltest>

RemoteRef HEAD

RemoteSha 578335a28dcfcee04c24a44dd031d025422afc80

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hazardcross	<i>Simulated survival data with crossing hazard functions from the piecewise exponential distribution</i>
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Description

The data frame `hazardcross` is obtained as follows. The survival time is generated from the piecewise exponential model displayed in the left column of Figure 1 in Chang and McKeague (2016). The censoring distributions (the same in each arm) is specified to be uniform with administrative censoring at $t = 10$, and a censoring rate of 25% in the first group.

Usage

```
hazardcross
```

Format

The `hazardcross` is a data frame with 100 observations of 3 variables, and has the following columns:

- `time` the observed times to first remission and censoring times
- `sensor` the censoring indicator
- `group` the grouping variable

References

H. Chang, I.W. McKeague, "Empirical likelihood based tests for stochastic ordering under right censorship," *Electronic Journal of Statistics*, Vol. 10, No. 2, pp. 2511-2536, (2016).

See Also

[nocrossings](#), [ptwiseELtest](#), [supELtest](#)

hazardcross_Weibull	<i>Simulated survival data with crossing hazard functions from the Weibull distribution</i>
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Description

The data frame `hazardcross_Weibull` is obtained as follows. The survival time is generated from the Weibull model displayed as the solid and dashed lines in the right panel of Figure 1 in Chang and McKeague (2019). The censoring distributions (the same in each arm) is specified to be uniform with administrative censoring at $t = 10$, and a censoring rate of 25% in the first group.

Usage

```
hazardcross_Weibull
```

Format

The `hazardcross_Weibull` is a data frame with 100 observations of 3 variables, and has the following columns:

- `time` the observed times to first remission and censoring times
- `sensor` the censoring indicator
- `group` the grouping variable

References

H. Chang, I.W. McKeague, "Nonparametric testing for multiple survival functions with non-inferiority margins," *Annals of Statistics*, Vol. 47, No. 1, pp. 205-232, (2019).

See Also

[nocrossings](#), [ptwiseELtest](#), [supELtest](#)

hepatitis	<i>Severe alcoholic hepatitis data</i>
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Description

The data frame `hepatitis` is obtained by digitizing the published Kaplan-Meier curves in Nguyen-Khac et al. (2011). The method of digitizing is described in Guyot et al. (2012). See [intELtest](#) for the application.

Usage

```
hepatitis
```

Format

The hepatitis is a data frame with 174 observations of 3 variables, and has the following columns:

- time the observed survival and censoring times
- censor the censoring indicator
- group the grouping variable

Source

Nguyen-Khac et al., "Glucocorticoids plus N-Acetylcysteine in Severe Alcoholic Hepatitis," *The New England Journal of Medicine*, Vol. 365, No. 19, pp. 1781-1789 (2011). <http://www.nejm.org/doi/full/10.1056/NEJMoa1101214#t=article>

References

P. Guyot, A. E. Ades, M. J. N. M. Ouwens, and N. J. Welton, "Enhanced secondary analysis of survival data: reconstructing the data from published Kaplan-Meier survival curves," *BMC Medical Research Methodology*, 12(1):9. <http://bmcmedresmethodol.biomedcentral.com/articles/10.1186/1471-2288-12-9>

- Nguyen-Khac et al., "Glucocorticoids plus N-Acetylcysteine in Severe Alcoholic Hepatitis," *The New England Journal of Medicine*, Vol. 365, No. 19, pp. 1781-1789 (2011). <http://www.nejm.org/doi/full/10.1056/NEJMoa1101214#t=article>
- P. Guyot, A. E. Ades, M. J. N. M. Ouwens, and N. J. Welton, "Enhanced secondary analysis of survival data: reconstructing the data from published Kaplan-Meier survival curves," *BMC Medical Research Methodology*, 12(1):9. <http://bmcmedresmethodol.biomedcentral.com/articles/10.1186/1471-2288-12-9>

See Also

[intELtest](#), [supELtest](#), [ptwiseELtest](#), [nocrossings](#)

intELtest

The integrated EL test

Description

intELtest gives a class of integrated EL statistics:

$$\sum_{i=1}^m w_i \cdot \{-2 \log R(t_i)\},$$

where $R(t)$ is the EL ratio that compares the survival functions at each given time t , w_i is the weight at each t_i , and $0 < t_1 < \dots < t_m < \infty$ are the (ordered) observed uncensored times at which the Kaplan-Meier estimate is positive and less than 1 for each sample.

Usage

```
intELtest(
  formula,
  data = NULL,
  group_order = NULL,
  t1 = 0,
  t2 = Inf,
  sided = 2,
  nboot = 1000,
  wt = "p.event",
  alpha = 0.05,
  seed = 1011,
  nlimit = 200
)
```

Arguments

formula	a formula object with a Surv object as the response on the left of the \sim operator and the grouping variable as the term on the right. The Surv object involves two variables: the observed survival and censoring times, and the censoring indicator, which takes a value of 1 if the observed time is uncensored and 0 otherwise. The grouping variable takes different values for different groups.
data	an optional data frame containing the variables in the formula: the observed survival and censoring times, the censoring indicator, and the grouping variable. If not found in data, the variables in the formula should be already defined by the user or in attached R objects. The default is the data frame with three columns of variables taken from the formula: column 1 contains the observed survival and censoring times, column 2 the censoring indicator, and column 3 the grouping variable.
group_order	a k -vector containing the values of the grouping variable, with the j -th element being the group hypothesized to have the j -th highest survival rates, $j = 1, \dots, k$. The default is the vector of sorted grouping variables.
t1	the first endpoint of a prespecified time interval, if any, to which the comparison of the survival functions is restricted. The default value is 0.
t2	the second endpoint of a prespecified time interval, if any, to which the comparison of the survival functions is restricted. The default value is ∞ .
sided	2 if two-sided test, and 1 if one-sided test. The default value is 2.
nboot	the number of bootstrap replications in calculating critical values for the tests. The default value is 1000.
wt	the name of the weight for the integrated EL statistics: "p.event", "dF", or "dt". The default is "p.event".
alpha	the pre-specified significance level of the tests. The default value is 0.05.
seed	the seed for the random number generator in R, for generating bootstrap samples needed to calculate the critical values for the tests. The default value is 1011.

`nlimit` a number used to calculate `nsplit = m/nlimit`, the number of parts into which the calculation of the `nboot` bootstrap replications is split. The use of this variable can make computation faster when the number of time points m is large. The default value for `nlimit` is 200.

Details

There are three options for the weight w_i :

- (`wt = "p.event"`)
This default option is an objective weight,

$$w_i = \frac{d_i}{n},$$

which assigns weight proportional to the number of events d_i at each observed uncensored time t_i . Here n is the total sample size.

- (`wt = "dF"`)
Inspired by the integral-type statistics considered in Barmi and McKeague (2013), another weight function is

$$w_i = \hat{F}(t_i) - \hat{F}(t_{i-1}),$$

for $i = 1, \dots, m$, where $\hat{F}(t) = 1 - \hat{S}(t)$, $\hat{S}(t)$ is the pooled KM estimator, and $t_0 \equiv 0$. This reduces to the objective weight when there is no censoring. The resulting I_n can be seen as an empirical version of the expected negative two times log EL ratio under H_0 .

- (`wt = "dt"`)
Inspired by the integral-type statistics considered in Pepe and Fleming (1989), another weight function is

$$w_i = t_{i+1} - t_i,$$

for $i = 1, \dots, m$, where $t_{m+1} \equiv t_m$. This gives more weight to the time intervals where there are fewer observed uncensored times, but can be affected by extreme observations.

Value

`intELtest` returns a `intELtest` object, a list with 15 elements:

- `call` the function call
- `teststat` the resulting integrated EL statistics
- `critval` the critical value based on bootstrap
- `pvalue` the p-value of the test
- `formula` the value of the input argument of `intELtest`
- `data` the value of the input argument of `intELtest`
- `group_order` the value of the input argument of `intELtest`
- `t1` the value of the input argument of `intELtest`
- `t2` the value of the input argument of `intELtest`
- `sided` the value of the input argument of `intELtest`
- `nboot` the value of the input argument of `intELtest`

- wt the value of the input argument of intELtest
- alpha the value of the input argument of intELtest
- seed the value of the input argument of intELtest
- nlimit the value of the input argument of intELtest

Methods defined for intELtest objects are provided for print and summary.

References

- H. Chang, I.W. McKeague, "Nonparametric testing for multiple survival functions with non-inferiority margins," *Annals of Statistics*, Vol. 47, No. 1, pp. 205-232, (2019).
- M. S. Pepe and T. R. Fleming, "Weighted Kaplan-Meier Statistics: A Class of Distance Tests for Censored Survival Data," *Biometrics*, Vol. 45, No. 2, pp. 497-507 (1989). https://www.jstor.org/stable/2531492?seq=1#page_scan_tab_contents
- H. E. Barmi and I.W. McKeague, "Empirical likelihood-based tests for stochastic ordering," *Bernoulli*, Vol. 19, No. 1, pp. 295-307 (2013). <https://projecteuclid.org/euclid.bj/1358531751>

See Also

[hepatitis](#), [supELtest](#), [ptwiseELtest](#), [nocrossings](#), [print.intELtest](#), [summary.intELtest](#)

Examples

```
library(survELtest)
intELtest(survival::Surv(hepatitis$time, hepatitis$censor) ~ hepatitis$group)

## OUTPUT:
## Call:
## intELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
## hepatitis$group)
##
## Two-sided integrated EL test statistic = 1.42, p = 0.007
```

nocrossings

The test that excludes the possibility of crossings or alternative orderings among the survival functions

Description

The test nocrossings should be used before one-sided testing via [intELtest](#) or [supELtest](#) to exclude the possibility of crossings or alternative orderings among the survival functions.

Usage

```
nocrossings(
  formula,
  data = NULL,
  group_order = NULL,
  t1 = 0,
  t2 = Inf,
  sided = 2,
  nboot = 1000,
  alpha = 0.05,
  seed = 1011,
  nlimit = 200
)
```

Arguments

formula	a formula object with a Surv object as the response on the left of the \sim operator and the grouping variable as the term on the right. The Surv object involves two variables: the observed survival and censoring times, and the censoring indicator, which takes a value of 1 if the observed time is uncensored and 0 otherwise. The grouping variable takes different values for different groups.
data	an optional data frame containing the variables in the formula: the observed survival and censoring times, the censoring indicator, and the grouping variable. If not found in data, the variables in the formula should be already defined by the user or in attached R objects. The default is the data frame with three columns of variables taken from the formula: column 1 contains the observed survival and censoring times, column 2 the censoring indicator, and column 3 the grouping variable.
group_order	a k -vector containing the values of the grouping variable, with the j -th element being the group hypothesized to have the j -th highest survival rates, $j = 1, \dots, k$. The default is the vector of sorted grouping variables.
t1	the first endpoint of a prespecified time interval, if any, to which the comparison of the survival functions is restricted. The default value is 0.
t2	the second endpoint of a prespecified time interval, if any, to which the comparison of the survival functions is restricted. The default value is ∞ .
sided	2 if two-sided test, and 1 if one-sided test. The default value is 2.
nboot	the number of bootstrap replications in calculating critical values for the tests. The default value is 1000.
alpha	the pre-specified significance level of the tests. The default value is 0.05.
seed	the seed for the random number generator in R, for generating bootstrap samples needed to calculate the critical values for the tests. The default value is 1011.
nlimit	a number used to calculate $n_{split} = m/nlimit$, the number of parts into which the calculation of the nboot bootstrap replications is split. The use of this variable can make computation faster when the number of time points m is large. The default value for nlimit is 200.

Value

nocrossings returns a nocrossings object, a list with 12 elements:

- call the function call
- decision 1 for rejection of the null hypothesis that there are crossings or alternative orderings among the survival functions, and 0 otherwise
- formula the value of the input argument of nocrossings
- data the value of the input argument of nocrossings
- group_order the value of the input argument of nocrossings
- t1 the value of the input argument of nocrossings
- t2 the value of the input argument of nocrossings
- sided the value of the input argument of nocrossings
- nboot the value of the input argument of nocrossings
- alpha the value of the input argument of nocrossings
- seed the value of the input argument of nocrossings
- nlimit the value of the input argument of nocrossings

Methods defined for nocrossings objects are provided for print and summary.

References

- H. Chang, I.W. McKeague, "Empirical likelihood based tests for stochastic ordering under right censorship," *Electronic Journal of Statistics*, Vol. 10, No. 2, pp. 2511-2536 (2016).
- H. Chang, I.W. McKeague, "Nonparametric testing for multiple survival functions with non-inferiority margins," *Annals of Statistics*, Vol. 47, No. 1, pp. 205-232, (2019).

See Also

[hepatitis](#), [intELtest](#), [supELtest](#), [ptwiseELtest](#), [print.nocrossings](#), [summary.nocrossings](#)

Examples

```
library(survELtest)
nocrossings(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)

## OUTPUT:
## Call:
## nocrossings(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
## Decision = 1
```

print.intELtest	<i>Print an intELtest object</i>
-----------------	----------------------------------

Description

Print the integrated EL statistics and the p-value of the test.

Usage

```
## S3 method for class 'intELtest'  
print(x, digits = max(3L, getOption("digits") - 3L), quiet = FALSE, ...)
```

Arguments

x	the result of a call to the intELtest function
digits	significant digits to print, the default value is max(3L, getOption("digits") - 3L)
quiet	a logical indicating whether to reduce the amount of output or not, the default value is FALSE
...	for future method

See Also

[hepatitis](#), [intELtest](#), [summary.intELtest](#)

Examples

```
library(survELtest)  
result = intELtest(survival::Surv(hepatitis$time, hepatitis$censor) ~ hepatitis$group)  
print(result)  
  
## OUTPUT:  
## Call:  
## intELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~  
## hepatitis$group)  
##  
## Two-sided integrated EL test statistic = 1.42, p = 0.007
```

print.nocrossings *Print a nocrossings object*

Description

Returns the decision for rejection of the null hypothesis that there are crossings or alternative orderings among the survival functions.

Usage

```
## S3 method for class 'nocrossings'  
print(x, digits = max(3L, getOption("digits") - 3L), quiet = FALSE, ...)
```

Arguments

x	the result of a call to the nocrossings function
digits	significant digits to print, the default value is max(3L, getOption("digits") - 3L)
quiet	a logical indicating whether to reduce the amount of output or not, the default value is FALSE
...	for future method

See Also

[hepatitis](#), [nocrossings](#), [summary.nocrossings](#)

Examples

```
library(survELtest)  
result = nocrossings(survival::Surv(hepatitis$time, hepatitis$censor)~  
                    hepatitis$group, sided = 1)  
print(result)  
  
## OUTPUT:  
## Call:  
## nocrossings(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~  
## hepatitis$group, sided = 1)  
##  
## Decision = 1
```

```
print.ptwiseELtest      Print a ptwiseELtest object
```

Description

Print some summary statistics for the observed uncensored time points, and the decisions, statistics, and critical values of the pointwise EL tests at those time points.

Usage

```
## S3 method for class 'ptwiseELtest'
print(x, digits = max(3L, getOption("digits") - 3L), quiet = FALSE, ...)
```

Arguments

x	the result of a call to the ptwiseELtest function
digits	significant digits to print, the default value is <code>max(3L, getOption("digits") - 3L)</code>
quiet	a logical indicating whether to reduce the amount of output or not, the default value is FALSE
...	for future method

See Also

[hepatitis](#), [ptwiseELtest](#), [summary.ptwiseELtest](#)

Examples

```
library(survELtest)
result = ptwiseELtest(survival::Surv(hepatitis$time, hepatitis$censor)~
                      hepatitis$group, sided = 1)
print(result)

## OUTPUT:
## Call:
## ptwiseELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
## hepatitis$group, sided = 1)
##
## Range of time_pts is from 5.2 to 153.1
## 30 out of 45 decisions are 1, the other 15 decisions are 0
## ----
## Summary of stat_ptwise:
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.000  2.293  3.694  4.263  6.288 10.360
## ----
## Summary of critval_ptwise:
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  2.117  2.346  2.483  2.509  2.669  2.951
```

```
print.supELtest      Print a supELtest object
```

Description

Print the maximally selected EL statistics and the p-value of the test.

Usage

```
## S3 method for class 'supELtest'
print(x, digits = max(3L, getOption("digits") - 3L), quiet = FALSE, ...)
```

Arguments

x	the result of a call to the supELtest function
digits	significant digits to print, the default value is max(3L, getOption("digits") - 3L)
quiet	a logical indicating whether to reduce the amount of output or not, the default value is FALSE
...	for future method

See Also

[hepatitis](#), [supELtest](#), [summary.supELtest](#)

Examples

```
library(survELtest)
nocrossings(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)

## OUTPUT:
## Call:
## nocrossings(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
## Decision = 1

## A decision value of 1 means the case of crossings or alternative orderings among the
## survival functions is excluded. Thus, we can proceed to the one-sided test.

result = supELtest(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)
print(result)

## OUTPUT:
## Call:
## supELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
```

```
## hepatitis$group, sided = 1)
##
## One-sided maximally selected EL test statistic = 10.36, p = 0.006
```

ptwiseELtest

The pointwise EL testing

Description

ptwiseELtest gives pointwise EL testing to compare the survival curves at each time point.

Usage

```
ptwiseELtest(
  formula,
  data = NULL,
  group_order = NULL,
  t1 = 0,
  t2 = Inf,
  sided = 2,
  nboot = 1000,
  alpha = 0.05,
  seed = 1011,
  nlimit = 200
)
```

Arguments

formula	a formula object with a Surv object as the response on the left of the \sim operator and the grouping variable as the term on the right. The Surv object involves two variables: the observed survival and censoring times, and the censoring indicator, which takes a value of 1 if the observed time is uncensored and 0 otherwise. The grouping variable takes different values for different groups.
data	an optional data frame containing the variables in the formula: the observed survival and censoring times, the censoring indicator, and the grouping variable. If not found in data, the variables in the formula should be already defined by the user or in attached R objects. The default is the data frame with three columns of variables taken from the formula: column 1 contains the observed survival and censoring times, column 2 the censoring indicator, and column 3 the grouping variable.
group_order	a k -vector containing the values of the grouping variable, with the j -th element being the group hypothesized to have the j -th highest survival rates, $j = 1, \dots, k$. The default is the vector of sorted grouping variables.
t1	the first endpoint of a prespecified time interval, if any, to which the comparison of the survival functions is restricted. The default value is 0.
t2	the second endpoint of a prespecified time interval, if any, to which the comparison of the survival functions is restricted. The default value is ∞ .

sided	2 if two-sided test, and 1 if one-sided test. The default value is 2.
nboot	the number of bootstrap replications in calculating critical values for the tests. The default value is 1000.
alpha	the pre-specified significance level of the tests. The default value is 0.05.
seed	the seed for the random number generator in R, for generating bootstrap samples needed to calculate the critical values for the tests. The default value is 1011.
nlimit	a number used to calculate $n_{split} = m/nlimit$, the number of parts into which the calculation of the nboot bootstrap replications is split. The use of this variable can make computation faster when the number of time points m is large. The default value for nlimit is 200.

Value

ptwiseELtest returns a ptwiseELtest object, a list with 12 elements:

- call the function call
- result_dataframe a dataframe with time_pts in the first column, decision in the second column, stat_ptwise in the third column and critval_ptwise in the fourth column.
 - time_pts a vector containing the observed uncensored time points at which the Kaplan—Meier estimate is positive and less than 1 for each sample.
 - decision a vector containing the decisions of the pointwise EL tests at time_pts. The decision at each of time_pts is 1 for rejection of the null hypothesis that the survival functions are the same at the specific time point, and 0 otherwise.
 - stat_ptwise a vector containing the pointwise EL statistics at time_pts.
 - critval_ptwise a vector containing the critical values for pointwise EL testing at time_pts.
- formula the value of the input argument of ptwiseELtest
- data the value of the input argument of ptwiseELtest
- group_order the value of the input argument of ptwiseELtest
- t1 the value of the input argument of ptwiseELtest
- t2 the value of the input argument of ptwiseELtest
- sided the value of the input argument of ptwiseELtest
- nboot the value of the input argument of ptwiseELtest
- alpha the value of the input argument of ptwiseELtest
- seed the value of the input argument of ptwiseELtest
- nlimit the value of the input argument of ptwiseELtest

Methods defined for ptwiseELtest objects are provided for print and summary.

See Also

[hepatitis](#), [intELtest](#), [supELtest](#), [nocrossings](#), [print.ptwiseELtest](#), [summary.ptwiseELtest](#)

Examples

```

library(survELtest)
ptwiseELtest(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)

## OUTPUT:
## Call:
## ptwiseELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
## Range of time_pts is from 5.2 to 153.1
## 30 out of 45 decisions are 1, the other 15 decisions are 0
## -----
## Summary of stat_ptwise:
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000  2.293  3.694  4.263  6.288 10.360
##   -----
## Summary of critval_ptwise:
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   2.117  2.346  2.483  2.509  2.669  2.951

```

summary.intELtest *Summary function for intELtest object*

Description

Returns a list containing the integrated EL statistics, the critical value based on bootstrap, and the p-value of the test.

Usage

```

## S3 method for class 'intELtest'
summary(object, digits = max(3L, getOption("digits") - 3L), quiet = FALSE, ...)

```

Arguments

object	the result of a call to the intELtest function
digits	significant digits to print, the default value is max(3L, getOption("digits") - 3L)
quiet	a logical indicating whether to reduce the amount of output or not, the default value is FALSE
...	for future method

Value

summary.intELtest returns a list with following components:

- call the statement used to create the intELtest object
- teststat the resulting integrated EL statistics
- critval the critical value based on bootstrap
- pvalue the p-value of the test
- sided the value of the input argument of intELtest
- alpha the value of the input argument of intELtest

See Also

[hepatitis](#), [intELtest](#), [print.intELtest](#)

Examples

```
library(survELtest)
result = intELtest(survival::Surv(hepatitis$time, hepatitis$censor) ~ hepatitis$group)
summary(result)

## OUTPUT:
## Call:
## intELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group)
##
## Two-sided integrated EL test statistic = 1.42, p = 0.007,
## critical value based on bootstrap = 0.875 at a significance level of 0.05
```

summary.nocrossings *Summary function for nocrossings object*

Description

Returns the decision for rejection of the null hypothesis that there are crossings or alternative orderings among the survival functions.

Usage

```
## S3 method for class 'nocrossings'
summary(object, digits = max(3L, getOption("digits") - 3L), quiet = FALSE, ...)
```

Arguments

object	the result of a call to the nocrossings function
digits	significant digits to print, the default value is max(3L, getOption("digits") - 3L)
quiet	a logical indicating whether to reduce the amount of output or not, the default value is FALSE
...	for future method

Value

summary.nocrossings returns a list with following components:

- call the statement used to create the nocrossings object
- decision 1 for rejection of the null hypothesis that there are crossings or alternative orderings among the survival functions, and 0 otherwise

See Also

[hepatitis](#), [nocrossings](#), [print.nocrossings](#)

Examples

```
library(survELtest)
result = nocrossings(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)
summary(result)

## OUTPUT:
## Call:
## nocrossings(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
## Decision = 1
```

summary.ptwiseELtest *Summary function for ptwiseELtest object*

Description

Returns a list with a data frame containing the observed uncensored time points, and the decisions, statistics, and critical values of the pointwise EL tests at those time points.

Usage

```
## S3 method for class 'ptwiseELtest'
summary(object, digits = max(3L, getOption("digits") - 3L), quiet = FALSE, ...)
```

Arguments

object	the result of a call to the ptwiseELtest function
digits	significant digits to print, the default value is max(3L, getOption("digits") - 3L)
quiet	a logical indicating whether to reduce the amount of output or not, the default value is FALSE
...	for future method

Value

summary.ptwiseELtest returns a list with following components:

- call the statement used to create the ptwiseELtest object
- result_dataframe a dataframe with time_pts in the first column, decision in the second column, stat_ptwise in the third column and critval_ptwise in the fourth column.
 - time_pts a vector containing the observed uncensored time points at which the Kaplan—Meier estimate is positive and less than 1 for each sample.
 - decision a vector containing the decisions of the pointwise EL tests at time_pts. The decision at each of time_pts is 1 for rejection of the null hypothesis that the survival functions are the same at the specific time point, and 0 otherwise.
 - stat_ptwise a vector containing the pointwise EL statistics at time_pts.
 - critval_ptwise a vector containing the critical values for pointwise EL testing at time_pts.

See Also

[hepatitis](#), [ptwiseELtest](#), [print.ptwiseELtest](#)

Examples

```
library(survELtest)
result = ptwiseELtest(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)
summary(result)

## OUTPUT:
## Call:
## ptwiseELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
##   time_pts decision stat_ptwise critval_ptwise
## 1      5.2         0      0.3005         2.951
## 2      9.7         0      0.0000         2.833
## 3     12.9         0      0.1627         2.748
## 4     14.0         0      0.6114         2.583
## 5     14.9         0      2.0010         2.780
## 6     15.7         1      3.7873         2.764
## 7     18.0         1      3.0722         2.652
## 8     18.9         0      1.8878         2.454
## 9     19.2         1      2.5896         2.339
## 10    19.7         0      1.6133         2.601
## 11    20.0         0      2.2393         2.383
## 12    21.7         1      3.6936         2.192
## 13    24.0         1      4.5083         2.300
## 14    24.9         1      5.3743         2.391
## 15    26.0         1      6.2879         2.253
## 16    26.9         1      9.2827         2.117
## 17    27.8         1     10.3581         2.209
## 18    28.0         1      6.9862         2.317
## 19    30.0         1      7.9190         2.346
```

## 20	31.2	1	6.5074	2.318
## 21	32.1	1	4.9709	2.310
## 22	34.1	1	5.7455	2.360
## 23	36.1	1	6.5627	2.244
## 24	44.9	1	5.4374	2.363
## 25	45.2	1	6.2240	2.416
## 26	47.8	1	7.0519	2.409
## 27	54.1	1	7.9198	2.427
## 28	54.9	1	6.7260	2.310
## 29	58.1	1	7.5667	2.456
## 30	59.8	1	7.2524	2.483
## 31	63.2	1	6.1770	2.511
## 32	70.4	1	5.2110	2.562
## 33	76.1	1	4.3461	2.683
## 34	80.1	1	3.5753	2.744
## 35	81.3	1	2.8926	2.467
## 36	82.1	0	2.2925	2.669
## 37	90.1	1	2.7908	2.543
## 38	92.1	0	2.2120	2.523
## 39	95.0	0	1.7079	2.755
## 40	99.0	0	2.1383	2.762
## 41	108.2	0	2.6206	2.652
## 42	109.9	1	3.1475	2.630
## 43	117.0	0	2.5398	2.646
## 44	148.8	1	3.0555	2.685
## 45	153.1	0	2.4658	2.774

summary.supELtest	<i>Summary function for supELtest object</i>
-------------------	--

Description

Returns a list containing the maximally selected EL statistics, the critical value based on bootstrap, and the p-value of the test.

Usage

```
## S3 method for class 'supELtest'
summary(object, digits = max(3L, getOption("digits") - 3L), quiet = FALSE, ...)
```

Arguments

object	the result of a call to the supEL test function
digits	significant digits to print, the default value is <code>max(3L, getOption("digits") - 3L)</code>
quiet	a logical indicating whether to reduce the amount of output or not, the default value is <code>FALSE</code>
...	for future method

Value

summary.supELtest returns a list with following components:

- call the statement used to create the supELtest object
- teststat the resulting integrated EL statistics
- critval the critical value based on bootstrap
- pvalue the p-value of the test
- sided the value of the input argument of supELtest
- alpha the value of the input argument of supELtest

See Also

[hepatitis](#), [supELtest](#), [print.supELtest](#)

Examples

```
library(survELtest)
nocrossings(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)

## OUTPUT:
## Call:
## nocrossings(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
## Decision = 1

## A decision value of 1 means the case of crossings or alternative orderings among the
## survival functions is excluded. Thus, we can proceed to the one-sided test.

result = supELtest(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)
summary(result)

## OUTPUT:
## Call:
## supELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
## One-sided maximally selected EL test statistic = 10.36, p = 0.006,
## critical value based on bootstrap = 6.289 at a significance level of 0.05
```

Description

supELtest provides the maximally selected EL statistics that is better adapted at detecting local differences:

$$\sup_{i=1,\dots,m} \{-2 \log R(t_i)\},$$

where $R(t)$ is the EL ratio that compares the survival functions at each given time t , and $0 < t_1 < \dots < t_m < \infty$ are the (ordered) observed uncensored times at which the Kaplan–Meier estimate is positive and less than 1 for each sample.

Usage

```
supELtest(
  formula,
  data = NULL,
  group_order = NULL,
  t1 = 0,
  t2 = Inf,
  sided = 2,
  nboot = 1000,
  alpha = 0.05,
  seed = 1011,
  nlimit = 200
)
```

Arguments

formula	a formula object with a Surv object as the response on the left of the \sim operator and the grouping variable as the term on the right. The Surv object involves two variables: the observed survival and censoring times, and the censoring indicator, which takes a value of 1 if the observed time is uncensored and 0 otherwise. The grouping variable takes different values for different groups.
data	an optional data frame containing the variables in the formula: the observed survival and censoring times, the censoring indicator, and the grouping variable. If not found in data, the variables in the formula should be already defined by the user or in attached R objects. The default is the data frame with three columns of variables taken from the formula: column 1 contains the observed survival and censoring times, column 2 the censoring indicator, and column 3 the grouping variable.
group_order	a k -vector containing the values of the grouping variable, with the j -th element being the group hypothesized to have the j -th highest survival rates, $j = 1, \dots, k$. The default is the vector of sorted grouping variables.
t1	the first endpoint of a prespecified time interval, if any, to which the comparison of the survival functions is restricted. The default value is 0.
t2	the second endpoint of a prespecified time interval, if any, to which the comparison of the survival functions is restricted. The default value is ∞ .
sided	2 if two-sided test, and 1 if one-sided test. The default value is 2.

nboot	the number of bootstrap replications in calculating critical values for the tests. The default value is 1000.
alpha	the pre-specified significance level of the tests. The default value is 0.05.
seed	the seed for the random number generator in R, for generating bootstrap samples needed to calculate the critical values for the tests. The default value is 1011.
nlimit	a number used to calculate $nsplit = m/nlimit$, the number of parts into which the calculation of the nboot bootstrap replications is split. The use of this variable can make computation faster when the number of time points m is large. The default value for nlimit is 200.

Value

supELtest returns a supELtest object, a list with 14 elements:

- call the function call
- teststat the resulting integrated EL statistics
- critval the critical value based on bootstrap
- pvalue the p-value of the test
- formula the value of the input argument of supELtest
- data the value of the input argument of supELtest
- group_order the value of the input argument of supELtest
- t1 the value of the input argument of supELtest
- t2 the value of the input argument of supELtest
- sided the value of the input argument of supELtest
- nboot the value of the input argument of supELtest
- alpha the value of the input argument of supELtest
- seed the value of the input argument of supELtest
- nlimit the value of the input argument of supELtest

Methods defined for supELtest objects are provided for print and summary.

References

- H. Chang, I.W. McKeague, "Empirical likelihood based tests for stochastic ordering under right censorship," *Electronic Journal of Statistics*, Vol. 10, No. 2, pp. 2511-2536 (2016).
- H. Chang, I.W. McKeague, "Nonparametric testing for multiple survival functions with non-inferiority margins," *Annals of Statistics*, Vol. 47, No. 1, pp. 205-232, (2019).

See Also

[hepatitis](#), [intELtest](#), [ptwiseELtest](#), [nocrossings](#), [print.supELtest](#), [summary.supELtest](#)

Examples

```

library(survELtest)
nocrossings(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)

## OUTPUT:
## Call:
## nocrossings(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
## Decision = 1

## A decision value of 1 means the case of crossings or alternative orderings among the
## survival functions is excluded. Thus, we can proceed to the one-sided test.

supELtest(survival::Surv(hepatitis$time, hepatitis$censor)~
  hepatitis$group, sided = 1)

## OUTPUT:
## Call:
## supELtest(formula = survival::Surv(hepatitis$time, hepatitis$censor) ~
##   hepatitis$group, sided = 1)
##
## One-sided maximally selected EL test statistic = 10.36, p = 0.006

```

threearm

Time to first remission data

Description

The data frame `threearm` is obtained by resampling from perturbed time-to-remission from patients in a three-arm randomized clinical trial for the treatment of major depression. See [nocrossings](#), [ptwiseELtest](#) and [supELtest](#) for the application.

Usage

```
threearm
```

Format

The `threearm` is a data frame with 664 observations of 3 variables, and has the following columns:

- `time` the observed times to first remission and censoring times
- `sensor` the censoring indicator
- `group` the grouping variable

See Also

[nocrossings](#), [ptwiseELtest](#), [supELtest](#)

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