Package 'kernhaz'

October 13, 2022

Type Package

Title Kernel Estimation of Hazard Function in Survival Analysis

Version 0.1.0

Description Producing kernel estimates of the unconditional and conditional hazard
function for right-censored data including methods of bandwidth selection.

Depends R(>= 3.2.0)

Imports rgl, foreach, doParallel, GA

Suggests survival

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2018-12-21 13:40:03 UTC

R topics documented:

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khazard   *Kernel estimate of hazard function for right-censored data*

Description

Kernel estimate of (unconditional) hazard function for right-censored data. Options include two methods for bandwidth selection.

Usage

```
khazard(times, delta, h = NULL, t = NULL, t.length = 100,
  tmin = NULL, tmax = NULL, kernel = "epanechnikov",
  type = "interior", parallel = FALSE, value = "CVML",
  h.method = "crossval", optim.method = "optimize",
  tol = ifelse(h.method == "crossval", 10^(-6), 1), run = 2, ...)
```

Arguments

times	vector of observed times
delta	vector of censoring indicator. 0 - censored, 1 - uncensored (dead)
h	bandwidth (scalar or vector). If missing, h is found using some bandwidth selection method.
t	vector of time points at which estimate is evaluated
t.length	number of grid points
tmin, tmax	minimum/maximum values for grid
kernel	kernel function, possible values are: "epanechnikov" (default), "gaussian", "rectangular", "quartic".
type	Type of kernel estimate. Possible types are: "exterior", "interior" (default).
parallel	allows parallel computation. Default is FALSE.
value	If h parameter is vector, this option controls output values. If "CVML" (default), the crossvalidation or log-likelihood values only are calculated. If "hazard", the hazard functions only are calculated. If "both" the crossvalidation or log-likelihood values and hazard function are calculated.
h.method	method for bandwidth selection. Possible methods are: "crossval" (default), "maxlike".
optim.method	method for numerical optimization of the crossvalidation or log-likelihood function. Possible methods are: "optimize" (default), "ga".
tol	the desired accuracy of optimization algorithm
run	the number of consecutive generations without any improvement in the best fitness value before the GA is stopped.
...	additional arguments of GA algorithm

Details

External type of kernel estimator is defined as the ratio of kernel estimator of the subdensity of the uncensored observations to the survival function of the observable time. Internal type of kernel estimator is based on a convolution of the kernel function with a nonparametric estimator of the cumulative hazard function (Nelson-Aalen estimator).

Value

Returns an object of class 'khazard' which is a list with fields

time.points	vector of time points at which estimate is evaluated
hazard	data frame of time points, hazard function values and bandwidth
h	bandwidth
CVML	value of crossvalidation or log-likelihood at h
details	description of used methods
GA.result	output of ga, object of class ga-class

References

Selingerova, I., Dolezelova, H., Horova, I., Katina, S., and Zelinka, J. (2016). Survival of Patients with Primary Brain Tumors: Comparison of Two Statistical Approaches. PloS one, 11(2), e0148733.

See Also

[plot.khazard](), [ga](), [optimize]()

Examples

```
library(survival)
fit<-khazard(times = lung$time,delta = lung$status-1)
```

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khazardcond   *Kernel estimate of conditional hazard function for right-censored data*

Description

Kernel estimate of conditional hazard function for right-censored data with one covariate. Options include two methods for bandwidth selection.

Usage

```
khazardcond(times, delta, covariate, h = NULL, t = NULL, x = NULL,
  tx = NULL, t.length = 100, x.length = 100, tmin = NULL,
  tmax = NULL, xmin = NULL, xmax = NULL, kernel = "epanechnikov",
  type = "interior", type.w = "nw", parallel = FALSE,
  h.method = "crossval", optim.method = "ga", tol = ifelse(h.method
  == "crossval", 10^(-6), 1), run = 2, ...)
```

Arguments

`times`	vector of observed times
`delta`	vector of censoring indicator. 0 - censored, 1 - uncensored (dead)
`covariate`	vector of covariate
`h`	bandwidth vector of length 2, first element is bandwidth for time and second for covariate. If missing, h is found using some bandwidth selection method.
`t`	vector of time points at which estimate is evaluated
`x`	vector of covariate points at which estimate is evaluated
`tx`	data frame of t and x at which estimate is evaluated
`t.length`	number of grid points of time
`x.length`	number of grid points of covariate
`tmin, tmax`	minimum/maximum values for grid of time
`xmin, xmax`	minimum/maximum values for grid of covariate
`kernel`	kernel function, possible values are: "epanechnikov" (default), "gaussian", "rectangular", "quartic".
`type`	Type of kernel estimate. Possible types are: "exterior", "interior" (default).
`type.w`	Type of weights. Default are Nadaraya-Watson weights.
`parallel`	allows parallel computation. Default is FALSE.
`h.method`	method for bandwidth selection. Possible methods are: "crossval" (default), "maxlike".
`optim.method`	method for numerical optimization of the crossvalidation or log-likelihood function. Possible methods are: "ga"(default).
`tol`	the desired accuracy of optimization algorithm
`run`	the number of consecutive generations without any improvement in the best fitness value before the GA is stopped.
`...`	additional arguments of GA algorithm

Details

External type of kernel estimator is defined as the ratio of kernel estimator of the conditional sub-density of the uncensored observations to the conditional survival function of the observable time. Internal type of kernel estimator is based on a convolution of the kernel function with a nonparametric estimator of the cumulative conditional hazard function.

Value

Returns an object of class 'khazardcond' which is a list with fields

`time.points`	vector of time points at which estimate is evaluated
`covariate.points`	
	vector of covariate points at which estimate is evaluated
`hazard`	matrix of hazard function values on grid or data.frame of time and covariate points and appropriate hazard values if hx is defined

h	bandwidth vector
CVML	value of crossvalidation or log-likelihood at h
details	description of used methods
GA.result	output of ga, object of class ga-class

References

Selingerova, I., Dolezelova, H., Horova, I., Katina, S., and Zelinka, J. (2016). Survival of Patients with Primary Brain Tumors: Comparison of Two Statistical Approaches. PloS one, 11(2), e0148733.

See Also

[plot.khazardcond](), [ga]()

Examples

```
library(survival)
fit<-khazardcond(times = lung$time,delta = lung$status-1,covariate = lung$age,h=c(200,20))
```

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plot.khazard	*Plot of kernel hazard estimate from an object of class khazard*

Description

Plot of kernel hazard estimate from an object of class khazard

Usage

```
## S3 method for class 'khazard'
plot(x, h = NULL, ylim, type, xlab, ylab, main, ...)
```

Arguments

x	Object of class khazard
h	bandwidth for which hazard function estimate will be plot if x$h is vector
ylim	Limits for the y axis.
type	type argument for plot.
xlab	Label for the x axis.
ylab	Label for the y axis.
main	Title of plot.
...	Additional arguments.

See Also

[khazard]()

Examples

```
library(survival)
fit<-khazard(times = lung$time,delta = lung$status-1)
plot(fit)

fit<-khazard(times = lung$time,delta = lung$status-1,h=c(100,150,200,250), value="both")
plot(fit,h=200)
```

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plot.khazardcond   *Plot of kernel conditional hazard estimate from an object of class khaz-
                              ardcond*

Description

Plot of kernel conditional hazard estimate from an object of class khazardcond

Usage

```
## S3 method for class 'khazardcond'
plot(x, type = "persp", zlim, xlab, ylab, zlab,
  main, ...)
```

Arguments

x	Object of class khazardcond
type	type of plot. Possible types are: "persp" (default), "persp3d", "contour".
zlim	Limits for the z axis.
xlab	Label for the x axis.
ylab	Label for the y axis.
zlab	Label for the z axis.
main	Title of plot.
...	Additional arguments.

See Also

[khazardcond](#)

Examples

```
library(survival)
fit<-khazardcond(times = lung$time,delta = lung$status-1,covariate = lung$age,h=c(200,20))
plot(fit)
```

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