Package ‘lbiassurv’

February 20, 2015

Version 1.1
Date 2013-05-23
Title Length-biased correction to survival curve estimation.
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Depends R (>= 2.15.0), actuar
Description The package offers various length-bias corrections to survival curve estimation.
License GPL (>= 2)

URL http://lbiassurv.r-forge.r-project.org/
Repository CRAN
Repository/R-Forge/Project lbiassurv
Repository/R-Forge/Revision 10
Repository/R-Forge/DateTimeStamp 2013-05-24 03:22:37
Date/Publication 2013-05-24 19:08:03
NeedsCompilation yes

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lbfit.nonpar  Fits a Vardi corrected survival curve, a nonparametric survival curve estimation.

Description
An extended version of the Kaplan-Miere estimator.

Usage
lbfit.nonpar(time, censor, boot = FALSE, boot.control = list(quantile = TRUE, use.median = FALSE, confidence.level = 0.95, iter = 1000), fit.control = list(iter = 500, tol = 1e-06))

Arguments
time The observed time as a vector.
censor The survival indicator, 1 if censored, 0 otherwise.
boot logical, for calculating bootstrap confidence bounds.
boot.control Bootstrap control parameters, as a list.
fit.control Nonparametric fit control parameters.

Details
A detailed description, or refer the reader to a work.

Value
The result of the function is an lbsurvfit object, including step functions for the nonparametric survival curve fit and its bootstrap confidence bounds.

Note
Bootstrapping is required if confidence bounds are needed.

Author(s)
V. P. Nia and P. J. Bergeron

References
Vardi Paper

See Also
lbfit.par, lbsample
Examples

```r
mydata = lbsample(20, family = "exponential", par = list(rate = 1))
noboot = lbfit.nonpar(time = mydata$time, censor = mydata$censor)
plot(noboot$survfun)
withboot = lbfit.nonpar(time = mydata$time, censor = mydata$censor, boot = TRUE)
x = seq(0, max(mydata$time) + 1, length = 500)
plot(x, withboot$survfun(x), type = "l", col = "blue", ylim = c(0, 1))
points(x, withboot$lowerfun(x), type = "l", col = "red")
points(x, withboot$upperfun(x), type = "l", col = "red")
```

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**lbfit.par**

*Fits parametric models*

**Description**

Will be combined with nonpar version soon.

**Usage**

```r
lbfit.par(time, censor, family, initial = list(shape, rate, meanlog, sdlog))
```

**Arguments**

- `time`: The observed time as a vector.
- `censor`: The survival indicator, 1 if censored, 0 otherwise.
- `family`: A string indicating the parametric family to fit. Options are `weibull`, `gamma`, `exponential`, `lognormal`, and `loglogistic`.
- `initial`: A list of initial parameters for optimization, `meanlog` and `sdlog` for lognormal and the `shape` and `rate` for the rest.

**Details**

See the master thesis of Jerome student.

**Value**

The list returned by the `optim` function.

**Note**

Write why and when you get NaNs.

**Author(s)**

V.P. Nia and P.J. Bergeron.
References

The thesis or an article here.

See Also

lbfit.nonpar,lbsample.

Examples

mydata=lbsample(500,family="exponential",par=list(rate=1))
lbfit.par(time=mydata$time,censor=mydata$censor,family="exponential",initial=list(shape=3,rate=3))

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lbsample

Generates gength bias samples from a parametric family.

Description

Some famous families are used

Usage

lbsample(n, family, par = list(shape, rate, meanlog, sdlog), censor.vec = rexp(n))

Arguments

n          The sample size.
family     Some families.
par         Parameters of the family.
censor.vec  A numeric vector of censoring. When the generated sample is bigger than the values of the vector, the function return 1 for censor, meaning that sample is right censored.

Details

Add some details if necessary.

Value

A list containing numeric time of survivals, the censor indicator, and the onset time.

Note

Add some notes about constraints on the parameters.

Author(s)

Pierre-Jerome Bergeron and Vahid Partovi Nia
*lbsample*

**References**

Thesis of Pierre-Jerome student.

**See Also**

`lbfit.nonpar, lbfit.par`.

**Examples**

```r
mydata = lbsample(500, family = "exponential", par = list(rate = 1))
hist(mydata$time)
```
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