Package 'lbiassurv'

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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)

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R topics documented:

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lbfit.nonpar	*Fits a Vardi corrected survival curve, a nonparametric survival cuve 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

```
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

```
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 Pjerome student.

Value

The list returned by the optim function.

Note

Write why and when you get NaNs.

Author(s)

V.P. Nia and 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

References

Thesis of Pierre-Jerome student.

See Also

lbfit.nonpar, lbfit.par.

Examples

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

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