Package ‘SurvTrunc’

July 28, 2018

Type Package
Title Analysis of Doubly Truncated Data
Version 0.1.0
Date 2018-07-13
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Description Package performs Cox regression and survival distribution function estimation when the survival times are subject to double truncation. The estimation procedure for each method involves inverse probability weighting, where the weights correspond to the inverse of the selection probabilities and are estimated using the survival times and truncation times only. Both methods require that the survival and truncation times are quasi-independent. A test for checking this independence assumption is also included in this package. The functions available in this package for Cox regression, survival distribution function estimation, and testing independence under double truncation are based on the following methods, respectively: Rennert and Xie (2017) <doi:10.1111/biom.12809>, Shen (2010) <doi:10.1007/s10463-008-0192-2>, Martin and Betensky (2005) <doi:10.1198/016214504000001538>.

License GPL-2
Encoding UTF-8
LazyData true
RoxygenNote 6.0.1
Depends survival
Imports stats, grDevices, graphics
NeedsCompilation no
Repository CRAN
Date/Publication 2018-07-28 16:40:08 UTC

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AIDS blood transfusion data

Description

Data collected by CDC data registry. Adults infected with virus from contaminated blood transfusion in April 1978. Event time is the induction time from HIV infection to AIDS. Infection time is time from blood transfusion to HIV infection. Data left truncated because only subjects who develop AIDS after 1982 are unobserved (as HIV unknown before 1982). Data also right truncated because cases reported after July 1, 1986 are not included in the sample to avoid inconsistent data and bias from reporting delay.

Usage

```r
data(AIDS)
```

Format

This data frame contains the following columns:

- **Induction.time** Months between HIV infection and development of AIDS (event time of interest)
- **Adult** Indicator of adult (1=adult,0=child)
- **Infection.time** Months from blood transfusion date (Apr 1, 1978) to HIV infection
- **L.time** Left truncation time: 45 - infection time
- **R.time** Right truncation time: Left truncation time + 54 months
- **status** Indicator of event occurrence, which is set to 1 since all subjects experience the event

Source


Examples

```r
data(AIDS)
```
Distribution function estimation under double truncation

dESCRIPTION

This function computes the NPMLE of the event time distribution and truncation time distribution, when the event times are subject to double truncation.

Usage

cdfDT(y, l, r, error = 1e-06, n.iter = 10000, boot = FALSE, 
    B.boot = 200, joint = FALSE, plot.cdf = FALSE, plot.joint = FALSE, 
    display = TRUE)

Arguments

- `y`: vector of event times
- `l`: vector of left truncation times
- `r`: vector of right truncation times
- `error`: prespecified error for convergence (default = 1e-6)
- `n.iter`: maximum number of iterations
- `boot`: Logical. Default=FALSE. If TRUE, the simple bootstrap method is applied to estimate the standard error and pointwise confidence intervals of the event time distribution
- `B.boot`: Numeric value for number of bootstrap resamples. Default is 200.
- `joint`: Logical. Default=FALSE. If TRUE, computes joint and marginal distributions of the truncation times
- `plot.cdf`: Logical. Default is FALSE. If TRUE, the estimated cumulative distribution and survival functions of the event times are plotted. If boot=TRUE, confidence intervals are also plotted.
- `plot.joint`: Logical. Default is FALSE. If TRUE, the estimated marginal distribution functions of the truncation times, and the joint distribution of the truncation times, are plotted. Note: Plot will only be displayed if both plot.joint=TRUE and joint=TRUE.
- `display`: Logical. Default is TRUE. If FALSE, output will not be displayed upon execution of function.

Details

Estimates the distribution function of the survival time in the presence of left and right truncation. Also estimates the joint cumulative distribution function and marginal cumulative distribution functions of the left and right truncation times. The computation is performed using the algorithm introduced in Shen (2010). This is an iterative algorithm that converges to the NPMLE after a number of iterations. Note that the survival, left, and right truncation times must be the same length. If either of these vectors have missing observations, the entire observation will be excluded.
Value

<table>
<thead>
<tr>
<th>time</th>
<th>Unique event times of the event time vector y</th>
</tr>
</thead>
<tbody>
<tr>
<td>n.event</td>
<td>Number of events that occurred at each timepoint</td>
</tr>
<tr>
<td>F</td>
<td>Estimated cumulative distribution function of Y at each distinct value of y</td>
</tr>
<tr>
<td>Survival</td>
<td>Estimated survival function of Y at each distinct value of y (equal to 1-F)</td>
</tr>
<tr>
<td>sigma.F</td>
<td>Bootstrapped standard error of F at each distinct value of y (displayed if boot=TRUE)</td>
</tr>
<tr>
<td>CI.lower.F</td>
<td>Estimated lower limits of the Wald confidence intervals for F (displayed if boot=TRUE).</td>
</tr>
<tr>
<td>CI.upper.F</td>
<td>Estimated upper limits of the Wald confidence intervals for F (displayed if boot=TRUE).</td>
</tr>
<tr>
<td>P.K</td>
<td>Probability of the observed vector y falling within a random truncation interval [L,R]</td>
</tr>
<tr>
<td>Joint.LR</td>
<td>Estimated joint distribution function of (L,R)</td>
</tr>
<tr>
<td>Marginal.L</td>
<td>Estimated marginal cumulative distribution function of L at each observed l</td>
</tr>
<tr>
<td>Marginal.R</td>
<td>Estimated marginal cumulative distribution function of R at each observed r</td>
</tr>
<tr>
<td>n.iterations</td>
<td>Number of iterations needed for convergence</td>
</tr>
<tr>
<td>max.iter_reached</td>
<td>0 indicates convergence, 1 indicates that number of iterations exceeded n.iter</td>
</tr>
</tbody>
</table>

References


Examples

#AIDS data set:
out=cdfdt(AIDS$Induction.time,AIDS$L.time,AIDS$R.time,plot.cdf=TRUE)
out

coxDT

Fit Cox Proportional Hazards Regression Model Under Double Truncation

Description

Fits a Cox proportional hazards regression model when the survival time is subject to both left and right truncation. Assumes that no censoring is present in the data.

Usage

coxDT(formula, L, R, data, subset, time.var = FALSE, subject = NULL,
B.SE.np = 200, CI.boot = FALSE, B.CI.boot = 2000, pvalue.boot = FALSE,
B.pvalue.boot = 500, B.pvalue.se.boot = 100, trunc.weight = 100,
print.weights = FALSE, error = 10^-6, n.iter = 1000)
Arguments

formula a formula object, with the response on the left of a \sim operator, and the terms on the right. The response must be a survival object as returned by the Surv function. NOTE: coxDT does not handle censoring.

L vector of left truncation times

R vector right truncation times

data mandatory data.frame matrix needed to interpret variables named in the formula

subset an optional vector specifying a subset of observations to be used in the fitting process. All observations are included by default.

time.var default = FALSE. If TRUE, specifies that time varying covariates are included in the model.

subject a vector of subject identification numbers. Only needed if time.var=TRUE (see example).

B.SE.np number of iterations for bootstrapped standard error (default = 200)

CI.boot requests bootstrap confidence intervals (default==FALSE)

B.CI.boot number of iterations for bootstrapped confidence intervals (default = 2000)

pvalue.boot requests bootstrap p-values (default==FALSE)

B.pvalue.boot number of iterations for numerator (estimate) of bootstrapped test statistic (default = 500)

B.pvalue.se.boot number of iterations for denominator (standard error) of bootstrapped test statistic (default = 100)

trunc.weight Truncates weights at a prespecified level (default=100). Trade off is a slight increase in bias for reduction in variance.

print.weights requests the output of nonparametric selection probabilities (default==FALSE)

error convergence criterion for nonparametric selection probabilities (default = 10e-6)

n.iter maximum number of iterations for computation of nonparametric selection probabilities (default = 1000)

Details

Fits a Cox proportional hazards model in the presence of left and right truncation by weighting each subject in the score equation of the Cox model by the probability that they are observed in the sample. These selection probabilities are computed nonparametrically. The estimation procedure here is performed using coxph survival and inserting these estimated selection probabilities in the 'weights' option. This method assumes that the survival and truncation times are independent. Furthermore, this method does not accommodate censoring. Note: If only left truncation is present, set R=\infty. If only right truncation is present, set L = -\infty.

Value

results.beta Displays the estimate, standard error, lower and upper 95% Wald confidence limits, Wald test statistic and corresponding p-value for each regression coefficient
CI  Method used for computation of confidence interval: Normal approximation (default) or bootstrap

p.value  Method used for computation of p-values: Normal approximation (default) or bootstrap

weights  If print.weights=TRUE, displays the weights used in the Cox model

References


Examples

++++++ Example: AIDS data set ++++
coxDT(Surv(Induction.time,status) ~ Adult,L.time,R.time,data=AIDS,B.SE.np=2)

# WARNING: To save computation time, number of bootstrap resamples for standard error set to 2.
# Note: The minimum recommendation is 200, which is the default setting.
++++++ Including time-dependent covariates ++++
# Accomodating time-dependent covariates in the model is similar to the accomodation in coxph

# The data set may look like the following:

# subject start stop event treatment test.score L.time R.time
# 1 T.10 T.11 1 X.1 Z.1 L.1 R.1
# 2 T.20 T.21 0 X.2 Z.21 L.2 R.2
# 2 T.21 T.22 1 X.2 Z.22 L.2 R.2
# ...

# Here the variable 'treatment' and the truncation times 'L.time' and 'R.time' stay the same
# from line to line. The variable 'test.score' will vary line to line. In this example,
# subject 1 has only one recorded measurement for test.score, and therefore only has one row
# of observations. Subject 2 has two recorded measurements for test score, and therefore has
# two rows of observations. In this example, it is assumed that the test score for subject 2
# is fixed at Z.21 between [T.20,T.21] and fixed at Z.22 between [T.21,T.22]. Notice that
# the event indicator is 0 in the first row of observations corresponding to subject 2,
# since they have not yet experienced the event. The status variable changes to 1 in the
# row where the event occurs.

# Note: Start time cannot preceed left truncation time and must be strictly less than stop time.

# example

test.data <- data.frame(
  list(subject.id = c(1, 2, 2, 3, 4, 4, 5, 6, 7, 7, 8, 8, 9, 10),
       start = c(3, 5, 7, 2, 1, 2, 6, 5, 6, 6, 7, 7, 17),
       stop = c(4, 7, 8, 5, 2, 6, 9, 8, 7, 7, 9, 9, 21),
       event = c(1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1),
       treatment = c(0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1),
       test.score = c(5, 6, 7, 4, 6, 9, 3, 4, 4, 7, 6, 4, 12),
       L.time = c(2, 4, 4, 2, 1, 1, 4, 5, 4, 3, 3, 1, 10),
       R.time = c(4, 7, 8, 5, 2, 6, 9, 8, 7, 7, 9, 9, 21)),
Description

This function tests for quasi-independence between the survival and truncation times. The survival and truncation times must be quasi-independent to use coxDT and cdfDT.

Usage

\texttt{indeptestDT(y, l, r)}

Arguments

\begin{itemize}
  \item \texttt{y} \hspace{1cm} \text{vector of event times}
  \item \texttt{l} \hspace{1cm} \text{vector of left truncation times}
  \item \texttt{r} \hspace{1cm} \text{vector of right truncation times}
\end{itemize}

Details

Testing for quasi-independence between the survival and truncation times using the conditional Kendall's tau introduced by Martin and Betensky (2005). More details are given in their paper.

Value

\begin{itemize}
  \item \texttt{tau} \hspace{1cm} \text{Conditional Kendall's tau for survival time and left truncation time and survival time and right truncation time}
  \item \texttt{X2} \hspace{1cm} \text{Chi-squared test statistic to test null hypothesis that survival and truncation times are quasi-independent. Default degrees of freedom (DF) is 2. If left and right truncation times perfectly correlated, DF = 1}
  \item \texttt{p} \hspace{1cm} \text{p-value for null hypothesis that survival and truncation times are quasi-independent}
\end{itemize}

References

Examples

# Generating independent survival and truncation times
set.seed(123)
y=rnorm(30); l=min(y)-abs(rnorm(30)); r=max(y)+abs(rnorm(30))

indeptestDT(y,l,r)

# Null hypothesis not rejected ==> not enough evidence to reject quasi-independence assumption
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