

Package ‘hds’

December 31, 2016

Type Package

Version 0.8.1

Title Hazard Discrimination Summary

Description Functions for calculating the hazard discrimination summary and its standard errors, as described in Liang and Heagerty (2016) <doi:10.1111/biom.12628>.

Date 2016-12-30

URL <https://github.com/liangcj/hds>

BugReports <https://github.com/liangcj/hds/issues>

Imports stats, survival, tensor

License GPL-2

LazyData TRUE

Depends R (>= 3.1.0)

RoxygenNote 5.0.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2016-12-31 16:32:12

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finda

*Estimate the time-varying coefficients from a local-in-time Cox model***Description**

finda estimates the time-varying coefficients $\beta(t)$ at a single time from a local-in-time Cox model. Think of it as a Cox model where the coefficients are allowed to vary with time. Further details can be found in Cai and Sun (2003) and Tian et al. (2005).

Usage

```
finda(tt, times, status, covars, start = rep(0, ncol(covars)), h = 400, ...)
```

Arguments

tt	Time to estimate $\beta(t)$ at
times	A vector of observed follow up times.
status	A vector of status indicators, usually 0=alive, 1=dead.
covars	A matrix or data frame of numeric covariate values, with a column for each covariate and each observation is on a separate row.
start	A vector of length p of starting values to be passed to <code>optim</code> for the numerical optimization procedure. p is the number of covariates. Defaults to all zeroes.
h	A single value on the time scale representing the bandwidth to use.
...	Additional parameters to pass to <code>optim</code> .

Details

The naming of the function `finda` stands for "find $a(t)$ ", where " $a(t)$ " is the notation used in Cai and Sun (2003) to represent the time-varying Cox model coefficients. We also refer to " $a(t)$ " as " $\beta(t)$ " through the documentation.

The user typically will not interact with this function, as `finda` is wrapped by `hds1c`.

Value

A vector of length p , where p is the number of covariates. The vector is the estimated $\beta(t)$ from the local-in-time Cox model at time `tt`.

References

Cai Z and Sun Y (2003). Local linear estimation for time-dependent coefficients in Cox's regression models. *Scandinavian Journal of Statistics*, 30: 93-111. doi:10.1111/1467-9469.00320

Tian L, Zucker D, and Wei LJ (2005). On the Cox model with time-varying regression coefficients. *Journal of the American Statistical Association*, 100(469):172-83. doi:10.1198/016214504000000845

hds	<i>Hazard discrimination summary estimator</i>
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Description

Returns hazard discrimination summary (HDS) estimates at all specified evaluation times. See Liang and Heagerty (2016) for details on HDS.

Usage

```
hds(times, status, m, evaltimes = times[order(times)], se = TRUE)
```

Arguments

times	A vector of observed follow up times.
status	A vector of status indicators, usually 0=alive, 1=dead.
m	A matrix or data frame of covariate values, with a column for each covariate and each observation is on a separate row. Non-numeric values are acceptable, as the values will be transformed into a numeric model matrix through <code>survival::coxph</code> .
evaltimes	A vector of times at which to estimate HDS. Defaults to all the times specified by the <code>times</code> vector. If there are a lot of observations, then you may want to enter in a sparser vector of times for faster computation.
se	TRUE or FALSE. TRUE: calculate and return standard error estimates. FALSE: do not calculate standard errors estimates and return NAs. Defaults to TRUE. May want to set to FALSE to save computation time if using this function to compute bootstrap standard errors.

Details

A wrapper for `hds_t`. Since `hds_t` only estimates HDS at one time point, this function calls `hds_t` multiple times to estimate the entire HDS curve. `hds` and `hds1c` are the main functions the user will interact with in this package.

The covariate values `m` are centered for numerical stability. This is particularly relevant for the standard error calculations.

Value

A data frame with three columns: 1) the evaluation times, 2) the HDS estimates at each evaluation time, and 3) the standard error estimates at each evaluation time

References

Liang CJ and Heagerty PJ (2016). A risk-based measure of time-varying prognostic discrimination for survival models. *Biometrics*. doi:10.1111/biom.12628

See Also[hdslc](#)**Examples**

```
## Not run:
head(hds(times = survival::pbc[1:312, 2],
      status = (survival::pbc[1:312, 3]==2)*1,
      m = survival::pbc[1:312, 5]))

hdsres <- hds(times=pbc5[,1], status=pbc5[,2], m=pbc5[,3:7])
hdslcres <- hdslc(times = pbc5[,1], status=pbc5[,2], m = pbc5[,3:7], h = 730)
Survt <- summary(survival::survfit(survival::Surv(pbc5[,1], pbc5[,2])~1))
Survtd <- cbind(Survt$time, c(0,diff(1-Survt$surv)))
tden <- density(x=Survtd[,1], weights=Survtd[,2], bw=100, kernel="epanechnikov")

par(mar=c(2.25,2.25,0,0)+0.1, mgp=c(1.25,0.5,0))
plot(c(hdslcres[,1], hdslcres[,1]), c(hdslcres[,2] - 1.96*hdslcres[,3],
      hdslcres[,2] + 1.96*hdslcres[,3]),
     type="n", xlab="days", ylab="HDS(t)", cex.lab=.75, cex.axis=.75,
     ylim=c(-3,15), xlim=c(0,3650))
polygon(x=c(hdsres[,1], hdsres[312:1,1]), col=rgb(1,0,0,.25), border=NA,
        fillOddEven=TRUE, y=c(hdsres[,2]+1.96*hdsres[,3],
        (hdsres[,2]-1.96*hdsres[,3])[312:1]))
polygon(x=c(hdslcres[,1], hdslcres[312:1, 1]), col=rgb(0,0,1,.25), border=NA,
        fillOddEven=TRUE, y=c(hdslcres[,2] + 1.96*hdslcres[,3],
        (hdslcres[,2] - 1.96*hdslcres[,3])[312:1]))
lines(hdsres[,1], hdsres[,2], lwd=2, col="red")
lines(hdslcres[,1], hdslcres[,2], lwd=2, col="blue")
abline(h=1, lty=3)
legend(x=1200, y=14, legend=c("Proportional hazards",
      "Local-in-time proportional hazards",
      "Time density"), col=c("red", "blue", "gray"),
      lwd=2, bty="n", cex=0.75)
with(tden, polygon(c(x, x[length(x):1]),
      c(y*3/max(y)-3.5, rep(-3.5, length(x))),
      col="gray", border=NA, fillOddEven=TRUE))

## End(Not run)
```

hdslc

*Hazard discrimination summary estimator***Description**

Returns local constant HDS estimates at all specified evaluation times. See Liang and Heagerty (2016) for details on HDS.

Usage

```
hdslc(times, status, m, evaltimes = times[order(times)], h = 1.06 *
      sd(times) * (length(times)^(-0.2)), se = TRUE)
```

Arguments

times	A vector of observed follow up times.
status	A vector of status indicators, usually 0=alive, 1=dead.
m	A matrix or data frame of covariate values, with a column for each covariate and each observation is on a separate row. Non-numeric values are acceptable, as the values will be transformed into a numeric model matrix through <code>survival::coxph</code> .
evaltimes	A vector of times at which to estimate HDS. Defaults to all the times specified by the <code>times</code> vector. If there are a lot of observations, then you may want to enter in a sparser vector of times for faster computation.
h	A single numeric value representing the bandwidth to use, on the time scale. The default bandwidth is a very ad hoc estimate using Silverman's rule of thumb
se	TRUE or FALSE. TRUE: calculate and return standard error estimates. FALSE: do not calculate standard errors estimates and return NAs. Defaults to TRUE. May want to set to FALSE to save computation time if using this function to compute bootstrap standard errors.

Details

A local constant version of `hds`. While `hds` estimates $HDS(t)$ assuming the Cox proportional hazards model, `hdslc` estimates $HDS(t)$ using a relaxed, local-in-time Cox model. Specifically, the hazard ratios are allowed to vary with time. See Cai and Sun (2003) and Tian Zucker Wei (2005) for details on the local-in-time Cox model.

Point estimates use `hdslc.fast` and standard errors use `hdslcse.fast`. `hdslc.fast` requires an estimate of $\beta(t)$ (time-varying hazard ratio), which is estimated using `finda()`; and subject specific survival, which is estimated using `sssf.fast()`. `hdslcse.fast` requires the same and in addition standard error estimates of $\beta(t)$, which are estimated using `betahatse.fast()`.

The covariate values `m` are centered for numerical stability. This is particularly relevant for the standard error calculations.

Value

A data frame with three columns: 1) the evaluation times, 2) the HDS estimates at each evaluation time, and 3) the standard error estimates at each evaluation time

References

- Liang CJ and Heagerty PJ (2016). A risk-based measure of time-varying prognostic discrimination for survival models. *Biometrics*. doi:10.1111/biom.12628
- Cai Z and Sun Y (2003). Local linear estimation for time-dependent coefficients in Cox's regression models. *Scandinavian Journal of Statistics*, 30: 93-111. doi:10.1111/1467-9469.00320

Tian L, Zucker D, and Wei LJ (2005). On the Cox model with time-varying regression coefficients. *Journal of the American Statistical Association*, 100(469):172-83. doi:10.1198/016214504000000845

See Also

[hds](#), [finda](#)

Examples

```
## Not run:
head(hdslc(times = survival::pbc[1:312, 2],
        status = (survival::pbc[1:312, 3]==2)*1,
        m = survival::pbc[1:312, 5]))

hdsres <- hds(times=pbc5[,1], status=pbc5[,2], m=pbc5[,3:7])
hdslcres <- hdslc(times = pbc5[,1], status=pbc5[,2], m = pbc5[,3:7], h = 730)
Survt <- summary(survival::survfit(survival::Surv(pbc5[,1], pbc5[,2])~1))
Survtd <- cbind(Survt$time, c(0,diff(1-Survt$surv)))
tden <- density(x=Survtd[,1], weights=Survtd[,2], bw=100, kernel="epanechnikov")

par(mar=c(2.25,2.25,0,0)+0.1, mgp=c(1.25,0.5,0))
plot(c(hdslcres[,1], hdslcres[,1]), c(hdslcres[,2] - 1.96*hdslcres[,3],
        hdslcres[,2] + 1.96*hdslcres[,3]),
     type="n", xlab="days", ylab="HDS(t)", cex.lab=.75, cex.axis=.75,
     ylim=c(-3,15), xlim=c(0,3650))
polygon(x=c(hdsres[,1], hdsres[312:1,1]), col=rgb(1,0,0,.25), border=NA,
        fillOddEven=TRUE, y=c(hdsres[,2]+1.96*hdsres[,3],
        (hdsres[,2]-1.96*hdsres[,3])[312:1]))
polygon(x=c(hdslcres[,1], hdslcres[312:1, 1]), col=rgb(0,0,1,.25), border=NA,
        fillOddEven=TRUE, y=c(hdslcres[,2] + 1.96*hdslcres[,3],
        (hdslcres[,2] - 1.96*hdslcres[,3])[312:1]))
lines(hdsres[,1], hdsres[,2], lwd=2, col="red")
lines(hdslcres[,1], hdslcres[,2], lwd=2, col="blue")
abline(h=1, lty=3)
legend(x=1200, y=14, legend=c("Proportional hazards",
        "Local-in-time proportional hazards",
        "Time density"), col=c("red", "blue", "gray"),
        lwd=2, bty="n", cex=0.75)
with(tden, polygon(c(x, x[length(x):1]),
        c(y*3/max(y)-3.5, rep(-3.5, length(x))),
        col="gray", border=NA, fillOddEven=TRUE))

## End(Not run)
```

hdslc.fast

Hazard discrimination summary estimate (local constant) at one time point

Description

hdslc.fast estimates HDS at a single time using the local-in-time proportional hazards model. See Cai and Sun (2003, Scandinavian Journal of Statistics) for details on the local-in-time PH model.

Usage

```
hdslc.fast(S, betahat, m)
```

Arguments

S	A vector of length nrow(m) (which is typically the number of observations n), where each value is the subject-specific survival at time t where t is implied by the choice of betahat.
betahat	A p x 1 vector of coefficient estimates at time t of interest from the local-in-time Cox model. Vector length p is the number of covariates. Typically the output from hdslc::finda is passed here.
m	A numeric n x p matrix of covariate values, with a column for each covariate and each observation is on a separate row.

Details

The user typically will not interact with this function. Rather, hdslc wraps this function and is what the user typically will use.

Value

The HDS estimate at times t, where t is implied by choice of S and betahat passed to hdslc.fast.

hdslcse.fast	<i>Hazard discrimination summary (local constant) standard error estimate</i>
--------------	---

Description

hdslcse.fast calculates an estimate of the variance for the local constant hazard discrimination summary estimator at a time t. The time t is implied by S, betahat, and betahatse

Usage

```
hdslcse.fast(S, betahat, m, betahatse)
```

Arguments

S	A vector of length $nrow(m)$ (which is typically the number of observations n), where each value is the subject-specific survival at time t where t is implied by the choice of <code>betahat</code> .
betahat	A $p \times 1$ vector of coefficient estimates at time t of interest from the local-in-time Cox model. Vector length p is the number of covariates. Typically the output from <code>hds1c::finda</code> is passed here.
m	A numeric $n \times p$ matrix of covariate values, with a column for each covariate and each observation is on a separate row.
betahatse	A $p \times p$ covariance matrix for <code>betahat</code> at time t

Details

The use will typically not interact with this function directly. Instead this function is wrapped by `hds1c`.

Value

Variance estimate that has not been normalized. To get a usable standard error estimate, divide the output of this function by the bandwidth and sample size, and then take the square root.

hds_t	<i>Hazard discrimination summary estimate at one time point</i>
-------	---

Description

`hds_t` estimates HDS at time t under the PH assumption

Usage

```
hds_t(t, L0hat, betahat, m)
```

Arguments

t	The time at which to calculate HDS
L0hat	A data frame with variable names of hazard and time. Typically the object returned by <code>basehaz</code> .
betahat	A vector of coefficient estimates from the Cox model. Typically the coefficients value from the <code>coxph</code> object returned by <code>coxph</code> .
m	A numeric matrix of covariate values, with a column for each covariate and each observation is on a separate row.

Details

The user typically will not interact with this function. Rather, `hds` is a wrapper for this function and is what the user typically will use.

pbc5

Cleaned up version of the Mayo PBC data.

Description

A cleaned up version of the Mayo PBC data from `survival::pbc`. Only the first 312 observations are used (the cases who participated in the randomized trial). Only five of the covariates (listed below) are used. Further, two of the covariates were log transformed.

Usage

`pbc5`

Format

A data frame with 312 rows and 7 variables:

time follow up time in days

status 1=death, 0=censored

age age in years

edema 0=no edema, 0.5=untreated or successfully treated, 1=edema despite diuretic therapy

bili log serum bilirubin level (original value from `survival::pbc` is unlogged)

albumin serum albumin

protime log standardized blood clotting time (original value from `survival::pbc` is unlogged)

Source

Cleaned up version of `survival::pbc`

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