

Package ‘HazardDiff’

October 12, 2022

Type Package

Title Conditional Treatment Effect for Competing Risks

Version 0.1.0

Date 2021-12-06

Maintainer Denise Rava <drava@ucsd.edu>

Description The conditional treatment effect for competing risks data in observational studies is estimated. While it is described as a constant difference between the hazard functions given the covariates, we do not assume specific functional forms for the covariates. Rava, D. and Xu, R. (2021) <[arXiv:2112.09535](https://arxiv.org/abs/2112.09535)>.

License GPL-2

Encoding UTF-8

RdMacros Rdpack

Imports ahaz, rootSolve, stats, survival, Rdpack (>= 0.7)

RoxygenNote 7.1.2

NeedsCompilation no

Author Denise Rava [aut, cre, cph],
Ronghui Xu [aut, ths]

Repository CRAN

Date/Publication 2021-12-21 20:12:05 UTC

R topics documented:

HazardDiff	2
Index	5

HazardDiff

*Conditional Treatment Effect for Competing Risks***Description**

This function estimates the conditional treatment effect for competing risks data in observational studies. The effect is described as a constant difference between the hazard functions given the covariates. The specific functional form for the covariates does not need to be assumed.

Usage

```
HazardDiff(data, type, ps, CL=.95, G="NonSpecified")
```

Arguments

data	DataFrame of survival data. First column needs to be the censored failure time and needs to be named 'time', second column needs to be the type of failure/event indicator (1=observed failure from primary risk, 2=observed failure from competing risk, 0=censored) and needs to be named 'status', third column needs to be the exposure (1 or 0) and the other columns are covariates.
type	If type=1, score 1 is used, if type=2, score 2 is used.
CL	Confidence level of the confidence interval.
ps	A vector of propensity scores, one for each observation.
G	a nxn dataframe with the censoring survival function. n is the number of observations in data. Every row of G corresponds to a different observation. Every column of G corresponds to a different censored failure time of the column 'time' of data. If not specified, the censoring survival function is not considered. If specified, type needs to be equal to 1.

Details

The conditional treatment effect on the primary risk

$$\beta_1 = \lambda_1(t|A = 1, Z) - \lambda_1(t|A = 0, Z)$$

and the conditional treatment effect on the competing risk

$$\beta_2 = \lambda_2(t|A = 1, Z) - \lambda_2(t|A = 0, Z)$$

are estimated.

Value

beta	A vector with two components. First component is the estimate of the conditional treatment effect on the primary risk. Second component is the estimate of the conditional treatment effect on the competing risk.
------	--

se	A vector with two components. First component is the standard error of the estimator of the conditional treatment effect on the primary risk. Second component is the standard error of the estimator of the conditional treatment effect on the competing risk.
CI	A matrix with two rows. First row contains the bounds of the confidence interval for the conditional treatment effect on the risk. Second row contains the bounds of the confidence interval for the conditional treatment effect on the competing risk.

Author(s)

Denise Rava and Ronghui Xu

References

Rava, D., Xu, R. "Doubly Robust Estimation of the Hazard Difference for Competing Risks Data", December 2021, arXiv:2112.09535

Examples

```
#simulating data
n=1000
Z1=1:n
Z2=Z1
A=Z1
time=Z1
status=Z1
x=status
c=status
beta1=0.1
beta2=0.1
for (i in 1:n)
{Z1[i]=runif(1,0,0.5)
Z2[i]=runif(1,0,0.5)
predt<-1/(1+exp(-Z1[i]-Z2[i]))
A[i]=rbinom(1,1,predt)
u=runif(1,0,1)
time[i]=-log(u)/(1.5+1.5*((Z1[i]))+1.5*((Z2[i]))+(beta1+beta2)*A[i])
status[i]=rbinom(1,1,1-((.5+.5*((Z1[i]))+.5*(Z2[i]))+(beta1)*A[i])/(1.5
+1.5*((Z1[i]))+1.5*((Z2[i]))+(beta1+beta2)*A[i]))+1
u=runif(1,0,1)
c[i]=runif(1,0,3)
x[i]=apply(cbind(time[i],c[i]),1,min)
status[i]<-ifelse(time[i]<c[i],status[i],0)}

data<-data.frame(time=x,status=status,A=A,Z1=Z1,Z2=Z2)

#estimating propensity score
mylogit <- glm(A ~ 1+Z1+Z2,data,family = binomial(link="logit"))
ps=predict(mylogit,newdata = data,type='response')
```

```
#score 1  
HazardDiff(data=data, type=1, ps=ps)  
#score 2  
HazardDiff(data=data, type=2, ps=ps)
```

Index

* **~HazardDifference**

HazardDiff, 2

* **~TreatmentEffect**

HazardDiff, 2

HazardDiff, 2