

Package ‘survIDINRI’

May 9, 2026

Type Package

Title IDI and NRI for Comparing Competing Risk Prediction Models with Censored Survival Data

Version 1.1-2

Date 2022-4-23

Author Hajime Uno, Tianxi Cai

Maintainer Hajime Uno <huno@jimmy.harvard.edu>

Description Performs inference for a class of measures to compare competing risk prediction models with censored survival data. The class includes the integrated discrimination improvement index (IDI) and category-less net reclassification index (NRI).

Depends survC1, survival

License GPL-2

Encoding UTF-8

LazyLoad yes

NeedsCompilation yes

Repository CRAN

Date/Publication 2022-04-23 07:10:02 UTC

Contents

| | |
|------------------------------|----------|
| survIDINRI-package | 2 |
| IDI.INF | 3 |
| IDI.INF.GRAPH | 5 |
| IDI.INF.OUT | 6 |
| Index | 7 |

survIDINRI-package *IDI and NRI for comparing competing risk prediction models with censored survival data*

Description

Performs inference for a class of measures to compare competing risk prediction models with censored survival data. The class includes the integrated discrimination improvement index (IDI) and category-less net reclassification index (NRI).

Details

Package: survIDINRI
Type: Package
Version: 1.1-2
Date: 2022-4-23
License: GPL-2

Author(s)

Hajime Uno, Tianxi Cai

Maintainer: Hajime Uno <huno@jimmy.harvard.edu>

References

Pencina MJ, D'Agostino RB, Steyerberg EW. Extensions of net reclassification improvement calculations to measure usefulness of new biomarkers. *Statistics in Medicine* 2011. doi:10.1002/sim.5647

Uno H, Tian L, Cai T, Kohane IS, Wei LJ. A unified inference procedure for a class of measures to assess improvement in risk prediction systems with survival data, *Statistics in Medicine* 2012. doi:10.1002/sim.5647

See Also

survC1-package

Examples

```
#--- sample data (pbc in survival package) ---  
D=subset(pbc, select=c("time","status","age","albumin","edema","protime","bili"))  
D$status=as.numeric(D$status==2)  
D=D[!is.na(apply(D,1,mean)),] ; dim(D)  
mydata=D[1:100,]  
  
t0=365*5
```

```

indata1=mydata;
indata0=mydata[,-7] ; n=nrow(D) ;
covs1<-as.matrix(indata1[,c(-1,-2)])
covs0<-as.matrix(indata0[,c(-1,-2)])

#--- inference ---
x<-IDI.INF(mydata[,1:2], covs0, covs1, t0, npert=200) ;

#--- results ---
IDI.INF.OUT(x) ;

#--- Graphical presentaion of the estimates ---
# IDI.INF.GRAPH(x) ;

```

IDI.INF

Inference for IDI, continuous NRI, and median improvement

Description

This function performs inference for IDI, continuous NRI, and median improvement. Censoring is adjusted by the inverse probability censoring weight. Proportional hazards models are used as working models.

Usage

```

IDI.INF(indata, covs0, covs1, t0, npert = 300,
npert.rand = NULL, seed1 = NULL, alpha = 0.05)

```

Arguments

| | |
|--------|---|
| indata | Time-to-event data. The number of columns should be 2. The 1st column should be time-to-event, and the 2nd column is event indicator (1=event, 0=censor). |
| covs0 | Covariates/predictors data for a base model (Model 0). Factor variables or character variables are not allowed. If any factor variable is involved in the set of predictors, use <code>model.matrix()</code> for dummy coding. <code>covs0</code> need to be a design matrix. Also missing value should not be included here. |
| covs1 | Covariates/predictors data for a new model (Model 1). Factor variables or character variables are not allowed. If any factor variable is involved in the set of predictors, use <code>model.matrix()</code> for dummy coding. <code>covs1</code> need to be a design matrix. Also missing value should not be included here. |
| t0 | A timepoint to define event=yes/no (case/control). Risk score is calculated as the event probability at <code>t0</code> for each model. |
| npert | The number of iterations for the perturbation-resampling. Default is 300. |

| | |
|-------------------------|---|
| <code>npert.rand</code> | If NULL (default), fresh random numbers will be generated in this routine. If a ($n \times m$) matrix is given as <code>npert.rand</code> , those numbers are used in the perturbation instead, where n is the number of subjects and m is the number of iterations of the resampling. The random numbers should be generated from a distribution with mean 1 and variance 1 independently. |
| <code>seed1</code> | A seed for generating random numbers for the perturbation-resampling. Default is NULL. |
| <code>alpha</code> | ($1-\alpha/2$) confidence interval will be calculated. A 0.95 confidence interval will be provided as a default. |

Value

| | |
|---------------------|--|
| <code>m1</code> | Result of IDI. Point and corresponding ($1-\alpha/2$) confidence interval are given |
| <code>m2</code> | Result of continuous-NRI. Point and corresponding ($1-\alpha/2$) confidence interval are given. Note that <code>m2</code> corresponds to the quantity defined as “ $1/2 \text{NRI}(>0)$ ” in Pencina et al.(2011) |
| <code>m3</code> | Result of median improvement in risk score. Point and corresponding ($1-\alpha/2$) confidence interval are given |
| <code>m1.est</code> | A vector with 3 elements. The 1st element is the point estimate of the IDI and the 2nd element is the average of risk score in “event” group, and the 3rd element is the average of risk score in “non-event” group. The 1st element is equal to the 2nd element minus the 3rd element. |
| <code>m2.est</code> | A vector with 3 elements. The 1st element is the point estimate of the continuous-NRI. The 2nd element is the proportion of patients in whom the risk scores with the new model were higher than the risk scores with the old model, among “event” group. The 3rd element is the same proportion but among “non-event” group. The 1st element is equal to the 2nd element minus the 3rd element. |
| <code>m3.est</code> | A vector with 3 elements. The 1st element is the point estimate of the median improvement and the 2nd element is the median of risk score in “event” group, and the 3rd element is the median of risk score in “non-event” group. The 1st element is equal to the 2nd element minus the 3rd element. |
| <code>m3.est</code> | A vector with 3 elements. The 1st element is the point estimate of the median improvement and the 2nd element is the median of risk score in “event” group, and the 3rd element is the median of risk score in “non-event” group. The 1st element is equal to the 2nd element minus the 3rd element. |
| <code>point</code> | An object used in <code>IDI.INF.GRAPH()</code> |

Note

`m2` corresponds to the quantity defined as “ $1/2 \text{NRI}(>0)$ ” in Pencina et al.(2011)

When the base model and the new model are nested, make sure that regression coefficients for the added predictors are significantly different from 0 in the new model, before using this function.

References

Pencina MJ, D'Agostino RB, Steyerberg EW. Extensions of net reclassification improvement calculations to measure usefulness of new biomarkers. *Statistics in Medicine* 2011. doi:10.1002/sim.5647

Uno H, Tian L, Cai T, Kohane IS, Wei LJ. A unified inference procedure for a class of measures to assess improvement in risk prediction systems with survival data, *Statistics in Medicine* 2012. doi:10.1002/sim.5647

See Also

Papers regarding the issue on evaluating nested models:

Kerr KF, McClellan RL, Brown ER, Lumley T. Evaluating the Incremental Value of New Biomarkers With Integrated Discrimination Improvement *American journal of epidemiology* 2011, 174(3):364-74.

Demler OV, Pencina MJ, D'Agostino RB. Misuse of DeLong test to compare AUCs for nested models. *Statistics in Medicine* 2012; online ahead of print.

Examples

```
#--- sample data (pbc in survival package) ---
D=subset(pbc, select=c("time","status","age","albumin","edema","protime","bili"))
D$status=as.numeric(D$status==2)
D=D[!is.na(apply(D,1,mean)),] ; dim(D)
mydata=D[1:100,]

t0=365*5
indata1=mydata;
indata0=mydata[,-7] ; n=nrow(D) ;
covs1<-as.matrix(indata1[,c(-1,-2)])
covs0<-as.matrix(indata0[,c(-1,-2)])

#--- inference ---
x<-IDI.INF(mydata[,1:2], covs0, covs1, t0, npert=200) ;

#--- results ---
IDI.INF.OUT(x) ;

#--- Graphical presentaion of the estimates ---
# IDI.INF.GRAPH(x) ;
```

IDI.INF.GRAPH

Function to display IDI and other measures in a graph

Description

This function generates a plot to graphically display IDI, continuous NRI, and median improvement

Usage

```
IDI.INF.GRAPH(x, main = NULL, xlab = NULL, ylab = NULL,
cex.main = NULL, cex.lab = NULL, ...)
```

Arguments

| | |
|----------|--|
| x | An object generated by IDI.INF |
| main | main title of graph |
| xlab | label of x-axis. The default is "s" |
| ylab | label of y-axis. The default is <code>expression(paste("pr(", hat(D)<=s, "))</code> |
| cex.main | size of the main title |
| cex.lab | size of the labels |
| ... | Arguments passed to <code>plot()</code> |

Details

This function provide a plot to graphically display IDI, continous-NRI and median improvement.

Examples

```
## see example in IDI.INF
```

| | |
|-------------|--------------------------------------|
| IDI.INF.OUT | <i>Function to print the summary</i> |
|-------------|--------------------------------------|

Description

This function disply a summary result performed by IDI.INF()

Usage

```
IDI.INF.OUT(x)
```

Arguments

| | |
|---|--------------------------------|
| x | An object generated by IDI.INF |
|---|--------------------------------|

Details

This function displays the point estimates of IDI, continous-NRI and median improvement, and corresponding (1-alpha) confidence intervals.

Examples

```
## see example in IDI.INF
```

Index

* **IDI**

survIDINRI-package, [2](#)

* **NRI**

survIDINRI-package, [2](#)

* **survival**

survIDINRI-package, [2](#)

IDI.INF, [3](#)

IDI.INF.GRAPH, [5](#)

IDI.INF.OUT, [6](#)

survIDINRI (survIDINRI-package), [2](#)

survIDINRI-package, [2](#)