Package ‘SvyNom’

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Type Package

Title Nomograms for Right-Censored Outcomes from Survey Designs

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Description

Builds, evaluates and validates a nomogram with survey data and right-censored outcomes.

Imports survival,rms,Hmisc,survey

License GPL-2

LazyLoad yes

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## SvyNom-package

**Nomograms for right-censored outcomes with complex survey data**

### Description

Builds, evaluates and validates a nomogram with survey data and right-censored outcomes.

### Details
There are three functions for the user svycox.nomogram, svycox.validate, svycox.calibrate

Author(s)

Marinela Capanu and Mithat Gonen
Maintainer: gonenm@mskcc.org

References


noNA

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Gastric cancer case-control study

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Description

Example dataset for the SvyNom package.

Usage

data(noNA)

Author(s)

Mithat Gonen, Marinela Capanu

Examples

data(noNA)
svycox.calibrate

Checking the calibration of a nomogram for a survey-weighted Cox model

Description
Checks the calibration of a nomogram for a survey-weighted Cox model.

Usage
svycox.calibrate(nom, timept = nom$pred.at, ngroup = 5)

Arguments
nom
a nomogram object from svycox.nomogram

timept
the time point at which calibration will take place; defaults to the time value of the prediction axis in the nomogram

ngroup
number of groups to be formed for validation purposes

Value
returns a matrix of calibration values and plots them

Author(s)
Mithat Gonen, Marinela Capanu

References

Examples
library(survey)
library(rms)
data(nonA)
dd=datadist(nonA)
options(datadist="dd")
dstr2=svydesign(id=-1, strata=group, prob=-inv_weight, fpc=-ssize, data=nonA)

mynom=svycox.nomogram(.design=dstr2, .model=Surv(survival,surv_cens)-ECOG+liver_only+Alb+Hb+Age+Differentiation+gt_1_m1site+lymph_only, .data=nonA, pred.at=24, fun.lab="Prob of 2 Yr OS")

svycox.calibrate(mynom)
svycox.nomogram

Builds a nomogram for a survey-weighted Cox model

Description

Builds a nomogram for a survey-weighted Cox model.

Usage

svycox.nomogram(.design, .model, .data, pred.at, fun.lab)

Arguments

.design represents a survey design object obtained with the package "survey"
.model indicates a Cox model specification
.data contains the data on which the model is to be fit (can not contain NAs)
pred.at specifies the time point at which the nomogram prediction axis will be drawn
fun.lab designate the label of the prediction axis

Details

In addition to the inputs, this function expects the following: 1) the input dataset (.data) cannot contain NAs. You can accomplish this using the na.omit function. See example. 2) datadist must be set. See examples and the documentation for the rms package. 3) survey design must have been saved in .design All of these requirements are explained in Capanu & Gonen (2015) in detail.

Value

A list including elements
nomog A nomogram object
preds predicted values from the model

In addition to what is listed below, the design and the fitted survey weighted Cox model (svy.cox), as well as the timepoint at which the nomogram prediction axis will be drawn (pred.at) are stored.

Author(s)

Mithat Gonen, Marinela Capanu

References

svycox.validate

Examples

```r
library(survey)
library(rms)
data(nona)
dd=datadist(nona)
options(datadist="dd")
dstr2=svydesign(id=-1, strata=group, prob=inv_weight, fpc=ssize, data=nona)
mynom=svycox.nomogram(.design=dstr2, .model=Surv(survival,surv_cens)=ECOG+liver_only+Alb+Hb+Age+
Differentiation+Gt_1_m1site+lymph_only, .data=nona, pred.at=24, fun.lab="Prob of 2 Yr OS")
plot(mynom$nomog)
```

svycox.validate  Validating a nomogram for a survey-weighted Cox model

Description

Validates a nomogram for a survey-weighted Cox model using bootstrap.

Usage

```r
svycox.validate(.boot.index, .nom, .data)
```

Arguments

- `.boot.index` a matrix of bootstrap sample indicators with the number of rows the same as the number of rows in the data on which the nomogram was created and the number of columns being the number of bootstrap samples
- `.nom` a nomogram object returned from svycox.nomogram
- `.data` contains the dataset on which the validation will take place

Details

Note that generating the bootstrap sample is design dependent and it is not part of the function. The user has to generate the bootstrap samples consistent with the design used. An example of how the bootstrap sample was generated for the dataset is presented in the reference below.

Value

prints the estimated optimism and returns the vector of optimism values for each bootstrap sample which can be used to summarize the validation with the measure of choice

References

Examples

bootit=200
library(survey)
library(rms)
data(noNA)
dd=datadist(noNA)
options(datadist="dd")
dstr2=svydesign(id=1, strata=group, prob=inv_weight, fpc=ssize, data=noNA)
mynom=svycox.nomogram(.design=dstr2, .model=Surv(survival,surv_cens)~ECOG+liver_only+Alb+Hb+Age+
Differentiation+Gt_1_m1site+lymph_only, .data=noNA, pred.at=24, fun.lab="Prob of 2 Yr OS")
cases=which(noNA$group=="long")
controls=which(noNA$group=="<24")
boot.index=matrix(NA,nrow(noNA),bootit)
for(i in 1:bootit){
  boot.index[,i]=c(sample(cases,replace=TRUE),sample(controls,replace=TRUE))
}
myval=svycox.validate(boot.index,mynom,noNA)
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