Package ‘CatPredi’

January 10, 2022

Type Package
Title Optimal Categorisation of Continuous Variables in Prediction Models
Version 1.3
Date 2022-01-10
Imports survival, rms, rgenoud, mgcv, stats, graphics
License GPL
NeedsCompilation no
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RoxygenNote 7.1.2
Repository CRAN
Date/Publication 2022-01-10 12:43:01 UTC

\textbf{R topics documented:}

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Description

Allows the user to categorise a continuous predictor variable in a logistic or a Cox proportional hazards regression setting, by maximising the discriminative ability of the model. The categorisation can be done either in a univariate or a multivariate setting.

Author(s)

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References


catpredi Function to obtain optimal cut points to categorise a continuous predictor variable in a logistic regression model

Description

Returns an object with the optimal cut points to categorise a continuous predictor variable in a logistic regression model

Usage

```
catpredi(formula, cat.var, cat.points = 1, data, method = c("addfor", "genetic"), range = NULL, correct.AUC = TRUE, control = controlcatpredi(), ...)```
Arguments

**formula**
An object of class `formula` giving the model to be fitted in addition to the continuous covariate is aimed to categorise. This argument allows the user to specify whether the continuous predictor should be categorised in a univariable context, or in presence of other covariates or cofounders, i.e in a multiple logistic regression model. For instance, Y ~ 1 indicates that the categorisation should be done in a univariable setting, with Y being the response variable. If the predictor variable is aimed to be categorised in a multivariable setting, this argument allows to specify whether the covariates should be modelled using linear or non linear effects. In the latest, the effects are estimated using the `mgcv` package.

**cat.var**
Name of the continuous variable to categorise.

**cat.points**
Number of cut points to look for.

**data**
Data frame containing all needed variables.

**method**
The algorithm selected to search for the optimal cut points. "addfor" if the AddFor algorithm is choosen and "genetic" otherwise.

**range**
The range of the continuous variable in which to look for the cut points. By default NULL, i.e, all the range.

**correct.AUC**
A logical value. If TRUE the bias corrected AUC is estimated.

**control**
Output of the controlcatpredi() function.

... Further arguments for passing on to the function `genoud` of the package `rgenoud`.

Value

Returns an object of class "catpredi" with the following components:

- **call**
the matched call.

- **method**
the algorithm selected in the call.

- **formula**
an object of class `formula` giving the model to be fitted in addition to the continuous covariate is aimed to categorise.

- **cat.var**
name of the continuous variable to categorise.

- **data**
the data frame with the variables used in the call.

- **correct.AUC**
The logical value used in the call.

- **results**
a list with the estimated cut points, AUC and bias corrected AUC.

- **control**
the control parameters used in the call.

For each of the methods used in the call, a list with the following components is obtained:

- "cutpoints" Estimated optimal cut points.
- "AUC" Estimated AUC.
- "AUC.cor" Estimated bias corrected AUC.

Author(s)

Irantzu Barrio, Maria Xose Rodriguez-Alvarez and Inmaculada Arostegui
References


See Also

See Also as `controlcatpredi`, `comp.cutpoints`, `plot.catpredi`, `summary.catpredi`.

Examples

```r
library(CatPredi)
set.seed(127)
# Simulate data
n = 200
# Predictor variable
xh <- rnorm(n, mean = 0, sd = 1)
xd <- rnorm(n, mean = 1.5, sd = 1)
x <- c(xh, xd)
# Response
y <- c(rep(0,n), rep(1,n))
# Covariate
zh <- rnorm(n, mean=1.5, sd=1)
zd <- rnorm(n, mean=1, sd=1)
z <- c(zh, zd)
# Data frame
df <- data.frame(y = y, x = x, z = z)

# Select optimal cut points using the AddFor algorithm
res.addfor <- catpredi.survival(formula = y ~ z, cat.var = "x", cat.points = 3,
data = df, method = "addfor", range=NULL, correct.AUC=FALSE)
```

---

catpredi.survival  
*Function to obtain optimal cut points to categorise a continuous predictor variable in a Cox proportional hazards regression model*

Description

Returns an object with the optimal cut points to categorise a continuous predictor variable in a Cox proportional hazards regression model.

Usage

catpredi.survival(formula, cat.var, cat.points = 1, data,  
method = c("addfor", "genetic"), conc.index = c("cindex", "cpe"),  
range = NULL, correct.index = TRUE, control = controlcatpredi.survival(), ...)
Arguments

**formula**
An object of class `formula` giving the model to be fitted in addition to the continuous covariate is aimed to categorise. The response must be a survival object as returned by the `Surv` function. This argument allows the user to specify whether the continuous predictor should be categorised in a univariable context, or in presence of other covariates or cofounders, i.e in a multiple Cox proportional hazards regression model. For instance, `Surv(SurvT,SurvS)~1` indicates that the categorisation should be done in a univariable setting.

**cat.var**
Name of the continuous variable to categorise.

**cat.points**
Number of cut points to look for.

**data**
Data frame containing all needed variables.

**method**
The algorithm selected to search for the optimal cut points. "addfor" if the AddFor algorithm is chosen and "genetic" otherwise.

**conc.index**
The concordance probability estimator selected for maximisation purposes. "cindex" if the c-index concordance probability is choosen and "cpe" otherwise. The c-index and CPE are estimated using the `rms` and `CPE` packages, respectively.

**range**
The range of the continuous variable in which to look for the cut points. By default NULL, i.e, all the range.

**correct.index**
A logical value. If TRUE the bias corrected concordance probability is estimated.

**control**
Output of the `controlcatpredi.survival()` function.

... Further arguments for passing on to the function `genoud` of the package `rgenoud`.

Value

Returns an object of class "catpredi.survival" with the following components:

**call**
the matched call.

**method**
the algorithm selected in the call.

**formula**
an object of class `formula` giving the model to be fitted in addition to the continuous covariate is aimed to categorise.

**cat.var**
name of the continuous variable to categorise.

**data**
the data frame with the variables used in the call.

**correct.index**
The logical value used in the call.

**results**
a list with the estimated cut points, concordance probability and bias corrected concordance probability.

**control**
the control parameters used in the call.

When the c-index concordance probability is choosen, a list with the following components is obtained for each of the methods used in the call:

"cutpoints" Estimated optimal cut points.
"Cindex" Estimated c-index.
"Cindex.cor" Estimated bias corrected c-index.
When the CPE concordance probability is choosen, a list with the following components is obtained for each of the methods used in the call:

"cutpoints"  Estimated optimal cut points.
"CPE"  Estimated CPE.
"CPE.cor"  Estimated bias corrected CPE.

Author(s)
Irantzu Barrio and Maria Xose Rodriguez-Alvarez

References


See Also

See Also \texttt{controlcatpredi.survival}, \texttt{comp.cutpoints.survival}, \texttt{plot.catpredi.survival}, \texttt{catpredi}.

Examples

```r
library(CatPredi)
library(survival)
set.seed(123)
#Simulate data
n = 500
tauc = 1
X <- rnorm(n=n, mean=0, sd=2)
SurvT <- exp(2*X + rweibull(n = n, shape=1, scale = 1)) + rnorm(n, mean=0, sd=0.25)
# Censoring time
CensTime <- runif(n=n, min=0, max=tauc)
# Status
SurvS <- as.numeric(SurvT <= CensTime)
# Data frame
dat <- data.frame(X = X, SurvT = pmin(SurvT, CensTime), SurvS = SurvS)

# Select optimal cut points using the AddFor algorithm
res <- catpredi.survival (formula= Surv(SurvT,SurvS)~1, cat.var="X", cat.points = 2, data = dat, method = "addfor", conc.index = "cindex", range = NULL, correct.index = FALSE)
```
**comp.cutpoints**

Selection of optimal number of cut points

**Description**

Compares two objects of class "catpredi".

**Usage**

```r
comp.cutpoints(obj1, obj2, V = 100)
```

**Arguments**

- **obj1**: an object inheriting from class "catpredi" for k number of cut points
- **obj2**: an object inheriting from class "catpredi" for k+1 number of cut points
- **V**: Number of bootstrap resamples. By default V=100

**Value**

This function returns an object of class "comp.cutpoints" with the following components:

- **AUC.cor.diff**: the difference of the bias corrected AUCs for the two categorical variables.
- **icb.auc.diff**: bootstrap based confidence interval for the bias corrected AUC difference.

**Author(s)**

Irantz Barrio, Maria Xose Rodriguez-Alvarez and Inmaculada Arostegui

**References**


**See Also**

See Also as `catpredi`.

**Examples**

```r
library(CatPredi)
set.seed(127)
#Simulate data
n = 100
#Predictor variable
xh <- rnorm(n, mean = 0, sd = 1)
xd <- rnorm(n, mean = 1.5, sd = 1)
x <- c(xh, xd)
```
# Response
y <- c(rep(0,n), rep(1,n))
# Data frame
df <- data.frame(y = y, x = x)

# Select 2 optimal cut points using the AddFor algorithm. Correct the AUC
res.addfor.k2 <- catpredi(formula = y ~ 1, cat.var = "x", cat.points = 2,
data = df, method = "addfor", range=NULL, correct.AUC=TRUE,
control=controlcatpredi(addfor.g=100))
# Select 3 optimal cut points using the AddFor algorithm. Correct the AUC
res.addfor.k3 <- catpredi(formula = y ~ 1, cat.var = "x", cat.points = 3,
data = df, method = "addfor", range=NULL, correct.AUC=TRUE,
control=controlcatpredi(addfor.g=100))
# Select optimal number of cut points
comp <- comp.cutpoints(res.addfor.k2, res.addfor.k3, V = 100)

---

comp.cutpoints.survival

Selection of optimal number of cut points

Description

Compares two objects of class "catpredi.survival"

Usage

comp.cutpoints.survival(obj1, obj2, V = 100)

Arguments

obj1       an object inheriting from class "catpredi.survival" for k number of cut points
obj2       an object inheriting from class "catpredi.survival" for k+1 number of cut points
V          Number of bootstrap resamples. By default V=100

Value

This function returns an object of class "comp.cutpoints.survival" with the following components:

CI.cor.diff  the difference of the bias corrected concordance probability for the two categorical variables.
icb.CI.diff  bootstrap based confidence interval for the bias corrected concordance probability difference.

Author(s)

Irantzu Barrio and Maria Xose Rodriguez-Alvarez
controlcatpredi

References


See Also

See Also as catpredi.survival.

Examples

library(CatPredi)
library(survival)
set.seed(123)

# Simulate data
n = 300
tauc = 1
X <- rnorm(n=n, mean=0, sd=2)
SurvT <- exp(2*X + rweibull(n = n, shape=1, scale = 1)) + rnorm(n, mean=0, sd=0.25)
# Censoring time
CensTime <- runif(n=n, min=0, max=tauc)
# Status
SurvS <- as.numeric(SurvT <= CensTime)
# Data frame
dat <- data.frame(X = X, SurvT = pmin(SurvT, CensTime), SurvS = SurvS)

# Select 2 optimal cut points using the AddFor algorithm. Correct the c-index
res.k2 <- catpredi.survival (formula= Surv(SurvT,SurvS)~1, cat.var="X", cat.points = 2,
data = dat, method = "addfor", conc.index = "cindex", range = NULL, correct.index = TRUE)
# Select 3 optimal cut points using the AddFor algorithm. Correct the c-index
res.k3 <- catpredi.survival (formula= Surv(SurvT,SurvS)~1, cat.var="X", cat.points = 3,
data = dat, method = "addfor", conc.index = "cindex", range = NULL, correct.index = TRUE)
# Select optimal number of cut points
comp <- comp.cutpoints.survival(res.k2, res.k3, V = 100)

controlcatpredi

Control function

Description

Function used to set several parameters to control the selection of the optimal cut points in a logistic regression model.
Usage

controlcatpredi.survival(min.p.cat = 1, addfor.g = 100, B = 50, b.method = c("ncoutcome", "coutcome"), print.gen = 0)

Arguments

min.p.cat Set the minimum number of individuals in each category
addfor.g Grid size for the AddFor algorithm
B Number of bootstrap replicates for the AUC bias correction procedure
b.method Allows to specify whether the bootstrap resampling should be done considering or not the outcome variable. The option "ncoutcome" indicates that the data is resampled without taking into account the response variable, while "coutcome" indicates that the data is resampled in regard to the response variable
print.gen corresponds to the argument print.level of the genoud function of the package rgenoud.

Value

A list with components for each of the possible arguments.

Author(s)

Irantzu Barrio, Maria Xose Rodriguez-Alvarez and Inmaculada Arostegui

References


See Also

See Also as catpredi.

description

Function used to set several parameters to control the selection of the optimal cut points in a Cox proportional hazards regression model

Usage

controlcatpredi.survival(min.p.cat = 5, addfor.g = 100, B = 50, b.method = c("ncoutcome", "coutcome"), print.gen = 0)
Arguments

min.p.cat  Set the minimum number of individuals in each category.
addfor.g  Grid size for the AddFor algorithm.
B  Number of bootstrap replicates for the AUC bias correction procedure
b.method  Allows to specify whether the bootstrap resampling should be done considering or not the outcome variable. The option "ncoutcome" indicates that the data is resampled without taking into account the response variable, while "coutcome" indicates that the data is resampled in regard to the response variable.
print.gen  Corresponds to the argument print.level of the genoud function of the package rgenoud.

Value

A list with components for each of the possible arguments.

Author(s)

Irantzu Barrio and Maria Xose Rodriguez-Alvarez

References


See Also

See Also as catpredi.survival.

Description

Plots the relationship between the predictor variable is aimed to categorise and the response variable based on a GAM model. Additionally, the optimal cut points obtained with the catpredi() function are drawn on the graph.

Usage

## S3 method for class 'catpredi'
plot(x, ...)

Arguments

x  An object of type catpredi.
...  Additional arguments to be passed on to other functions. Not yet implemented.
This function returns the plot of the relationship between the predictor variable and the outcome.

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See Also as `catpredi`.

```r
library(CatPredi)
set.seed(127)
#Simulate data
n = 100
#Predictor variable
xh <- rnorm(n, mean = 0, sd = 1)
xd <- rnorm(n, mean = 1.5, sd = 1)
x <- c(xh, xd)
#Response
y <- c(rep(0,n), rep(1,n))
# Data frame
df <- data.frame(y = y, x = x)

# Select optimal cut points using the AddFor algorithm
res.addfor <- catpredi(formula = y ~ 1, cat.var = "x", cat.points = 3,
data = df, method = "addfor", range = NULL, correct.AUC = FALSE)
# Plot
plot(res.addfor)
```

Plot the optimal cut points.

Plots the functional form of the predictor variable we want to categorise. Additionally, the optimal cut points obtained with the catpredi.survival() function are drawn on the graph.
## S3 method for class 'catpredi.survival'
plot(x, ...)

### Arguments

- **x**: An object of type catpredi.survival.
- **...**: Additional arguments to be passed on to other functions. Not yet implemented.

### Value

This function returns the plot of the relationship between the predictor variable and the outcome.

### Author(s)

Irantzu Barrio and Maria Xose Rodriguez-Alvarez

### References


### See Also

See Also as `catpredi.survival`.

### Examples

```r
library(CatPredi)
library(survival)
set.seed(123)
# Simulate data
n = 500
tauc = 1
X <- rnorm(n=n, mean=0, sd=2)
SurvT <- exp(2*X + rweibull(n = n, shape=1, scale = 1)) + rnorm(n, mean=0, sd=0.25)
# Censoring time
CensTime <- runif(n=n, min=0, max=tauc)
# Status
SurvS <- as.numeric(SurvT <= CensTime)
# Data frame
dat <- data.frame(X = X, SurvT = pmin(SurvT, CensTime), SurvS = SurvS)

# Select optimal cut points using the AddFor algorithm
res <- catpredi.survival (Formula= Surv(SurvT,SurvS)~1, cat.var="X", cat.points = 2, data = dat, method = "addfor", conc.index = "cindex", range = NULL, correct.index = FALSE)
# Plot
plot(res)
```
summary.catpredi

Summary method for catpredi objects

Description

Produces a summary of a catpredi object. The following are printed: the call to the catpredi() function; the estimated optimal cut points obtained with the method selected and the estimated AUC and bias corrected AUC (if the argument correct.AUC is TRUE) for the categorised variable.

Usage

```r
## S3 method for class 'catpredi'
summary(object, digits = 4, ...)
```

Arguments

- `object` an object of class catpredi as produced by catpredi()
- `digits` .
- `...` further arguments passed to or from other methods.

Value

Returns an object of class "summary.catpredi" with the same components as the catpredi function (see `catpredi`). plus:

- `fit.gam` fitted model according to the model specified in the call, based on the function `gam` of the package `mgcv`.

Author(s)

Irantzu Barrio, Maria Xose Rodriguez-Alvarez and Inmaculada Arostegui

References


See Also

See Also as `catpredi`.
Examples

```r
library(CatPredi)
set.seed(127)
# Simulate data
n = 200
# Predictor variable
xh <- rnorm(n, mean = 0, sd = 1)
xd <- rnorm(n, mean = 1.5, sd = 1)
x <- c(xh, xd)
# Response
y <- c(rep(0,n), rep(1,n))
# Covariate
zh <- rnorm(n, mean=1.5, sd=1)
zd <- rnorm(n, mean=1, sd=1)
z <- c(zh, zd)
# Data frame
df <- data.frame(y = y, x = x, z = z)

# Select optimal cut points using the AddFor algorithm
res.addfor <- catpredi(formula = y ~ z, cat.var = "x", cat.points = 2,
data = df, method = "addfor", range=NULL, correct.AUC=FALSE)
# Summary
summary(res.addfor)
```

**Description**

Produces a summary of a 'catpredi.survival' object. The following are printed: the call to the catpredi.survival() function; the estimated optimal cut points obtained with the method and concordance probability estimator selected and the estimated and bias corrected concordance probability for the categorised variable (whenever the argument correct.index is set to TRUE).

**Usage**

```r
## S3 method for class 'catpredi.survival'
summary(object, digits = 4, ...)
```

**Arguments**

- `object` an object of class "catpredi.survival" as produced by catpredi.survival()
- `digits` .
- `...` further arguments passed to or from other methods.
Value

Returns an object of class "summary.catpredi.survival" with the same components as the catpredi.survival function (see catpredi.survival).

Author(s)

Irantzu Barrio and Maria Xose Rodriguez-Alvarez

References


See Also

See Also as catpredi.survival.

Examples

library(CatPredi)
library(survival)
set.seed(123)
# Simulate data
  n = 500
tauc = 1
X <- rnorm(n=n, mean=0, sd=2)
SurvT <- exp(2*X + rweibull(n = n, shape=1, scale = 1)) + rnorm(n, mean=0, sd=0.25)
# Censoring time
CensTime <- runif(n=n, min=0, max=tauc)
# Status
SurvS <- as.numeric(SurvT <= CensTime)
# Data frame
dat <- data.frame(X = X, SurvT = pmin(SurvT, CensTime), SurvS = SurvS)

# Select optimal cut points using the AddFor algorithm
res <- catpredi.survival (formula= Surv(SurvT,SurvS)~1, cat.var="X", cat.points = 2, data = dat, method = "addfor", conc.index = "cindex", range = NULL, correct.index = FALSE)
# Summary
summary(res)
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