Package ‘thregI’
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Description Fit a threshold regression model for Interval Censored Data based on the first-hitting-time of a boundary by the sample path of a Wiener diffusion process. The threshold regression methodology is well suited to applications involving survival and time-to-event data.
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**bcos  Breast Cosmesis Data**

**Description**

94 early breast cancer patients who had been treated with primary radiation therapy and adjuvant chemotherapy and with radiotherapy alone for the treatment. A patient due to monitored weekly or monthly for a clinically observable change in breast cancer status and may return with a changed status. For this case, we know the changed status is between \((L, R]\).

**Usage**

- `bcos`

**Format**

- `id`: subject recorded in the data set
- `left`: breast cancer status return with a changed status after time \(L\)
- `right`: breast cancer status return with a changed status after time \(R\)
- `treatment`: Radiation = radiation therapy, RadChemo = radiation therapy with chemotherapy

**References**


**hdsp  NASAs Hypobaric Decompression Sickness Data**

**Description**

Time to onset of grade IV VGE was collected by volunteers who underwent denitrogenation test procedures before being uncovered to a hypobaric environment. This data set contains with 238 subjects and several covariates were recorded periodically monitor for a changed status is between \((L, R]\).

**Usage**

- `hdsp`

**Format**
id: subject recorded in the data set
Age: recorded age (ranged from 20 to 54)
Sex: (males = 1; females = 0)
TR360: (ranged from 1.04 to 1.89)
Noadyn: (ambulatory, Noadyn=1; lower body adynamic, Noadyn=0)
right: return with a grade IV VGE changed status before time \( R \)
left: return with a grade IV VGE changed status after time \( L \)

References


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hr.thregI

*perform hazard ratio for threshold regression model*

---

Description

Returns the hazard ratios at a selected time for specified scenarios of the threshold regression model.

Usage

```r
## S3 method for class 'thregI'
hr(object, var, timevalue, scenario)
```

Arguments

- **object**: a thregI object.
- **var**: specifies the categorical variable which is required for the hazard ratios. Transform this variable into factor variable that has been used in thregI(). The lower level of the factor variable of var is the reference level of hazard ratio.
- **timevalue**: specifies the desired time at which the hazard ratios would like to be had. A vector is allowed for this argument.
- **scenario**: specifies the values of all variables that considered in the thregI() except variable of var.
Examples

#load the data "bcos"
data("bcos", package="thregI")

#transform the "treatment" variable into factor variable f.treatment
bcos$f.treatment=factor(bcos$treatment)

#fit the threshold regression model on the factor variable f.treatment
fit<-thregI(Surv(left, right, type='interval2')~f.treatment|f.treatment,data=bcos)

#hazard ratio of the radiation group vs. the radiation with chemotherapy at fifth month
hr.thregI(fit, var = f.treatment, timevalue = 5)

hr.thregIcure

perform hazard ratio for threshold regression cure-rate model

Description

Returns the hazard ratios at a selected time for specified scenarios of the threshold regression cure-rate model.

Usage

## S3 method for class 'thregIcure'
hr(object, var, timevalue, scenario)

Arguments

object
  a thregIcure object.

var
  specifies the name of the variable which is required to be categorical for which the hazard ratios are to be calculated. The use of the var argument is similar to that in the hr.thregI() function.

timevalue
  specifies the desired time at which the hazard ratios would like to be had. A vector is allowed for this argument.

scenario
  specifies the values of all variables that considered in the thregIcure function except variable of var.

Examples

#load the data "hdsd"
data("hdsd", package="thregI")

#transform categorical variable Noadyn into factor variable f.noadyn
hdsd$f.noadyn=factor(hdsd$Noadyn)

#fit the threshold regression cure-rate model
#the covariates are TR360, Noadyn, Sex and Age
fit<-thregIcure(Surv(left, right, type='interval2')~f.noadyn|TR360|Sex+Age, data=hdsd)

#calculate the hazard ratios for categorical variable Noadyn
#specified scenario of TR360=1.5, Male, Age=30 at time one
hr.thregIcure(fit, var = f.noadyn, timevalue = 1, scenario=TR360(1.5)+Sex(1)+Age(30))

### Description

Display the graphs of the estimated survival, hazard or density function at different levels of a categorical variable which has been included in the threshold regression model by thregI(). There are three options, "sv", "hz" and "ds" are for survival, hazard and density function, respectively.

### Usage

```r
## S3 method for class 'thregI'
plot(x, var, scenario, graph, nolegend=0, nocolor=0, ...)
```

### Arguments

- **x**: a thregI object.
- **var**: specifies the name of the variable which is required to be categorical. For each level of which (survival, hazard, density) the plots would be generated at given scenario specified by the scenario argument.
- **scenario**: specifies a scenario for predicted plots.
- **graph**: specifies the type of curves to be generated. The "sv" option is to plot survival function, the "hz" option is to plot hazard function and the "ds" option is to plot density function.
- **nolegend**: set nolegend to be 1 when no need for legend. Users can add legends by themselves after set nolegend=1.
- **nocolor**: set nocolor to be 1 if users would like to have all curves in black.
- **...**: for future methods

### Examples

```r
#load the data "bcos"
data("bcos", package="thregI")

# transform the "treatment" variable into factor variable f.treatment
bcos$f.treatment=factor(bcos$treatment)

# fit the threshold regression model on the factor variable f.treatment
fit<-thregI(Surv(left, right, type='interval2')|f.treatment, data=bcos)
```
# estimated survival function at all levels of a categorical variable
plot.thregI(fit, var = f.treatment, graph = "sv", nocolor = 1)

# estimated hazard function at all levels of a categorical variable
plot.thregI(fit, var = f.treatment, graph = "hz", nocolor = 1)

# estimated density function at all levels of a categorical variable
plot.thregI(fit, var = f.treatment, graph = "ds", nocolor = 1)

---

**plot.thregIcure**  
plot survival, hazard and density curves

---

**Description**
Display the graphs of the estimated survival, hazard or density function at different levels of a categorical variable which has been included in the threshold regression cure-rate model by thregIcure(). There are three options, "sv", "hz" and "ds" are for survival, hazard and density function, respectively.

**Usage**
```r
## S3 method for class 'thregIcure'
plot(x, var, scenario, graph, nolegend=0, nocolor=0,...)
```

**Arguments**
- `x`: a thregIcure object.
- `var`: specifies the name of the variable which is required to be categorical. The use of the var argument is the same as that in the plot.thregI().
- `scenario`: specifies a scenario for predicted plots.
- `graph`: specifies the type of curves to be generated. The "hz" option is to plot hazard function accommodated a cure rate, the "sv" option is to plot survival function accommodated a cure rate and the "ds" option is to plot density function accommodated a cure rate.
- `nolegend`: The use of the nolegend argument is the same as that in the plot.thregI().
- `nocolor`: The use of the nolegend argument is the same as that in the plot.thregI().
- `...`: for future methods

**Examples**
```r
# load the data "hdsd"
data("hdsd", package="thregI")

# transform categorical variable Noadyn into factor variable f.noadyn
hdsd$f.noadyn=factor(hdsd$Noadyn)
```
predict.thregI

predict the initial health status value and the drift value of the health process

Description
Display the predicted values of threshold regression coefficients, density probability, survival probability, and hazard rate at the desired time and specified scenario; or, display the predicted values for all subjects corresponding to subjects scenario values at the desired time.

Usage
## S3 method for class 'thregI'
predict(object, timevalue, scenario, ...)

Arguments
object  a thregI object.
timevalue  specifies the desired time at which the predicted values of threshold regression coefficients, density probability, survival probability, and hazard rate.
scenario  specifies the values of all predictors considered in the thregI() and the dummy of the categorical variable of var. The predicted values at a specified time value for all subjects are calculated by the covariate values for each subject are used as their corresponding scenario values if ignore this argument.

...  for future methods

Examples
#load the data "bcos"
data("bcos", package="thregI")

# transform the treatment variable into factor variable f.treatment
bcos$f.treatment=factor(bcos$treatment)

# fit the threshold regression model on the factor variable f.treatment
fit<-thregI(Surv(left, right, type='interval2')~f.treatment,f.treatment,data=bcos)

# calculate the predicted values for y0, mu, f, s and h
predict.thregIcure

# for the specified scenario that the treatment classification is 1 at time fifth month.
predict.thregI(fit, timevalue = 5, scenario=f.treatmentRadiation(1))

predict.thregIcure  predict the initial health status value, the drift value of the health process and cure rate

Description

Display the predicted values of threshold regression coefficients, non-cure rate, density probability, survival probability and hazard rate at the desired time and specified scenario; or, display the predicted values for all subjects corresponding to subjects scenario values at the desired time.

Usage

## S3 method for class 'thregIcure'
predict(object,timevalue,scenario,...)

Arguments

object  a thregIcure object.
timevalue  specifies the desired time at which the predicted values of threshold regression coefficients, non-cure rate, density probability, survival probability, and hazard rate.
scenario  specifies the values of all predictors considered in the thregIcure() and the dummy of the categorical variable of var. The use of the scenario argument is the same as that in the predit.thregI().
...
	for future methods

Examples

#load the data "hdsd"
data("hdsd", package="thregI")

# transform categorical variable Noadyn into factor variable f.noadyn
hdsd$f.noadyn=factor(hdsd$Noadyn)

# fit the threshold regression cure-rate model
# the covariates are TR360, Noadyn, Sex and Age
fit<-thregIcure(Surv(left, right, type='interval2')~f.noadyn|TR360|Sex+Age, data=hdsd)

# calculate the predicted values
# subject is ambulatory (Noadyn=1), TR360 = 1.5, male and 30 years old
# note that f.noadyn1 is the name of non-reference group
predict.thregIcure(fit, timevalue = 1, scenario=f.noadyn1(1)+TR360(1.5)+Sex(1)+Age(30))
print.thregI  

**print method for thregI objects**

Description

Produces a printed summary of a fitted thregI function

Usage

```r
## S3 method for class 'thregI'
print(x, digits=max(options()$digits - 4, 3), ...)
```

Arguments

- `x` the result of a call to `thregI`
- `digits` significant digits to print
- `...` For future methods

print.thregIcure  

**print method for thregIcure objects**

Description

produces a printed summary of a fitted thregIcure function

Usage

```r
## S3 method for class 'thregIcure'
print(x, digits=max(options()$digits - 4, 3), ...)
```

Arguments

- `x` the result of a call to `thregIcure`
- `digits` significant digits to print
- `...` For future methods
thregI

*fit threshold regression for interval-censored data*

### Description

Extend right-censored data of Xiao et al. (2015) into interval-censored data. Fit a threshold regression model for interval-censored data and calculate the prediction of the initial health status value and the drift value of the health process.

### Usage

```r
thregI(formula, data)
```

### Arguments

- **formula**: a formula object, which has the response on the left of a ~ operator, and the explanation variables on the right. The response must be a survival object as returned by the `Surv()` function. The | operator on the left-hand side is used for the linear regression function of \( \ln y_0 \) and right-hand side is for specifying explanation variables of \( \mu \). A constant \( \ln y_0 \) or \( \mu \) is allowed, let 0 or 1 as a placeholder on the left or right of the | operator.

- **data**: a data frame must contains two time points (\( L \) and \( R \)) in which to through the `Surv()` of R package survival by type = interval2 and interpret the variables named in the formula.

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### References


### Examples

```r
#load the data "bcos"
data("bcos", package="thregI")

#transform the "treatment" variable into factor variable f.treatment
bcos$f.treatment=factor(bcos$treatment)

#fit the threshold regression model on the factor variable f.treatment
fit<-thregI(Surv(left, right, type='interval2')~f.treatment|f.treatment, data=bcos)
fit
```
thregIcure  

fit threshold regression cure-rate model for interval-censored data

---

Description

Fit a threshold regression cure-rate model for interval-censored data and calculate the prediction of the initial health status value, the drift value of the health process and cure rate. Whether the accommodated cure rate exists by goodness-of-fit test compared with the 'thregI'.

Usage

```r
thregIcure(formula, data)
```

Arguments

- `formula`: a formula object, which has the similar format to that in the `thregI()`. There are two | operators, on the left-hand side | operator is used for the linear regression function of $lny_0$ and specifying explanation variables of $\mu$. On the right of right-hand side | operator is used for specifying explanation variables of $logit(p)$. A constant $lny_0$, $\mu$ or $logit(p)$ is allowed.
- `data`: a data frame has the same format as that in the `thregI()`.

Examples

```r
# load the data "hdsd"
#data("hdsd", package="thregI")

data(hdsd, package="thregI")

# transform the Noadyn variable into factor variable f.noadyn
hdsd$f.noadyn=factor(hdsd$Noadyn)

# fit the threshold regression cure-rate model
# the covariates are TR360, Noadyn, Sex and Age
fit<-thregIcure(Surv(left, right, type='interval2')~f.noadyn+TR360|f.noadyn+TR360|f.noadyn+TR360+Sex+Age, data=hdsd)

fit

# note that p-value of the goodness of fit test return by thregIcure function
```
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