Package ‘crskdiag’

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Title Diagnostics for Fine and Gray Model
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Description Provides the implementation of analytical and graphical approaches for checking the assumptions of the Fine and Gray model.
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R topics documented:

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Create a competing risks object.

**Description**

Combines observed time and cause indicator to be a competing risks object. For internal use only.

**Usage**

`crsk(t, ic)`

**Arguments**

- **t** A vector of observed times.
- **ic** A vector of cause indicators.

**dat1**

Simulated competing risks data contains covariate with non-linear functional form

**Description**

Simulated data with 300 subjects and 4 variates: time, cause, z1 and z2.

**Format**

The data has 300 rows and 4 columns.

- **time** a numeric vector of event or censoring times.
- **cause** a numeric vector code of survival status. 1: failure from the cause of interest; 2: failure from other causes; 0: censored.
- **z1** a numeric vector with continuous values.
- **z2** a numeric vector with continuous values.

**Source**

Simulated data
Simulated competing risks data with time-varying covariate

Description

Simulated data with 300 subjects and 4 variates: time, cause, z1 and z2.

Format

The data has 300 rows and 4 columns.

- **time**: a numeric vector of event or censoring times.
- **cause**: a numeric vector code of survival status. 1: failure from the cause of interest; 2: failure from other causes; 0: censored.
- **z1**: a numeric vector with the values of 0 and 1.
- **z2**: a numeric vector with continuous values.

Source

Simulated data

Checking Fine and Gray subdistribution hazards model with cumulative sums of residuals

Description

Provides with a class of analytical methods and graphical approaches for checking the assumptions of the Fine and Gray subdistribution hazards model based on the cumulative sums of residuals. It validates the model in three aspects: proportionality of hazard ratio, the linear functional form, and the link function.

Usage

```r
diag_crr(formula, data, test = c("lin", "prop"), N.it = 20, n.sim = 1000, n.plot = 10, seed = NULL, minor_included = 1)
```

Arguments

- **formula**: a formula object, with the response on the left of a ~ operator, and the terms on the right. The response must be a competing risks object as returned by the Crsk function.
- **data**: a dataset contains the time, causes of event, and the covariates. For the causes, 0 is censoring, 1 is the cause of interest, 2 is all other causes.
test type of diagnostic method used in the test. One test at a time. "lin" generates the results of testing linear functional form for each covariate and link function. "prop" generates the results of testing proportionality for each covariate and overall proportionality.

Nit number of iterations in model estimation. Default is 20.
n.sim number of iterations in the analytical diagnostics. Default is 1000.
n.plot number of plots of simulated processes used in the graphical diagnostics. Default is 10.
seed a seed used in generating the simulated processes.
minor_included include the minor term in FG model if TRUE. Default is TRUE.

Details
More details about the model diagnostic procedures can be found in Li, Scheike and Zhang (2015).

Value

- test type of diagnostic method used in the test.
- varname covariate names.
- used total sample size used in analysis. Subject with missing value will be excluded from analysis.
- NJP total number of unique time points for the cause of interest.
- TJP unique time points for the cause of interest leading by a zero.
- n.plot number of plots of simulated processes used in the graphical diagnostics.
- beta estimated regression coefficients.
- beta.se estimated standard errors for regression coefficients.
- dlamb0 a vector of estimated cumulative baseline subdistribution hazards at observed failure times.
- pval p-values of the model diagnostic test.
- mav maximum value of the cumulative residual process (lin) or standardized residual process (prop).
- B cumulative residual process (lin) or standardized cumulative residual process (prop). Used for plot functions.
- uniX unique values of the covariates. Used for plot and available only when test="lin".
- TC number of unique covariates. Available only when test="lin".

Author(s)
Jianing Li

References
**diag_lin**

*See Also*

`diag_lin`, `diag_prop`, `plot.diaglin`, `plot.diagprop`, `print.diaglin`, `print.diagprop`

**Examples**

```r
data(dat1)
out1 <- diag_crr(Crsk(time,cause)~z1+z2, data=dat1, test="lin", seed=1234)
print(out1)
plot(out1)

data(dat2)
out2 <- diag_crr(Crsk(time,cause)~z1+z2, data=dat2, test="prop", seed=1234)
print(out2)
plot(out2)
```

**Description**

Diagnostics for the linear functional form and the link function

Checks the linear functional form and the log-log link function assumptions of the Fine and Gray model. For internal use only.

**Usage**

```r
diag_lin(t, ic, z, n.total, Nit, n.sim, n.plot, seed, minor_included)
```

**Arguments**

- `t`: a vector of observed times.
- `ic`: a vector of cause indicators.
- `z`: a matrix of covariates for fitting the model.
- `n.total`: total number of samples
- `Nit`: number of iterations for model estimation. Default is 20.
- `n.sim`: number of iterations in the analytical diagnostics. Default is 1000.
- `n.plot`: number of plots of simulated processes used in the graphical diagnostics. Default is 10.
- `seed`: a seed used in generating the simulated processes.
- `minor_included`: include the minor term in FG model if TRUE. Default is TRUE.

**Details**

More details can be found in Li, Scheike and Zhang (2015).
diag_prop

Value

a "diaglin" class object.

Author(s)

Jianing Li

References


See Also

diag_crr, plot.diaglin, print.diaglin

Description

Checks the proportionality assumptions of the Fine and Gray model. For internal use only.

Usage

diag_prop(t, ic, z, n.total, Nit, n.sim, n.plot, seed, minor_included)

Arguments

t a vector of observed times.
ic a vector of cause indicators.
z a matrix of covariates for fitting the model.
n.total total number of samples
Nit number of iterations for model estimation. Default is 20.
n.sim number of iterations in the analytical diagnostics. Default is 1000.
n.plot number of plots of simulated processes used in the graphical diagnostics. Default is 10.
seed a seed used in generating the simulated processes.
minor_included include the minor term in FG model if TRUE. Default is TRUE.

Details

More details can be found in Li, Scheike and Zhang (2015).
Value

a "diagprop" class object.

Author(s)

Jianing Li

References


See Also

`diag_crr`, `plot.diaglin`, `print.diaglin`

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**plot.diaglin**

*Plot diaglin object*

Description

Plots the observed and simulated cumulative sums of residuals in testing linear functional form for each covariate and link function for the fitted Fine and Gray model.

Usage

```r
## S3 method for class 'diaglin'
plot(x, col = c("red", "black"), lty = c(1, 2), lwd = c(2, 1), txt.pos=c(0.85,0.1), lgd.pos="topright", x=lim=NULL, ylim=NULL, select=NULL, ...) 
```

Arguments

- `x`: a diaglin object.
- `col`: colors of the plots. The first element is used for observed process, and the second element is used for simulated processes.
- `lty`: line types of the plots. The first element is used for observed process, and the second element is used for simulated processes.
- `lwd`: line widths of the plots. The first element is used for observed process, and the second element is used for simulated processes.
- `txt.pos`: the horizontal and vertical positions of the p-value. The assigned numbers represents the percentage in the x-y panel.
- `lgd.pos`: the position of the legend.
- `xlim`: the x limitation of the plots
- `ylim`: the y limitation of the plots
select the covariate needs to be plotted. Valid value is an integer from 1 to the number of covariates plus 1. For example, if the number of covariates is 3, then 1, 2, 3 indicates the plots of checking corresponding covariates in the formula, and 4 indicates the plot of checking the link function. Multiple values are allowed additional arguments to plot()

See Also
diag_lin, print.diaglin

Examples
library(crskdiag)
data(dat1)
out1 <- diag_crr(Crsk(time,cause)-z1+z2, data=dat1, test="lin", seed=1234)
plot(out1)

plot.diagprop

Plot diagprop object

Description
Plots the observed and simulated cumulative sums of residuals in testing the proportionality assumption for the fitted Fine and Gray model.

Usage
```r
## S3 method for class 'diagprop'
plot(x, col = c("red", "black"), lty = c(1, 2), lwd = c(2, 1), txt.pos=c(0.85, 0.1), lgd.pos="topright", xlim=NULL, ylim=NULL, select=NULL, ...)
```

Arguments
- **x**: a diagprop object.
- **col**: colors of the plots. The first element is used for observed process, and the second element is used for simulated processes.
- **lty**: line types of the plots. The first element is used for observed process, and the second element is used for simulated processes.
- **lwd**: line widths of the plots. The first element is used for observed process, and the second element is used for simulated processes.
- **txt.pos**: the horizontal and vertical positions of the p-value. The assigned numbers represent the percentage in the x-y panel.
- **lgd.pos**: the position of the legend.
- **xlim**: the x limitation of the plots
- **ylim**: the y limitation of the plots
select the covariate needs to be plotted. Valid value is an integer from 1 to the number of covariates plus 1. For example, if the number of covariates is 3, then 1, 2, 3 indicates the plots of checking corresponding covariates in the formula, and 4 indicates the plot of checking the link function. Multiple values are allowed additional arguments to plot()

See Also
diag_prop, print.diagprop

Examples
library(crskdiag)
data(dat2)
out2 <- diag_crr(Crsk(time,cause)~z1+z2, data=dat2, test="prop", seed=1234)
plot(out2)

print.diaglin

Print diaglin object

Description
Prints the p-values of testing linear functional form for each covariate and the p-value of testing link function.

Usage
## S3 method for class 'diaglin'
print(x, ...)

Arguments
x a diaglin object
... additional arguments to print()

See Also
diag_lin, plot.diaglin

Examples
library(crskdiag)
data(dat1)
out1 <- diag_crr(Crsk(time,cause)~z1+z2, data=dat1, test="lin", seed=1234)
print(out1)
**print.diagprop**

*Print diagprop object*

**Description**

Prints the p-values of testing proportionality of the subdistribution hazards for each covariate and the p-value of overall proportionality.

**Usage**

```r
## S3 method for class 'diagprop'
print(x, ...)
```

**Arguments**

- `x`: a diagprop object
- `...`: additional arguments to print()

**See Also**

- [diag_prop](#), [plot.diagprop](#)

**Examples**

```r
library(crskdiag)
data(dat2)
out2 <- diag_crr(Crsk(time, cause)~z1+z2, data=dat2, test="prop", seed=1234)
print(out2)
```
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