

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.

License GPL (>= 2)

NeedsCompilation yes

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Crsk	<i>Create a competing risks object.</i>
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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	<i>Simulated competing risks data contains covariate with non-linear functional form</i>
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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

dat2	<i>Simulated competing risks data with time-varying covariate</i>
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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

diag_crr	<i>Checking Fine and Gray subdistribution hazards model with cumulative sums of residuals</i>
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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

```
diag_crr(formula, data, test = c("lin", "prop"), Nit = 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

- Li, Jianing, Thomas H. Scheike, and Mei-Jie Zhang. "Checking Fine and Gray subdistribution hazards model with cumulative sums of residuals." *Lifetime data analysis* 21.2 (2015): 197-217.
- Fine, Jason P., and Robert J. Gray. "A proportional hazards model for the subdistribution of a competing risk." *Journal of the American statistical association* 94.446 (1999): 496-509.

See Also

[diag_lin](#), [diag_prop](#), [plot.diaglin](#), [plot.diagprop](#), [print.diaglin](#), [print.diagprop](#)

Examples

```
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)
```

diag_lin

Diagnostics for the linear functional form and the link function

Description

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

Usage

```
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).

Value

a "diaglin" class object.

Author(s)

Jianing Li

References

Li, Jianing, Thomas H. Scheike, and Mei-Jie Zhang. "Checking Fine and Gray subdistribution hazards model with cumulative sums of residuals." *Lifetime data analysis* 21.2 (2015): 197-217.

See Also

[diag_crr](#), [plot.diaglin](#), [print.diaglin](#)

diag_prop

Diagnostic of the proportionality

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

Li, Jianing, Thomas H. Scheike, and Mei-Jie Zhang. "Checking Fine and Gray subdistribution hazards model with cumulative sums of residuals." *Lifetime data analysis* 21.2 (2015): 197-217.

See Also

[diag_crr](#), [plot.diaglin](#), [print.diaglin](#)

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

```
## 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", xlim=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

```
## 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 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_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	<i>Print diaglin object</i>
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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)
```

<code>print.diagprop</code>	<i>Print diagprop object</i>
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Description

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

Usage

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

Arguments

<code>x</code>	a <code>diagprop</code> object
<code>...</code>	additional arguments to <code>print()</code>

See Also

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

Examples

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

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