Package 'idmTPreg'

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Type Package

Title Regression Model for Progressive Illness Death Data

Version 1.1

Date 2018-02-23

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Depends R (>= 3.4.0), survival, foreach, doParallel

Imports graphics, utils, stats

Description Modeling of regression effects for transition probabilities in a
progressive illness-death model. Azarang, Scheike, and de Una-
Alvarez (2017) <doi:10.1002/sim.7245>.

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LazyLoad yes

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idmTPreg-package   *Regression Model for Progressive Illness Death Data*

Description

Modeling of regression effects for transition probabilities in a progressive illness-death model. Azarang, Scheike, and de Una-Alvarez (2017) <doi:10.1002/sim.7245>.

Details

The DESCRIPTION file:

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Author(s)

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References

Azarang, L. Scheike, TH. and de Una-Alvarez, J. (2017) *Direct modeling of regression effects for transition probabilities in the progressive illness-death model* Statistics in Medicine **36**, 1964 − 1976.

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colonTPreg	*The colon cancer data*

Description

Colon cancer data with 929 rows and 8 columns. There is one row per person. The original data have 16 columns and two records per person and are available as part of survival Package. These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent.

Usage

```
data("colonTPreg")
```

Format

A data frame with 929 observations on the following 8 variables.

id identification variable.

Zt recurrence free survival time, that is the minimum of recurrence, death, and censoring time.

Tt total survival time, time to death or censoring

delta1 recurrence free survival indicator, 0=alive and recurrence free, 1=dead or relapsed.

delta status indicator, 0=alive, 1=dead.

Nodes number of lymph nodes with detectable cancer.

Age age in years.

treatment a factor with levels Obs, Lev and Lev+5FU

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iddata	*Transforming a Simple Illness-Death Dataset into a Proper Data Frame to be Used Inside* TPreg *Function*

Description

Converts a raw illness-death dataset to a data frame which can be passed into TPreg function.

Usage

```
iddata(Stime, Sind, Iltime, Ilind, covar, ...)
```

Arguments

Stime	the possibly censored total survival time.
Sind	the indicator of uncensored total survival time.
Iltime	the arrival time to the intermediate state, for example diseased, recurrence, or relapse time.
Ilind	the indicator of visiting intermediate state.
covar	a vector of covariates.
...	arguments to be passed to methods.

Value

iddata returns an object of class data frame, containing at least the following components:

id	identification variable
Zt	the possibly censored sojourn time in initial state
delta1	the indicator of uncensored sojourn time in initial state
Tt	the possibly censored total survival time
delta	the indicator of uncensored total survival time
covar	a vector of covariates

Examples

```
Stime <- c(10, 20, 34, 12, 30)
Sind <- c(1, 0, 0, 1, 1)
Iltime <- c(7, 20, 28, 12, 30)
Ilind <- c(1, 0, 1, 0, 0)
covar <- c(20, 25, 57, 36, 46)
mydata <- iddata(Stime, Sind, Iltime, Ilind, covar)
mydata
```

---

plot.TPreg *Plotting a TPreg object*

Description

Makes a plot for the estimated effect of covariate(s) on pre-specified transition probabilities together with 95% confidence bands along time, from time s to time t.

Usage

```
## S3 method for class 'TPreg'
plot(x, covar, rug = TRUE, main, ylab, xlab, Ylim, ...)
```

Arguments

x	an object of class TPreg
covar	a character vector of the name(s) of covariate(s)
rug	if TRUE (default), it adds a rug representation of times between time s and time t.
main	an overall title for the plot
ylab	a title for the y axis
xlab	a title for the x axis
Ylim	a list of y limits
...	arguments to be passed to methods.

See Also

[TPreg](), and generic functions [print.TPreg](), and [summary.TPreg]().

Examples

```
data(colonTPreg)

co13 <- TPreg( ~ Age + Nodes + treatment, colonTPreg, link = "logit", s = 0, R = 9, t = 1200,
  by = 110, trans = "13", ncores = 1)
plot(co13, covar = "Nodes", Ylim = list(c(-0.5,0.5)))


co11 <- TPreg( ~ Age + Nodes + treatment, colonTPreg, link = "logit", s = 0, by = 10,
  R = 199, t = 365*5, trans = "11")
plot(co11, covar = c("Age", "Nodes", "treatmentLev", "treatmentLev.5FU"),
Ylim = list(c(-0.1,0.1), c(-0.5,0.5), c(-2,2), c(-2,2)))
```

---

print.TPreg   *Printing the model fits*

Description

Provides the details about the estimated effect of covariate(s) on pre-specified transition probabilities for given s and t.

Usage

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

Arguments

x   an object of class TPreg.

...   arguments to be passed to methods.

Details

print.TPreg formats the coefficients, standard errors, etc. The coefficients component of the result gives the estimated coefficients, their estimated standard errors, their confidence bands, and the p-values. The print method returns the aforementioned results for the specified s and t.

Value

print.TPreg returns a list with the following components:

Call   the matched call.

Transition   the specified transition(s).

(s,t)   the vector of current time and future time for the transition probabilities.

Coefficients   the matrix of coefficients, standard errors, lower confidence limits, upper confidence limits and p-values.

Also, trans= "all" will return Coefficients 11, Coefficients 12, Coefficients 13, and Coefficients 23.

See Also

[TPreg](#), and generic functions [summary.TPreg](#), and [plot.TPreg](#).

Examples

```
## For examples see example TPreg.
```

---

summary.TPreg	*Summarizing Details of the Estimated Effects on the Transition Probabilities in a Progressive Illness-Death Model*

Description

Gives details about the estimated effect of covariate(s) on pre-specified transition probabilities for a progressive illness-death model for a sequence of time from a given s to a given t.

Usage

```
## S3 method for class 'TPreg'
summary(object, ...)
```

Arguments

object	an object of class TPreg.
...	arguments to be passed to methods.

Details

summary.TPreg formats the coefficients, standard errors, etc. for the jump times already fixed by 's', 't', 'by' arguments, corresponding to the possible transition. The jump times come out in the first column of these components.

Value

summary.TPreg returns a list with at least the following components:

Call	the matched call.
Transition(s)	the specified transition(s).
(s,t)	the vector of current time and future time for the transition probabilities.
Coefficients	the matrix of selected jump times and their corresponding coefficients.
Standard Errors	the matrix of selected jump times and their corresponding standard errors.
Lower limits	the matrix of selected jump times and their corresponding lower confidence bands.
Upper limits	the matrix of selected jump times and their corresponding upper confidence bands.
p.values	the matrix of selected jump times and their corresponding p-values.

for Transitions = "11", "12", "13", "23", summary.TPreg gives Coefficients, Standard Errors, Lower limits, Upper limits, and p-values for each of Transition 11, Transition 12, Transition 13 and Transition 23.

See Also

TPreg, and generic functions print.TPreg and plot.TPreg.

Examples

```
## For examples see example TPreg.
```

| TPreg | *Regression Modeling of Transition Probabilities in a Progressive Illness-Death Model* |

Description

Fits a semi-parametric regression model to estimate the effects on transition probabilities in a (possibly non-Markov) progressive illness-death model for a sequence of time.

Usage

```
TPreg(formula, data, link, s = 0, t = NULL, R = 199, by = NULL, trans, ncores = NULL)
```

Arguments

formula	an object of class formula which specifies the covariates. For example formula = ~ age + sex.
data	a data.frame of iddata class or a data.frame in which other than covariates five variables; id, Zt, delta1, Tt, delta are included.
link	a link function for binomial family which are logit, probit and cauchit, (corresponding to logistic, normal and Cauchy CDFs respectively).
s	the current time for the transition probabilities; default is zero which reports the occupation probabilities.
t	the Future time for the transition probabilities; default is NULL which is the largest uncensored sojourn time in the initial state.
R	the number of bootstrap replicates. Default is 199.
by	number: increment of the sequence from time s to time t.The default is NULL which is $\lfloor (\max(Zt)-\min(Zt))/q_{0.01}(Zt) \rfloor$, where $q_{0.01}(.)$ is the sample quantile corresponding to 0.01 probability and $\lfloor x \rfloor$ gives the largest integer less than or equal to x. A binomial regression at every byth time between s and t is performed. by=1 reports all binomial regression results for each jump time, corresponding to the specified transition(s), between s and t. By increasing by we skip some times. In order to save the time, for a relatively large dataset a relatively big by is recommended.
trans	the possible transition(s) for a progressive illness-death model. For trans argument there are five options: "11", "12", "13", "23", and "all".
ncores	the number of cores to use for parallel execution. Default is the number of CPU cores on the current host.

Value

TPreg returns an object of class TPreg. An object of class TPreg is a list containing at least the following components:

co   the list of:

- 'transition' the transition,
- 'time' the jump times,
- 'coefficients' the estimated effects ,
- 'SD' standard errors,
- 'LWL' lower confidence limits,
- 'UPL' upper confidence limits,
- 'p.value' p-values.

call   the matched call.

transition   the transition, this is equal to the transition in co unless for trans="all"

s   the current time for the transition probability.

t   the future time for the transition probability.

n.misobs   the number of missing observations.

In addition, trans="all" will have four lists: co11, co12, co13, and co23 instead of co and will give the information for all possible transitions in the progressive illness death model

References

Azarang, L. Scheike, TH. and de Una-Alvarez, J. (2017) *Direct modeling of regression effects for transition probabilities in the progressive illness-death model*, Statistics in Medicine **36**, $1964 - 1976$.

See Also

print.TPreg, summary.TPreg, and plot.TPreg as generic functions.

Examples

```
data(colonTPreg)

co11 <- TPreg( ~ Age + Nodes + treatment, colonTPreg, link = "logit", s = 50, R = 19, t = 200,
trans = "11", ncores = 1)
co11
summary(co11)
```

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