Package: smcure (via r-universe)

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Type Package

Title Fit Semiparametric Mixture Cure Models

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Description An R-package for Estimating Semiparametric PH and AFT Mixture Cure Models.

Depends survival, stats, graphics

License GPL-2

LazyLoad yes

RoxygenNote 7.1.2

Encoding UTF-8

NeedsCompilation no

Repository CRAN

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Contents

`bmt` *Bone marrow transplant study*

Description

Bone marrow transplant study which is widely used in the AFTMC model

Usage

```
data(bmt)
```

Format

There were 46 patients in the allogeneic treatment and 44 patients in the autologous treatment group

`Time` time to event

`Status` censor indicator, 0 for censored and 1 for uncensored

`TRT` 1 for autologous treatment group; 0 for allogeneic treatment group

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`coefsmcure` *Retrieves the estimated coefficients from object*

Description

Retrieving coefficients, printing method, and summary mthod for a smcure object.

Usage

```
coefsmcure(x,...)
```

Arguments

`x`	an object from smcure function
`...`	Further arguments to be passed to the printsmcure function.

`e1684` *Eastern Cooperative Oncology Group (ECOG) data*

Description

Eastern Cooperative Oncology Group (ECOG) data used for modeling PH semicure model

Usage

```
data(e1684)
```

Format

A data frame with 284 observations on the following 5 variables.

`TRT`	0=control group, 1=IFN treatment group
`FAILTIME`	observed relapse-free time
`FAILCENS`	relapse-free censor indicator
`AGE`	continuous variable, which is centered to the mean
`SEX`	0 for male, 1 fopr female

`em` *EM algorithm*

Description

EM algorithm used in the mixture cure model by assuming a latent indicator of uncure. Detailed estimation methods can be found in the reference section

Usage

```
em(Time, Status, X, Z, offsetvar, b, beta, model, link, emmax, eps)
```

Arguments

`Time`	time to event of interest
`Status`	status indicator, 0=alive, 1=dead
`X`	a vector or matrix of covariates corresponding to latency part
`Z`	a vector or matrix of covariates corresponding to incidence part
`offsetvar`	offset variable
`b`	initial value for parameter b
`beta`	initial value for parameter beta
`model`	either "ph" or "aft"

`link`	specifies the link in incidence part. The "logit", "probit" or complementary loglog ("cloglog") links are available. By default link = "logit".
`emmax`	specifies the maximum iteration number. If the convergence criterion is not met, the EM iteration will be stopped after emmax iterations and the estimates will be based on the last maximum likelihood iteration. The default emmax = 100.
`eps`	sets the convergence criterion. The default is eps = 1e-7. The iterations are considered to be converged when the maximum relative change in the parameters and likelihood estimates between iterations is less than the value specified.

`plotpredictsmcure` *Plot predicted smcure object*

Description

plot predicted survival curve(s) from the estimated mixture cure model

Usage

```
plotpredictsmcure(object, type = "S", xlab = "Time",
ylab = "Predicted Survival Probability",
model = c("ph", "aft"), ...)
```

Arguments

`object`	an object of the predictsmcure function
`type`	type of plot. "S" means steps plot.
`xlab`	a label for the x axis
`ylab`	a label for the y axis
`model`	either "ph" or "aft"
`...`	Further options in plotfunction can be passed to the plotpredictsmcure function

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`predictsmcure` *prediction of semicure model*

Description

Prediction of semicure model

Usage

```
predictsmcure(object, newX, newZ, model = c("ph", "aft"), ...)
```

Arguments

`object`	an object of smcure
`newX`	new value(s) of X
`newZ`	new value(s) of Z
`model`	either 'ph' or 'aft'
`...`	further arguments to be passed to the predictsmcure function

Details

Predicted population survival function can be calculated by the following equation

$$S_{pop}(t) = \pi + (1 - \pi) * S(t)$$

`printsmcure` *Print smcure object*

Description

Output of smcure object

Usage

```
printsmcure(x, Var, ...)
```

Arguments

`x`	an object of smcure
`Var`	If it is TRUE, the program returns standard error by bootstrap method. If set to False, the program only returns estimators of coefficients. By default, Var = TRUE
`...`	Further arguments to be passed to the printsmcure function.

`smcure` *Title*

Description

Title

Usage

```
smcure(
  formula,
  cureform,
  offset = NULL,
  data,
  na.action = na.omit,
  model = c("aft", "ph"),
  link = "logit",
  Var = TRUE,
  emmax = 50,
  eps = 1e-07,
  nboot = 100
)
```

Arguments

`formula`	a formula object
`cureform`	specifies the variables in the incidence
`offset`	variable(s) with coefficient 1 in PH model or AFT model
`data`	a data.frame in which to interpret the variables named in the formula and cureform
`na.action`	a missing-data filter function. By default na.action = na.omit
`model`	specifies your model ph or aft
`link`	incidence part
`Var`	By default Var = TRUE
`emmax`	maximum iteration number
`eps`	convergence criterion
`nboot`	number of bootstrap sampling

Value

a smcure object

Examples

```
data(e1684)
pd <- smcure(Surv(FAILTIME,FAILCENS)~TRT+SEX+AGE,
cureform=~TRT+SEX+AGE,data=e1684,model="ph",
Var = FALSE)
printsmcure(pd,Var = FALSE)
```

`smsurv` *Estimation of the baseline survival*

Description

This R-program uses the Breslow method to estimate baseline survival of PH mixture cure model and AFT mixture cure model.

Usage

```
smsurv(Time, Status, X, beta, w, model)
```

Arguments

`Time`	this is the follow up time for "ph" model. If model is "aft", then this is residual.
`Status`	The status indicator, normally 0=alive, 1=dead
`X`	effects of covariates of uncured patients
`beta`	initial beta from coxph
`w`	conditional probability of the ith individual remains uncured at the mth iteration. We use Status as initial value
`model`	specifies your model, it can be "ph" or "aft"

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