Package ‘smcure’

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**bmt**  
*Bone marrow transplant study*

**Description**

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

**Usage**

```r
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 method for a smcure object.

**Usage**

```r
coopsmcure(x,...)
```

**Arguments**

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

eem(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

predictsmcure

prediction of smcure model

Description
Prediction of smicure model

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

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

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 cure-
        form
  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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time</td>
<td>this is the follow up time for &quot;ph&quot; model. If model is &quot;aft&quot;, then this is residual.</td>
</tr>
<tr>
<td>Status</td>
<td>The status indicator, normally 0=alive, 1=dead</td>
</tr>
<tr>
<td>X</td>
<td>effects of covariates of uncured patients</td>
</tr>
<tr>
<td>beta</td>
<td>initial beta from coxph</td>
</tr>
<tr>
<td>w</td>
<td>conditional probability of the ith individual remains uncured at the mth iteration. We use Status as initial value</td>
</tr>
<tr>
<td>model</td>
<td>specifies your model, it can be &quot;ph&quot; or &quot;aft&quot;</td>
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