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smcure-package

Semiparametric mixture cure model

Description

An R package to fit semiparametric PH mixture cure model or AFT mixture cure model

Details

Package: smcure
Type: Package
Version: 2.0
Date: 2012-02-05
License: GPL-2
LazyLoad: yes

Author(s)

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References


**bmt**

*Bone marrow transplant study*

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**Description**

Bone marrow transplant study for the refractory acute lymphoblastic leukemia patients which is widely used in the AFTMC model (Kersey, et al., 1987)

**Usage**

```r
data(bmt)
```

**Format**

There were 90 patients in total, where 46 patients in the allogeneic treatment group and 44 patients in the autologous treatment group

- **Time**  time to death
- **Status** censoring indicator, 1=event of interest happens, and 0=censoring
- **TRT**  1 for autologous treatment group; 0 for allogeneic treatment group

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**coefsmcure**

*Retrieves the estimated coefficients from object*

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**Description**

Retrieving coefficients from a smcure object.

**Usage**

```r
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**

The melanoma data from the Eastern Cooperative Oncology Group (ECOG) phase III clinical trial e1684 which is used for modeling semicure PH mixture cure model (Kirkwood, et al., 1996)

**Usage**

```r
data(e1684)
```

**Format**

There were 284 patients in this study with the following 5 variables.

- **TRT**: 0=control group, 1=IFN treatment group
- **FAILTIME**: observed relapse-free time
- **FAILCENS**: censoring indicator, 1=event of interest happens, and 0=censoring
- **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 status. Detailed estimation methods can be found in the reference section.

**Usage**

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

**Arguments**

- **Time**: time to event of interest
- **Status**: censoring indicator, 1=event of interest happens, and 0=censoring
- **X**: a vector or matrix of covariates corresponding to the latency part
- **Z**: a vector or matrix of covariates corresponding to the 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**

```r
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

**See Also**

`smcure`, `printsmcure`, `predictsmcure`
### predictsmcure

**Prediction of semicure model**

**Description**

Prediction of survival probability from the smcure in order to pass subjects to `plotpredictsmcure()`.

**Usage**

```r
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

\[
\hat{S}_{\text{pop}}(t) = \hat{\pi} + (1 - \hat{\pi}) \hat{S}(t)
\]

where \( \hat{S}(t) \) is the estimated survival function for the uncured patients based on the PH or AFT model.

**See Also**

- smcure, printsmcure, plotpredictsmcure

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### printsmcure

**Print smcure object**

**Description**

Output of smcure object.

**Usage**

```r
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.

Semiparametric mixture cure model

Description

Fit semiparametric PH mixture cure model or AFT mixture cure model by the EM algorithm

Usage

```
smcure(formula, cureform, offset = NULL, data, na.action = na.omit,
model = c("aft", "ph"), link = "logit", Var = TRUE,
emmax = 50, eps = 1e-7, nboot = 100)
```

Arguments

- `formula`: a formula object, specifying the variables included in the latent on the right. The response must be a survival object as returned by the Surv function.
- `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.
- `model`: specifies your model, it can be "ph" or "aft"
- `link`: specifies the link in incidence part. The "logit", "probit" or complementary loglog ("cloglog") links are available. By default link = "logit".
- `Var`: If it is TRUE, the program returns Std.Error by bootstrap method. If set to False, the program only returns estimators of coefficients. By default, Var = TRUE
- `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.
- `nboot`: specifies the number of bootstrap sampling. The default nboot = 100.
smrank

Rank function

Description

Rank estimating equation used in the M-step of the EM algorithm for the AFT mixture cure model.

Usage

smrank(beta, Time, X, n, w, Status)

Arguments

beta unknown parameters corresponding to latency part
Time time to event of interest
X a vector or matrix of covariates corresponding to latency part
n total number of observations

Value

See printsmcure for returned values

See Also

printsmcure, predictsmcure, plotpredictsmcure

Examples

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

# plot predicted survival curves for male with median centered age by treatment groups
predm=predictsmcure(pd,newX=cbind(c(1,0),c(0,0),c(0.579,0.579)),
newZ=cbind(c(1,0),c(0,0),c(0.579,0.579)),model="ph")
plotpredictsmcure(predm,model="ph")

data(bmt)
# fit AFT mixture cure model
bmtfit <- smcure(formula = Surv(Time, Status) ~ TRT, cureform = -TRT, data = bmt,
model = "aft", Var = FALSE)
printsmcure(bmtfit,Var = FALSE)

# plot predicted Survival curves by treatment groups
predbmt=predictsmcure(bmtfit,newX=c(0,1),newZ=c(0,1),model="aft")
plotpredictsmcure(predbmt,model="aft")
smsurv

\[ w \text{ conditional probability of the individual remaining uncured} \]
\[ \text{Status censoring indicator, } 1=\text{event of interest happens, and } 0=\text{censoring} \]

Description

The estimated baseline survival function based on the Breslow method, which is used in order to update the E-step in the EM algorithm.

Usage

\texttt{smsurv(Time, Status, X, beta, w, model)}

Arguments

\texttt{Time} this is the follow up time for "ph" model. If model is "aft", then this is residual log \( t - \beta x \).
\texttt{Status} censoring indicator, 1=\text{event of interest happens, and } 0=\text{censoring}
\texttt{X} effects of covariates of uncured patients
\texttt{beta} initial beta from coxph
\texttt{w} conditional probability of the ith individual remains uncured at the mth iteration. We use Status as initial value
\texttt{model} specifies your model, it can be "ph" or "aft"
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