

Package ‘smcure’

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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

License GPL-2

LazyLoad yes

Collate 'coefsmcure.R' 'em.R' 'plotpredictsmcure.R' 'predictsmcure.R'
'printsmcure.R' 'smcure.R' 'smrank.R' 'smsurv.R'

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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

Kersey, et al., Comparison of autologous and allogeneic bone marrow trans-plantation for treatment of high-risk refractory acute lymphoblastic leukemia. *New England Journal of Medicine*, 317 (8), 461-467, 1987.

Kirkwood, et al., Interferon alfa-2b adjuvant therapy of high-risk resected cutaneous melanoma: the eastern cooperative oncology group trial est 1684. *Journal of Clinical Oncology*, 14 (1), 7, 1996.

J. Zhang and Y. Peng. A new estimation method for the semiparametric accelerated failure time mixture cure model. *Statistics in Medicine*, 26(16):3157-3171, 2007.

Peng, Y., Dear, K. B. G., 2000. A nonparametric mixture model for cure rate estimation. *Biometrics* 56 (1), 237-243.

C. Cai, et al., smcure: An R-Package for estimating semiparametric mixture cure models, *Computer Methods and Programs in Biomedicine*. (2012), <http://dx.doi.org/10.1016/j.cmpb.2012.08.013>.

 bmt

Bone marrow transplant study

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

```
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

coefsmcure	<i>Retrieves the estimated coefficients from object</i>
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Description

Retrieving coefficients from a smcure object.

Usage

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

Arguments

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

e1684	<i>Eastern Cooperative Oncology Group (ECOG) data</i>
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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

```
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

```
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

```
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

```
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

$$\hat{S}_{pop}(t) = \hat{\pi} + (1 - \hat{\pi})\hat{S}(t)$$

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

printsmcure	<i>Print smcure object</i>
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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	<i>Semiparametric mixture cure model</i>
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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-07, 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.
na.action	a missing-data filter function. By default na.action = na.omit.
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.

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")

```

smrank	<i>Rank function</i>
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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
w	conditional probability of the individual remaining uncured
Status	censoring indicator, 1=event of interest happens, and 0=censoring

smsurv	<i>Estimation of the baseline survival</i>
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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

```
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 $\log t - \beta\mathbf{x}$.
Status	censoring indicator, 1=event of interest happens, and 0=censoring
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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