Package ‘smcure’

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       Mixture Cure Models
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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

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**References**


**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

Retrieves the estimated coefficients from object

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

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

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

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em

\textit{EM algorithm}

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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

\texttt{em(Time, Status, X, Z, offsetvar, b, beta, model, link, emmax, eps)}

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time</td>
<td>time to event of interest</td>
</tr>
<tr>
<td>Status</td>
<td>censoring indicator, 1=event of interest happens, and 0=censoring</td>
</tr>
<tr>
<td>X</td>
<td>a vector or matrix of covariates corresponding to the latency part</td>
</tr>
<tr>
<td>Z</td>
<td>a vector or matrix of covariates corresponding to the incidence part</td>
</tr>
<tr>
<td>offsetvar</td>
<td>offset variable</td>
</tr>
<tr>
<td>b</td>
<td>initial value for parameter b</td>
</tr>
<tr>
<td>beta</td>
<td>initial value for parameter beta</td>
</tr>
<tr>
<td>model</td>
<td>either &quot;ph&quot; or &quot;aft&quot;</td>
</tr>
<tr>
<td>link</td>
<td>specifies the link in incidence part. The &quot;logit&quot;, &quot;probit&quot; or complementary loglog (&quot;cloglog&quot;) links are available. By default link = &quot;logit&quot;.</td>
</tr>
<tr>
<td>emmax</td>
<td>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.</td>
</tr>
<tr>
<td>eps</td>
<td>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.</td>
</tr>
</tbody>
</table>
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

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

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

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.

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smcure | 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-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 = predictmcure(bmtfit, newx = c(0, 1), newz = c(0, 1), model = "aft")
plotpredictmcure(predbmt, model = "aft")

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**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
- **w**: conditional probability of the individual remaining uncured
- **Status**: censoring indicator, 1=event of interest happens, and 0=censoring

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**smsurv**  
*Estimation of the baseline survival*

**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 \( \log t - \beta x \).

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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