

# 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

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**Repository** <https://rxpharmstat.r-universe.dev>

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<code>bmt</code>	<i>Bone marrow transplant study</i>
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### 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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<code>coefsmcure</code>	<i>Retrieves the estimated coefficients from object</i>
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### Description

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

### Usage

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

### Arguments

`x` an object from `smcure` function

`...` Further arguments to be passed to the `printsmcure` function.

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 e1684

*Eastern Cooperative Oncology Group (ECOG) data*


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**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

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 em

*EM algorithm*


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**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.

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plotpredictsmcure      *Plot predicted smcure object*

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### 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*

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### 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

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

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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.

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 smcure

*Title*


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## 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)
```

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smsurv

*Estimation of the baseline survival*

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**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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