Package ‘mixcure’

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Imports boot, flexsurv, survey, gam, timereg

License GPL-3

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**mixcure-package**  
*Mixture cure models*

**Description**  
Fit various mixture cure models

**Details**  
This package fits various mixture cure model using existing R packages.

**Author(s)**  
Yingwei Peng

**References**  


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**coef.mixcure**  
*Retrieve coefficients from mixture cure models*

**Description**  
Retrieve coefficients from mixture cure models

**Usage**  
```r
## S3 method for class 'mixcure'
coef(object, ...)
```

**Arguments**  
- `object`:
  a mixcure object
- `...`:
  for compatibility purpose. Not used.
leukaemia

Value

a list of two components:

- latency: a vector of coefficients in the latency model
- incidence: a vector of coefficients in the incidence model

Author(s)

Yingwei Peng

See Also

mixcure

Examples

data(leukaemia)
z1 <- mixcure(Surv(time, cens) ~ transplant, ~ transplant, data = leukaemia, savedata = TRUE)
coef(z1)

leukaemia

Data from leukaemia patients with bone marrow transplants

Description

This data set is used in the examples of this package.

Usage

data(leukaemia)

Format

A data.frame object with columns:

- time: Relapse Free Survival Time.
- cens: Relapse Indicator with 1-Relapsed, 0-Disease Free.

Source

Examples

data(leukaemia)

mixcure

Description

Fit some parametric and semiparametric mixture cure models

Usage

mixcure(
  lformula, 
  iformula, 
  data, 
  lmodel, 
  imodel, 
  postuncure = NULL, 
  emmax = 100, 
  eps = 1e-04, 
  savedata = FALSE, 
  debug = FALSE
)

Arguments

lformula a formula specifying the latency model
iformula a formula specifying the incidence model
data a data frame in which to interpret the variables named in the formulas in lmodel

lmodel a list of at least one component: fun, a text string specifying R function to fit the latency model. Other arguments to the function specified in fun can be added to the list. If lmodel is not supplied, the default is lmodel = list(fun = "coxph") and it fits the semiparametric PH latency model to the data. Other latency models currently implemented include

• fun = "survfit" (for nonparametric mixture cure models),
• fun = "survreg" (for parametric mixture cure models),
• fun = "flexsurvreg" (for parametric mixture cure models),
• fun = "flexsurvspline" (for parametric mixture cure models),
• fun = "cox.aalen" (for semiparametric multiplicative-additive hazards models),
• fun = "prop.odds" (for semiparametric proportional odds models).
R functions for other regression models for survival data can be added as long as they meet certain criteria. See details on how a new regression model for survival data can be added.

**imoto**
a list of at least one component: fun, a text string specifying the R function to fit the incidence model. Other arguments to the function specified in fun can be added to the list. If imodel is not supplied, the default is imodel = list(fun = "glm", family = binomial()) and it fits the logistic regression as the incidence model to the data. The other incidence model currently implemented is fun = "gam". R functions for other regression models as the incidence model can be added as long as they meet certain criteria. See details on how a new regression model for incidence model can be added.

A covariate may be used in both lformula and iformula. A model with the intercept term only in iformula assumes that there are cured patients and that the cure rates are the same for all patients.

**postuncure**
a vector of initial probabilities of being uncured for all subjects

**emmax**
the maximum number of EM iterations

**eps**
tolerance for EM convergence. Iteration stops once the relative change in log likelihoods is less than eps.

**savedata**
If TRUE, the data set will be stored in the final object. It is mainly used for bootstrap in summary() to get standard errors. Default is FALSE.

**debug**
for debug purpose.

**Details**

This function fits mixture cure models, where the latency and incidence parts of the mixture cure models can be fit using existing R regression functions. We implemented the logistic regression and the generalized additive model for the incidence part and the semiparametric proportional hazards and additive hazards models and the parametric failure time models for the latency parts. To include a new regression model xxx() for the incidence part, you need to add the following functions:

- incidence.xxx()
- coef.incidence.xxx()
- loglik.incidence.xxx()
- curepred.incidence.xxx()

To include a new regression model xxx() for the latency part, you need to add the following functions:

- latency.xxx()
- coef.latency.xxx()
- loglik.latency.xxx()
- survpred.latency.xxx()

When mixcure program ends, it may produce warning messages such as "In eval(expr, envir, enclos) : non-integer #successes in a binomial glm!." The message is due to the fact that glm is picky when it comes to specifying binomial models. It warns if it detects that the number of trials or successes
is non-integer, but it still fits the model properly. If you want to suppress the warning (and you’re
sure it’s not a problem), use family=quasibinomial instead.

This package requires the following R packages: survival, boot, survey and any packages that
provide the latency and incidence models.

Value

a list consists of the following components:

ifit      the final fit from the model for cure probability.
lfit      the final fit from the model for failure time of uncured subjects
survprob  the final estimate of the survival probability for each subject at its own observed
time if uncured
postuncure the final estimate of the posterior uncure probability for each subject based its
observed values. The prior uncure probability can be obtained from ifit$uncureprob
em        a matrix containing the iterations of the EM algorithm and convergence errors
(for debug purpose)

Author(s)

Yingwei Peng

References

Hall, 2020

Scheike, T. H., editors, Handbook of Survival Analysis, Handbooks of Modern Statistical Methods
series, chapter 6, pages 113-134. Chapman & Hall, Boca Raton, FL, USA, 2014

Peng, Y. Fitting semiparametric cure models. Computational Statistics & Data Analysis, 41: 481-
490, 2003

See Also

summary.mixcure, predict.mixcure, plot.predict.mixcure

Examples

data(leukaemia)
z = mixcure(Surv(time, cens) ~ transplant, ~ transplant, data = leukaemia)
plot.predict.mixcure  Plot method for the prediction of mixture cure models

Description

Plot the predicted survival function curves from mixture cure models

Usage

## S3 method for class 'predict.mixcure'
plot(
  x, 
  type = "l", 
  add = FALSE, 
  which = 1:nrow(x$cure), 
  curemark = FALSE, 
  conditional = FALSE, 
  xlab, 
  ylab, 
  ylim = c(0, 1), 
  lty = seq(along = which), 
  ... 
)

Arguments

x  an object from predict.mixcure

type  line type. The default is type = "l"

add  if add = FALSE (default), a plot is shown in a new graphics window. Otherwise, an existing window is used.

which  a vector of row numbers for which the survival probabilities will be drawn. The default is to draw the survival probabilities for all rows.

curemark  if curemark = TRUE, a line will be drawn at a height that is equal to the cure rate

conditional  if conditional = FALSE (default), the unconditional survival probabilities will be drawn. Otherwise, the survival probabilities of uncured subjects will be drawn.

xlab  the label for x axis

ylab  the label for y axis

ylim  the range for y axis

lty  the line types for survival curves from different groups

...  other standard graphics parameters can be set here.
Details
This function plots survival probabilities for each row in newdata. The survival probabilities can be conditional probabilities for uncured subjects or unconditional survival probabilities, the latter will level off at estimated cure rates.

Value
a graphics window will be opened and drawn.

Author(s)
Yingwei Peng

See Also
mixcure predict.mixcure

Examples

data(leukaemia)
plot(predict(mixcure(Surv(time, cens) ~ transplant, ~ transplant,
data = leukaemia), newdata = leukaemia[1, ], times = 0:2000))
Value

A list with the following components:

- **cure**: a matrix of 2 columns and the same number of rows as `newdata`. The first column is uncure rates for the rows in `newdata` and the second column is cure rates for the rows in `newdata`.
- **uncuresurv**: a list with the number of components equal to the rows of `newdata`. Each component is a vector of the estimated survival probabilities at times for a subject if uncured.
- **surv**: similar to `uncuresurv` except that the survival probabilities are the unconditional survival probabilities.
- **times**: a vector of times at which the survival probabilities will be predicted.

Author(s)

Yingwei Peng

See Also

mixcure

Examples

```r
data(leukaemia)
predict(mixcure(Surv(time, cens) ~ transplant, ~ transplant, data = leukaemia),
newdata = leukaemia[1, ], times = 0:2000)
```

---

### print.mixture

**Print method for mixture cure models**

Description

Print method for mixture cure models.

Usage

```r
## S3 method for class 'mixcure'
print(x, ...)
```

Arguments

- `x` : a mixcure object
- `...` : further arguments passed to or from other methods.
residuals.mixcure

Author(s)
Yingwei Peng

See Also
mixcure

Examples

```r
data(leukaemia)
z1 = mixcure(Surv(time, cens) ~ transplant, ~ transplant, data = leukaemia,
savedata = TRUE)
print(z1)
```

residuals.mixcure  Residuals for mixture cure models

Description
Obtain residuals for the mixture cure models

Usage
```r
## S3 method for class 'mixcure'
residuals(
  object,
  data,
            "M3", "D2"),
  type2 = c("residuals", "partial"),
  model = c("latency", "incidence"),
  ...
)
```

Arguments

- `object`: an object of mixcure
- `data`: the data used to obtain mixcure object.
- `type`: residuals type. WLCH is a modified residual proposed in Wileyto et al (2013). The rest types of residuals are defined in the same way as in the classic survival models.
- `type2`: residual type, either "residuals" for regular residuals or "partial" for partial residuals.
- `model`: if "latency" (default), residuals for latency model are generated. Otherwise, "incidence" means that residuals for incidence model are generated.
- `...`: for compatibility purpose. Not used.
Details

This function computes residuals for the fitted model from mixcure().

Value

It is a list containing at least the following components:

- **type**: residuals type
- **residuals**: residuals of the model

Author(s)

Yingwei Peng

References


See Also

mixcure

Examples

```r
data(leukaemia)
residuals(mixcure(Surv(time, cens) ~ transplant, ~ transplant,
data = leukaemia), data = leukaemia, type = "Martingale")
```
Arguments

- **object**: A mixcure object
- **R**: the number of boot samples required to calculate bootstrap variances.
- **index**: An argument used in censboot function in boot package to specify the columns in data that store survival times and censoring indicators.
- ... other parameters to be passed into print function.

Details

censboot in boot package is called to calculate bootstrap variances.

Value

A modified mixcure object with extra components:

- **varboot**: a censboot object
- **stderr**: standard errors of parameters in mixcure
- **R**: the number of bootstrap samples used

Author(s)

Yingwei Peng

See Also

mixcure

Examples

data(leukaemia)
# To reduce running time of this example, R is set to 2.
summary(mixcure(Surv(time, cens) ~ transplant, ~ transplant, data = leukaemia, savedata = TRUE), R = 2)
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