

Package ‘TransModel’

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Type Package

Title Fit Linear Transformation Models for Right Censored Data

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Description A unified estimation procedure for the analysis of right censored data using linear transformation models.

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TransModel-package *Fit Linear Transformation Models for Right Censored Data*

Description

Semiparametric analysis for linear transformation model, such as the proportional hazards model and the proportional odds model, is fitted based on a unified method proposed in Chen(2002) for right censored survival data.

Details

The main function TransModel gives estimates for coefficients and covariance matrix for the predictors in the linear transformation model. Print and summary method can be applied to the returned object.

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References

Kani Chen, et al., Semiparametric analysis of transformation models with censored data. *Biometrika*, 89(3), 659-668, 2002.

PH_exam *Data example for proportional hazard model.*

Description

This data set is randomly generated from the proportional hazards transformation model as an example.

Usage

```
data(PH_exam)
```

Format

A data frame containing survival time, right censoring indicator, predictors gender and age, and a trivial variable called error.

`plot.predict.TransModel`*Plot the predicted survival curve with confidence interval/band.*

Description

Survival curve with confidence interval or confidence band will be plotted for the returned object from `predict.TransModel`.

Usage

```
## S3 method for class 'predict.TransModel'  
plot(x, CI = FALSE, CB = FALSE, ...)
```

Arguments

<code>x</code>	An object from the function <code>predict.TransModel</code> .
<code>CI</code>	Whether a 100(1-alpha)% pointwise confidence interval will be added to the survival curve.
<code>CB</code>	Whether a 100(1-alpha)% confidence band will be added to the survival curve.
<code>...</code>	Other plot arguments.

Note

Either `CI` or `CB` is set to be `TRUE` in this plot method, the object from `predict.TransModel` needs to have the argument `CICB.st` to be `TRUE` as well. Otherwise, no confidence interval or band will be added to the plot.

`PO_examp`*Data example for proportional odds model.*

Description

This data set is randomly generated from the proportional odds transformation model as an example.

Usage

```
data(PO_examp)
```

Format

A data frame containing survival time, right censoring indicator, predictors gender and age, and a trivial variable called error.

predict.TransModel	<i>Predict survival probabilities with confidence intervals and confidence bands</i>
--------------------	--

Description

Calculate survival probabilities, confidence intervals and confidence bands in the estimated transformation model. If new time points is not specified, event times in the original data set will be used. If no new covariate values are specified, zeros will be used and the baseline survival probabilities will be calculated.

Usage

```
## S3 method for class 'TransModel'
predict(object, ...)
```

Arguments

object	An object returned from the function TransModel.
...	Other arguments including: newdata: a vector containing the values for each covariate variables specified in the model. If not specified, 0 will be used for all variables. new.time: vector of ordered time points to be used for survival probability calculation. If null, distinct event time points in the original dataset will be used. alpha: used to determine the confidence level of the predicted confidence interval/band for the survival curve. The default value is 0.05, corresponding to a 95% confidence level.

Value

time	ordered time points on which survival probabilities are calculated.
survival	predicted survival probabilities.
low.ci	the lower limit of confidence interval.
up.ci	the upper limit of confidence interval.
low.cb	the lower limit of confidence band.
up.cb	the upper limit of confidence band.

Note

The values low.ci, up.ci, low.cb and up.cb will be returned only if CICB.st=TRUE in the original model.

Examples

```

data(PH_examp)
mod1<-TransModel(formula=Surv(time,status)~gender+age,data=PH_examp,r=0)
# Predict survival probability
pred1<-predict(mod1,newdata=c(0,1))
pred2<-predict(mod1,newdata=c(1,1))
plot(pred1)
lines(pred2$time,pred2$survival,type="s",col=2)

### Not Run ###
# survival estimate with 95% pointwise CI and overall CB
# mod1<-TransModel(formula=Surv(time,status)~gender+age,data=PH_examp,r=0,CICB.st=TRUE,num.sim=50)
# pred1<-predict(mod1,newdata=c(0,1))
# plot(pred1,lty=1,col=1,CI=TRUE,CB=TRUE)
# Change the confidence level to 90%
# pred1<-predict(mod1,newdata=c(0,1),alpha=0.1)

```

```
print.summary.TransModel
```

Print method for the summary output of TransModel.

Description

A summary table with coefficient estimates, standard error and p-values will be printed.

Usage

```
## S3 method for class 'summary.TransModel'
print(x, ...)
```

Arguments

x	An object from the function summary.TransModel.
...	Other print arguments.

```
print.TransModel
```

Print method for the function TransModel.

Description

Estimated coefficients and covariance matrix will be printed for the fitted linear transformation model from TransModel.

Usage

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

Arguments

x An object from the function TransModel.
 ... Other arguments to be specified for the print function.

summary.TransModel *Summary results for fitting the linear transformation model*

Description

A summary table contains the coefficient estimates, standard errors, test statistics and p values in the linear transformation model.

Usage

```
## S3 method for class 'TransModel'
summary(object, ...)
```

Arguments

object An object returned from the function TransModel.
 ... Other arguments to be specified for the summary function.

Value

coefficients The summary table.

Examples

```
data(veteran)
fit<-TransModel(Surv(time,status)~karno+as.factor(celltype),data=veteran,r=0,subset=(prior==0))
summary(fit)

fit0<-TransModel(Surv(time,status)~1,data=veteran,r=0,subset=(prior==0)) #the null model
summary(fit0)
```

TransModel	<i>Main function for fitting the linear transformation models for right censored data</i>
------------	---

Description

This function is used to fit a linear transformation model, such as the proportional hazards model or proportional odds model, to the right censored survival data.

Usage

```
TransModel(formula = formula(data), data = parent.frame(), r, CICB.st, subset,
dx, iter.max, num.sim)
```

Arguments

formula	A survival formula based on the Surv() function, containing survival time, right censoring indicator and covariates.
data	Data set with all the variables needed in formula.
r	Parameter in the hazard function, used to define different linear models. See details for more information.
CICB.st	Whether or not the perturbation for deriving the confidence intervals and confidence bands of survival estimates will be done. The default value is FALSE.
subset	Conditions for subsetting the dataset.
dx	Convergence tolerance. Default is 0.001.
iter.max	Maximum number of iterations before convergence. Default is 100.
num.sim	The number of perturbation, only works when CICB.st=TRUE. Default is 200.

Details

In the linear transformation model $H(t) = -b'z + e$, the hazard function for error term e is defined as: $h(x) = \exp(x) / (1 + r \cdot \exp(x))$, where the parameter r must be a non-negative value and can be changed for different models. For example, $r=0$ refers to the proportional hazards model and $r=1$ refers to a proportional odds model. The default value for r is 0.

Value

coefficients	Estimated coefficients for covariates in the specified linear transformation model.
vcov	Estimated covariance matrix for the coefficients.
converged	Convergence status, 0 indicates converged, and number of iterations used for convergence.

References

Kani Chen, et al., Semiparametric analysis of transformation models with censored data. *Biometrika*, 89(3), 659-668, 2002.

Examples

```

beta0 = c(1,-1)
# Fit proportional hazards model
data(PH_examp)
mod1<-TransModel(formula=Surv(time,status)~gender+age,data=PH_examp,r=0)
print(mod1)
summary(mod1)
mod1$coefficients
mod1$vcov
mod1$converged

# Fit proportional odds model
data(PO_examp)
mod2=TransModel(Surv(time,status)~gender+age,data=PO_examp,r=1)
print(mod2)
summary(mod2)

```

TransModel.default *Default method for function TransModel.*

Description

Default method for function TransModel.

Usage

```

## Default S3 method:
TransModel(formula = formula(data), data = parent.frame(),r=0,
CICB.st=FALSE,subset,dx=0.001,iter.max=100,num.sim=200)

```

Arguments

formula	A survival formula based on Surv function, containing survival time, right censoring indicator and covariates.
data	Data set with all the variables needed in formula.
r	Parameter in the hazard function, used to define different transformation models. Must be a non-negative value. The default value is 0.
CICB.st	Whether or not the perturbation for the confidence interval and confidence bands will be done. The default value is FALSE.
subset	Conditions for subsetting the dataset.
dx	Upbound of convergence limit. Default is 0.001.
iter.max	Maximum number of iterations before convergence. Default is 100.
num.sim	The number of perturbation, only works when CICB.st=TRUE. Default is 200.

veteran

Veterans Administration Lung Cancer study

Description

Randomised trial of two treatment regimens for lung cancer. This is a standard survival analysis data set.

Usage

```
data(veteran)
```

Format

trt: 1=standard 2=test celltype: 1=squamous, 2=smallcell, 3=adeno, 4=large time: survival time
status: censoring status karno: Karnofsky performance score (100=good) diagtime: months from
diagnosis to randomisation age: in years prior: prior therapy 0=no, 1=yes

Source

D Kalbfleisch and RL Prentice (1980), *The Statistical Analysis of Failure Time Data*. Wiley, New York.

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