Package 'YPPE'

July 21, 2025

Title Yang and Prentice Model with Piecewise Exponential Baseline Distribution

Version 1.0.1

Description Semiparametric modeling of lifetime data with crossing survival curves via Yang and Prentice model with piecewise exponential baseline distribution. Details about the model can be found in Demarqui and Mayrink (2019) <doi:10.48550/arXiv.1910.02406>. Model fitting carried out via likelihood-based and Bayesian approaches. The package also provides point and interval estimation for the crossing survival times.

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URL `https://github.com/fndemarqui/YPPE`

BugReports `https://github.com/fndemarqui/YPPE/issues`

Encoding UTF-8

LazyData true

Biarch true

Depends R (>= 3.4.0), survival

Imports methods, MASS, Formula, Rcpp (>= 0.12.0), rstan (>= 2.18.1), rstantools (>= 2.0.0)

LinkingTo BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

SystemRequirements GNU make

RoxygenNote 7.0.2

Suggests testthat

NeedsCompilation yes

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Repository CRAN

Date/Publication 2020-01-09 20:40:03 UTC

Contents

`YPPE-package` *The 'YPPE' package.*

Description

Semiparametric modeling of lifetime data with crossing survival curves via Yang and Prentice model with piecewise exponential baseline distribution curves. Details about the model can be found in Demarqui and Mayrink (2019) <arXiv:1910.02406>. Model fitting carried out via likelihood-based and Bayesian approaches. The package also provides point and interval estimation for the crossing survival times.

References

Demarqui, F. N. and Mayrink, V. D. (2019). A fully likelihood-based approach to model survival data with crossing survival curves. <arXiv:1910.02406>

Stan Development Team (2019). RStan: the R interface to Stan. R package version 2.19.2. https://mc-stan.org

Yang, S. and Prentice, R. L. (2005). Semiparametric analysis of short-term and long-term hazard ratios with two-sample survival data. Biometrika 92, 1-17.

`coef` *Generic S3 method coef*

Description

Generic S3 method coef

Usage

```
coef(object, ...)
```

Arguments

`object`	a fitted model object
`...`	further arguments passed to or from other methods.

Value

the estimated regression coefficients

`coef.yppe` *Estimated regression coefficients*

Description

Estimated regression coefficients

Usage

```
## S3 method for class 'yppe'
coef(object, ...)
```

Arguments

`object`	an object of the class yppe
`...`	further arguments passed to or from other methods

Value

the estimated regression coefficients

`confint` *Generic S3 method confint*

Description

Generic S3 method confint

Usage

```
confint(object, ...)
```

Arguments

`object`	a fitted model object
`...`	further arguments passed to or from other methods.

Value

the estimated regression coefficients

`confint.yppe` *Confidence intervals for the regression coefficients*

Description

Confidence intervals for the regression coefficients

Usage

```
## S3 method for class 'yppe'
confint(object, level = 0.95, ...)
```

Arguments

`object`	an object of the class yppe
`level`	the confidence level required
`...`	further arguments passed to or from other methods

Value

100(1-alpha) confidence intervals for the regression coefficients

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`crossTime` *Generic S3 method crossTime*

Description

Generic S3 method crossTime

Usage

```
crossTime(object, ...)
```

Arguments

`object`	a fitted model object
`...`	further arguments passed to or from other methods.

Value

the crossing survival time

`crossTime.yppe` *Computes the crossing survival times*

Description

Computes the crossing survival times

Usage

```
## S3 method for class 'yppe'
crossTime(object, newdata1, newdata2, conf.level = 0.95, nboot = 4000, ...)
```

Arguments

`object`	an object of class yppe
`newdata1`	a data frame containing the first set of explanatory variables
`newdata2`	a data frame containing the second set of explanatory variables
`conf.level`	level of the confidence/credible intervals
`nboot`	number of bootstrap samples (default nboot=4000); ignored if approach="bayes".
`...`	further arguments passed to or from other methods.

Value

the crossing survival time

Examples

```
# ML approach:
library(YPPE)
mle <- yppe(Surv(time, status)~arm, data=ipass, approach="mle")
summary(mle)
newdata1 <- data.frame(arm=0)
newdata2 <- data.frame(arm=1)
tcross <- crossTime(mle, newdata1, newdata2)
tcross
ekm <- survfit(Surv(time, status)~arm, data=ipass)
newdata <- data.frame(arm=0:1)
St <- survfit(mle, newdata)
time <- sort(ipass$time)
plot(ekm, col=1:2)
lines(time, St[[1]])
lines(time, St[[2]], col=2)
abline(v=tcross, col="blue")

# Bayesian approach:
bayes <- yppe(Surv(time, status)~arm, data=ipass, approach="bayes")
summary(bayes)
newdata1 <- data.frame(arm=0)
newdata2 <- data.frame(arm=1)
tcross <- crossTime(bayes, newdata1, newdata2)
tcross
ekm <- survfit(Surv(time, status)~arm, data=ipass)
newdata <- data.frame(arm=0:1)
St <- survfit(bayes, newdata)
time <- sort(ipass$time)
plot(ekm, col=1:2)
lines(time, St[[1]])
lines(time, St[[2]], col=2)
abline(v=tcross, col="blue")
```

`gastric` *Gastric cancer data set*

Description

Data set from a clinical trial conducted by the Gastrointestinal Tumor Study Group (GTSG) in 1982. The data set refers to the survival times of patients with locally nonresectable gastric cancer. Patients were either treated with chemotherapy combined with radiation or chemotherapy alone.

Format

A data frame with 90 rows and 3 variables:

- time: survival times (in days)

- status: failure indicator (1 - failure; 0 - otherwise)
- trt: treatments (1 - chemotherapy + radiation; 0 - chemotherapy alone)

Author(s)

Fabio N. Demarqui <`fndemarqui@est.ufmg.br`>

References

Gastrointestinal Tumor Study Group. (1982) A Comparison of Combination Chemotherapy and Combined Modality Therapy for Locally Advanced Gastric Carcinoma. Cancer 49:1771-7.

`ipass` *IRESSA Pan-Asia Study (IPASS) data set*

Description

Reconstructed IPASS clinical trial data reported in Argyropoulos and Unruh (2015). Although reconstructed, this data set preserves all features exhibited in references with full access to the observations from this clinical trial. The data base is related to the period of March 2006 to April 2008. The main purpose of the study is to compare the drug gefitinib against carboplatin/paclitaxel doublet chemotherapy as first line treatment, in terms of progression free survival (in months), to be applied to selected non-small-cell lung cancer (NSCLC) patients.

Format

A data frame with 1217 rows and 3 variables:

- time: progression free survival (in months)
- status: failure indicator (1 - failure; 0 - otherwise)
- arm: (1 - gefitinib; 0 - carboplatin/paclitaxel doublet chemotherapy)

Author(s)

Fabio N. Demarqui <`fndemarqui@est.ufmg.br`>

References

Argyropoulos, C. and Unruh, M. L. (2015). Analysis of time to event outcomes in randomized controlled trials by generalized additive models. PLOS One 10, 1-33.

`print.summary.yppe` *Print the summary.yppe output*

Description

Print the summary.yppe output

Usage

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

Arguments

`x`	an object of the class summary.yppe.
`...`	further arguments passed to or from other methods.

Value

a summary of the fitted model.

`summary.yppe` *Summary for the yppe model*

Description

Summary for the yppe model

Usage

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

Arguments

`object`	an objecto of the class ’yppe’.
`...`	further arguments passed to or from other methods.

`survfit` *Generic S3 method survfit*

Description

Generic S3 method survfit

Usage

```
survfit(object, ...)
```

Arguments

`object`	a fitted model object
`...`	further arguments passed to or from other methods.

Value

the crossing survival time

`survfit.yppe` *Survival function for the YPPE model*

Description

Survival function for the YPPE model

Usage

```
## S3 method for class 'yppe'
survfit(object, newdata, ...)
```

Arguments

`object`	an object of the class yppe
`newdata`	a data frame containing the set of explanatory variables.
`...`	further arguments passed to or from other methods.

Value

a list containing the estimated survival probabilities.

Examples

```
# ML approach:
library(YPPE)
mle <- yppe(Surv(time, status)~arm, data=ipass, approach="mle")
summary(mle)
ekm <- survfit(Surv(time, status)~arm, data=ipass)
newdata <- data.frame(arm=0:1)
St <- survfit(mle, newdata)
time <- sort(ipass$time)
plot(ekm, col=1:2)
lines(time, St[[1]])
lines(time, St[[2]], col=2)

# Bayesian approach:
bayes <- yppe(Surv(time, status)~arm, data=ipass, approach="bayes")
summary(bayes)
ekm <- survfit(Surv(time, status)~arm, data=ipass)
newdata <- data.frame(arm=0:1)
St <- survfit(bayes, newdata)
time <- sort(ipass$time)
plot(ekm, col=1:2)
lines(time, St[[1]])
lines(time, St[[2]], col=2)
```

`timeGrid` *Time grid*

Description

Time grid

Usage

```
timeGrid(time, status, n_int = NULL)
```

Arguments

`time`	Vector of failure times
`status`	Vector of failure indicators
`n_int`	Optional. Number of intervals. If `NULL`, the number of intervals is set to be equal to the number of distinct observed failure times.

Value

Time grid.

`vcov` *Generic S3 method vcov*

Description

Generic S3 method vcov

Usage

```
vcov(object, ...)
```

Arguments

`object`	a fitted model object
`...`	further arguments passed to or from other methods.

Value

the variance-covariance matrix associated the regression coefficients.

`vcov.yppe` *Covariance of the regression coefficients*

Description

Covariance of the regression coefficients

Usage

```
## S3 method for class 'yppe'
vcov(object, ...)
```

Arguments

`object`	an object of the class yppe
`...`	further arguments passed to or from other methods.

Value

the variance-covariance matrix associated with the regression coefficients.

`yppe` *Fits the Yang and Prentice model with baseline distribution modelled by the piecewise exponential distribution.*

Description

Fits the Yang and Prentice model with baseline distribution modelled by the piecewise exponential distribution.

Usage

```
yppe(
  formula,
  data,
  n_int = NULL,
  rho = NULL,
  tau = NULL,
  hessian = TRUE,
  approach = c("mle", "bayes"),
 hyper_parms = list(h1_gamma = 0, h2_gamma = 4, mu_psi = 0, sigma_psi = 4, mu_phi = 0,
    sigma_phi = 4, mu_beta = 0, sigma_beta = 4),
  ...
)
```

Arguments

`formula`	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`data`	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which yppe is called.
`n_int`	number of intervals of the PE distribution. If NULL, default value (square root of n) is used.
`rho`	the time grid of the PE distribution. If NULL, the function timeGrid is used to compute rho.
`tau`	the maximum time of follow-up. If NULL, tau = max(time), where time is the vector of observed survival times.
`hessian`	logical; If TRUE (default), the hessian matrix is returned when approach="mle".
`approach`	approach to be used to fit the model (mle: maximum likelihood; bayes: Bayesian approach).
`hyper_parms`	a list containing the hyper-parameters of the prior distributions (when approach = "bayes"). If not specified, default values are used.
`...`	Arguments passed to either ‘rstan::optimizing‘ or ‘rstan::sampling‘ .

Value

yppe returns an object of class "yppe" containing the fitted model.

Examples

```
# ML approach:
library(YPPE)
mle <- yppe(Surv(time, status)~arm, data=ipass, approach="mle")
summary(mle)

# Bayesian approach:
bayes <- yppe(Surv(time, status)~arm, data=ipass, approach="bayes")
summary(bayes)
```

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