

Package ‘spsurv’

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Type Package

Title Bernstein Polynomial Based Semiparametric Survival Analysis

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Description A set of reliable routines to ease semiparametric survival regression modeling based on Bernstein polynomials. 'spsurv' includes proportional hazards, proportional odds and accelerated failure time frameworks for right-censored data. RV Panaro (2020) <[doi:10.48550/arXiv.2003.10548](https://doi.org/10.48550/arXiv.2003.10548)>.

License GPL-3

Biarch true

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spsurv-package	<i>The 'spsurv' package.</i>
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Description

A set of flexible routines to allow semiparametric survival regression modeling based on Bernstein polynomial, including Bernstein based proportional hazards model (BPPH), Bernstein polynomial based proportional odds model (BPPO) and Bernstein based accelerated failure time model (BPAFT) for right-censored data.

Details

`sppb` fits semi-parametric models for time-to-event survival data. Non-informative right-censoring assumption is available. Any user-defined Bernstein polynomial can be user-defined using an arbitrary degree, i.e. highest basis polynomials order.

The framework takes advantage of fully likelihood methods since the polynomial parameters are used to estimate the baseline functions. Even so, this is said to be semi-parametric since this approach does not rely on any distribution. Unlike the Cox model, the BP based models provide smooth hazard and survival curve estimates.

Value

none

Author(s)

Renato Valladares Panaro (renatovp@ime.usp.br).

References

- Panaro R.V. (2020). `spsurv`: An R package for semi-parametric survival analysis. arXiv preprint arXiv:2003.10548.
- Demarqui, F. N., & Mayrink, V. D. (2019). A fully likelihood-based approach to model survival data with crossing survival curves. arXiv preprint arXiv:1910.02406.
- Demarqui, F. N., Mayrink, V. D., & Ghosh, S. K. (2019). An Unified Semiparametric Approach to Model Lifetime Data with Crossing Survival Curves. arXiv preprint arXiv:1910.04475.
- Osman, M., & Ghosh, S. K. (2012). Nonparametric regression models for right-censored data using Bernstein polynomials. *Computational Statistics & Data Analysis*, 56(3), 559-573.
- Lorentz, G. G. (1953). Bernstein polynomials. American Mathematical Society.

bp.basis

Bernstein basis polynomials calculations

Description

Bernstein basis polynomials calculations

Usage

```
bp.basis(time, degree, tau = max(time))
```

Arguments

time	a vector of times.
degree	Bernstein polynomial degree
tau	must be greater than times maximum value observed.

Value

A list containing matrices `b` and `B` corresponding BP basis and corresponding tau value used to compute them.

bpaft

Bernstein Polynomial Based Accelerated Failure Time Model

Description

Fits the BPAFT model to time-to-event data.

Usage

```
bpaft(formula, degree, data, approach = c("mle", "bayes"), ...)
```

Arguments

<code>formula</code>	a <code>Surv</code> object with time to event observations, right censoring status and explanatory terms.
<code>degree</code>	Bernstein polynomial degree.
<code>data</code>	a <code>data.frame</code> object.
<code>approach</code>	Bayesian or maximum likelihood estimation methods, default is <code>approach = "mle"</code> .
<code>...</code>	further arguments passed to or from other methods

Value

An object of class `'spbp'`.

See Also

[spbp](#), [bpph](#) and [bppp](#) for other BP based models.

Examples

```
library("spsurv")
data("veteran")

fit <- bpaft(Surv(time, status) ~ karno + celltype,
data = veteran)

summary(fit)
```

bpph*Bernstein Polynomial Based Proportional Hazards Model*

Description

Fits the BPPH model to time-to-event data.

Usage

```
bpph(formula, degree, data, approach = c("mle", "bayes"), ...)
```

Arguments

formula	a Surv object with time to event observations, right censoring status and explanatory terms.
degree	Bernstein polynomial degree.
data	a data.frame object.
approach	Bayesian or maximum likelihood estimation methods, default is approach = "mle".
...	further arguments passed to or from other methods

Value

An object of class 'spbp'.

See Also

[spbp](#), [bppp](#) and [bpafit](#) for other BP based models.

Examples

```
library("spsurv")
data("veteran")

fit <- bpph(Surv(time, status) ~ karno + factor(celltype),
data = veteran)

summary(fit)
```

 bppp

Bernstein Polynomial Based Proportional Odds Model

Description

Fits the BPPO model to time-to-event data.

Usage

```
bppo(formula, degree, data, approach = c("mle", "bayes"), ...)
```

Arguments

formula	a Surv object with time-to-event observations, right censoring status and explanatory terms.
degree	Bernstein polynomial degree.
data	a data.frame object.
approach	Bayesian or maximum likelihood estimation methods, default is approach = "mle".
...	further arguments passed to or from other methods

Value

An object of class 'spbp'.

See Also

[spbp](#), [bpph](#) and [bpafit](#) for other BP based models.

Examples

```
library("spsurv")
data("veteran")

fit <- bppo(Surv(time, status) ~ karno + celltype,
  data = veteran)

summary(fit)
```

coef	<i>Generic S3 method coef</i>
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Description

Generic S3 method coef

Usage

```
coef(spbp, ...)
```

Arguments

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

Value

the estimated regression coefficients

coef.spbp	<i>Estimated regression coefficients</i>
-----------	--

Description

Estimated regression coefficients

Usage

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

Arguments

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

Value

the estimated regression coefficients

confint	<i>Generic S3 method confint</i>
---------	----------------------------------

Description

Generic S3 method confint

Usage

```
confint(sbp, ...)
```

Arguments

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

Value

the estimated regression coefficients

confint.sbp	<i>Confidence intervals for the regression coefficients</i>
-------------	---

Description

Confidence intervals for the regression coefficients

Usage

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

Arguments

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

Value

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

extract	<i>Generic S3 method extract</i>
---------	----------------------------------

Description

Generic S3 method extract

Usage

```
extract(spbp, ...)
```

Arguments

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

Value

extract the MCMC chain values of a Bayesian fit.

extract.spbp	<i>Extract method for fitted spbp models</i>
--------------	--

Description

Extract samples from a fitted [spbp](#) model.

Usage

```
## S3 method for class 'spbp'
extract(spbp, pars = c("beta", "gamma"), ...)
```

Arguments

spbp	an object of class ‘spbp’ result of a spbp fit.
pars	parameters to be selected.
...	arguments inherent from extract .

Value

see [extract](#).

See Also

[spbp](#), [stan_dens.spbp](#), [traceplot.spbp](#)

Examples

```
library("spsurv")
data("veteran")

fit <- bpph(Surv(time, status) ~ karno + factor(celltype),
data = veteran)

extract(fit)
```

itsamp

Inverse Transform Sampling To Generate Time-to-event Data From Parametric Models

Description

Random survival times generation for the weibull or log-logistic distributions with parameters ‘scale’ and ‘shape’.

Usage

```
itsamp(
  n,
  beta = c(2, -1),
  event_scale = 10,
  censor_scale = 4,
  features = data.frame(x1 = rnorm(n, 0), x2 = rnorm(n, 0)),
  shape = 2,
  model = c("ph", "po", "aft"),
  dist = c("weibull", "llogis"),
  censor = TRUE
)
```

Arguments

n	integer; sample size
beta	vector of regression coefficients
event_scale, censor_scale	event and censoring scale parameters
features	matrix of features (columns)
shape	event and censoring distribution shape
model	either "ph" (default) or "aft" for weibull and "po" or "aft" for log-logistic distribution
dist	"weibull" or "llogis"
censor	logical; if ‘TRUE’, censoring is required, that is mean(status) > 0

Details

`sim_surv` returns weibull (log-logistic) randomly generated survival times. According to Collett (2003), the accelerated failure time model encompasses a wide variety of parametric models, including weibull and log-logistic models.

Value

data.frame of `'ncol(x) + 2'` columns in which the survival times are the response variable denoted by `'y'`, `'status'` indicates failure (0 = failure) and the features are appended to the next columns.

See Also

[spbp](#)

Examples

```
rows <- 200

categorical <- rbinom(rows, size = 3, prob = .5)
x <- data.frame(numerical = rnorm(rows),
  cat0 = as.numeric(categorical == 0),
  cat1 = as.numeric(categorical == 1),
  cat2 = as.numeric(categorical == 2),
  cat3 = as.numeric(categorical == 3))

newdata <- itsamp(n = rows, beta = c(1, -2, .5, .1, 1),
  features = x, model = 'ph', dist = 'weibull')
```

mode

Calculate the posterior mode

Description

Calculate the posterior mode

Usage

```
mode(ext)
```

Arguments

`ext` `rstan` extracted sample.

Value

A vector containing the posterior mode of each sample.

model.matrix.spbp	<i>Model.matrix method for fitted spbp models</i>
-------------------	---

Description

Model.matrix of a fitted [spbp](#) model.

Usage

```
## S3 method for class 'spbp'
model.matrix(
  object,
  data = eval(object$call$data, envir = parent.frame()),
  ...
)
```

Arguments

object	an object of class ‘spbp’, see spbp .
data	data.frame object.
...	arguments inherent from model.matrix .

Value

The explanatory variables matrix.

See Also

[spbp](#), [model.matrix](#)

Examples

```
library("spsurv")
data("veteran")

fit <- bpph(Surv(time, status) ~ karno + factor(celltype),
  data = veteran)

model.matrix(fit)
```

print.sbp

Bernstein Polynomial Based Regression Object Print

Description

Bernstein Polynomial Based Regression Object Print

Usage

```
## S3 method for class 'sbp'
print(
  x,
  digits = max(getOption("digits") - 4, 3),
  signif.stars = getOption("show.signif.stars"),
  ...
)
```

Arguments

x	an object of class sbp
digits	number of digits to display
signif.stars	see getOption
...	further arguments passed to or from other methods

Value

none

print.summary.bpaft.bayes

Bernstein Polynomial Based Regression Object Summary BPAFT Bayes

Description

Bernstein Polynomial Based Regression Object Summary BPAFT Bayes

Usage

```
## S3 method for class 'summary.bpaft.bayes'
print(...)
```

Arguments

...	further arguments passed to or from other methods
-----	---

Value

none

print.summary.bpaft.mle

Bernstein Polynomial Based Regression Object Summary BPAFT MLE

Description

Bernstein Polynomial Based Regression Object Summary BPAFT MLE

Usage

```
## S3 method for class 'summary.bpaft.mle'  
print(...)
```

Arguments

... further arguments passed to or from other methods

Value

none

print.summary.bpph.bayes

Bernstein Polynomial Based Regression Object Summary BPPH Bayes

Description

Bernstein Polynomial Based Regression Object Summary BPPH Bayes

Usage

```
## S3 method for class 'summary.bpph.bayes'  
print(...)
```

Arguments

... further arguments passed to or from other methods

Value

none

`print.summary.bpph.mle`

Bernstein Polynomial Based Regression Object Summary BPPH MLE

Description

Bernstein Polynomial Based Regression Object Summary BPPH MLE

Usage

```
## S3 method for class 'summary.bpph.mle'  
print(...)
```

Arguments

... further arguments passed to or from other methods

Value

none

`print.summary.bppo.bayes`

Bernstein Polynomial Based Regression Object Summary BPPO Bayes

Description

Bernstein Polynomial Based Regression Object Summary BPPO Bayes

Usage

```
## S3 method for class 'summary.bppo.bayes'  
print(...)
```

Arguments

... further arguments passed to or from other methods

Value

none

```
print.summary.bppo.mle
```

Bernstein Polynomial Based Regression Object BPPO MLE

Description

Bernstein Polynomial Based Regression Object BPPO MLE

Usage

```
## S3 method for class 'summary.bppo.mle'  
print(...)
```

Arguments

... further arguments passed to or from other methods

Value

none

```
print.summary.spbp.bayes
```

Bernstein Polynomial Based Regression Object Summary Bayes

Description

Bernstein Polynomial Based Regression Object Summary Bayes

Usage

```
## S3 method for class 'summary.spbp.bayes'  
print(x, digits = max(getOption("digits") - 4, 3), ...)
```

Arguments

x a summary.spbp.bayes object
digits number of digits to display.
... further arguments passed to or from other methods

Value

none

print.summary.spbp.mle

Bernstein Polynomial Based Regression Object Summary MLE

Description

Bernstein Polynomial Based Regression Object Summary MLE

Usage

```
## S3 method for class 'summary.spbp.mle'
print(
  x,
  digits = max(getOption("digits") - 4, 3),
  signif.stars = getOption("show.signif.stars"),
  ...
)
```

Arguments

x	a summary.spbp.mle object
digits	number of digits to display.
signif.stars	see getOption
...	further arguments passed to or from other methods

Value

none

residuals.spbp	<i>BP based models residuals.</i>
----------------	-----------------------------------

Description

Residuals for a fitted [spbp](#) model.

Usage

```
## S3 method for class 'spbp'
residuals(object, type = c("cox-snell"), ...)
```

Arguments

object	an object of class 'spbp' result of a spbp fit.
type	type of residuals, default is "cox-snell"
...	further arguments passed to or from other methods

See Also

[spbp.](#)

Examples

```
library("spsurv")
data("veteran")

fit <- bpph(Surv(time, status) ~ karno + factor(celltype),
  data = veteran)

residuals(fit)
```

spbp

spbp: The BP Based Survival Analysis Function

Description

Semiparametric Survival Analysis Using Bernstein Polynomial

Usage

```
spbp(formula, ...)
```

Arguments

formula	a Surv object with time to event, status and explanatory terms.
...	Arguments passed to ‘rstan::sampling’ (e.g. iter, chains) or ‘rstan::optimizing’.

Details

Fits Bernstein Polynomial based Proportional regression to survival data.

Value

An object of class ‘spbp’.

See Also

[spbp.default](#)

[spbp.default](#), [bpph](#), [bppp](#), [bpafit](#), <https://mc-stan.org/users/documentation/>

Examples

```
library("spsurv")
data("veteran") ## imports from survival package

fit_mle <- spbp(Surv(time, status) ~ karno + factor(celltype),
  data = veteran, model = "po")
summary(fit_mle)

fit_bayes <- spbp(Surv(time, status) ~ karno + factor(celltype),
  data = veteran, model = "po", approach = "bayes",
  cores = 1, iter = 300, chains = 1,
  priors = list(beta = c("normal(0,4)"),
    gamma = "lognormal(0,4)"))

summary(fit_bayes)
```

spbp.default

spbp: The BP Based Semiparametric Survival Analysis Function

Description

spbp: The BP Based Semiparametric Survival Analysis Function

Usage

```
## Default S3 method:
spbp(
  formula,
  degree,
  data,
  approach = c("mle", "bayes"),
  model = c("ph", "po", "aft"),
  priors = list(beta = c("normal(0,4)"), gamma = "lognormal(0,10)"),
  scale = TRUE,
  cores = parallel::detectCores(),
  ...
)
```

Arguments

formula	a Surv object with time to event, status and explanatory terms
degree	Bernstein Polynomial degree
data	a data.frame object
approach	Bayesian or Maximum Likelihood estimation methods, default is approach = "bayes"

model	Proportional Hazards or Proportional Odds BP based regression, default is model = "ph"
priors	prior settings for the Bayesian approach; 'normal' or 'cauchy' for beta; 'gamma', 'inv_gamma' or 'lognormal' for gamma (BP coefficients)
scale	logical; indicates whether to center and scale the data
cores	number of core threads to use
...	further arguments passed to or from other methods

Value

An object of class spbp

stan_dens	<i>Generic S3 method extract</i>
-----------	----------------------------------

Description

Generic S3 method extract

Usage

```
stan_dens(spbp, ...)
```

Arguments

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

Value

the density plot of a MCMC chain.

stan_dens.spbp	<i>Density plots method for fitted spbp models</i>
----------------	--

Description

Posterior density of samples from a fitted [spbp](#) model.

Usage

```
## S3 method for class 'spbp'  
stan_dens(spbp, pars = c("beta", "gamma"), ...)
```

Arguments

spbp	the result of a spbp fit.
pars	parameters to be selected.
...	arguments inherent from stan_dens .

Value

see [stan_dens](#).

See Also

[spbp](#), [traceplot.spbp](#), [extract.spbp](#)

Examples

```
library("spsurv")
data("veteran")

fit <- bpph(Surv(time, status) ~ karno + factor(celltype),
data = veteran)

stan_dens(fit)
```

summary.spbp

Bernstein Polynomial Based Regression Object Summary

Description

Bernstein Polynomial Based Regression Object Summary

Usage

```
## S3 method for class 'spbp'
summary(object, interval = 0.95, ...)
```

Arguments

object	an object of class spbp
interval	interval coverage (confidence or credibility)
...	further arguments passed to or from other methods

Value

An object of class analogous to for e.g. 'summary.bppo.bayes'.

survivor	<i>Generic S3 method vcov</i>
----------	-------------------------------

Description

Generic S3 method vcov

Usage

```
survivor(spbp, ...)
```

Arguments

spbp	an object of class spbp
...	further arguments passed to or from other methods

Value

estimates survival for each dataset individual (line). Spbp Object Observed Survival

See Also

[spbp](#), [itsamp](#)

traceplot	<i>Generic S3 method traceplot</i>
-----------	------------------------------------

Description

Generic S3 method traceplot

Usage

```
traceplot(spbp, ...)
```

Arguments

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

Value

the traceplot of a MCMC chain.

traceplot.spbp	<i>Traceplot method for fitted spbp models</i>
----------------	--

Description

Traceplot of a Bayesian fit [spbp](#).

Usage

```
## S3 method for class 'spbp'  
traceplot(spbp, pars = c("beta", "gamma"), ...)
```

Arguments

spbp	an object of class ‘spbp’ result of a spbp fit.
pars	parameters to be selected.
...	arguments inherent from traceplot .

Value

see [traceplot](#).

See Also

[spbp](#), [stan_dens.spbp](#), [extract.spbp](#)

Examples

```
library("spsurv")  
data("veteran")  
  
fit <- bph(Surv(time, status) ~ karno + factor(celltype),  
data = veteran)  
  
traceplot(fit)
```

vcov	<i>Generic S3 method vcov</i>
------	-------------------------------

Description

Generic S3 method vcov

Usage

```
vcov(sbp, ...)
```

Arguments

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

Value

the variance-covariance matrix associated the regression coefficients.

vcov.sbp	<i>Covariance of the regression coefficients</i>
----------	--

Description

Covariance of the regression coefficients

Usage

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

Arguments

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

Value

the variance-covariance matrix associated with the regression coefficients.

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