

Package: SemiParamBernsteinDepCS (via r-universe)

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Type Package

Title Semiparametric Bayesian Regression for Dependent Current Status Data

Version 0.1.0

Description Implements a semiparametric Bayesian regression framework using Bernstein polynomial baseline models for analyzing dependent current status data. The package accommodates proportional hazards (PH) and proportional odds (PO) regression models with Archimedean copulas ('Gumbel', 'Frank', and 'Clayton') to model the joint dependence structure between event and observation or censoring times. Estimation is performed using a Robust Adaptive Metropolis (RAM) Markov Chain Monte Carlo ('MCMC') algorithm. Model comparison metrics including Deviance Information Criterion ('DIC') and posterior summaries with Highest Posterior Density ('HPD') intervals and Kendall's tau are provided. Methodological details are described in Sharma and Balakrishnan (2026)
<doi:10.1080/02664763.2026.2701921>.

License GPL (>= 3)

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Imports stats, graphics

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

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NeedsCompilation no

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copula_kendall_tau	<i>Compute Kendall's Tau for Copula Families</i>
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Description

Compute Kendall's Tau for Copula Families

Usage

copula_kendall_tau(alpha, copula = c("gumbel", "frank", "clayton"))

Arguments

- alpha Copula parameter.
- copula Character string specifying the copula family.

Value

Numeric value of Kendall's tau correlation coefficient.

Examples

```
copula_kendall_tau(2.0, "gumbel")
copula_kendall_tau(1.5, "clayton")
copula_kendall_tau(3.0, "frank")
```

`fit_semiparam_bernstein_depcs`*Fit Semiparametric Bayesian Regression for Dependent Current Status Data*

Description

Fits a semiparametric Bayesian regression model using Bernstein polynomials and Archimedean copulas for dependent current status survival data. Supports Proportional Hazards (PH) and Proportional Odds (PO) models.

Usage

```
fit_semiparam_bernstein_depcs(  
  formula_Y = NULL,  
  formula_T = NULL,  
  data = NULL,  
  time = NULL,  
  status = NULL,  
  delta = NULL,  
  X_Y = NULL,  
  X_T = NULL,  
  model_type = c("PH", "PO"),  
  copula = c("gumbel", "frank", "clayton"),  
  order_m = 2,  
  order_m_Y = NULL,  
  order_m_T = NULL,  
  nu_Y = NULL,  
  nu_T = NULL,  
  n_iter = 2000,  
  n_burn = 500,  
  thin = 1,  
  seed = NULL,  
  priors = NULL  
)
```

```
fit_bernstein_depcs(  
  formula_Y = NULL,  
  formula_T = NULL,  
  data = NULL,  
  time = NULL,  
  status = NULL,  
  delta = NULL,  
  X_Y = NULL,  
  X_T = NULL,  
  model_type = c("PH", "PO"),  
  copula = c("gumbel", "frank", "clayton"),
```

```

    order_m = 2,
    order_m_Y = NULL,
    order_m_T = NULL,
    nu_Y = NULL,
    nu_T = NULL,
    n_iter = 2000,
    n_burn = 500,
    thin = 1,
    seed = NULL,
    priors = NULL
  )

```

Arguments

formula_Y	Formula for current status outcome and event covariates, e.g., $\text{delta} \sim x_1 + x_2$.
formula_T	Formula for observation time and censoring covariates, e.g., $\text{time} \sim x_1 + x_2$.
data	Data frame containing variables in formulas.
time	Vector of observation times (if formulas not provided).
status	Vector of observation time censoring indicators (1 = uncensored/event for T, 0 = administrative censoring).
delta	Vector of current status indicators (1 = $Y \leq T$, 0 = $Y > T$).
X_Y	Design matrix for event time Y covariates.
X_T	Design matrix for observation time T covariates.
model_type	Character string, either "PH" for Proportional Hazards or "PO" for Proportional Odds.
copula	Copula family for dependence structure: "gumbel", "frank", or "clayton".
order_m	Order of Bernstein polynomial baseline model (default 2).
order_m_Y	Order of Bernstein polynomial for Y (defaults to order_m).
order_m_T	Order of Bernstein polynomial for T (defaults to order_m).
nu_Y	Upper bound of time domain for Y (defaults to $\max(\text{time}) * 1.05$).
nu_T	Upper bound of time domain for T (defaults to $\max(\text{time}) * 1.05$).
n_iter	Total MCMC iterations (default 2000).
n_burn	Burn-in iterations to discard (default 500).
thin	Thinning interval (default 1).
seed	Optional random seed.
priors	List of prior hyperparameters.

Value

An object of class `semiparam_bernstein_depcs` containing MCMC chains, posterior summaries, DIC, log-likelihood, and model specifications.

Examples

```
set.seed(123)
dat <- sim_bernstein_deps(n = 100, model_type = "PH", copula = "gumbel")
fit <- fit_semiparam_bernstein_deps(
  formula_Y = delta ~ x1 + x2,
  formula_T = time ~ x1 + x2,
  data = dat,
  model_type = "PH",
  copula = "gumbel",
  order_m = 2,
  n_iter = 500,
  n_burn = 100
)
print(fit)
summary(fit)
```

pbcs_deps

Primary Biliary Cirrhosis (PBC) Dependent Current Status Dataset

Description

A benchmark dataset containing clinical trial information from Primary Biliary Cirrhosis (PBC) patients used to analyze dependent current status data.

Usage

```
data(pbc_deps)
```

Format

A data frame with 100 rows and 8 variables:

time Survival/observation time in days.

status Censoring indicator for survival time (1 = dead, 0 = censored).

delta Current status indicator for hepatomegaly onset (1 = present, 0 = absent).

age Patient age in years.

sex Patient gender (1 = male, 0 = female).

ascites Presence of ascites (1 = yes, 0 = no).

bilirubin Serum bilirubin level in mg/dl.

albumin Serum albumin level in g/dl.

Source

Mayo Clinic trial data on Primary Biliary Cirrhosis (PBC), adapted for dependent current status analysis in Sharma and Balakrishnan (2026) <doi:10.1080/02664763.2026.2701921>.

plot.semiparam_bernstein_depcs

Plot Predicted Survival Curves or Diagnostics

Description

Plot Predicted Survival Curves or Diagnostics

Usage

```
## S3 method for class 'semiparam_bernstein_depcs'
plot(x, type = c("survival", "trace", "hazard"), ...)
```

Arguments

x	An object of class semiparam_bernstein_depcs.
type	Character string indicating plot type: "survival", "trace", or "hazard".
...	Additional graphic parameters.

Value

Invisible NULL.

predict.semiparam_bernstein_depcs

Predict Survival and Cumulative Hazards for New Data

Description

Computes predicted marginal survival curves $S_Y(t | X_{\text{new}})$ and $S_T(t | X_{\text{new}})$ with HPD intervals.

Usage

```
## S3 method for class 'semiparam_bernstein_depcs'
predict(object, newdata = NULL, times = NULL, prob = 0.95, ...)
```

Arguments

object	An object of class semiparam_bernstein_depcs.
newdata	Optional data frame or list containing new covariate values. If NULL, uses average covariate values.
times	Grid of time points to evaluate predictions. If NULL, defaults to 50 points over $[0, \text{nu}]$.
prob	Credible interval level (default 0.95).
...	Additional arguments.

Value

A list containing predicted survival probabilities and HPD bounds for Y and T.

Examples

```
set.seed(123)
dat <- sim_bernstein_depcs(n = 100, model_type = "PH", copula = "gumbel")
fit <- fit_semiparam_bernstein_depcs(
  formula_Y = delta ~ x1 + x2,
  formula_T = time ~ x1 + x2,
  data = dat,
  n_iter = 500,
  n_burn = 100
)
pred <- predict(fit, times = seq(0.1, 2, length.out = 10))
```

```
print.semiparam_bernstein_depcs
```

Print Summary of Fitted SemiParamBernsteinDepCS Model

Description

Print Summary of Fitted SemiParamBernsteinDepCS Model

Usage

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

Arguments

x	An object of class semiparam_bernstein_depcs.
...	Additional arguments passed to print.

Value

Invisible x.

sim_bernstein_depcs *Simulate Dependent Current Status Data*

Description

Generates synthetic current status data with dependent censoring based on copula models and Weibull/Bernstein marginal distributions.

Usage

```
sim_bernstein_depcs(
  n = 200,
  model_type = c("PH", "PO"),
  copula = c("gumbel", "frank", "clayton"),
  alpha = NULL,
  beta_Y = c(0.5, -0.3),
  beta_T = c(-0.2, 0.4),
  scale_Y = 1,
  shape_Y = 1.5,
  scale_T = 1,
  shape_T = 1.2,
  admin_censor = 3,
  seed = NULL
)
```

Arguments

n	Sample size (integer, default 200).
model_type	Character string, either "PH" for Proportional Hazards or "PO" for Proportional Odds.
copula	Copula family: "gumbel", "frank", or "clayton".
alpha	Copula dependence parameter (default 2.0 for Gumbel/Clayton, 3.0 for Frank).
beta_Y	Numeric vector of true regression coefficients for Y (default c(0.5, -0.3)).
beta_T	Numeric vector of true regression coefficients for T (default c(-0.2, 0.4)).
scale_Y	Scale parameter for Weibull baseline Y (default 1.0).
shape_Y	Shape parameter for Weibull baseline Y (default 1.5).
scale_T	Scale parameter for Weibull baseline T (default 1.0).
shape_T	Shape parameter for Weibull baseline T (default 1.2).
admin_censor	Administrative censoring time limit (default 3.0).
seed	Optional random seed.

Value

A data frame containing simulated columns: time, status, delta, x1, x2.

Examples

```
set.seed(42)
dat <- sim_bernstein_depcs(n = 50, model_type = "PH", copula = "gumbel")
head(dat)
```

```
summary.semiparam_bernstein_depcs
```

Summarize Fitted SemiParamBernsteinDepCS Model

Description

Summarize Fitted SemiParamBernsteinDepCS Model

Usage

```
## S3 method for class 'semiparam_bernstein_depcs'
summary(object, prob = 0.95, ...)
```

Arguments

object	An object of class semiparam_bernstein_depcs.
prob	Credible interval level (default 0.95).
...	Additional arguments.

Value

A summary table object.

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