# Package: PICBayes (via r-universe)

October 17, 2024

**Title** Bayesian Models for Partly Interval-Censored Data

**Version** 1.0

**Date** 2021-08-04

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**Description** Contains functions to fit proportional hazards (PH) model
to partly interval-censored (PIC) data (Pan et al. (2020)
<doi:10.1177/0962280220921552>), PH model with spatial frailty
to spatially dependent PIC data (Pan and Cai (2021)
<doi:10.1080/03610918.2020.1839497>), and mixed effects PH
model to clustered PIC data. Each random intercept/random
effect can follow both a normal prior and a Dirichlet process
mixture prior. It also includes the corresponding functions for
general interval-censored data.

**License** GPL (>= 2)

**Depends** R (>= 3.5.0), coda, MCMCpack, survival

**LazyLoad** yes

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2021-08-05 07:50:17 UTC

# Contents

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PICBayes–package          *Bayesian Models for Partly Interval-Censored Data and General Interval-Censored Data*

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### Description

Contains functions to fit proportional hazards (PH) model to partly interval-censored (PIC) data (Pan et al. (2020) <doi:10.1177/0962280220921552>), PH model with spatial frailty to spatially dependent PIC data (Pan and Cai (2021) <doi:10.1080/03610918.2020.1839497>), and mixed effects PH model to clustered PIC data. Each random intercept/random effect can follow both a normal prior and a Dirichlet process mixture prior. It also includes the corresponding functions for general interval-censored data.

### Details

| | |
|---|---|
| Package: | PICBayes |
| Type: | Package |
| Version: | 1.0 |
| Date: | 2021-08-04 |
| License: | GPL>=2 |
| LazyLoad: | yes |

**Author(s)**

Chun Pan

Maintainer: Chun Pan <chunpan2003@hotmail.com>

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C *Adjacency matrix of 46 South Carolina counties*

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**Description**

The adjacency matrix of the 46 South Carolina counties. C[i,j] = 1 if county i and county j share boundaries; 0 if not. C[i,i] = 0.

**Usage**

```
data(C)
```

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clusterIC_int *PH model with random intercept for clustered general interval-censored data*

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**Description**

Fit a Bayesian semiparametric PH model with random intercept for clustered general interval-censored data. Random intercept follows a normal distribution $N(0, \text{tau}^{-1})$.

**Usage**

```
clusterIC_int(L, R, y, xcov, IC, scale.designX, scaled, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_tau, b_tau, beta_iter, phi_iter,
beta_cand, phi_cand, beta_sig0, x_user, total, burnin, thin, conf.int, seed)
```

**Arguments**

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |

| | |
|---|---|
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| a_tau | The shape parameter of Gamma prior for random intercept precision tau. |
| b_tau | The rate parameter of Gamma prior for random intercept precision tau. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for phi_i. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for beta_r. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for phi_i. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

## Details

The baseline cumulative hazard is approximated by a linear combination of I-splines:

sum_{l=1}^{K}(gamma_l*b_l(t)).

For a binary prdictor, we sample e^{beta_r}, with Gamma prior.

The regression coefficient beta_r for a continuous predictor and random intercept phi_i are sampled using MH algorithm. During the initial beta_iter iterations, sd of the proposal distribution is beta_cand. Afterwards, proposal sd is set to be the sd of available MCMC draws. Same method for phi_i.

## Value

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A total by p matrix of MCMC draws of beta_r, r=1, ..., p. |

| parsurv0 | A total by length(grids) matrix, each row contains the baseline survival at grids from one iteration. |
|---|---|
| parsurv | A total by length(grids)*G matrix, each row contains the survival at grids from one iteration. G is the number of sets of user-specified covariate values. |
| parphi | A total by I matrix of MCMC draws of phi_i, i=1,...,I. |
| partau | A total by 1 vector of MCMC draws of tau. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at grids. |
| S_m | The estimated survival at grids with user-specified covariate values x_user. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

### Author(s)

Chun Pan

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| clusterIC_int_DP | *PH model with random intercept for clustered general interval-censored data* |
|---|---|

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### Description

Fit a Bayesian semiparametric PH model with random intercept for clustered general interval-censored data. Random intercept follows a Dirithlet process mixture distribution.

### Usage

```
clusterIC_int_DP(L, R, y, xcov, IC, scale.designX, scaled, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_alpha, b_alpha, H, a_tau_star,
b_tau_star, beta_iter, phi_iter, beta_cand, phi_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

### Arguments

| L | The vector of left endpoints of the observed time intervals. |
|---|---|
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored. |
| xcov | The covariate matrix for the p predictors. |

| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
|---|---|
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| a_alpha | The shape parameter of Gamma prior for alpha. |
| b_alpha | The rate parameter of Gamma prior for alpha. |
| H | The number of distinct components in DP mixture prior under blocked Gibbs sampler. |
| a_tau_star | The shape parameter of G_0 in DP mixture prior. |
| b_tau_star | The rate parameter of G_0 in DP mixture prior. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for phi_i. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for beta_r. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for phi_i. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

## Details

DP mixture prior:

$phi\_i \sim N(0, tau\_\{i\}^\{-1\})$

$tau\_\{i\} \sim G$

$G \sim DP(alpha, G\_\{0\})$

G_{0}=Gamma(a_tau_star,b_tau_star)

tau_{h}^{*}~G_{0}, h=1,...,H

The blocked Gibbs sampler proposed by Ishwaran and James (2001) is used to sample from the posteriors under the DP mixture prior.

## Value

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A `total` by p matrix of MCMC draws of `beta_r`, r=1, ..., p. |
| parsurv0 | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| paralpha | A `total` by 1 vector of MCMC draws of `alpha`. |
| parphi | A `total` by I matrix of MCMC draws of `phi_i`, i=1,...,I. |
| partau_star | A `total` by H matrix of MCMC draws of `tau_star`. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

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| clusterIC_trt | *PH model with random intercept and random treatment for clustered general interval-censored data* |
|---|---|

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## Description

Fit a Bayesian semiparametric PH model with random intercept and random treatment for clustered general interval-censored data. Each random effect follows a normal distribution N(0, tau^{-1}).

**Usage**

```
clusterIC_trt(L, R, y, xcov, IC, scale.designX, scaled, xtrt, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_tau, b_tau, a_tau_trt,
b_tau_trt, beta_iter, phi_iter, beta_cand, phi_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

**Arguments**

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| xtrt | The covariate that has a random effect. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| a_tau | The shape parameter of Gamma prior for random intercept precision tau. |
| b_tau | The rate parameter of Gamma prior for random intercept precision tau. |
| a_tau_trt | The shape parameter of Gamma prior for random treatment precision tau_trt. |
| b_tau_trt | The rate parameter of Gamma prior for random treatment precision tau_trt. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for phi_i. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for beta_r. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for phi_i. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |

| | |
|---|---|
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

## Details

The baseline cumulative hazard is approximated by a linear combination of I-splines:

sum_{l=1}^{K}(gamma_l*b_l(t)).

For a binary prdictor, we sample e^{beta_r}, with Gamma prior.

The regression coefficient beta_r for a continuous predictor, random intercept phi_i, and random treatment phi_trt_i are sampled using MH algorithm. During the initial beta_iter iterations, sd of the proposal distribution is beta_cand. Afterwards, proposal sd is set to be the sd of available MCMC draws. Same method for phi_i and phi_trt_i.

## Value

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A total by p matrix of MCMC draws of beta_r, r=1, ..., p. |
| parsurv0 | A total by length(grids) matrix, each row contains the baseline survival at grids from one iteration. |
| parsurv | A total by length(grids)*G matrix, each row contains the survival at grids from one iteration. G is the number of sets of user-specified covariate values. |
| parphi | A total by I matrix of MCMC draws of phi_i, i=1,...,I. |
| parphi_trt | A total by I matrix of MCMC draws of phi_trt_i, i=1,...,I. |
| partau | A total by 1 vector of MCMC draws of tau. |
| partau_trt | A total by 1 vector of MCMC draws of tau_trt. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at grids. |
| S_m | The estimated survival at grids with user-specified covariate values x_user. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

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| clusterIC_trt_DP | *PH model with random intercept and random treatment for clustered general interval-censored data* |
|---|---|

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**Description**

Fit a Bayesian semiparametric PH model with random intercept and random treatment for clustered general interval-censored data. Each random effect follows a Dirichlet process mixture distribution.

**Usage**

```
clusterIC_trt_DP(L, R, y, xcov, IC, scale.designX, scaled, xtrt, area, binary,
I, order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_alpha, b_alpha, H,
a_tau_star, b_tau_star, a_alpha_trt, b_alpha_trt, H_trt, a_tau_trt_star,
b_tau_trt_star, beta_iter, phi_iter, beta_cand, phi_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

**Arguments**

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| xtrt | The covariate that has a random effect. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| a_alpha | The shape parameter of Gamma prior for alpha. |

| b_alpha | The rate parameter of Gamma prior for `alpha`. |
|---|---|
| H | The number of distinct components in DP mixture prior under blocked Gibbs sampler. |
| a_tau_star | The shape parameter of `G_0` in DP mixture prior. |
| b_tau_star | The rate parameter of `G_0` in DP mixture prior. |
| a_alpha_trt | The shape parameter of Gamma prior for `alpha_trt`. |
| b_alpha_trt | The rate parameter of Gamma prior for `alpha_trt`. |
| H_trt | The number of distinct components in DP mixture prior under blocked Gibbs sampler for random treatment. |
| a_tau_trt_star | The shape parameter of `G_0` in DP mixture prior for random treatment. |
| b_tau_trt_star | The rate parameter of `G_0` in DP mixture prior for random treatment. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for `beta_r`. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for `phi_i`. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for `beta_r`. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for `phi_i`. |
| beta_sig0 | The sd of the prior normal distribution for `beta_r`. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for `beta_r`. |
| seed | A user-specified random seed. |

## Details

Both random intercept and random treatment follow its own DP mixture prior. DP mixture prior:

`phi_i~N(0,tau_{i}^{-1})`

`tau_{i}~G`

`G~DP(alpha,G_{0})`

`G_{0}=Gamma(a_tau_star,b_tau_star)`

`tau_{h}^{*}~G_{0}, h=1,...,H`

The blocked Gibbs sampler proposed by Ishwaran and James (2001) is used to sample from the posteriors under the DP mixture prior.

## Value

a list containing the following elements:

| N | The sample size. |
|---|---|
| parbeta | A `total` by p matrix of MCMC draws of `beta_r`, r=1, ..., p. |

| | |
|---|---|
| parsurv0 | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| paralpha | A `total` by 1 vector of MCMC draws of `alpha`. |
| paralpha_trt | A `total` by 1 vector of MCMC draws of `alpha_trt`. |
| parphi | A `total` by I matrix of MCMC draws of phi_i, i=1,...,I. |
| parphi_trt | A `total` by I matrix of MCMC draws of phi_trt_i, i=1,...,I. |
| partau_star | A `total` by H matrix of MCMC draws of `tau_star`. |
| partau_trt_star | |
| | A `total` by H_trt matrix of MCMC draws of `tau_trt_star`. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

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clusterIC_Z                      *Mixed effects PH model for clustered general interval-censored data*

---

## Description

Fit a Bayesian semiparametric mixed effects PH model for clustered general interval-censored data. Each random effect follows a normal distribution N(0, tau^{-1}).

## Usage

```
clusterIC_Z(L, R, y, xcov, IC, scale.designX, scaled, zcov, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_tau, b_tau, beta_iter, phi_iter,
beta_cand, phi_cand, beta_sig0, x_user, total, burnin, thin, conf.int, seed)
```

**Arguments**

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored; 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| zcov | The design matrix for the q random effects. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for `gamma_l`. |
| b_eta | The rate parameter of Gamma prior for `gamma_l`. |
| a_ga | The shape parameter of Gamma prior for `e^{beta_r}`. |
| b_ga | The rate parameter of Gamma prior for `e^{beta_r}`. |
| a_tau | The shape parameter of Gamma prior for random intercept precision `tau`. |
| b_tau | The rate parameter of Gamma prior for random intercept precision `tau`. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for `beta_r`. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for `phi_i`. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for `beta_r`. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for `phi_i`. |
| beta_sig0 | The sd of the prior normal distribution for `beta_r`. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for `beta_r`. |
| seed | A user-specified random seed. |

## Details

The mixed effects PH model is:

h(t_{ij}|x_{ij},z_{ij})=h_{0}(t_{ij})exp(beta'x_{ij}+phi_{i}'z_{ij}),

for the jth subject in the ith cluster.

Each of the q random effects is sampled using MH algorithm separately.

## Value

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A `total` by p matrix of MCMC draws of beta_r, r=1, ..., p. |
| parsurv0 | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

---

clusterIC_Z_DP                 *Mixed effects PH model for clustered general interval-censored data*

---

## Description

Fit a Bayesian semiparametric mixed effects PH model for clustered general interval-censored data. Each random effect follows a DP mixture distribution.

## Usage

```
clusterIC_Z_DP(L, R, y, xcov, IC, scale.designX, scaled, zcov, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_alpha, b_alpha, H,
a_tau_star, b_tau_star, beta_iter, phi_iter, beta_cand, phi_cand,
beta_sig0, x_user, total, burnin, thin, conf.int, seed)
```

## Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| zcov | The design matrix for the q random effects. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for `gamma_l`. |
| b_eta | The rate parameter of Gamma prior for `gamma_l`. |
| a_ga | The shape parameter of Gamma prior for `e^{beta_r}`. |
| b_ga | The rate parameter of Gamma prior for `e^{beta_r}`. |
| a_alpha | The shape parameter of Gamma prior for `alpha`. |
| b_alpha | The rate parameter of Gamma prior for `alpha`. |
| H | The number of distinct components in DP mixture prior under blocked Gibbs sampler. |
| a_tau_star | The shape parameter of `G_0` in DP mixture prior. |
| b_tau_star | The rate parameter of `G_0` in DP mixture prior. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for `beta_r`. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for `phi_i`. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for `beta_r`. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for `phi_i`. |
| beta_sig0 | The sd of the prior normal distribution for `beta_r`. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for `beta_r`. |
| seed | A user-specified random seed. |

**Details**

The mixed effects PH model is:

`h(t_{ij}|x_{ij},z_{ij})=h_{0}(t_{ij})exp(beta'x_{ij}+phi_{i}'z_{ij})`,

for the jth subject in the ith cluster.

Each of the q random effects is sampled using MH algorithm separately.

**Value**

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A `total` by p matrix of MCMC draws of `beta_r`, r=1, ..., p. |
| parsurv0 | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| paralpha | A `total` by q vector of MCMC draws of `alpha`. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

**Author(s)**

Chun Pan

---

| | |
|---|---|
| clusterPIC_int | *PH model with random intercept for clustered partly interval-censored data* |

---

**Description**

Fit a Bayesian semiparametric PH model with random intercept for clustered partly interval-censored data. Random intercept follows a normal distribution `N(0, tau^{-1})`.

**Usage**

```
clusterPIC_int(L, R, y, xcov, IC, scale.designX, scaled, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_tau, b_tau, beta_iter,
phi_iter, beta_cand, phi_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

## Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| a_tau | The shape parameter of Gamma prior for random intercept precision tau. |
| b_tau | The rate parameter of Gamma prior for random intercept precision tau. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for phi_i. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for beta_r. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for phi_i. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

**Details**

The baseline cumulative hazard is approximated by a linear combination of I-splines:

`sum_{l=1}^{K}(gamma_l*b_l(t)).`

The baseline hazard is approximated by a linear combination of basis M-splines:

`sum_{l=1}^{K}(gamma_l*M_l(t)).`

For a binary prdictor, we sample e^{beta_r}, with Gamma prior.

The regression coefficient `beta_r` for a continuous predictor and random intercept `phi_i` are sampled using MH algorithm. During the initial `beta_iter` iterations, sd of the proposal distribution is `beta_cand`. Afterwards, proposal sd is set to be the sd of available MCMC draws. Same method for `phi_i`.

**Value**

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A `total` by p matrix of MCMC draws of beta_r, r=1, ..., p. |
| parsurv0 | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| parphi | A `total` by I matrix of MCMC draws of phi_i, i=1,...,I. |
| partau | A `total` by 1 vector of MCMC draws of `tau`. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

**Author(s)**

Chun Pan

**Examples**

```
# Number of iterations set to very small for CRAN automatic testing
data(da3)
try3<-PICBayes(formula=Surv(L,R,type='interval2')~x1+x2,data=data.frame(da3),
model='clusterPIC_int',area=da3[,6],IC=da3[,7],scale.designX=TRUE,scale=c(1,0),
binary=c(0,1),I=25,C=C,nn=nn,order=3,knots=c(0,2,6,max(da3[,1:2],na.rm=TRUE)+1),
grids=seq(0.1,10.1,by=0.1),a_eta=1,b_eta=1,a_ga=1,b_ga=1,a_tau=1,b_tau=1,
```

```
beta_iter=11,phi_iter=11,beta_cand=rep(1,2),phi_cand=1,beta_sig0=10,
x_user=NULL,total=60,burnin=10,thin=1,conf.int=0.95,seed=1)
```

---

| clusterPIC_int_DP | *PH model with random intercept for clustered partly interval-censored data data* |
|---|---|

---

## Description

Fit a Bayesian semiparametric PH model with random intercept for clustered partly interval-censored data. Random intercept follows a Dirithlet process mixture distribution.

## Usage

```
clusterPIC_int_DP(L, R, y, xcov, IC, scale.designX, scaled, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_alpha, b_alpha, H, a_tau_star,
b_tau_star, beta_iter, phi_iter, beta_cand, phi_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

## Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for `gamma_l`. |
| b_eta | The rate parameter of Gamma prior for `gamma_l`. |
| a_ga | The shape parameter of Gamma prior for `e^{beta_r}`. |
| b_ga | The rate parameter of Gamma prior for `e^{beta_r}`. |

| a_alpha    | The shape parameter of Gamma prior for `alpha`. |
|------------|--------------------------------------------------|
| b_alpha    | The rate parameter of Gamma prior for `alpha`. |
| H          | The number of distinct components in DP mixture prior under blocked Gibbs sampler. |
| a_tau_star | The shape parameter of `G_0` in DP mixture prior. |
| b_tau_star | The rate parameter of `G_0` in DP mixture prior. |
| beta_iter  | The number of initial iterations in the Metropolis-Hastings sampling for `beta_r`. |
| phi_iter   | The number of initial iterations in the Metropolis-Hastings sampling for `phi_i`. |
| beta_cand  | The sd of the proposal normal distribution in the initial MH sampling for `beta_r`. |
| phi_cand   | The sd of the proposal normal distribution in the initial MH sampling for `phi_i`. |
| beta_sig0  | The sd of the prior normal distribution for `beta_r`. |
| x_user     | The user-specified covariate vector at which to estimate survival function(s). |
| total      | The number of total iterations. |
| burnin     | The number of burnin. |
| thin       | The frequency of thinning. |
| conf.int   | The confidence level of the CI for `beta_r`. |
| seed       | A user-specified random seed. |

## Details

DP mixture prior:

`phi_i~N(0,tau_{i}^{-1})`

`tau_{i}~G`

`G~DP(alpha,G_{0})`

`G_{0}=Gamma(a_tau_star,b_tau_star)`

`tau_{h}^{*}~G_{0}`, h=1,...,H

The blocked Gibbs sampler proposed by Ishwaran and James (2001) is used to sample from the posteriors under the DP mixture prior.

## Value

a list containing the following elements:

| N         | The sample size. |
|-----------|-------------------|
| parbeta   | A `total` by p matrix of MCMC draws of `beta_r`, r=1, ..., p. |
| parsurv0  | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv   | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| paralpha  | A `total` by 1 vector of MCMC draws of `alpha`. |
| parphi    | A `total` by I matrix of MCMC draws of `phi_i`, i=1,...,I. |

| partau_star | A total by H matrix of MCMC draws of `tau_star`. |
|---|---|
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

## Examples

```
# Number of iterations set to very small for CRAN automatic testing
data(da3)
try4<-PICBayes(formula=Surv(L,R,type='interval2')~x1+x2,data=data.frame(da3),
model='clusterPIC_int_DP',area=da3[,6],IC=da3[,7],scale.designX=TRUE,
scale=c(1,0),binary=c(0,1),I=25,C=C,order=3,
knots=c(0,2,6,max(da3[,1:2],na.rm=TRUE)+1),grids=seq(0.1,10.1,by=0.1),
a_eta=1,b_eta=1,a_ga=1,b_ga=1,a_alpha=1,b_alpha=1,H=5,a_tau_star=1,
b_tau_star=1,beta_iter=11,phi_iter=11,beta_cand=rep(1,2),phi_cand=1,
beta_sig0=10,x_user=NULL,total=60,burnin=10,thin=1,conf.int=0.95,seed=1)
```

---

| clusterPIC_trt | *PH model with random intercept and random treatment for clustered partly interval-censored data* |
|---|---|

---

## Description

Fit a Bayesian semiparametric PH model with random intercept and random treatment for clustered partly interval-censored data. Each random effect follows a normal distribution N(0, tau^{-1}).

## Usage

```
clusterPIC_trt(L, R, y, xcov, IC, scale.designX, scaled, xtrt, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_tau, b_tau, a_tau_trt,
b_tau_trt, beta_iter, phi_iter, beta_cand, phi_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

**Arguments**

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| xtrt | The covariate that has a random effect. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for `gamma_l`. |
| b_eta | The rate parameter of Gamma prior for `gamma_l`. |
| a_ga | The shape parameter of Gamma prior for $e^{\beta_r}$. |
| b_ga | The rate parameter of Gamma prior for $e^{\beta_r}$. |
| a_tau | The shape parameter of Gamma prior for random intercept precision `tau`. |
| b_tau | The rate parameter of Gamma prior for random intercept precision `tau`. |
| a_tau_trt | The shape parameter of Gamma prior for random treatment precision `tau_trt`. |
| b_tau_trt | The rate parameter of Gamma prior for random treatment precision `tau_trt`. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for `beta_r`. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for `phi_i`. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for `beta_r`. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for `phi_i`. |
| beta_sig0 | The sd of the prior normal distribution for `beta_r`. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for `beta_r`. |
| seed | A user-specified random seed. |

## Details

The baseline cumulative hazard is approximated by a linear combination of I-splines:

`sum_{l=1}^{K}(gamma_l*b_l(t)).`

The baseline hazard is approximated by a linear combination of basis M-splines:

`sum_{l=1}^{K}(gamma_l*M_l(t)).`

For a binary prdictor, we sample `e^{beta_r}`, with Gamma prior.

The regression coefficient `beta_r` for a continuous predictor, random intercept `phi_i`, and random treatment `phi_trt_i` are sampled using MH algorithm. During the initial `beta_iter` iterations, sd of the proposal distribution is `beta_cand`. Afterwards, proposal sd is set to be the sd of available MCMC draws. Same method for `phi_i` and `phi_trt_i`.

## Value

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A `total` by p matrix of MCMC draws of `beta_r`, r=1, ..., p. |
| parsurv0 | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| parphi | A `total` by I matrix of MCMC draws of `phi_i`, i=1,...,I. |
| parphi_trt | A `total` by I matrix of MCMC draws of `phi_trt_i`, i=1,...,I. |
| partau | A `total` by 1 vector of MCMC draws of `tau`. |
| partau_trt | A `total` by 1 vector of MCMC draws of `tau_trt`. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

## Examples

```
# Number of iterations set to very small for CRAN automatic testing
data(da4)
try5<-PICBayes(formula=Surv(L,R,type='interval2')~x1+x2,data=data.frame(da4),
model='clusterPIC_trt',xtrt=da4[,5],area=da4[,6],IC=da4[,7],
scale.designX=TRUE,scaled=c(1,0),binary=c(0,1),I=25,order=3,
knots=c(0,2,6,max(da4[,1:2],na.rm=TRUE)+1),grids=seq(0.1,10.1,by=0.1),
a_eta=1,b_eta=1,a_ga=1,b_ga=1,a_tau=1,b_tau=1,a_tau_trt=1,b_tau_trt=1,
beta_iter=11,phi_iter=11,beta_cand=c(1,1),phi_cand=1,
beta_sig0=10,x_user=NULL,total=60,burnin=10,thin=1,conf.int=0.95,seed=1)
```

---

clusterPIC_trt_DP           *PH model with random intercept and random treatment for clustered*
                            *partly interval-censored data*

---

## Description

Fit a Bayesian semiparametric PH model with random intercept and random treatment for clustered
partly interval-censored data. Each random effect follows a Dirichlet process mixture distribution
N(0, tau^{-1}).

## Usage

```
clusterPIC_trt_DP(L, R, y, xcov, IC, scale.designX, scaled, xtrt, area, binary,
I, order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_alpha, b_alpha, H,
a_tau_star, b_tau_star, a_alpha_trt, b_alpha_trt, H_trt, a_tau_trt_star,
b_tau_trt_star, beta_iter, phi_iter, beta_cand, phi_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

## Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| xtrt | The covariate that has a random effect. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |

| I | The number of clusters. |
|---|---|
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| a_alpha | The shape parameter of Gamma prior for alpha. |
| b_alpha | The rate parameter of Gamma prior for alpha. |
| H | The number of distinct components in DP mixture prior under blocked Gibbs sampler. |
| a_tau_star | The shape parameter of G_0 in DP mixture prior. |
| b_tau_star | The rate parameter of G_0 in DP mixture prior. |
| a_alpha_trt | The shape parameter of Gamma prior for alpha_trt. |
| b_alpha_trt | The rate parameter of Gamma prior for alpha_trt. |
| H_trt | The number of distinct components in DP mixture prior under blocked Gibbs sampler for random treatment. |
| a_tau_trt_star | The shape parameter of G_0 in DP mixture prior for random treatment. |
| b_tau_trt_star | The rate parameter of G_0 in DP mixture prior for random treatment. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for phi_i. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for beta_r. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for phi_i. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

## Details

Both random intercept and random treatment follow its own DP mixture prior. DP mixture prior:

phi_i~N(0,tau_{i}^{-1})

tau_{i}~G

G~DP(alpha,G_{0})

G_{0}=Gamma(a_tau_star,b_tau_star)

tau_{h}^{*}~G_{0}, h=1,...,H

The blocked Gibbs sampler proposed by Ishwaran and James (2001) is used to sample from the posteriors under the DP mixture prior.

## Value

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A total by p matrix of MCMC draws of beta_r, r=1, ..., p. |
| parsurv0 | A total by length(grids) matrix, each row contains the baseline survival at grids from one iteration. |
| parsurv | A total by length(grids)*G matrix, each row contains the survival at grids from one iteration. G is the number of sets of user-specified covariate values. |
| paralpha | A total by 1 vector of MCMC draws of alpha. |
| paralpha_trt | A total by 1 vector of MCMC draws of alpha_trt. |
| parphi | A total by I matrix of MCMC draws of phi_i, i=1,...,I. |
| parphi_trt | A total by I matrix of MCMC draws of phi_trt_i, i=1,...,I. |
| partau_star | A total by H matrix of MCMC draws of tau_star. |
| partau_trt_star | |
| | A total by H_trt matrix of MCMC draws of tau_trt_star. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at grids. |
| S_m | The estimated survival at grids with user-specified covariate values x_user. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

## Examples

```
# Number of iterations set to very small for CRAN automatic testing
data(da4)
try2<-PICBayes(formula=Surv(L,R,type='interval2')~x1+x2,data=data.frame(da4),
model='clusterPIC_trt_DP', scale.designX=TRUE,scaled=c(1,0),IC=da4[,7],xtrt=da4[,5],
area=da4[,6],binary=c(0,1),I=25,order=3,knots=c(0,2,6,max(da4[,1:2],na.rm=TRUE)+1),
grids=seq(0.1,10.1,by=0.1),a_eta=1,b_eta=1,a_ga=1,b_ga=1,
a_alpha=1,b_alpha=1,H=5,a_alpha_trt=1,b_alpha_trt=1,H_trt=5,
a_tau_star=1,b_tau_star=1,a_tau_trt_star=1,b_tau_trt_star=1,
beta_iter=11,phi_iter=11,beta_cand=rep(1,2),phi_cand=1,beta_sig0=10,
x_user=NULL,total=60,burnin=10,thin=1,conf.int=0.95,seed=1)
```

---

| clusterPIC_Z | *Mixed effects PH model for clustered partly interval-censored data* |
|---|---|

---

### Description

Fit a Bayesian semiparametric mixed effects PH model for clustered partly interval-censored data with random effects for one or more predictors. Each random effect follows a normal distribution N(0, tau^{-1}).

### Usage

```
clusterPIC_Z(L, R, y, xcov, IC, scale.designX, scaled, zcov, area, binary, I,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_tau, b_tau, beta_iter,
phi_iter, beta_cand, phi_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

### Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| zcov | The design matrix for the q random effects. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for `gamma_l`. |
| b_eta | The rate parameter of Gamma prior for `gamma_l`. |
| a_ga | The shape parameter of Gamma prior for $e^{beta_r}$. |
| b_ga | The rate parameter of Gamma prior for $e^{beta_r}$. |
| a_tau | The shape parameter of Gamma prior for random intercept precision tau. |
| b_tau | The rate parameter of Gamma prior for random intercept precision tau. |

| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
|---|---|
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for phi_i. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for beta_r. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for phi_i. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

## Details

The mixed effects PH model is:

$h(t_{ij}|x_{ij},z_i) = h_0(t_{ij})\exp(beta'x_{ij}+phi_i'z_i),$

for the jth subject in the ith cluster.

Each of the q random effects is sampled using MH algorithm separately.

## Value

a list containing the following elements:

| N | The sample size. |
|---|---|
| parbeta | A total by p matrix of MCMC draws of beta_r, r=1, ..., p. |
| parsurv0 | A total by length(grids) matrix, each row contains the baseline survival at grids from one iteration. |
| parsurv | A total by length(grids)*G matrix, each row contains the survival at grids from one iteration. G is the number of sets of user-specified covariate values. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at grids. |
| S_m | The estimated survival at grids with user-specified covariate values x_user. |
| grids | The sequance of points where baseline survival functions is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

## Examples

```
# Number of iterations set to very small for CRAN automatic testing
data(da4)
J=rep(1,nrow(da4))
zcov=cbind(J,da4[,4]) # The 4th column of da4 is x1.
try7<-PICBayes(formula=Surv(L,R,type='interval2')~x1+x2,data=data.frame(da4),
model='clusterPIC_Z',IC=da4[,7],scale.designX=TRUE,scaled=c(1,0),zcov=zcov,
area=da4[,6],binary=c(0,1),I=25,order=3,knots=c(0,2,6,max(da4[,1:2],na.rm=TRUE)+1),
grids=seq(0.1,10.1,by=0.1),a_eta=1,b_eta=1,a_ga=1,b_ga=1,a_tau=1,b_tau=1,
beta_iter=11,phi_iter=11,beta_cand=c(1,1),phi_cand=1,beta_sig0=10,
x_user=NULL,total=30,burnin=10,thin=1,conf.int=0.95,seed=1)
```

---

clusterPIC_Z_DP　　　　　　*Mixed effects PH model for clustered partly interval-censored data*

---

## Description

Fit a Bayesian semiparametric mixed effects PH model for clustered partly interval-censored data with random effects for one or more predictors. Each random effect follows a DP mixture distribution.

## Usage

```
clusterPIC_Z_DP(L, R, y, xcov, IC, scale.designX, scaled, zcov, area, binary, I, order,
knots, grids, a_eta, b_eta, a_ga, b_ga, a_alpha, b_alpha, H,
a_tau_star, b_tau_star, beta_iter, phi_iter, beta_cand, phi_cand,
beta_sig0, x_user, total, burnin, thin, conf.int, seed)
```

## Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| zcov | The design matrix for the q random effects. |
| area | The vector of cluster ID. |
| binary | The vector indicating whether each covariate is binary. |
| I | The number of clusters. |

| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
|---|---|
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| a_alpha | The shape parameter of Gamma prior for alpha. |
| b_alpha | The rate parameter of Gamma prior for alpha. |
| H | The number of distinct components in DP mixture prior under blocked Gibbs sampler. |
| a_tau_star | The shape parameter of G_0 in DP mixture prior. |
| b_tau_star | The rate parameter of G_0 in DP mixture prior. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for phi_i. |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for beta_r. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for phi_i. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

## Details

The mixed effects PH model is:

$h(t_{ij}|x_{ij},z_{i})=h_{0}(t_{ij})exp(beta'x_{ij}+phi_{i}'z_{i})$,

for the jth subject in the ith cluster.

Each of the q random effects is sampled using MH algorithm separately.

## Value

a list containing the following elements:

| N | The sample size. |
|---|---|
| parbeta | A total by p matrix of MCMC draws of beta_r, r=1, ..., p. |
| parsurv0 | A total by length(grids) matrix, each row contains the baseline survival at grids from one iteration. |

| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| --- | --- |
| paralpha | A `total` by q vector of MCMC draws of `alpha`. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival function is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

## Examples

```
# Number of iterations set to very small for CRAN automatic testing
data(da4)
J=rep(1,nrow(da4))
zcov=cbind(J,da4[,4])
try8<-PICBayes(formula=Surv(L,R,type='interval2')~x1+x2,data=data.frame(da4),
model='clusterPIC_Z_DP',IC=da4[,7],scale.designX=TRUE,scaled=c(1,0),zcov=zcov,
area=da4[,6],binary=c(0,1),I=25,order=3,knots=c(0,2,6,max(da4[,1:2],na.rm=TRUE)+1),
grids=seq(0.1,10.1,by=0.1),a_eta=1,b_eta=1,a_ga=1,b_ga=1,a_alpha=1,b_alpha=1,H=5,
a_tau_star=1,b_tau_star=1,beta_iter=11,phi_iter=11,beta_cand=1,phi_cand=1,
beta_sig0=10,x_user=NULL,total=20,burnin=10,thin=1,conf.int=0.95,seed=1)
```

---

| coef.PICBayes | *Coef method for a PICBayes model* |
| --- | --- |

---

## Description

Extracts estimated regression coefficients.

## Usage

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

## Arguments

| object | The class PICBayes object. |
| --- | --- |
| ... | Other arguments if any. |

## Value

An object of class `coef`.

---

da1 *Partly interva-censored data*

---

## Description

A simulated partly interval-censored data set based on:

`lambda(t|x)=lambda_{0}(t)exp(x1+x2).`

## Usage

```
data(da1)
```

## Format

| | |
|---|---|
| L: | Left endpoints of observed time intervals. |
| R: | Right endpoints of observed time intervals. |
| y: | Censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| X1: | Covariate 1. |
| X2: | Covariate 2. |
| IC: | General interval-censored indicator: 1=general interval-censored, 0=exact. |
| ID: | Subject ID. |

---

da2 *Clustered partly interva-censored data*

---

## Description

A simulated clsutered partly interval-censored data set based on PH model with spatial frailty:

`lambda(t|x)=lambda_{0}(t)exp(x1+x2+phi).`

## Usage

```
data(da2)
```

## Format

L:      Left endpoints of observed time intervals.
R:      Right endpoints of observed time intervals.
y:      Censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact.
X1:     Covariate 1.
X2:     Covariate 2.
area:   Cluster ID.
IC:     General interval-censored indicator: 1=general interval-censored, 0=exact.
ID:     Subject ID.

---

da3                     *Clustered partly interva-censored data*

---

### Description

A simulated clsutered partly interval-censored data set based on PH model with random intercept:

`lambda(t|x)=lambda_{0}(t)exp(x1+x2+phi).`

### Usage

`data(da3)`

### Format

L:      Left endpoints of observed time intervals.
R:      Right endpoints of observed time intervals.
y:      Censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact.
X1:     Covariate 1.
X2:     Covariate 2.
area:   Cluster ID.
IC:     General interval-censored indicator: 1=general interval-censored, 0=exact.
ID:     Subject ID.

---

da4                          *Clustered partly interva-censored data*

---

### Description

A simulated clsutered partly interval-censored data set based on PH model with random intercept
and random effect for x2:

```
lambda(t|x)=lambda_{0}(t)exp(x1+x2+phi+phi_trt*x2).
```

### Usage

```
data(da4)
```

### Format

| | |
|---|---|
| L: | Left endpoints of observed time intervals. |
| R: | Right endpoints of observed time intervals. |
| y: | Censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| X1: | Covariate 1. |
| X2: | Covariate 2. |
| area: | Cluster ID. |
| IC: | General interval-censored indicator: 1=general interval-censored, 0=exact. |
| ID: | Subject ID. |

---

IC                          *PH model for general interval-censored data*

---

### Description

Fit a Bayesian semiparametric PH model to general interval-censored data.

### Usage

```
IC(L, R, y, xcov, IC, scale.designX, scaled, binary, order, knots, grids,
a_eta, b_eta, a_ga, b_ga, beta_iter, beta_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

**Arguments**

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| binary | The vector indicating whether each covariate is binary. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| beta_cand | The sd of the proposal normal distribution in the MH sampling for beta_r. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

**Details**

The baseline cumulative hazard is approximated by a linear combination of I-splines:

sum_{l=1}^{K}(gamma_l*b_l(t)).

For a binary prdictor, we sample e^{beta_r}, with Gamma prior.

The regression coefficient beta_r for a continuous predictor is sampled using MH algorithm. During the initial beta_iter iterations, sd of the proposal distribution is beta_cand. Afterwards, proposal sd is set to be the sd of available MCMC draws.

## Value

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A `total` by `p` matrix of MCMC draws of `beta_r`, r=1, ..., p. |
| parsurv0 | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival functions is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

## References

Pan, C., Cai, B., and Wang, L. (2020). A Bayesian approach for analyzing partly interval-censored data under the proportional hazards model. *Statistical Methods in Medical Research*,

DOI: 10.1177/0962280220921552.

---

| logLik.PICBayes | *LogLik method for a PICBayes model* |
|---|---|

---

## Description

The log-likelihood of the observed partly interval-censored data estimated by log pseudo-marginal likelihood.

## Usage

```
## S3 method for class 'PICBayes'
logLik(object, ...)
```

## Arguments

| | |
|---|---|
| object | Class PICBayes object. |
| ... | Other arguments if any. |

## Value

An object of class logLik.

---

mCRC                            *Colorectal cancer data*

---

## Description

A progression-free survival data set derived by the author from a phase 3 metastatic colorectal cancer clinical trial.

## Usage

```
data(mCRC)
```

## Format

| | |
|---|---|
| L: | Left endpoints of observed time intervals. |
| R: | Right endpoints of observed time intervals. |
| y: | Censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| TRT_C: | Treatment arm: 0 = FOLFIRI alone, 1 = Panitumumab + FOLFIRI. |
| KRAS_C: | Tumor KRAS mutation status: 0 = wild-type, 1 = mutant. |
| SITE: | Clinical site where a patient is treated. |
| IC: | General interval-censored indicator: 1=general interval-censored, 0=exact. |
| ID: | Subject ID. |

---

PIC                      *PH model for partly interval-censored data*

---

## Description

Fit a Bayesian semiparametric PH model to partly interval-censored data.

## Usage

```
PIC(L, R, y, xcov, IC, scale.designX, scaled, binary, order, knots, grids,
a_eta, b_eta, a_ga, b_ga, beta_iter, beta_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

## Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| binary | The vector indicating whether each covariate is binary: 1=binary, 0=not. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| beta_cand | The sd of the proposal normal distribution in the MH sampling for beta_r. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

## Details

The baseline cumulative hazard is approximated by a linear combination of I-splines:

sum_{l=1}^{K}(gamma_l*b_l(t)).

The baseline hazard is approximated by a linear combination of basis M-splines:

sum_{l=1}^{K}(gamma_l*M_l(t)).

For a binary prdictor, we sample e^{beta_r}, with Gamma prior.

The regression coefficient beta_r for a continuous predictor is sampled using MH algorithm. During the initial beta_iter iterations, sd of the proposal distribution is beta_cand. Afterwards, proposal sd is set to be the sd of available MCMC draws.

## Value

a list containing the following elements:

| | |
|---|---|
| N | The sample size. |
| parbeta | A `total` by p matrix of MCMC draws of beta_r, r=1, ..., p. |
| parsurv0 | A `total` by `length(grids)` matrix, each row contains the baseline survival at `grids` from one iteration. |
| parsurv | A `total` by `length(grids)*G` matrix, each row contains the survival at `grids` from one iteration. G is the number of sets of user-specified covariate values. |
| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival functions is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

## References

Pan, C., Cai, B., and Wang, L. (2020). A Bayesian approach for analyzing partly interval-censored data under the proportional hazards model. *Statistical Methods in Medical Research*,

DOI: 10.1177/0962280220921552.

## Examples

```
# Number of iterations set to very small for CRAN automatic testing
data(da1)
try1<-PICBayes(formula=Surv(L,R,type='interval2')~x1+x2,data=data.frame(da1),
model='PIC',IC=da1[,6],scale.designX=TRUE,scale=c(1,0),binary=c(0,1),
order=3,knots=c(0,2,6,max(da1[,1:2],na.rm=TRUE)+1),grids=seq(0.1,10.1,by=0.1),
a_eta=1,b_eta=1,a_ga=1,b_ga=1,beta_iter=11,beta_cand=1,beta_sig0=10,
x_user=NULL,total=60,burnin=10,thin=1,conf.int=0.95,seed=1)
```

---

PICBayes           *Bayesian models for partly interval-censored data and general interval-censored data*

---

### Description

Calls one of the 16 functions to fit the correspoinding model.

### Usage

```
PICBayes(L, ...)

## Default S3 method:
PICBayes(L,R,y,xcov,IC,model,scale.designX,scaled,xtrt,zcov,
area,binary,I,C,nn,order=3,knots,grids,a_eta=1,b_eta=1,a_ga=1,b_ga=1,a_lamb=1,
b_lamb=1,a_tau=1,b_tau=1,a_tau_trt=1,b_tau_trt=1,a_alpha=1,b_alpha=1,H=5,
a_tau_star=1,b_tau_star=1,a_alpha_trt=1,b_alpha_trt=1,H_trt=5,
a_tau_trt_star=1,b_tau_trt_star=1,beta_iter=1001,phi_iter=1001,
beta_cand,phi_cand,beta_sig0=10,x_user=NULL,
total=6000,burnin=1000,thin=1,conf.int=0.95,seed=1,...)

## S3 method for class 'formula'
PICBayes(formula, data, ...)
```

### Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| model | A character string specifying the type of model. See details. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| xtrt | The covariate that has a random effect. |
| zcov | The design matrix for the q random effects. |
| area | The vector of cluster ID. |
| I | The number of areas. |
| C | The adjacency matrix. |
| nn | The vector of number of neighbors for each area. |

| | |
|---|---|
| binary | The vector indicating whether each covariate is binary. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for `gamma_l`. |
| b_eta | The rate parameter of Gamma prior for `gamma_l`. |
| a_ga | The shape parameter of Gamma prior for `e^{beta_r}`. |
| b_ga | The rate parameter of Gamma prior for `e^{beta_r}`. |
| a_lamb | The shape parameter of Gamma prior for spatial precision `lambda`. |
| b_lamb | The rate parameter of Gamma prior for spatial precision `lambda`. |
| a_tau | The shape parameter of Gamma prior for random intercept precision `tau`. |
| b_tau | The rate parameter of Gamma prior for random intercept precision `tau`. |
| a_tau_trt | The shape parameter of Gamma prior for random treatment precision `tau_trt`. |
| b_tau_trt | The rate parameter of Gamma prior for random treatment precision `tau_trt`. |
| a_alpha | The shape parameter of Gamma prior for `alpha`. |
| b_alpha | The rate parameter of Gamma prior for `alpha`. |
| H | The number of distinct components in DP mixture prior under blocked Gibbs sampler. |
| a_tau_star | The shape parameter of `G_0` in DP mixture prior. |
| b_tau_star | The rate parameter of `G_0` in DP mixture prior. |
| a_alpha_trt | The shape parameter of Gamma prior for `alpha_trt`. |
| b_alpha_trt | The rate parameter of Gamma prior for `alpha_trt`. |
| H_trt | The number of distinct components in DP mixture prior under blocked Gibbs sampler for random treatment. |
| a_tau_trt_star | The shape parameter of `G_0` in DP mixture prior for random treatment. |
| b_tau_trt_star | The rate parameter of `G_0` in DP mixture prior for random treatment. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for `beta_r`. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for `phi_i`. |
| beta_cand | The sd of the proposal normal distribution in the MH sampling for `beta_r`. |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for `phi_i`. |
| beta_sig0 | The sd of the prior normal distribution for `beta_r`. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for `beta_r`. |
| seed | A user-specified random seed. |
| formula | A formula expression with the response returned by the Surv function in the survival package. |
| data | A data frame that contains the variables named in the formula argument. |
| ... | Other arguments if any. |

**Details**

Possible values are "PIC", "spatialPIC", "clusterPIC_int", "clusterPIC_int_DP", "clusterPIC_trt", "clusterPIC_trt_DP", "clusterPIC_Z", and "clusterPIC_Z_DP" for partly interval-censored data; and "IC", "spatialIC", "clusterIC_int", "clusterIC_int_DP", "clusterIC_trt", "clusterIC_trt_DP", "clusterIC_Z", and "clusterIC_Z_DP" for general interval-censored data.

**Value**

An object of class `PICBayes`. Refere to each specific function for its specific values.

**Author(s)**

Chun Pan

---

plot.PICBayes            *Plot method for a PICBayes model*

---

**Description**

Plot estimated baseline survival function at `grids`.

**Usage**

```
## S3 method for class 'PICBayes'
plot(x, y, ...)
```

**Arguments**

| | |
|---|---|
| x | A sequence of points (`grids`) where baseline survival probabilities are estimated. |
| y | Estiamted baseline survival at `grids`. |
| ... | Other arguments if any. |

**Value**

A plot of baseline survival function.

---

| spatialIC | *PH model for spatial general interval-censored data* |

---

### Description

Fit a Bayesian semiparametric PH model with spatial frailty for spatially dependent general interval-censored data.

### Usage

```
spatialIC(L, R, y, xcov, IC, scale.designX, scaled, area, binary, I, C, nn,
order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_lamb, b_lamb, beta_iter,
phi_iter, beta_cand, beta_sig0, x_user, total, burnin, thin, conf.int, seed)
```

### Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| area | The vector of area ID. |
| I | The number of areas. |
| C | The adjacency matrix. |
| nn | The vector of number of neighbors for each area. |
| binary | The vector indicating whether each covariate is binary. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |
| grids | A sequence of points at which baseline survival function is to be estimated. |
| a_eta | The shape parameter of Gamma prior for $gamma\_l$. |
| b_eta | The rate parameter of Gamma prior for $gamma\_l$. |
| a_ga | The shape parameter of Gamma prior for $e^{beta\_r}$. |
| b_ga | The rate parameter of Gamma prior for $e^{beta\_r}$. |
| a_lamb | The shape parameter of Gamma prior for spatial precision $lambda$. |
| b_lamb | The rate parameter of Gamma prior for spatial precision $lambda$. |

| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
|-----------|----------------------------------------------------------------------------------|
| phi_iter  | The number of initial iterations in the Metropolis-Hastings sampling for phi_i.  |
| beta_cand | The sd of the proposal normal distribution in the MH sampling for beta_r.        |
| beta_sig0 | The sd of the prior normal distribution for beta_r.                              |
| x_user    | The user-specified covariate vector at which to estimate survival function(s).   |
| total     | The number of total iterations.                                                  |
| burnin    | The number of burnin.                                                            |
| thin      | The frequency of thinning.                                                       |
| conf.int  | The confidence level of the CI for beta_r.                                       |
| seed      | A user-specified random seed.                                                    |

## Details

The baseline cumulative hazard is approximated by a linear combination of I-splines:

sum_{l=1}^{K}(gamma_l*b_l(t)).

For a binary prdictor, we sample e^{beta_r}, with Gamma prior.

The regression coefficient beta_r for a continuous predictor is sampled using MH algorithm. During the initial beta_iter iterations, sd of the proposal distribution is beta_cand. Afterwards, proposal sd is set to be the sd of available MCMC draws.

## Value

a list containing the following elements:

| N        | The sample size.                                                                                                                              |
|----------|---------------------------------------------------------------------------------------------------------------------------------------------|
| parbeta  | A total by p matrix of MCMC draws of beta_r, r=1, ..., p.                                                                                    |
| parsurv0 | A total by length(grids) matrix, each row contains the baseline survival at grids from one iteration.                                        |
| parsurv  | A total by length(grids)*G matrix, each row contains the survival at grids from one iteration. G is the number of sets of user-specified covariate values. |
| parphi   | A total by I matrix of MCMC draws of phi_i, i=1,...,I.                                                                                       |
| parlamb  | A total by 1 matrix of MCMC draws of lambda.                                                                                                 |
| coef     | A vector of regression coefficient estimates.                                                                                                |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates.                                                                  |
| coef_ci  | The credible intervals for the regression coefficients.                                                                                      |
| S0_m     | The estimated baseline survival at grids.                                                                                                    |
| S_m      | The estimated survival at grids with user-specified covariate values x_user.                                                                 |
| grids    | The sequance of points where baseline survival functions is estimated.                                                                       |
| DIC      | Deviance information criterion.                                                                                                              |
| NLLK     | Negative log pseudo-marginal likelihood.                                                                                                     |

## Author(s)

Chun Pan

## References

Pan, C. and Cai, B. (2020). A Bayesian model for spatial partly interval-censored data. *Communications in Statistics - Simulation and Computation*, DOI: 10.1080/03610918.2020.1839497.

---

spatialPIC                    *PH model for spatial partly interval-censored data*

---

## Description

Fit a Bayesian semiparametric PH model with spatial frailty for spatially dependent partly interval-censored data.

## Usage

```
spatialPIC(L, R, y, xcov, IC, scale.designX, scaled, area, binary, I,
C, nn, order, knots, grids, a_eta, b_eta, a_ga, b_ga, a_lamb, b_lamb,
beta_iter, phi_iter, beta_cand, beta_sig0, x_user,
total, burnin, thin, conf.int, seed)
```

## Arguments

| | |
|---|---|
| L | The vector of left endpoints of the observed time intervals. |
| R | The vector of right endponts of the observed time intervals. |
| y | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| xcov | The covariate matrix for the p predictors. |
| IC | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| scale.designX | The TRUE or FALSE indicator of whether or not to scale the design matrix X. |
| scaled | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| area | The vector of area ID. |
| I | The number of areas. |
| C | The adjacency matrix. |
| nn | The vector of number of neighbors for each area. |
| binary | The vector indicating whether each covariate is binary. |
| order | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| knots | A sequence of knots to define the basis I-splines. |

| grids | A sequence of points at which baseline survival function is to be estimated. |
|---|---|
| a_eta | The shape parameter of Gamma prior for gamma_l. |
| b_eta | The rate parameter of Gamma prior for gamma_l. |
| a_ga | The shape parameter of Gamma prior for e^{beta_r}. |
| b_ga | The rate parameter of Gamma prior for e^{beta_r}. |
| a_lamb | The shape parameter of Gamma prior for spatial precision lambda. |
| b_lamb | The rate parameter of Gamma prior for spatial precision lambda. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for beta_r. |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for phi_i. |
| beta_cand | The sd of the proposal normal distribution in the MH sampling for beta_r. |
| beta_sig0 | The sd of the prior normal distribution for beta_r. |
| x_user | The user-specified covariate vector at which to estimate survival function(s). |
| total | The number of total iterations. |
| burnin | The number of burnin. |
| thin | The frequency of thinning. |
| conf.int | The confidence level of the CI for beta_r. |
| seed | A user-specified random seed. |

## Details

The baseline cumulative hazard is approximated by a linear combination of I-splines:

sum_{l=1}^{K}(gamma_l*b_l(t)).

The baseline hazard is approximated by a linear combination of basis M-splines:

sum_{l=1}^{K}(gamma_l*M_l(t)).

For a binary prdictor, we sample e^{beta_r}, with Gamma prior.

The regression coefficient beta_r for a continuous predictor is sampled using MH algorithm. During the initial beta_iter iterations, sd of the proposal distribution is beta_cand. Afterwards, proposal sd is set to be the sd of available MCMC draws.

## Value

a list containing the following elements:

| N | The sample size. |
|---|---|
| parbeta | A total by p matrix of MCMC draws of beta_r, r=1, ..., p. |
| parsurv0 | A total by length(grids) matrix, each row contains the baseline survival at grids from one iteration. |
| parsurv | A total by length(grids)*G matrix, each row contains the survival at grids from one iteration. G is the number of sets of user-specified covariate values. |
| parphi | A total by I matrix of MCMC draws of phi_i, i=1,...,I. |
| parlamb | A total by 1 matrix of MCMC draws of lambda. |

| coef | A vector of regression coefficient estimates. |
| coef_ssd | A vector of sample standard deviations of regression coefficient estimates. |
| coef_ci | The credible intervals for the regression coefficients. |
| S0_m | The estimated baseline survival at `grids`. |
| S_m | The estimated survival at `grids` with user-specified covariate values `x_user`. |
| grids | The sequance of points where baseline survival functions is estimated. |
| DIC | Deviance information criterion. |
| NLLK | Negative log pseudo-marginal likelihood. |

## Author(s)

Chun Pan

## References

Pan, C. and Cai, B. (2020). A Bayesian model for spatial partly interval-censored data. *Communications in Statistics - Simulation and Computation*, DOI: 10.1080/03610918.2020.1839497.

## Examples

```
data(C)
data(da2)
nn<-apply(C,1,sum)
# Number of iterations set to very small for CRAN automatic testing
try2<-PICBayes(formula=Surv(L,R,type='interval2')~x1+x2,data=data.frame(da2),
model='spatialPIC',area=da2[,6],IC=da2[,7],scale.designX=TRUE,scale=c(1,0),
binary=c(0,1),I=46,C=C,nn=nn,order=3,knots=c(0,2,6,max(da2[,1:2],na.rm=TRUE)+1),
grids=seq(0.1,10.1,by=0.1),a_eta=1,b_eta=1,a_ga=1,b_ga=1,a_lamb=1,b_lamb=1,
beta_iter=11,phi_iter=11,beta_cand=1,beta_sig0=10,
x_user=NULL,total=50,burnin=10,thin=1,conf.int=0.95,seed=1)
```

---

| summary.PICBayes | *Summary method for a PICBayes model* |

---

## Description

Present output from function [PICBayes](#).

## Usage

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

## Arguments

| object | Class PICBayes object. |
| ... | Other arguments if any. |

## Value

An object of class summary.

---

SurvtoLR                        *Transform Surv object to data matrix with L and R columns*

---

## Description

Take a [Surv](Surv) object and transforms it into a data matrix with two columns, L and R, representing the left and right points of observed time intervals. For right-censored data, R = NA.

## Usage

```
SurvtoLR(x)
```

## Arguments

x                        a [Surv](Surv) object

## Details

The input Surv object should be in the form of Surv(L,R,type='interval2'), where R = NA for right-censored data.

## Value

A data matrix with two variables:

L                        left-points of observed time intervals

R                        right-points of observed time intervals

## References

Michael P. Fay, Pamela A. Shaw (2010). Exact and Asymptotic Weighted Logrank Tests for Interval Censored Data: The interval R Package. *Journal of Statistical Software*, **36** 1-34.

## Examples

```
library(survival)
L<-c(45,6,0,46)
R<-c(NA,10,7,NA)
y<-Surv(L,R,type='interval2')
SurvtoLR(y)
```

# Index