

# Package ‘PICBayes’

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**Title** Bayesian Models for Partly 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](https://doi.org/10.1177/0962280220921552)>), PH model with spatial frailty to spatially dependent PIC data (Pan and Cai (2021) <[doi:10.1080/03610918.2020.1839497](https://doi.org/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

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## Contents

PICBayes-package	2
C	3
clusterIC_int	3
clusterIC_int_DP	5
clusterIC_trt	7
clusterIC_trt_DP	10
clusterIC_Z	12
clusterIC_Z_DP	14
clusterPIC_int	16
clusterPIC_int_DP	19
clusterPIC_trt	21

clusterPIC_trt_DP . . . . .	24
clusterPIC_Z . . . . .	27
clusterPIC_Z_DP . . . . .	29
coef.PICBayes . . . . .	31
da1 . . . . .	32
da2 . . . . .	32
da3 . . . . .	33
da4 . . . . .	34
IC . . . . .	34
logLik.PICBayes . . . . .	36
mCRC . . . . .	37
PIC . . . . .	37
PICBayes . . . . .	40
plot.PICBayes . . . . .	42
spatialIC . . . . .	43
spatialPIC . . . . .	45
summary.PICBayes . . . . .	47
SurvtoLR . . . . .	48
<b>Index</b>	<b>49</b>

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PICBayes-package	<i>Bayesian Models for Partly Interval-Censored Data and General Interval-Censored Data</i>
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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

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C

*Adjacency matrix of 46 South Carolina counties***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)

clusterIC\_int

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

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

**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 endpoints 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_1.
b_eta	The rate parameter of Gamma prior for gamma_1.
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 predictor, 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 $\phi_i$ , $i=1,\dots,I$ .
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 $x_{\text{user}}$ .
grids	The sequence 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	<i>PH model with random intercept for clustered general interval-censored data</i>
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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 endpoints 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_1.
b_eta	The rate parameter of Gamma prior for gamma_1.
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 $G_{\emptyset}$ in DP mixture prior.
b_tau_star	The rate parameter of $G_{\emptyset}$ 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:

$$\phi_i \sim N(0, \tau_i^{-1})$$

$$\tau_i \sim G$$

$$G \sim DP(\alpha, G_{\emptyset})$$

$G_{\{0\}} = \text{Gamma}(a_{\text{tau\_star}}, b_{\text{tau\_star}})$

$\text{tau}_{\{h\}}^{\{*\}} \sim G_{\{0\}}, h=1, \dots, H$

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 $\beta_r, r=1, \dots, p$ .
parsurv0	A total by $\text{length}(\text{grids})$ matrix, each row contains the baseline survival at grids from one iteration.
parsurv	A total by $\text{length}(\text{grids}) * G$ 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 $\phi_i, i=1, \dots, I$ .
partau_star	A total by H matrix of MCMC draws of $\text{tau\_star}$ .
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 $x_{\text{user}}$ .
grids	The sequence 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	<i>PH model with random intercept and random treatment for clustered general interval-censored data</i>
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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  $N(\theta, \text{tau}^{\{-1\}})$ .

**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 endpoints 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 <sub>1</sub> .
b_eta	The rate parameter of Gamma prior for gamma <sub>1</sub> .
a_ga	The shape parameter of Gamma prior for e <sup>{beta<sub>r</sub>}</sup> .
b_ga	The rate parameter of Gamma prior for e <sup>{beta<sub>r</sub>}</sup> .
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 <sub>trt</sub> .
b_tau_trt	The rate parameter of Gamma prior for random treatment precision tau <sub>trt</sub> .
beta_iter	The number of initial iterations in the Metropolis-Hastings sampling for beta <sub>r</sub> .
phi_iter	The number of initial iterations in the Metropolis-Hastings sampling for phi <sub>i</sub> .
beta_cand	The sd of the proposal normal distribution in the initial MH sampling for beta <sub>r</sub> .
phi_cand	The sd of the proposal normal distribution in the initial MH sampling for phi <sub>i</sub> .
beta_sig0	The sd of the prior normal distribution for beta <sub>r</sub> .
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 predictor, 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 $\beta_r$ , $r=1, \dots, p$ .
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 $\phi_i$ , $i=1, \dots, I$ .
parphi_trt	A total by I matrix of MCMC draws of $\phi_{trt_i}$ , $i=1, \dots, I$ .
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 sequence 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	<i>PH model with random intercept and random treatment for clustered general interval-censored data</i>
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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 endpoints 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 $\gamma_{1l}$ .
b_eta	The rate parameter of Gamma prior for $\gamma_{1l}$ .
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 $G_{\emptyset}$ in DP mixture prior.
b_tau_star	The rate parameter of $G_{\emptyset}$ 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 $G_{\emptyset}$ in DP mixture prior for random treatment.
b_tau_trt_star	The rate parameter of $G_{\emptyset}$ 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:

$$\phi_i \sim N(0, \tau_i^{-1})$$

$$\tau_i \sim G$$

$$G \sim DP(\alpha, G_{\emptyset})$$

$$G_{\emptyset} = \text{Gamma}(a_{\tau\_star}, b_{\tau\_star})$$

$$\tau_{\{h\}^*} \sim G_{\emptyset}, h=1, \dots, H$$

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 sequence of points where baseline survival function is estimated.
DIC	Deviance information criterion.
NLLK	Negative log pseudo-marginal likelihood.

**Author(s)**

Chun Pan

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  $N(\theta, \tau^{-1})$ .

**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 endpoints 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 $\gamma_{1.}$ .
b_eta	The rate parameter of Gamma prior for $\gamma_{1.}$ .
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  $j$ th subject in the  $i$ th 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 $\beta_r$ , $r=1, \dots, p$ .
parsurv0	A total by $\text{length}(\text{grids})$ matrix, each row contains the baseline survival at grids from one iteration.
parsurv	A total by $\text{length}(\text{grids}) * G$ 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 $x_{\text{user}}$ .
grids	The sequence 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\_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 endpoints 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 $\gamma_{1l}$ .
b_eta	The rate parameter of Gamma prior for $\gamma_{1l}$ .
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 $G_{\theta}$ in DP mixture prior.
b_tau_star	The rate parameter of $G_{\theta}$ 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  $j$ th subject in the  $i$ th 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 $\beta_r$ , $r=1, \dots, p$ .
parsurv0	A total by <code>length(grids)</code> matrix, each row contains the baseline survival at grids from one iteration.
parsurv	A total by <code>length(grids)*G</code> 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 sequence 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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clusterPIC_int	<i>PH model with random intercept for clustered partly interval-censored data</i>
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**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 endpoints 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 $\gamma_{1i}$ .
b_eta	The rate parameter of Gamma prior for $\gamma_{1i}$ .
a_ga	The shape parameter of Gamma prior for $e^{\beta_{ri}}$ .
b_ga	The rate parameter of Gamma prior for $e^{\beta_{ri}}$ .
a_tau	The shape parameter of Gamma prior for random intercept precision $\tau_i$ .
b_tau	The rate parameter of Gamma prior for random intercept precision $\tau_i$ .
beta_iter	The number of initial iterations in the Metropolis-Hastings sampling for $\beta_{ri}$ .
phi_iter	The number of initial iterations in the Metropolis-Hastings sampling for $\phi_{ii}$ .
beta_cand	The sd of the proposal normal distribution in the initial MH sampling for $\beta_{ri}$ .
phi_cand	The sd of the proposal normal distribution in the initial MH sampling for $\phi_{ii}$ .
beta_sig0	The sd of the prior normal distribution for $\beta_{ri}$ .
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 $\beta_{ri}$ .
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 predictor, 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 $\beta_r$ , $r=1, \dots, p$ .
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 $\phi_i$ , $i=1, \dots, I$ .
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 sequence 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)
```

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clusterPIC_int_DP	<i>PH model with random intercept for clustered partly interval-censored data data</i>
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### 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 endpoints 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 <sub>1</sub> .
b_eta	The rate parameter of Gamma prior for gamma <sub>1</sub> .
a_ga	The shape parameter of Gamma prior for e <sup>{beta<sub>r</sub>}</sup> .
b_ga	The rate parameter of Gamma prior for e <sup>{beta<sub>r</sub>}</sup> .

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 $G_{\emptyset}$ in DP mixture prior.
b_tau_star	The rate parameter of $G_{\emptyset}$ 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:

$$\phi_i \sim N(0, \tau_i^{-1})$$

$$\tau_i \sim G$$

$$G \sim DP(\alpha, G_{\emptyset})$$

$$G_{\emptyset} = \text{Gamma}(a_{\tau\_star}, b_{\tau\_star})$$

$$\tau_h \sim G_{\emptyset}, h=1, \dots, H$$

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 sequence 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)
```

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clusterPIC_trt	<i>PH model with random intercept and random treatment for clustered partly interval-censored data</i>
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**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  $N(\theta, \tau^{-1})$ .

**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 endpoints 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 <sub>1</sub> .
b_eta	The rate parameter of Gamma prior for gamma <sub>1</sub> .
a_ga	The shape parameter of Gamma prior for e <sup>{beta<sub>r</sub>}</sup> .
b_ga	The rate parameter of Gamma prior for e <sup>{beta<sub>r</sub>}</sup> .
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 <sub>trt</sub> .
b_tau_trt	The rate parameter of Gamma prior for random treatment precision tau <sub>trt</sub> .
beta_iter	The number of initial iterations in the Metropolis-Hastings sampling for beta <sub>r</sub> .
phi_iter	The number of initial iterations in the Metropolis-Hastings sampling for phi <sub>i</sub> .
beta_cand	The sd of the proposal normal distribution in the initial MH sampling for beta <sub>r</sub> .
phi_cand	The sd of the proposal normal distribution in the initial MH sampling for phi <sub>i</sub> .
beta_sig0	The sd of the prior normal distribution for beta <sub>r</sub> .
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 <sub>r</sub> .
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 predictor, 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 $\beta_r$ , $r=1, \dots, p$ .
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 $\phi_i$ , $i=1, \dots, I$ .
parphi_trt	A total by I matrix of MCMC draws of $\phi_{trt_i}$ , $i=1, \dots, I$ .
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 sequence 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)
```

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clusterPIC_trt_DP	<i>PH model with random intercept and random treatment for clustered partly interval-censored data</i>
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**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  $N(\theta, \tau^{-1})$ .

**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 endpoints 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_1.
b_eta	The rate parameter of Gamma prior for gamma_1.
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 $G_{\theta}$ in DP mixture prior.
b_tau_star	The rate parameter of $G_{\theta}$ 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 $G_{\theta}$ in DP mixture prior for random treatment.
b_tau_trt_star	The rate parameter of $G_{\theta}$ 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:

$$\phi_i \sim N(0, \tau_i^{-1})$$

$$\tau_i \sim G$$

$$G \sim DP(\alpha, G_{\theta})$$

$$G_{\theta} = \text{Gamma}(a_{\tau\_star}, b_{\tau\_star})$$

$$\tau_{\{h\}^*} \sim G_{\theta}, h=1, \dots, H$$

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 $\beta_r$ , $r=1, \dots, p$ .
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 $\phi_i$ , $i=1, \dots, I$ .
parphi_trt	A total by I matrix of MCMC draws of $\phi_{trt_i}$ , $i=1, \dots, I$ .
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 sequence 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 endpoints 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 $\gamma_1$ .
b_eta	The rate parameter of Gamma prior for $\gamma_1$ .
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  $j$ th subject in the  $i$ th 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, $r=1, \dots, p$ .
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 sequence 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 endpoints 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_1.
b_eta	The rate parameter of Gamma prior for gamma_1.
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 $G_{\theta}$ in DP mixture prior.
b_tau_star	The rate parameter of $G_{\theta}$ 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:

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

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 sequence 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	<i>Partly interval-censored data</i>
-----	--------------------------------------

---

**Description**

A simulated partly interval-censored data set based on:

$$\lambda(t|x) = \lambda_{\{0\}}(t) \exp(x_1 + x_2).$$

**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	<i>Clustered partly interval-censored data</i>
-----	--

---

**Description**

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

$$\lambda(t|x) = \lambda_{\{0\}}(t) \exp(x_1 + x_2 + \phi).$$

**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 interval-censored data*


---

### Description

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

$$\lambda(t|x) = \lambda_{\{0\}}(t) \exp(x_1 + x_2 + \phi).$$

### 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 interval-censored data*


---

### Description

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

$$\lambda(t|x) = \lambda_{\{0\}}(t) \exp(x_1 + x_2 + \phi + \phi_{trt} * x_2).$$

### 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 endpoints 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 $\gamma_{1l}$ .
b_eta	The rate parameter of Gamma prior for $\gamma_{1l}$ .
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:

$$\sum_{l=1}^K (\gamma_{1l} * b_{1l}(t)).$$

For a binary predictor, 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 $\beta_r, r=1, \dots, p$ .
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 sequence 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 endpoints 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_1.
b_eta	The rate parameter of Gamma prior for gamma_1.
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 predictor, 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 $\beta_r$ , $r=1, \dots, p$ .
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 $x_{\text{user}}$ .
grids	The sequence 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 corresponding 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 endpoints 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 $\gamma_{1l}$ .
b_eta	The rate parameter of Gamma prior for $\gamma_{1l}$ .
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 $G_{\emptyset}$ in DP mixture prior.
b_tau_star	The rate parameter of $G_{\emptyset}$ 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 $G_{\emptyset}$ in DP mixture prior for random treatment.
b_tau_trt_star	The rate parameter of $G_{\emptyset}$ 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 endpoints 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 $\gamma_{1l}$ .
b_eta	The rate parameter of Gamma prior for $\gamma_{1l}$ .
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 predictor, 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 sequence 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 endpoints 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 $\gamma_{l=1}$ .
b_eta	The rate parameter of Gamma prior for $\gamma_{l=1}$ .
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:

$$\sum_{l=1}^K (\gamma_{l=1} * b_l(t)).$$

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

$$\sum_{l=1}^K (\gamma_{l=1} * M_l(t)).$$

For a binary predictor, 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 $\beta_r$ , $r=1, \dots, p$ .
parsurv0	A total by $\text{length}(\text{grids})$ matrix, each row contains the baseline survival at grids from one iteration.
parsurv	A total by $\text{length}(\text{grids}) * G$ 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 $\phi_i$ , $i=1, \dots, I$ .
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 sequence 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](#) 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](#) 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

C, [3](#)  
clusterIC\_int, [3](#)  
clusterIC\_int\_DP, [5](#)  
clusterIC\_trt, [7](#)  
clusterIC\_trt\_DP, [10](#)  
clusterIC\_Z, [12](#)  
clusterIC\_Z\_DP, [14](#)  
clusterPIC\_int, [16](#)  
clusterPIC\_int\_DP, [19](#)  
clusterPIC\_trt, [21](#)  
clusterPIC\_trt\_DP, [24](#)  
clusterPIC\_Z, [27](#)  
clusterPIC\_Z\_DP, [29](#)  
coef.PICBayes, [31](#)

da1, [32](#)  
da2, [32](#)  
da3, [33](#)  
da4, [34](#)

IC, [34](#)

logLik.PICBayes, [36](#)

mCRC, [37](#)

PIC, [37](#)  
PICBayes, [40](#), [47](#)  
PICBayes-package, [2](#)  
plot.PICBayes, [42](#)

spatialIC, [43](#)  
spatialPIC, [45](#)  
summary.PICBayes, [47](#)  
Surv, [48](#)  
SurvtoLR, [48](#)