

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)

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

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^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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^{β_r} , with Gamma prior.

The regression coefficient β_r for a continuous predictor and random intercept ϕ_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 ϕ_i .

Value

a list containing the following elements:

| | |
|---------|--|
| N | The sample size. |
| parbeta | A total by p matrix of MCMC draws of β_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 ϕ_i , $i=1,\dots,I$. |
| partau | A total by 1 vector of MCMC draws of τ . |
| 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_int_DP | <i>PH model with random intercept for clustered general interval-censored data</i> |
|------------------|--|

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^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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 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 $\phi_i, i=1, \dots, I$. |
| 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

| | |
|---------------|---|
| clusterIC_trt | <i>PH model with random intercept and random treatment for clustered general interval-censored data</i> |
|---------------|---|

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 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 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. |
| 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 predictor, we sample e^{β_r} , with Gamma prior.

The regression coefficient β_r for a continuous predictor, random intercept ϕ_i , and random treatment ϕ_{trt_i} are sampled using MH algorithm. During the initial β_{iter} iterations, sd of the proposal distribution is β_{cand} . Afterwards, proposal sd is set to be the sd of available MCMC draws. Same method for ϕ_i and ϕ_{trt_i} .

Value

a list containing the following elements:

| | |
|------------|--|
| N | The sample size. |
| parbeta | A total by p matrix of MCMC draws of β_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 ϕ_i , $i=1, \dots, I$. |
| parphi_trt | A total by I matrix of MCMC draws of ϕ_{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

| | |
|------------------|---|
| clusterIC_trt_DP | <i>PH model with random intercept and random treatment for clustered general interval-censored data</i> |
|------------------|---|

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 γ_{1l} . |
| b_eta | The rate parameter of Gamma prior for γ_{1l} . |
| a_ga | The shape parameter of Gamma prior for e^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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 β_r . |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for ϕ_i . |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for β_r . |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for ϕ_i . |
| beta_sig0 | The sd of the prior normal distribution for β_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 β_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 β_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_{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_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 γ_{1l} . |
| b_eta | The rate parameter of Gamma prior for γ_{1l} . |
| a_ga | The shape parameter of Gamma prior for e^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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_{θ} in DP mixture prior. |
| b_tau_star | The rate parameter of G_{θ} in DP mixture prior. |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for β_r . |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for ϕ_i . |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for β_r . |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for ϕ_i . |
| beta_sig0 | The sd of the prior normal distribution for β_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 β_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 β_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 q vector of MCMC draws of α . |
| 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

| | |
|----------------|---|
| clusterPIC_int | <i>PH model with random intercept for clustered partly interval-censored data</i> |
|----------------|---|

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 γ_{1i} . |
| b_eta | The rate parameter of Gamma prior for γ_{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 τ_i . |
| b_tau | The rate parameter of Gamma prior for random intercept precision τ_i . |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for β_{ri} . |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for ϕ_{ii} . |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for β_{ri} . |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for ϕ_{ii} . |
| beta_sig0 | The sd of the prior normal distribution for β_{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 β_{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^{β_r} , with Gamma prior.

The regression coefficient β_r for a continuous predictor and random intercept ϕ_i are sampled using MH algorithm. During the initial β_{iter} iterations, sd of the proposal distribution is β_{cand} . Afterwards, proposal sd is set to be the sd of available MCMC draws. Same method for ϕ_i .

Value

a list containing the following elements:

| | |
|----------|--|
| N | The sample size. |
| parbeta | A total by p matrix of MCMC draws of β_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 ϕ_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)
```

| | |
|-------------------|--|
| clusterPIC_int_DP | <i>PH model with random intercept for clustered partly interval-censored data data</i> |
|-------------------|--|

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 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:

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

$$\tau_i \sim G$$

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

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

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

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)
```

| | |
|----------------|--|
| clusterPIC_trt | <i>PH model with random intercept and random treatment for clustered partly interval-censored data</i> |
|----------------|--|

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 $\gamma_{1.}$. |
| b_eta | The rate parameter of Gamma prior for $\gamma_{1.}$. |
| a_ga | The shape parameter of Gamma prior for e^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_r} . |
| a_tau | The shape parameter of Gamma prior for random intercept precision τ . |
| b_tau | The rate parameter of Gamma prior for random intercept precision τ . |
| a_tau_trt | The shape parameter of Gamma prior for random treatment precision τ_{trt} . |
| b_tau_trt | The rate parameter of Gamma prior for random treatment precision τ_{trt} . |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for β_r . |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for ϕ_i . |
| beta_cand | The sd of the proposal normal distribution in the initial MH sampling for β_r . |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for ϕ_i . |
| beta_sig0 | The sd of the prior normal distribution for β_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 β_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^{β_r} , with Gamma prior.

The regression coefficient β_r for a continuous predictor, random intercept ϕ_i , and random treatment ϕ_{trt_i} are sampled using MH algorithm. During the initial β_{iter} iterations, sd of the proposal distribution is β_{cand} . Afterwards, proposal sd is set to be the sd of available MCMC draws. Same method for ϕ_i and ϕ_{trt_i} .

Value

a list containing the following elements:

| | |
|------------|--|
| N | The sample size. |
| parbeta | A total by p matrix of MCMC draws of β_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 ϕ_i , $i=1, \dots, I$. |
| parphi_trt | A total by I matrix of MCMC draws of ϕ_{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)
```

| | |
|-------------------|--|
| clusterPIC_trt_DP | <i>PH model with random intercept and random treatment for clustered partly interval-censored data</i> |
|-------------------|--|

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^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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_{θ} in DP mixture prior. |
| b_tau_star | The rate parameter of G_{θ} 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_{θ} in DP mixture prior for random treatment. |
| b_tau_trt_star | The rate parameter of G_{θ} 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 β_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 ϕ_i , $i=1, \dots, I$. |
| parphi_trt | A total by I matrix of MCMC draws of ϕ_{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 γ_{1l} . |
| b_eta | The rate parameter of Gamma prior for γ_{1l} . |
| a_ga | The shape parameter of Gamma prior for e^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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 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^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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_{θ} in DP mixture prior. |
| b_tau_star | The rate parameter of G_{θ} 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 x_2 :

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

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_1. |
| b_eta | The rate parameter of Gamma prior for gamma_1. |
| a_ga | The shape parameter of Gamma prior for e^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_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 predictor, we sample e^{β_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 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.

| | |
|----------------------------|---|
| <code>y</code> | The vector of censoring indicator: 0=left-censored, 1=interval-censored, 2=right-censored, 3=exact. |
| <code>xcov</code> | The covariate matrix for the p predictors. |
| <code>IC</code> | The vector of general interval-censored indicator: 1=general interval-censored, 0=exact. |
| <code>scale.designX</code> | The TRUE or FALSE indicator of whether or not to scale the design matrix X . |
| <code>scaled</code> | The vector indicating whether each covariate is to be scaled: 1=to be scaled, 0=not. |
| <code>binary</code> | The vector indicating whether each covariate is binary: 1=binary, 0=not. |
| <code>order</code> | The degree of basis I-splines: 1=linear, 2=quadratic, 3=cubic, etc. |
| <code>knots</code> | A sequence of knots to define the basis I-splines. |
| <code>grids</code> | A sequence of points at which baseline survival function is to be estimated. |
| <code>a_eta</code> | The shape parameter of Gamma prior for γ_{l1} . |
| <code>b_eta</code> | The rate parameter of Gamma prior for γ_{l1} . |
| <code>a_ga</code> | The shape parameter of Gamma prior for e^{β_r} . |
| <code>b_ga</code> | The rate parameter of Gamma prior for e^{β_r} . |
| <code>beta_iter</code> | The number of initial iterations in the Metropolis-Hastings sampling for β_r . |
| <code>beta_cand</code> | The sd of the proposal normal distribution in the MH sampling for β_r . |
| <code>beta_sig0</code> | The sd of the prior normal distribution for β_r . |
| <code>x_user</code> | The user-specified covariate vector at which to estimate survival function(s). |
| <code>total</code> | The number of total iterations. |
| <code>burnin</code> | The number of burnin. |
| <code>thin</code> | The frequency of thinning. |
| <code>conf.int</code> | The confidence level of the CI for β_r . |
| <code>seed</code> | A user-specified random seed. |

Details

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

$$\sum_{l=1}^K (\gamma_{l1} * b_{l1}(t)).$$

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

$$\sum_{l=1}^K (\gamma_{l1} * M_{l1}(t)).$$

For a binary predictor, we sample e^{β_r} , with Gamma prior.

The regression coefficient β_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 β_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.

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 γ_{1l} . |
| b_eta | The rate parameter of Gamma prior for γ_{1l} . |
| a_ga | The shape parameter of Gamma prior for e^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_r} . |
| a_lamb | The shape parameter of Gamma prior for spatial precision λ . |
| b_lamb | The rate parameter of Gamma prior for spatial precision λ . |
| a_tau | The shape parameter of Gamma prior for random intercept precision τ . |
| b_tau | The rate parameter of Gamma prior for random intercept precision τ . |
| a_tau_trt | The shape parameter of Gamma prior for random treatment precision τ_{trt} . |
| b_tau_trt | The rate parameter of Gamma prior for random treatment precision τ_{trt} . |
| a_alpha | The shape parameter of Gamma prior for α . |
| b_alpha | The rate parameter of Gamma prior for α . |
| 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 α_{trt} . |
| b_alpha_trt | The rate parameter of Gamma prior for α_{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 β_r . |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for ϕ_i . |
| beta_cand | The sd of the proposal normal distribution in the MH sampling for β_r . |
| phi_cand | The sd of the proposal normal distribution in the initial MH sampling for ϕ_i . |
| beta_sig0 | The sd of the prior normal distribution for β_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 β_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 γ_{1l} . |
| b_eta | The rate parameter of Gamma prior for γ_{1l} . |
| a_ga | The shape parameter of Gamma prior for e^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_r} . |
| a_lamb | The shape parameter of Gamma prior for spatial precision λ . |
| b_lamb | The rate parameter of Gamma prior for spatial precision λ . |

| | |
|-----------|--|
| 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^{β_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^{β_r} . |
| b_ga | The rate parameter of Gamma prior for e^{β_r} . |
| a_lamb | The shape parameter of Gamma prior for spatial precision λ . |
| b_lamb | The rate parameter of Gamma prior for spatial precision λ . |
| beta_iter | The number of initial iterations in the Metropolis-Hastings sampling for β_r . |
| phi_iter | The number of initial iterations in the Metropolis-Hastings sampling for ϕ_i . |
| beta_cand | The sd of the proposal normal distribution in the MH sampling for β_r . |
| beta_sig0 | The sd of the prior normal distribution for β_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 β_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^{β_r} , with Gamma prior.

The regression coefficient β_r for a continuous predictor is sampled using MH algorithm. During the initial β_iter iterations, sd of the proposal distribution is β_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 β_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 ϕ_i , $i=1, \dots, I$. |
| parlamb | A total by 1 matrix of MCMC draws of λ . |

| | |
|----------|--|
| 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)
```


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