

# Package ‘BayesFBHborrow’

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**Title** Bayesian Dynamic Borrowing with Flexible Baseline Hazard Function

**Version** 2.0.1

**Description** Allows Bayesian borrowing from a historical dataset for time-to-event data. A flexible baseline hazard function is achieved via a piecewise exponential likelihood with time varying split points and smoothing prior on the historic baseline hazards. The method is described in Scott and Lewin (2024)  [<doi:10.48550/arXiv.2401.06082>](https://doi.org/10.48550/arXiv.2401.06082).

**License** Apache License ( $\geq 2$ )

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<code>.beta.MH.RW.glm</code>	<i>Beta MH RW sampler from freq PEM fit</i>
------------------------------	---

---

**Description**

Sample beta from RW sampler

**Usage**

`.beta.MH.RW.glm(df, beta, beta_count, cprop_beta)`

**Arguments**

<code>df</code>	Data frame with indicators
<code>beta</code>	vector of parameters
<code>beta_count</code>	count number of accepted proposals
<code>cprop_beta</code>	proposal scalar

**Value**

beta, either old or new move

---

<code>.beta_MH_MALA</code>	<i>Proposal beta with a Metropolis Adjusted Langevin (MALA)</i>
----------------------------	---

---

**Description**

Proposal beta with a Metropolis Adjusted Langevin (MALA)

**Usage**

`.beta_MH_MALA(df, beta, bp, cprop_beta, beta_count)`

**Arguments**

df	Data frame with indicators
beta	vector of parameters
bp	number of covariates
cprop_beta	proposal variance standard deviation
beta_count	count number of accepts

**Value**

updated beta vector

---

<i>.beta_MH_NR</i>	<i>Newton Raphson MH move</i>
--------------------	-------------------------------

---

**Description**

Sample beta from RW sampler

**Usage**

```
.beta_MH_NR(df, beta, bp, cprop_beta, beta_count)
```

**Arguments**

df	Data frame with indicators
beta	vector of parameters
bp	number of covariates
cprop_beta	proposal scalar
beta_count	count number of accepts

**Value**

updated beta

---

.beta\_MH\_RW                      *Beta Metropolis-Hastings Random walk move*

---

**Description**

Update beta via a Metropolis-Hastings Random Walk move

**Usage**

.beta\_MH\_RW(df, beta, bp, cprop\_beta, beta\_count)

**Arguments**

df                      data.frame from dataframe\_fun()  
beta                    beta values  
bp                      number of covariates  
cprop\_beta            hyperparameter for beta proposal standard deviation  
beta\_count            number of moves done for beta

**Value**

beta, either old or new move

---

.beta\_mom                      *Mean for MALA using derivative for beta proposal*

---

**Description**

Mean for MALA using derivative for beta proposal

**Usage**

.beta\_mom(df, k, beta, bp, cprop\_beta)

**Arguments**

df                      Data frame with indicators  
k                        index for beta  
beta                    vector of parameters  
bp                      number of covariates  
cprop\_beta            proposal standard dev

**Value**

proposal mean

---

.beta_mom.NR.fun	<i>First and second derivative of target for mode and variance of proposal</i>
------------------	--

---

**Description**

First and second derivative of target for mode and variance of proposal

**Usage**

```
.beta_mom.NR.fun(df, k, beta, bp, cprop_beta)
```

**Arguments**

df	Data frame with indicators
k	index
beta	vector of parameters
bp	number of covariates
cprom_beta	proposal variance standard deviation

**Value**

First and second derivative mode and variance

---

.birth_move	<i>Birth move in RJMCMC</i>
-------------	-----------------------------

---

**Description**

Calculates new values of x when proposing another split point, based on a weighted mean, as  $x_{\text{new}}/x \leftarrow (1-U)/U$

**Usage**

```
.birth_move(U, sj, s_star, sjm1, x, j)
```

**Arguments**

U	uniform random number
sj	upcoming split point location, j
s_star	new split point location, *
sjm1	previous split point location, j-1
x	vector of parameter values, length J + 1
j	split point

**Value**

vector with adjusted parameter values after additional split point, length J + 2

---

.dataframe\_fun            *Create data.frame for piecewise exponential models*

---

**Description**

Construct a split data.frame for updated split points

**Usage**

.dataframe\_fun(Y, I, X, s, lambda, bp, J)

**Arguments**

- Y                    time-to-event
- I                    censor indicator
- X                    design Matrix
- s                    split point locations, including start and end (length J + 2)
- lambda            baseline Hazards (length J+1)
- bp                   number of covariates
- J                    number of split points

**Value**

data.frame with columns c(tstart, id, X1,..., Xp, Y, I, lambda)

---

.death\_move            *Death move in RJMCMC*

---

**Description**

Calculates new values of x when proposing the death of a split point

**Usage**

.death\_move(sjp1, sj, sjm1, x, j)

**Arguments**

sjp1	upcoming split point location, $J + 1$
sj	split point location to be removed, $j$
sjm1	previous split point location, $j-1$
x	vector of parameter values, length $J + 1$
j	split point

**Value**

vector with adjusted parameter values after removal of split point, length  $J$

---

<code>.glmFit</code>	<i>Fit frequentist piecewise exponential model for MLE and information matrix of beta</i>
----------------------	---

---

**Description**

Compute MLE for PEM

**Usage**

```
.glmFit(df)
```

**Arguments**

df	Data frame with time-to-event, censoring indicator and covariates
----	---

**Value**

beta MLE and inverse of information matrix

---

<code>.ICAR_calc</code>	<i>Calculate covariance matrix in the MVN-ICAR</i>
-------------------------	--

---

**Description**

Calculate covariance matrix in the MVN-ICAR

**Usage**

```
.ICAR_calc(s, J, clam)
```



**Arguments**

- s split points,  $J + 2$
- J number of split points
- clam controls neighbor interactions, in range (0, 1)

**Value**

$\text{Sigma}_s = (I - W)^{-1} * Q, W, Q$

---

.input\_check                    *Input checker*

---

**Description**

Checks inputs before Gibbs sampler is run

**Usage**

```
.input_check(  
  Y,  
  Y_0,  
  X,  
  X_0,  
  tuning_parameters,  
  initial_values = NULL,  
  hyperparameters  
)
```

**Arguments**

- Y current time-to-event data
- Y\_0 historical time-to-event data
- X design Matrix
- X\_0 design Matrix for historical data
- tuning\_parameters list of tuning parameters
- initial\_values list of initial values (optional)
- hyperparameters list of hyperparameters

**Value**

a print statement

---

`.J_RJMCMC`*RJMCMC (with Bayesian Borrowing)*

---

**Description**

Metropolis-Hastings Green Reversible Jump move, with Bayesian Borrowing

**Usage**

```
.J_RJMCMC(  
  df_hist,  
  df_curr,  
  Y,  
  Y_0,  
  I,  
  I_0,  
  X,  
  X_0,  
  lambda,  
  lambda_0,  
  beta,  
  beta_0,  
  mu,  
  sigma2,  
  tau,  
  s,  
  J,  
  Jmax,  
  bp,  
  bp_0,  
  clam_smooth,  
  a_tau = NULL,  
  b_tau = NULL,  
  c_tau = NULL,  
  d_tau = NULL,  
  type,  
  p_0 = NULL,  
  phi,  
  pi_b,  
  maxSj  
)
```

**Arguments**

<code>df_hist</code>	data_frame containing historical data.
<code>df_curr</code>	data_frame containing current trial data.

Y	data.
Y_0	historical data.
I	censoring indicator.
I_0	historical trial censoring indicator.
X	design matrix.
X_0	historical trial design matrix.
lambda	baseline hazard.
lambda_0	historical trial baseline hazard.
beta	current trial parameters.
beta_0	historical trial parameters.
mu	prior mean for baseline hazard.
sigma2	prior variance hyperparameter for baseline hazard.
tau	borrowing parameter.
s	split point locations, $J + 2$ .
J	number of split points.
Jmax	maximum number of split points.
bp	number of covariates in current trial.
bp_0	number of covariates in historical trial.
clam_smooth	neighbor interactions, in range (0, 1), for ICAR update.
a_tau	tau hyperparameter.
b_tau	tau hyperparameter.
c_tau	tau hyperparameter.
d_tau	tau hyperparameter.
type	choice of borrowing, "mix", "uni", or any other string for borrowing on every baseline hazard without mixture.
p_0	mixture ratio.
phi	J hyperparameter.
pi_b	probability of birth move.
maxSj	maximal time point, either current or historic.

**Value**

list of proposed J and s, with adjusted values of lambda, lambda\_0, tau, Sigma\_s, and data\_frames for historical and current trial data.

---

*.J\_RJMCMC\_NoBorrow*      *RJMCMC (without Bayesian Borrowing)*

---

### **Description**

Metropolis-Hastings Green Reversible Jump move, without Bayesian Borrowing

### **Usage**

```
.J_RJMCMC_NoBorrow(  
  df,  
  Y_0,  
  I_0,  
  X_0,  
  lambda_0,  
  beta_0,  
  mu,  
  sigma2,  
  s,  
  J,  
  Jmax,  
  bp_0,  
  clam_smooth,  
  phi,  
  pi_b  
)
```

### **Arguments**

<code>df</code>	data_frame
<code>Y_0</code>	data
<code>I_0</code>	censoring indicator
<code>X_0</code>	design matrix
<code>lambda_0</code>	baseline hazard
<code>beta_0</code>	historical trial parameters
<code>mu</code>	prior mean for baseline hazard
<code>sigma2</code>	prior variance hyperparameter for baseline hazard
<code>s</code>	split point locations, $J + 2$
<code>J</code>	number of split points
<code>Jmax</code>	maximum number of split points
<code>bp_0</code>	number of covariates in historical trial
<code>clam_smooth</code>	neighbor interactions, in range (0, 1), for ICAR update
<code>phi</code>	J hyperparameter
<code>pi_b</code>	probability of birth move

**Value**

list of proposed J and s, with adjusted values of lambda, lambda\_0, tau, Sigma\_s, and data\_frames for historical and current trial data

---

.lambda_0_MH_cp	<i>Lambda_0 MH step, proposal from conditional conjugate posterior</i>
-----------------	--

---

**Description**

Lambda\_0 MH step, proposal from conditional conjugate posterior

**Usage**

```
.lambda_0_MH_cp(
  df_hist,
  Y_0,
  I_0,
  X_0 = NULL,
  s,
  beta_0 = NULL,
  mu,
  sigma2,
  lambda,
  lambda_0,
  tau,
  bp_0 = 0,
  J,
  clam,
  a_lam = 0.01,
  b_lam = 0.01,
  lambda_0_count = 0,
  lambda_0_move = 0
)
```

**Arguments**

- df\_hist            data.frame from dataframe\_fun()
- Y\_0                historical trial data
- I\_0                historical trial censoring indicator
- X\_0                historical trial design matrix
- s                  split point locations, (J+2)
- beta\_0            parameter value for historical covariates
- mu                 prior mean for baseline hazard
- sigma2            prior variance hyperparameter for baseline hazard

lambda	baseline hazard
lambda_0	historical baseline hazard
tau	borrowing parameter
bp_0	number of covariates, length(beta_0)
J	number of split points
clam	controls neighbor interactions, in range (0, 1)
a_lam	lambda hyperparameter, default is 0.01
b_lam	lambda hyperparameter, default is 0.01
lambda_0_count	number of total moves for lambda_0
lambda_0_move	number of accepted moves for lambda_0

**Value**

list of updated (if accepted) lambda\_0 and data.frames, as well as the number of accepted moves

---

```
.lambda_0_MH_cp_NoBorrow
```

*Lambda\_0 MH step, proposal from conditional conjugate posterior*

---

**Description**

Lambda\_0 MH step, proposal from conditional conjugate posterior

**Usage**

```
.lambda_0_MH_cp_NoBorrow(
  df_hist,
  Y_0,
  I_0,
  X_0 = NULL,
  s,
  beta_0 = NULL,
  mu,
  sigma2,
  lambda_0,
  bp_0 = 0,
  J,
  clam,
  a_lam = 0.01,
  b_lam = 0.01,
  lambda_0_count = 0,
  lambda_0_move = 0
)
```

**Arguments**

<code>df_hist</code>	data.frame from <code>dataframe_fun()</code>
<code>Y_0</code>	historical trial data
<code>I_0</code>	historical trial censoring indicator
<code>X_0</code>	historical trial design matrix
<code>s</code>	split point locations, (J+2)
<code>beta_0</code>	parameter value for historical covariates
<code>mu</code>	prior mean for baseline hazard
<code>sigma2</code>	prior variance hyperparameter for baseline hazard
<code>lambda_0</code>	baseline hazard
<code>bp_0</code>	number of covariates, <code>length(beta_0)</code>
<code>J</code>	number of split points
<code>clam</code>	controls neighbor interactions, in range (0, 1)
<code>a_lam</code>	lambda hyperparameter, default is 0.01
<code>b_lam</code>	lambda hyperparameter, default is 0.01
<code>lambda_0_count</code>	number of total moves for <code>lambda_0</code>
<code>lambda_0_move</code>	number of accepted moves for <code>lambda_0</code>

**Value**

list of updated (if accepted) `lambda_0` and data.frames, as well as the number of accepted moves

---

<code>.lambda_conj_prop</code>	<i>Propose lambda from a gamma conditional conjugate posterior proposal</i>
--------------------------------	---

---

**Description**

Propose lambda from a gamma conditional conjugate posterior proposal

**Usage**

```
.lambda_conj_prop(df, beta, j, bp, alam = 0.01, blam = 0.01)
```

**Arguments**

<code>df</code>	data.frame from <code>dataframe_fun()</code>
<code>beta</code>	parameter value for beta
<code>j</code>	current split point
<code>bp</code>	number of covariates
<code>alam</code>	lambda hyperparameter, default set to 0.01
<code>blam</code>	lambda hyperparameter, default set to 0.01

**Value**

list containing proposed lambda, shape and rate parameters

---

<code>.lambda_MH_cp</code>	<i>Lambda MH step, proposal from conditional conjugate posterior</i>
----------------------------	--

---

**Description**

Lambda MH step, proposal from conditional conjugate posterior

**Usage**

```
.lambda_MH_cp(
  df_hist,
  df_curr,
  Y,
  I,
  X,
  s,
  beta,
  beta_0 = NULL,
  mu,
  sigma2,
  lambda,
  lambda_0,
  tau,
  bp,
  bp_0 = 0,
  J,
  a_lam = 0.01,
  b_lam = 0.01,
  lambda_move = 0,
  lambda_count = 0,
  alpha = 0.3
)
```

**Arguments**

<code>df_hist</code>	data.frame from <code>dataframe_fun()</code>
<code>df_curr</code>	data.frame from <code>dataframe_fun()</code>
<code>Y</code>	data
<code>I</code>	censoring indicator
<code>X</code>	design matrix
<code>s</code>	split point locations, $J + 2$
<code>beta</code>	parameter value for covariates



beta_0	parameter value for historical covariates
mu	prior mean for baseline hazard
sigma2	prior variance hyperparameter for baseline hazard
lambda	baseline hazard
lambda_0	historical baseline hazard
tau	borrowing parameter
bp	number of covariates, length(beta)
bp_0	number of covariates, length(beta_0)
J	number of split points
a_lam	lambda hyperparameter
b_lam	lambda hyperparameter
lambda_move	number of accepted lambda moves
lambda_count	total number of lambda moves
alpha	power parameter

**Value**

list of updated (if accepted) lambda and data.frames, as well as the number of accepted moves

---

.lgamma\_ratio                      *Calculate log gamma ratio for two different parameter values*

---

**Description**

Calculate log gamma ratio for two different parameter values

**Usage**

.lgamma\_ratio(x1, x2, shape, rate)

**Arguments**

x1	old parameter value
x2	proposed parameter value
shape	shape parameter
rate	rate parameter

**Value**

log gamma ratio

---

```
.llikelihood_ratio_beta
```

*Loglikelihood ratio calculation for beta parameters*

---

**Description**

Compute log likelihood for beta update

**Usage**

```
.llikelihood_ratio_beta(df, beta, beta_new)
```

**Arguments**

df	data.frame from dataframe_fun()
beta	beta values
beta_new	proposed beta values

**Value**

likelihood ratio

---

```
.llikelihood_ratio_lambda
```

*Log likelihood for lambda / lambda\_0 update*

---

**Description**

Log likelihood for lambda / lambda\_0 update

**Usage**

```
.llikelihood_ratio_lambda(df, df_prop, beta)
```

**Arguments**

df	data.frame from dataframe_fun()
df_prop	proposal data.frame
beta	parameter value for beta

**Value**

log likelihood ratio for lambda

---

.logsumexp                      *Computes the logarithmic sum of an exponential*

---

**Description**

Computes the logarithmic sum of an exponential

**Usage**

.logsumexp(x)

**Arguments**

x                      set of log probabilities

**Value**

the logarithmic sum of an exponential

---

.log\_likelihood                  *Log likelihood function*

---

**Description**

Log likelihood function

**Usage**

.log\_likelihood(df, beta)

**Arguments**

df                      data.frame containing data, time split points, and lambda  
beta                    coefficients for covariates

**Value**

log likelihood given lambdas and betas

---

`.lprop.dens.beta.NR`    *log Gaussian proposal density for Newton Raphson proposal*

---

**Description**

log Gaussian proposal density for Newton Raphson proposal

**Usage**

```
.lprop.dens.beta.NR(beta.prop, mu_old, var_old)
```

**Arguments**

<code>beta.prop</code>	beta proposal
<code>mu_old</code>	density mean
<code>var_old</code>	density variance

**Value**

log Gaussian density

---

`.lprop_density_beta`    *Log density of proposal for MALA*

---

**Description**

Log density of proposal for MALA

**Usage**

```
.lprop_density_beta(beta_prop, mu, cprop_beta)
```

**Arguments**

<code>beta_prop</code>	proposal beta
<code>mu</code>	mean of proposal distribution
<code>cprop_beta</code>	proposal standard dev

**Value**

log density

---

.ltau\_dprior                      *Calculate log density tau prior*

---

**Description**

Calculate log density tau prior

**Usage**

.ltau\_dprior(tau, a\_tau, b\_tau, c\_tau = NULL, d\_tau = NULL, p\_0 = NULL, type)

**Arguments**

tau	current value(s) of tau
a_tau	tau hyperparameter
b_tau	tau hyperparameter
c_tau	tau hyperparameter
d_tau	tau hyperparameter
p_0	mixture ratio
type	choice of borrowing, "mix", "uni", or any other string for borrowing on every baseline hazard without mixture

**Value**

log density of tau

---

.mu\_update                      *Calculate mu posterior update*

---

**Description**

Calculate mu posterior update

**Usage**

.mu\_update(Sigma\_s, lambda\_0, sigma2, J)

**Arguments**

Sigma_s	VCV matrix (j + 1) x (j + 1).
lambda_0	Baseline hazard.
sigma2	Scale variance.
J	Number of split point.

**Value**

mu update from Normal.

---

.normalize_prob	<i>Normalize a set of probability to one, using the the log-sum-exp trick</i>
-----------------	---

---

**Description**

Normalize a set of probability to one, using the the log-sum-exp trick

**Usage**

.normalize\_prob(x)

**Arguments**

x                    set of log probabilities

**Value**

normalized set of log probabilities

---

.nu_sigma_update	<i>Calculates nu and sigma2 for the Gaussian Markov random field prior, for a given split point j</i>
------------------	---

---

**Description**

Calculates nu and sigma2 for the Gaussian Markov random field prior, for a given split point j

**Usage**

.nu\_sigma\_update(j, lambda\_0, mu, sigma2, W, Q, J)

**Arguments**

j	current split point
lambda_0	historical baseline hazard
mu	prior mean for baseline hazard
sigma2	prior variance hyperparameter for baseline hazard
W	influence from right and left neighbors
Q	individual effect of neighborhood
J	number of split points

**Value**

nu and sigma2

---

.plot\_hist *Plot histogram from MCMC samples*

---

### Description

Plots a histogram of the given discrete MCMC samples

### Usage

```
.plot_hist(  
  samples,  
  title = "",  
  xlab = "Values",  
  ylab = "Frequency",  
  color = "black",  
  fill = "blue",  
  binwidth = 0.05,  
  scale_x = FALSE  
)
```

### Arguments

samples	data.frame containing the discrete MCMC samples
title	title of the plot, default is none
xlab	x-label of the plot, default is "Values"
ylab	y-label of the plot, default is "Frequency"
color	outline color for the bars, default is "black"
fill	fill color, default is "blue"
binwidth	width of the histogram bins, default is 0.5
scale_x	option to scale the x-axis, suitable for discrete samples, default is FALSE

### Value

a ggplot2 object

---

`.plot_matrix`*Plot smoothed baseline hazards*

---

**Description**

Plot mean and given quantiles of a matrix. Can also be used to plot derivatives of the baseline hazard, such as estimated cumulative hazard and survival function.

**Usage**

```
.plot_matrix(
  x_lim,
  y,
  percentiles = c(0.05, 0.95),
  title = "",
  xlab = "",
  ylab = "",
  color = "blue",
  fill = "blue",
  linewidth = 1,
  alpha = 0.2,
  y2 = NULL,
  color2 = "red",
  fill2 = "red"
)
```

**Arguments**

<code>x_lim</code>	time grid
<code>y</code>	samples
<code>percentiles</code>	percentiles to include in plot, default is <code>c(0.025, 0.975)</code>
<code>title</code>	optional, add title to plot
<code>xlab</code>	optional, add xlabel
<code>ylab</code>	optional, add ylabel
<code>color</code>	color of the mid line, default is blue
<code>fill</code>	color of the percentiles, default is blue
<code>linewidth</code>	thickness of the plotted line, default is 1
<code>alpha</code>	opacity of the percentiles, default is 0.2
<code>y2</code>	(optional) second set of samples for comparison
<code>color2</code>	(optional) color of the mid line, default is red
<code>fill2</code>	(optional) color of the percentiles, default is red

**Value**

a `ggplot2` object



---

.plot\_trace                      *Plot MCMC trace*

---

### Description

Creates a trace plot of given MCMC samples.

### Usage

```
.plot_trace(  
  x_lim,  
  samples,  
  title = "",  
  xlab = "",  
  ylab = "",  
  color = "black",  
  linewidth = 1  
)
```

### Arguments

x_lim	x-axis of the plot
samples	samples from MCMC
title	optional, add title to plot
xlab	optional, add xlabel
ylab	optional, add ylabel
color	color of the mid line, default is black
linewidth	thickness of the plotted line, default is 1

### Value

a ggplot2 object

---

.predictive\_hazard              *Predictive hazard from BayesFBHborrow object*

---

### Description

Predictive hazard from BayesFBHborrow object

### Usage

```
.predictive_hazard(out_slam, x_pred, beta_samples)
```

**Arguments**

out\_slam        samples from the smoothed baseline hazard  
 x\_pred         set of predictors to be used for calculating the predictive hazard  
 beta\_samples    samples of the covariates

**Value**

matrix of the predictive hazard

---

`.predictive_hazard_ratio`

*Predictive hazard ratio (HR) from BayesFBHborrow object*

---

**Description**

Predictive hazard ratio (HR) from BayesFBHborrow object

**Usage**

`.predictive_hazard_ratio(x_pred, beta_samples)`

**Arguments**

x\_pred         set of predictors to be used for calculating the predictive HR  
 beta\_samples    samples of the covariates

**Value**

posterior samples for expectation and credible intervals

---

`.predictive_survival`    *Predictive survival from BayesFBHborrow object*

---

**Description**

Predictive survival from BayesFBHborrow object

**Usage**

`.predictive_survival(grid_width, out_slam, x_pred, beta_samples)`

**Arguments**

`grid_width`      size of time step  
`out_slam`        samples from the smoothed baseline hazard  
`x_pred`          set of predictors to be used for calculating the predictive survival  
`beta_samples`    samples of the covariates

**Value**

matrix of the predictive survival

---

`.set_hyperparameters`    *Set tuning parameters*

---

**Description**

Set tuning parameters

**Usage**

`.set_hyperparameters(hyperparameters = NULL, model_choice)`

**Arguments**

`hyperparameters`      list of hyperparameters, could contain any combination of the listed hyperparameters  
`model_choice`        choice of model, could be either of 'mix', 'uni' or 'all'

**Value**

filled list of `tuning_parameters`

---

`.set_tuning_parameters`      *Set tuning parameters*

---

**Description**

Set tuning parameters

**Usage**

`.set_tuning_parameters(tuning_parameters = NULL, borrow, X, X_0 = NULL)`

**Arguments**

tuning_parameters	list of tuning_parameters, could contain any combination of the listed tuning parameters
borrow	choice of borrow, could be TRUE or FALSE
X	design matrix for concurrent trial
X_0	design matrix for historical trial

**Value**

filled list of tuning\_parameters

---

*.shuffle\_split\_point\_location*

*Metropolis Hastings step: shuffle the split point locations (with Bayesian borrowing)*

---

**Description**

Metropolis Hastings step: shuffle the split point locations (with Bayesian borrowing)

**Usage**

```
.shuffle_split_point_location(
  df_hist,
  df_curr,
  Y_0,
  I_0,
  X_0,
  lambda_0,
  beta_0,
  Y,
  I,
  X,
  lambda,
  beta,
  s,
  J,
  bp_0,
  bp,
  clam_smooth,
  maxSj
)
```

**Arguments**

<code>df_hist</code>	dataframe containing historical trial data and parameters
<code>df_curr</code>	data.frame containing current trial data and parameters
<code>Y_0</code>	historical trial data
<code>I_0</code>	historical trial censoring indicator
<code>X_0</code>	historical trial design matrix
<code>lambda_0</code>	historical baseline hazard
<code>beta_0</code>	historical parameter vector
<code>Y</code>	data
<code>I</code>	censoring indicator
<code>X</code>	design matrix
<code>lambda</code>	baseline hazard
<code>beta</code>	parameter vector
<code>s</code>	split point locations, $J + 2$
<code>J</code>	number of split points
<code>bp_0</code>	number of covariates in historical trial
<code>bp</code>	number of covariates in current trial
<code>clam_smooth</code>	neighbor interactions, in range (0, 1), for ICAR update
<code>maxSj</code>	the smallest of the maximal time points, $\min(\max(Y), \max(Y_0))$

**Value**

list containing new split points, updated `Sigma_s` and data.frames for historic and current trial data

---

`.shuffle_split_point_location_NoBorrow`

*Metropolis Hastings step: shuffle the split point locations (without Bayesian borrowing)*

---

**Description**

Metropolis Hastings step: shuffle the split point locations (without Bayesian borrowing)

**Usage**

```
.shuffle_split_point_location_NoBorrow(  
  df,  
  Y_0,  
  I_0,  
  X_0,  
  lambda_0,
```

```

    beta_0,
    s,
    J,
    bp_0,
    clam_smooth
)

```

**Arguments**

df	dataframe containing trial data and parameters
Y_0	data
I_0	censoring indicator
X_0	design matrix
lambda_0	baseline hazard
beta_0	parameter vector
s	split point locations, $J + 2$
J	number of split points
bp_0	number of covariates in historical trial
clam_smooth	neighbor interactions, in range (0, 1), for ICAR update

**Value**

list containing new split points, updated Sigma\_s and data.frames for historic and current trial data

---

<i>.sigma2_update</i>	<i>Calculate sigma2 posterior update</i>
-----------------------	--

---

**Description**

Calculate sigma2 posterior update

**Usage**

```
.sigma2_update(mu, lambda_0, Sigma_s, J, a_sigma, b_sigma)
```

**Arguments**

mu	mean.
lambda_0	Baseline hazard.
Sigma_s	VCV matrix $(j + 1) \times (j + 1)$ .
J	Number of split point.
a_sigma	Hyperparameter a.
b_sigma	Hyperparameter b.

**Value**

sigma2 draw from IG

---

.smooth\_hazard      *Smoothed hazard function*

---

**Description**

Smoothed hazard function

**Usage**

```
.smooth_hazard(out_slam, beta_samples = NULL)
```

**Arguments**

out\_slam      samples from GibbsMH of the baseline hazard  
beta\_samples    samples from GibbsMH from the treatment effect

**Value**

smoothed function for the baseline hazard

---

.smooth\_survival      *Smoothed survival curve*

---

**Description**

Smoothed survival curve

**Usage**

```
.smooth_survival(grid_width, out_slam, beta_samples = NULL)
```

**Arguments**

grid\_width      step size  
out\_slam      samples from GibbsMH of the baseline hazard  
beta\_samples    samples from GibbsMH from the treatment effect

**Value**

smoothed survival function

---

`.tau_update`*Sample tau from posterior distribution*

---

**Description**

Sample tau from posterior distribution

**Usage**

```
.tau_update(
  lambda_0,
  lambda,
  J,
  s,
  a_tau,
  b_tau,
  c_tau = NULL,
  d_tau = NULL,
  p_0 = NULL,
  type
)
```

**Arguments**

<code>lambda_0</code>	historical baseline hazard
<code>lambda</code>	baseline hazard
<code>J</code>	number of split points
<code>s</code>	split point locations, $J + 2$
<code>a_tau</code>	Inverse Gamma hyperparameter
<code>b_tau</code>	Inverse Gamma hyperparameter
<code>c_tau</code>	Inverse Gamma hyperparameter
<code>d_tau</code>	Inverse Gamma hyperparameter
<code>p_0</code>	mixture ratio
<code>type</code>	choice of borrowing, "mix", "uni", or any other string for borrowing on every baseline hazard without mixture

**Value**

list containing tau and new mixture ratio



---

 BayesFBHborrow

*BayesFBHborrow: Run MCMC for a piecewise exponential model*


---

## Description

Main function of the BayesFBHborrow package. This generic function calls the correct MCMC sampler for time-to-event Bayesian borrowing.

## Usage

```
BayesFBHborrow(
  data,
  data_hist = NULL,
  borrow = TRUE,
  model_choice,
  tuning_parameters,
  hyperparameters,
  lambda_hyperparameters,
  iter,
  warmup_iter,
  refresh,
  verbose,
  max_grid
)
```

## Arguments

<code>data</code>	data.frame containing atleast three vectors of "tte" (time-to-event) and "event" (censoring), and covariates "X_i" (where i should be a number/ indicator of the covariate)
<code>data_hist</code>	data.frame containing atleast two vectors of "tte" (time-to-event) and "event" (censoring), with the option of adding covariates named "X_0_i" (where i should be a number/ indicator of the covariate), for historical data
<code>borrow</code>	TRUE (default), will run the model with borrowing
<code>model_choice</code>	choice of which borrowing model to use out of 'mix', 'uni' or 'all'
<code>tuning_parameters</code>	list of "cprop_beta" ("cprop_beta_0" for historical data), "alpha", "Jmax", and "pi_b". Default is ("Jmax" = 5, "clam_smooth" = 0.8, "cprop_beta" = 0.5, "cprop_beta_0" = 0.5, "pi_b" = 0.5)
<code>hyperparameters</code>	list containing the hyperparameters c("a_tau", "b_tau", "c_tau", "d_tau", "type", "p_0", "a_sigma", "b_sigma"). Default is list("a_tau" = 1, "b_tau" = 1, "c_tau" = 1, "d_tau" = 0.001, "type" = "mix", "p_0" = 0.5, "a_sigma" = 2, "b_sigma" = 2, "phi" = 3)

lambda_hyperparameters	contains two hyperparameters (a_lambda and b_lambda) used for the update of lambda and lambda_0. Default is c(0.01, 0.01)
iter	number of iterations for MCMC sampler
warmup_iter	number of warmup iterations (burn-in) for MCMC sampler.
refresh	number of iterations between printed screen updates
verbose	FALSE (default), choice of output, if TRUE will output intermittent results into console
max_grid	grids size for the smoothed baseline hazard

**Value**

a nested list of two items, 'out' and 'plots'. The list 'out' will contain all the samples of the MCMC chain, as well as acceptance ratios. The latter, 'plots', contains plots (and data) of the smoothed baseline hazard, smoothed survival, a histogram of the sampled number of split points, and the trace plot of the treatment effect beta\_1

**Examples**

```
set.seed(123)
# Load the example data
data(piecewise_exp_cc, package = "BayesFBHborrow")
data(piecewise_exp_hist, package = "BayesFBHborrow")

# Set your tuning parameters
tuning_parameters <- list("Jmax" = 5,
                        "pi_b" = 0.5,
                        "cprop_beta" = 3.25,
                        "alpha" = 0.4)

# Set hyperparameters to default, with the borrowing model "mix"
out <- BayesFBHborrow(data = piecewise_exp_cc, data_hist = piecewise_exp_hist,
                    model_choice = 'mix', tuning_parameters = tuning_parameters,
                    iter = 2, warmup_iter = 0)

# Create a summary of the output
summary(out$out, estimator = "out_fixed")

# Plot the predictive curves for the treatment group
plots <- plot(out$out, out$out$time_grid, x_pred = c(1))
```

---

BayesFBHborrow.NoBorrow

*Run the MCMC sampler without Bayesian Borrowing*

---

**Description**

Main function of the BayesFBHborrow package. This generic function calls the correct MCMC sampler for time-to-event without Bayesian borrowing.

**Usage**

```
## S3 method for class 'NoBorrow'
BayesFBHborrow(
  data,
  data_hist = NULL,
  borrow = FALSE,
  model_choice = "no_borrow",
  tuning_parameters = NULL,
  hyperparameters = NULL,
  lambda_hyperparameters = list(a_lambda = 0.01, b_lambda = 0.01),
  iter = 2000,
  warmup_iter = 2000,
  refresh = 0,
  verbose = FALSE,
  max_grid = 2000
)
```

**Arguments**

<code>data</code>	data.frame containing atleast three vectors of "tte" (time-to-event) and "event" (event indicator), and covariates "X_i" (where i should be a number/ indicator of the covariate)
<code>data_hist</code>	NULL (not used)
<code>borrow</code>	FALSE (default), will run the model with borrowing
<code>model_choice</code>	'no_borrow' (default), for no borrowing
<code>tuning_parameters</code>	list of "cprop_beta", "Jmax", and "pi_b". Default is ("Jmax" = 5, "cprop_beta" = 0.5, "pi_b" = 0.5)
<code>hyperparameters</code>	list containing the hyperparameters c("a_sigma", "b_sigma", "phi", "clam_smooth"). Default is list("a_sigma" = 2, "b_sigma" = 2, "phi" = 3, "clam_smooth" = 0.8)
<code>lambda_hyperparameters</code>	contains two hyperparameters ("a_lambda" and "b_lambda") used for the update of lambda, default is c(0.01, 0.01)
<code>iter</code>	number of iterations for MCMC sampler. Default is 2000
<code>warmup_iter</code>	number of warmup iterations (burn-in) for MCMC sampler. Default is 2000
<code>refresh</code>	number of iterations between printed console updates. Default is 0
<code>verbose</code>	FALSE (default), choice of output, if TRUE will output intermittent results into console
<code>max_grid</code>	grid size for the smoothed baseline hazard. Default is 2000

**Value**

a nested list of two items, 'out' and 'plots'. The list 'out' will contain all the samples of the MCMC chain, as well as acceptance ratios. The latter, 'plots', contains plots (and data) of the smoothed baseline hazard, smoothed survival, a histogram of the sampled number of split points, and the trace plot of the treatment effect  $\beta_1$

**Examples**

```

set.seed(123)
# Load the example data
data(piecewise_exp_cc, package = "BayesFBHborrow")

# Set your tuning parameters
tuning_parameters <- list("Jmax" = 5,
                        "cprop_beta" = 3.25)

# Set initial values to default
out <- BayesFBHborrow(piecewise_exp_cc, NULL, borrow = FALSE,
                     tuning_parameters = tuning_parameters,
                     iter = 2, warmup_iter = 0)

```

---

BayesFBHborrow.WBorrow

*Run the MCMC sampler with Bayesian Borrowing*

---

**Description**

Main function of the BayesFBHborrow package. This generic function calls the correct MCMC sampler for time-to-event Bayesian borrowing.

**Usage**

```

## S3 method for class 'WBorrow'
BayesFBHborrow(
  data,
  data_hist,
  borrow = TRUE,
  model_choice = "mix",
  tuning_parameters = NULL,
  hyperparameters = NULL,
  lambda_hyperparameters = list(a_lambda = 0.01, b_lambda = 0.01),
  iter = 2000,
  warmup_iter = 2000,
  refresh = 0,
  verbose = FALSE,
  max_grid = 2000
)

```

**Arguments**

data	data.frame containing atleast three vectors called "tte" (time-to-event), "event" (censoring), and covariates "X_i" (where i should be a number/ indicator of the covariate)
------	--

<code>data_hist</code>	data.frame containing atleast two vectors called "tte" (time-to-event) and "event" (censoring), with the option of adding covariates named "X_0_i" (where i should be a number/ indicator of the covariate), for historical data
<code>borrow</code>	TRUE (default), will run the model with borrowing
<code>model_choice</code>	choice of which borrowing model to use out of 'mix', 'uni' or 'all'
<code>tuning_parameters</code>	list of "cprop_beta" ("cprop_beta_0" for historical data), "alpha", "Jmax", and "pi_b". Default is ("Jmax" = 5, "clam_smooth" = 0.8, "cprop_beta" = 0.5, "cprop_beta_0" = 0.5, "pi_b" = 0.5)
<code>hyperparameters</code>	list containing the hyperparameters c("a_tau", "b_tau", "c_tau", "d_tau", "type", "p_0", "a_sigma", "b_sigma"). Default is list("a_tau" = 1, "b_tau" = 1, "c_tau" = 1, "d_tau" = 0.001, "type" = "mix", "p_0" = 0.5, "a_sigma" = 2, "b_sigma" = 2, "phi" = 3)
<code>lambda_hyperparameters</code>	contains three hyperparameters (a_lambda, b_lambda) used for the update of lambda and lambda_0. Default is c(0.01, 0.01)
<code>iter</code>	number of iterations for MCMC sampler. Default is 2000
<code>warmup_iter</code>	number of warmup iterations (burn-in) for MCMC sampler. Default is 2000
<code>refresh</code>	number of iterations between printed console updates. Default is 0
<code>verbose</code>	FALSE (default), choice of output, if TRUE will output intermittent results into console
<code>max_grid</code>	grid size for the smoothed baseline hazard. Default is 2000

### Value

a nested list of two items, 'out' and 'plots'. The list 'out' will contain all the samples of the MCMC chain, as well as acceptance ratios. The latter, 'plots', contains plots (and data) of the smoothed baseline hazard, smoothed survival, a histogram of the sampled number of split points, and the trace plot of the treatment effect  $\beta_1$

### Examples

```
set.seed(123)
# Load the example data
data(piecewise_exp_cc, package = "BayesFBHborrow")
data(piecewise_exp_hist, package = "BayesFBHborrow")

# Set your tuning parameters
tuning_parameters <- list("Jmax" = 5,
                        "pi_b" = 0.5,
                        "cprop_beta" = 3.25,
                        "alpha" = 0.4)

# Set hyperparameters to default, with the borrowing model "mix"
out <- BayesFBHborrow(data = piecewise_exp_cc, data_hist = piecewise_exp_hist,
                     model_choice = 'mix', tuning_parameters = tuning_parameters,
```

```

iter = 2, warmup_iter = 0)

# Create a summary of the output
summary(out$out, estimator = "out_fixed")

# Plot the predictive curves for the treatment group
plots <- plot(out$out, out$out$time_grid, x_pred = c(1))

```

---

coef.BayesFBHborrow     *Extract mean posterior values*

---

### Description

S3 method for class "BayesFBHborrow", returns the mean posterior values for the fixed parameters

### Usage

```

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

```

### Arguments

object	MCMC sample object from BayesFBHborrow()
...	other arguments, see coef.default()

### Value

mean values of given samples

### Examples

```

data(weibull_cc, package = "BayesFBHborrow")

# Set your tuning parameters
tuning_parameters <- list("Jmax" = 5,
                          "pi_b" = 0.5,
                          "cprop_beta" = 0.5)

# run the MCMC sampler
out <- BayesFBHborrow(weibull_cc, NULL, tuning_parameters = tuning_parameters,
                      iter = 3, warmup_iter = 1)

# Plot the posterior mean values of the fixed parameters
coef(out$out)

```

---

GibbsMH

*S3 generic, calls the correct GibbsMH sampler*


---

### Description

An MCMC sampler for Bayesian borrowing with time-to-event data. We obtain a flexible baseline hazard function by making the split points random within a piecewise exponential model and using a Gaussian Markov random field prior to smooth the baseline hazards. Only calls the sampler and does not run any input checks. Best practice is to call `BayesFBHborrow()`, if the user is not familiar with the model at hand.

### Usage

```
GibbsMH(
  Y,
  I,
  X,
  Y_0 = NULL,
  I_0 = NULL,
  X_0 = NULL,
  tuning_parameters,
  hyperparameters,
  lambda_hyperparameters,
  iter,
  warmup_iter,
  refresh,
  max_grid
)
```

### Arguments

Y	data
I	event indicator
X	design matrix
Y_0	historical data, default is NULL
I_0	historical event indicator, default is NULL
X_0	historical design matrix, default is NULL
tuning_parameters	list of "cprop_beta" ("cprop_beta_0" for historical data), "alpha", "Jmax", and "pi_b".
hyperparameters	list containing the hyperparameters c("a_tau", "b_tau", "c_tau", "d_tau", "type", "p_0", "a_sigma", "b_sigma"). Default is list("a_tau" = 1, "b_tau" = 1, "c_tau" = 1, "d_tau" = 0.001, "type" = "mix", "p_0" = 0.5, "a_sigma" = 2, "b_sigma" = 2, "phi" = 3)

<code>lambda_hyperparameters</code>	contains two hyperparameters ( <code>a_lambda</code> and <code>b_lambda</code> ) used for the update of <code>lambda</code> and <code>lambda_0</code>
<code>iter</code>	number of iterations for MCMC sampler, excluding warmup, default is 2000
<code>warmup_iter</code>	number of warmup iterations (burn-in) for MCMC sampler, default is 2000
<code>refresh</code>	number of iterations between printed screen updates, default is 500
<code>max_grid</code>	grid size for the smoothed baseline hazard, default is 2000

### Value

depending on if the user wishes to borrow; returns a list with values after each iteration for parameters: `out_fixed` (`J`, `mu`, `sigma2`, `beta`), `lambda`, `lambda_0`, `tau`, `s`, as well as tuning values of the total number of accepts: `lambda_move`, `lambda_0_move` and `beta_move`. Also included is the `out_slam` which contains the shrunk estimate of the baseline hazard.

### Examples

```
set.seed(123)
# Load example data and set your initial values and hyper parameters
data(weibull_cc, package = "BayesFBHborrow")
data(weibull_hist, package = "BayesFBHborrow")

# The datasets consists of 3 (2) columns named "tte", "event" and "X"
# (only for concurrent). To explicitly run the sampler, extract the samples as
# following
Y <- weibull_cc$tte
I <- weibull_cc$event
X <- matrix(weibull_cc$X_trt)

Y_0 <- weibull_hist$tte
I_0 <- weibull_hist$event
X_0 <- NULL

# Specify hyperparameters and tuning parameters
hyper <- list("a_tau" = 1,
             "b_tau" = 0.001,
             "c_tau" = 1,
             "d_tau" = 1,
             "type" = 'all',
             "p_0" = 0.5,
             "a_sigma" = 2,
             "b_sigma" = 2,
             "clam_smooth" = 0.5,
             "phi" = 3)

tuning_parameters <- list("Jmax" = 5,
                        "pi_b" = 0.5,
                        "cprop_beta" = 0.5,
                        "alpha" = 0.4)

output <- GibbsMH(Y, I, X, Y_0, I_0, X_0,
```



```
tuning_parameters, hyper,
iter = 5, warmup_iter = 1)
```

---

GibbsMH.NoBorrow

*GibbsMH sampler, without Bayesian Borrowing*


---

## Description

An MCMC sampler for time-to-event data, without Bayesian Borrowing. We obtain a flexible baseline hazard function by making the split points random within a piecewise exponential model and using a Gaussian Markov random field prior to smooth the baseline hazards. Only calls the sampler and does not run any input checks. Best practice is to call `BayesFBHborrow()`, if the user is not familiar with the model at hand.

## Usage

```
## S3 method for class 'NoBorrow'
GibbsMH(
  Y,
  I,
  X = NULL,
  Y_0 = NULL,
  I_0 = NULL,
  X_0 = NULL,
  tuning_parameters,
  hyperparameters = list(a_sigma = 1, b_sigma = 1, phi = 3, clam_smooth = 0.8),
  lambda_hyperparameters = list(a_lambda = 0.01, b_lambda = 0.01),
  iter = 1500L,
  warmup_iter = 10L,
  refresh = 0,
  max_grid = 2000L
)
```

## Arguments

Y	data
I	event indicator
X	design matrix
Y_0	historical data, default is NULL
I_0	historical event indicator, default is NULL
X_0	historical design matrix, default is NULL
tuning_parameters	list of "cprop_beta", "Jmax", and "pi_b"
hyperparameters	list containing the hyperparameters c("a_sigma", "b_sigma", "clam_smooth", "phi").

lambda_hyperparameters	contains two hyperparameters (a_lambda and b_lambda) used for the update of lambda, default is c(0.01, 0.01)
iter	number of iterations for MCMC sampler, excluding warmup, default is 2000
warmup_iter	number of warmup iterations (burn-in) for MCMC sampler, default is 2000
refresh	number of iterations between printed screen updates, default is 500
max_grid	grid size for the smoothed baseline hazard, default is 2000

### Value

list with values after each iteration for parameters: out\_fixed (J, mu, sigma2, beta), lambda, s, as well as tuning values of the total number of accepts: lambda\_move and beta\_move. Also included is the out\_slam which contains the shrunk estimate of the baseline hazard.

### Examples

```
set.seed(123)
# Load example data and set your hyper parameters
data(weibull_cc, package = "BayesFBHborrow")
data(weibull_hist, package = "BayesFBHborrow")

# The datasets consists of 3 (2) columns named "tte", "event" and "X".
# To explicitly run the sampler, extract the samples as following
Y <- weibull_cc$tte
I <- weibull_cc$event
X <- matrix(weibull_cc$X_trt)

# Specify hyperparameters and tuning parameters
hyper <- list("a_sigma" = 2,
             "b_sigma" = 2,
             "clam_smooth" = 0.5,
             "phi" = 3)

tuning_parameters <- list("Jmax" = 5,
                        "pi_b" = 0.5,
                        "cprop_beta" = 0.5)

# Set initial values to 'NULL' for default settings
output <- GibbsMH(Y, I, X, NULL, NULL, NULL,
                 tuning_parameters = tuning_parameters, hyperparameters = hyper,
                 iter = 5, warmup_iter = 1)
```

## Description

An MCMC sampler for Bayesian borrowing with time-to-event data. We obtain a flexible baseline hazard function by making the split points random within a piecewise exponential model and using a Gaussian Markov random field prior to smooth the baseline hazards. Only calls the sampler and does not run any input checks. Best practice is to call `BayesFBHborrow()`, if the user is not familiar with the model at hand.

## Usage

```
## S3 method for class 'WBorrow'
GibbsMH(
  Y,
  I,
  X,
  Y_0,
  I_0,
  X_0,
  tuning_parameters = NULL,
  hyperparameters = list(a_tau = 1, b_tau = 0.001, c_tau = 1, d_tau = 1, type = "mix",
    p_0 = 0.8, a_sigma = 1, b_sigma = 1, phi = 3, clam_smooth = 0.8),
  lambda_hyperparameters = list(a_lambda = 0.01, b_lambda = 0.01),
  iter = 150L,
  warmup_iter = 10L,
  refresh = 0,
  max_grid = 2000L
)
```

## Arguments

Y	data
I	event indicator
X	design matrix
Y_0	historical data
I_0	historical event indicator
X_0	historical design matrix
tuning_parameters	list of "cprop_beta" ("cprop_beta_0" for historical data), "alpha", "Jmax", and "pi_b".
hyperparameters	list containing the hyperparameters c("a_tau", "b_tau", "c_tau", "d_tau", "type", "p_0", "a_sigma", "b_sigma"). Default is list("a_tau" = 1, "b_tau" = 1, "c_tau" = 1, "d_tau" = 0.001, "type" = "mix", "p_0" = 0.5, "a_sigma" = 2, "b_sigma" = 2, "phi" = 3)
lambda_hyperparameters	contains two hyperparameters (a_lambda and b_lambda) used for the update of lambda and lambda_0. Default is c(0.01, 0.01)

<code>iter</code>	number of iterations for MCMC sampler, excluding warmup, default is 2000
<code>warmup_iter</code>	number of warmup iterations (burn-in) for MCMC sampler, default is 2000
<code>refresh</code>	number of iterations between printed screen updates, default is 500
<code>max_grid</code>	grid size for the smoothed baseline hazard, default is 2000

### Value

list with values after each iteration for parameters: `out_fixed` ( $J$ ,  $\mu$ ,  $\sigma^2$ ,  $\beta$ ),  $\lambda$ ,  $\lambda_0$ ,  $\tau$ ,  $s$ , as well as tuning values of the total number of accepts: `lambda_move`, `lambda_0_move` and `beta_move`. Also included is the `out_slam` which contains the shrunk estimate of the baseline hazard.

### Examples

```
set.seed(123)
# Load example data and set your initial values and hyper parameters
data(weibull_cc, package = "BayesFBHborrow")
data(weibull_hist, package = "BayesFBHborrow")

# The datasets consists of 3 (2) columns named "tte", "event" and "X"
# (only for concurrent). To explicitly run the sampler, extract the samples as
# following
Y <- weibull_cc$tte
I <- weibull_cc$event
X <- matrix(weibull_cc$X_trt)

Y_0 <- weibull_hist$tte
I_0 <- weibull_hist$event
X_0 <- NULL

# Specify hyperparameters and tuning parameters
hyper <- list("a_tau" = 1,
             "b_tau" = 0.001,
             "c_tau" = 1,
             "d_tau" = 1,
             "type" = "all",
             "p_0" = 0.5,
             "a_sigma" = 2,
             "b_sigma" = 2,
             "clam_smooth" = 0.5,
             "phi" = 3)

tuning_parameters <- list("Jmax" = 5,
                        "pi_b" = 0.5,
                        "cprop_beta" = 0.5,
                        "alpha" = 0.4)

output <- GibbsMH(Y, I, X, Y_0, I_0, X_0, tuning_parameters = tuning_parameters,
                 hyperparameters = hyper, iter = 5, warmup_iter = 1)
```

---

group_summary	<i>Create group level data</i>
---------------	--------------------------------

---

## Description

Aggregate individual level data into group level data

## Usage

```
group_summary(Y, I, X, s)
```

## Arguments

Y	data
I	censoring indicator
X	design matrix
s	split points, $J + 2$

## Value

list of group level data

## Examples

```
set.seed(111)
# Load example data and set your initial values and hyper parameters
data(weibull_cc, package = "BayesFBHborrow")
data(weibull_hist, package = "BayesFBHborrow")

Y <- weibull_cc$tte
I <- weibull_cc$event
X <- weibull_cc$X_trt

# Say we want to know the group level data for the following split points
s <- quantile(Y, c(0, 0.45, 0.65, 1), names = FALSE)

group_summary(Y, I, X, s)
```

```
init_lambda_hyperparameters  
    Initialize lambda hyperparameters
```

---

### Description

Propose lambda hyperparameters for the choice of initial values for lambda

### Usage

```
init_lambda_hyperparameters(group_data, s, w = 0.5)
```

### Arguments

group_data	group level data
s	split points
w	weight

### Value

shape and rate for the estimated lambda distribution

### Examples

```
set.seed(111)  
# Load example data and set your initial values and hyper parameters  
data(weibull_cc, package = "BayesFBHborrow")  
data(weibull_hist, package = "BayesFBHborrow")  
  
Y <- weibull_cc$tte  
I <- weibull_cc$event  
X <- weibull_cc$X_trt  
  
# Say we want to know the group level data for the following split points  
s <- quantile(Y, c(0, 0.45, 0.65, 1), names = FALSE)  
  
group_data <- group_summary(Y, I, NULL, s)  
init_lambda_hyperparameters(group_data, s)
```

---

piecewise\_exp\_cc      *Example data, simulated from a piecewise exponential model.*

---

### Description

Data is simulated for a concurrent trial with three columns named "tte" (time-to-event), "event" (event indicator), and "X\_trt" (treatment indicator). It was simulated using the following parameters:

### Usage

```
data(piecewise_exp_cc)
```

### Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 250 rows and 3 columns.

### Examples

```
data(piecewise_exp_cc)
survival_model <- survival::survfit(survival::Surv(tte, event) ~ X_trt, data = piecewise_exp_cc)
line_colors <- c("blue", "red") # Adjust colors as needed
line_types <- 1:length(unique(piecewise_exp_cc$X_trt))
plot(survival_model, col = line_colors, lty = line_types,
     xlab = "Time (tte)", ylab = "Survival Probability",
     main = "Kaplan-Meier Survival Curves by Treatment")
```

---

piecewise\_exp\_hist      *Example data, simulated from a piecewise exponential model.*

---

### Description

Data is simulated for a historical trial with two columns named "tte" (time-to-event) and "event" (event indicator). It was simulated using the following parameters:

### Usage

```
data(piecewise_exp_hist)
```

### Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 100 rows and 2 columns.

**Examples**

```

data(piecewise_exp_cc)
data(piecewise_exp_hist)
piecewise_exp_hist$X_trt <- 0
survival_model <- survival::survfit(survival::Surv(tte, event) ~ X_trt,
                                   data = rbind(piecewise_exp_cc,
                                                piecewise_exp_hist))
line_colors <- c("blue", "red", "green") # Adjust colors as needed
line_types <- 1:length(unique(piecewise_exp_cc$X_trt))
plot(survival_model, col = line_colors, lty = line_types,
     xlab = "Time (tte)", ylab = "Survival Probability",
     main = "Kaplan-Meier Survival Curves by Treatment")

```

---

plot.BayesFBHborrow *Plot the MCMC results*

---

**Description**

S3 object which produces predictive probabilities of the survival, hazard, and hazard ratio for a given set of predictors

**Usage**

```

## S3 method for class 'BayesFBHborrow'
plot(x, x_lim, x_pred = NULL, ...)

```

**Arguments**

x	object of class "BayesFBHborrow" to be visualized
x_lim	x-axis to be used for plot, set to NULL to use default from MCMC sampling
x_pred	vector of chosen predictors
...	other plotting arguments, see .plot_matrix() for more information

**Value**

nested list of 'plots' (posterior predictive hazard, survival, and hazard ratio) as well as their samples.

**Examples**

```

data(weibull_cc, package = "BayesFBHborrow")

# Set your tuning parameters
tuning_parameters <- list("Jmax" = 5,
                         "pi_b" = 0.5,
                         "cprop_beta" = 0.5)

# run the MCMC sampler
out <- BayesFBHborrow(weibull_cc, NULL, tuning_parameters = tuning_parameters,

```



```

iter = 3, warmup_iter = 1)

# for the treatment group
plots <- plot(out$out, out$out$time_grid, x_pred = c(1))

```

---

```
summary.BayesFBHborrow
```

*Summarize fixed MCMC results*

---

## Description

S3 method for with borrowing. Returns summary of mean, median and given percentiles for the one dimensional parameters.

## Usage

```

## S3 method for class 'BayesFBHborrow'
summary(
  object,
  estimator = NULL,
  percentiles = c(0.025, 0.25, 0.75, 0.975),
  ...
)

```

## Arguments

object	MCMC sample object from BayesFBHborrow()
estimator	The type of estimator to summarize, could be "fixed", "lambda", "lambda_0" or "s". The default is NULL and will print a summary of the output list.
percentiles	Given percentiles to output, default is c(0.025, 0.25, 0.75, 0.975)
...	other arguments, see summary.default

## Value

summary of the given estimator

## Examples

```

data(piecewise_exp_cc, package = "BayesFBHborrow")

# Set your tuning parameters
tuning_parameters <- list("Jmax" = 5,
  "pi_b" = 0.5,
  "cprop_beta" = 0.5)

# run the MCMC sampler
out <- BayesFBHborrow(piecewise_exp_cc, NULL, tuning_parameters = tuning_parameters,
  iter = 3, warmup_iter = 1)

```

```
# Create a summary of the output
summary(out$out, estimator = "out_fixed")
```

---

```
weibull_cc
```

*Example data, simulated from a Weibull distribution.*

---

### Description

Data is simulated for a concurrent trial with three columns named "tte" (time-to-event), "event" (event indicator), and "X\_trt" (treatment indicator). It was simulated by drawing samples from a Weibull with  $\kappa = 1.5$  (shape) and  $\nu = 0.4$  (scale)

### Usage

```
data(weibull_cc)
```

### Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 250 rows and 3 columns.

### Examples

```
data(weibull_cc)
survival_model <- survival::survfit(survival::Surv(tte, event) ~ X_trt, data = weibull_cc)
line_colors <- c("blue", "red") # Adjust colors as needed
line_types <- 1:length(unique(weibull_cc$X_trt))
plot(survival_model, col = line_colors, lty = line_types,
     xlab = "Time (tte)", ylab = "Survival Probability",
     main = "Kaplan-Meier Survival Curves by Treatment")
```

---

```
weibull_hist
```

*Example data, simulated from a Weibull distribution*

---

### Description

Data is simulated for a historical trial with two columns named "tte" (time-to-event) and "event" (event indicator). It was simulated using the following parameters:

### Usage

```
data(weibull_hist)
```

### Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 100 rows and 2 columns.

**Examples**

```
data(weibull_cc)
data(weibull_hist)
weibull_hist$X_trt <- 0
survival_model <- survival::survfit(survival::Surv(tte, event) ~ X_trt,
                                   data = rbind(weibull_cc,
                                                weibull_hist))
line_colors <- c("blue", "red", "green") # Adjust colors as needed
line_types <- 1:length(unique(weibull_cc$X_trt))
plot(survival_model, col = line_colors, lty = line_types,
     xlab = "Time (tte)", ylab = "Survival Probability",
     main = "Kaplan-Meier Survival Curves by Treatment")
```

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