Package 'BayesFBHborrow'

July 18, 2026

Title Bayesian Dynamic Borrowing with Flexible Baseline Hazard Function

Version 2.0.14

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 (2026) <doi:10.1093/biostatistics/kxag006>, and a paper focused on the software is in Scott, Axillus, Lewin and Izmirlian (2026) <doi:10.48550/arXiv.2408.04327>.

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Contents

BayesFBHborrow 2
coef.BayesFBHborrow 7
Combine 8

genBFBHBdat 9
group_summary 11
init_lambda_hyperparameters 12
plot.BayesFBHborrow 13
read_haz_mcmc_smpls 15
summary.BayesFBHborrow 16
update.BayesFBHborrow 17
xifinder 20

Index **22**

`BayesFBHborrow` *Fit the Bayesian Flexible Baseline Hazard Model with Borrowing via MCMC/MH*

Description

Fits the Bayesian Flexible Baseline Hazard Model with Borrowing via MCMC/MH. Each sample in the Gibbs sampler is a piecewise exponential model, with prior over number and location of split points. Accommodates borrowing over a historical control arm as well as G-computation.

Usage

```
BayesFBHborrow(formula = NULL, data, data_hist = NULL, subset, na.action,
               CntlOnly = FALSE, model_choice = "mix", tuning_parameters = NULL,
               hyperparameters = NULL, iter = 1000, warmup_iter = 100,
               refresh = 0, verbose = FALSE, max_grid = 2000, standardise = TRUE,
               G_compute = FALSE, preprocess = TRUE, fnm_cnd_blh = "cnd_blh",
               fnm_mgnl_haz0 = "mgnl_haz0", fnm_mgnl_haz1 = "mgnl_haz1",
               dbg = FALSE, ...)
```

Arguments

`formula`	Optional but most likely preferred. When using the formula/data interface, specify the formula in the form typically used in other survival models e.g. Surv(TOS, Event) ~ Trt + Oth + Covs + etc The first listed covariate must be the treatment variable. The rest can be continuous or factor.
`data`	Required. The current trial/study data.frame with a treated and a control arm. For the formula/data interface, there is no naming convention for variables as the user specifies these with the formula. For the data only interface, you must name the time to event variable 'tte', and the event variable 'event'. All covariates including the treatment indicator must have the 'X_' prefix.
`data_hist`	When fitting the full model with borrowing, the historical controls data.frame with variables named to agree with the current trial data.frame specified in the 'data' argument. Comments above regarding the formula/data versus data only interface apply here as well.
`subset`	When using the formula/data interface, you may also use `subset` and `na.action` as you do in other statistical routines in R.

`na.action` When using the formula/data interface, you may also use `subset` and `na.action` as you do in other statistical routines in R.

`CntlOnly` Set to `TRUE` when running the model with on the historical controls dataset only. The default value is `FALSE`.

`model_choice` Borrowing method. Determine the borrowing per split point by specifying the option "mix" (default) for a mixture of inverse gamma densities or "uni" for a single inverse gamma density. Otherwise, determine the borrowing once for all split points by specifying the option "all".

`tuning_parameters`
list with components `cprop_beta` (`cprop_beta_0` for historical data), `a_lambda`, `b_lambda`, `pi_b` and `alpha`. Default is `list(cprop_beta=1.1, cprop_beta_0=1.1, a_lambda=0.01, b_lambda=0.01, pi_b=0.5, alpha=0.4)`. The most important for the user are `cprop_beta` and `cprop_beta_0`. Starting at the default values, the user must adjust these values up or down in a series of test runs (`iter=200`) so that `beta_acc_ratio` and `beta_0_acc_ratio` (in the output list) are between 0.3 and 0.4. The relationship between `cprop_beta` parameters and the acceptance ratios is inverse.

`hyperparameters`
list with components `beta_prior`, `beta_0_prior`, `a_tau`, `b_tau`, `c_tau`, `d_tau`, `type`, `p_0`, `a_sigma`, `b_sigma`, `phi`, `clam_smooth`, `Jmax`. Default is `list(beta_prior=10^2, beta_0_prior=10^2, a_tau=1, b_tau=0.001, c_tau=1, d_tau=5, type="mix", p_0=0.8, a_sigma=1, b_sigma=1, phi=3, clam_smooth=0.7, Jmax=5)`.

`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` Whether or not to print the progress to the console every `refresh` iterations. Defaults to `FALSE`.

`max_grid` Grid size for the smoothed baseline hazard. Default value is 2000.

`standardise` Whether or not to normalize the current trial baseline hazard to unity and apply the same normalization constant to the historical data. Default is `TRUE`.

`G_compute` If set to `TRUE` when treatment effect and pretreatment covariates are entered into the model (current trial only or current trial with borrowing), results are displayed as a marginal estimand computed via g-computation. This setting affects the behavior of the ‘coef‘ and ‘summary‘ methods and thus the ‘print‘ method. The default is `FALSE` which results in display of a conditional estimand.

`preprocess` Controls the interpretation of the ’baseline’ hazard consequent to recoding of the input dataset(s). When set to `TRUE`, all continuous variables will be centered at their mean over the dataset in the `data` argument, and factor variables will be centered to their mean under a hypothetical design having balanced levels for each factor. This defaults to `TRUE` and works with either the formula/data interface or the data only interface. If complete control over recoding is desired, one must use the data only interface together with `preprocess=FALSE`. This is the only way to include interactions.

`fnm_cnd_blh` Binary files generated during run time which are given a default name prefix with a random hex suffix. The collection of "snapped to common grid" samples

from the posterior distribution of the baseline hazards is a matrix of dimension `max_grid` by `iter`. Adding updated columns to this very large matrix would result in memory caching and for this reason, these are written out to binary files during the run of the MCMC, and then read back in during the final sumarization. This file is for the conditional baseline hazard. These files are available to the user for computing any functional of the posterior distribution. See the documentation for the `read_haz_mcmc_smpls` function.

`fnm_mgnl_haz0` Binary files generated during run time which are given a default name prefix with a random hex suffix. The collection of "snapped to common grid" samples from the posterior distribution of the baseline hazards is a matrix of dimension `max_grid` by `iter`. Adding updated columns to this very large matrix would result in memory caching and for this reason, these are written out to binary files during the run of the MCMC, and then read back in during the final sumarization. This file is for the control arm log-log marginal hazard. These files are available to the user for computing any functional of the posterior distribution. See the documentation for the `read_haz_mcmc_smpls` function.

`fnm_mgnl_haz1` Binary files generated during run time which are given a default name prefix with a random hex suffix. The collection of "snapped to common grid" samples from the posterior distribution of the baseline hazards is a matrix of dimension `max_grid` by `iter`. Adding updated columns to this very large matrix would result in memory caching and for this reason, these are written out to binary files during the run of the MCMC, and then read back in during the final sumarization. This file is for the treated arm log-log marginal hazard. These files are available to the user for computing any functional of the posterior distribution. See the documentation for the `read_haz_mcmc_smpls` function.

`dbg` When running in command line mode, set to `TRUE` in order to enable line by line debugging.

`...` Other arguments as needed.

Details

BayesFBHborrow implements our semiparametric Bayesian borrowing model allowing inferences on a current trial with commensurate Bayesian borrowing from a set of historical controls. The model supports covariate adjusted borrowing, which can reduce prior-data conflict and improve power when differences in outcomes are attributable to changes in covariate distribution. As the treatment effect estimator is non-collapsible, the marginal hazard ratio can be estimated via Bayesian G-computation, while still permitting an adjusted analysis to account for control group drift.

Value

`Y` Times on study in the 'data' argument data.frame, scaled to unit event rate.

`I` Event indicators in the 'data' argument data.frame

`X` Treatment indicator and pretreatment covariates in the 'data' argument data.frame, recoded if 'prepocess' is TRUE.

`Y_0` Times on study in the 'data_hist' argument data.frame, scaled to unit event rate.

`I_0` Event indicators in the 'data_hist' argument data.frame

X_0	Pretreatment covariates in the 'data_hist' argument data.frame, recoded if 'prepocess' is TRUE.
samples	An 'iter' by ncol(X) + 3*J + 4 matrix containing all post warmup samples from the MCMC sampler: the model coefficients, the number of split points, hyperparameters mu and sigma2, the locations of all split points and the values of the piecewise exponential hazards corresponding to the current trial and to the historical controls data distributions.
surv_dat	Median together with 95 percent credible interval of posterior samples of the per arm conditional hazards/survival functions, per arm marginal hazard/survival functions, and marginal treatment effect at each time point on the fine meshed grid of length 'max_grid'.
MTE_dens_dfs	kernel density estimates for samples of the posterior distribution of the marginal treatment effect at information fraction 25, 50, 75 and 100 percent.
T.if	Times on study at 25, 50, 75 and 100 percent information.
fnms	File names of binary files of snapped to fine meshed grid hazard function samples from the posterior. Provided for calculating custom functionals of the hazard function posterior distribution.
beta_acc_ratio	Metropolis-Hastings algorithm acceptance ratio for current data model coefficients. Find value of cprop_beta in tuning_parameters which results in this being between 0.30 and 0.40.
beta_0_acc_ratio	Metropolis-Hastings algorithm acceptance ratio for historical data model coefficients. Find value of cprop_beta in tuning_parameters which results in this being between 0.30 and 0.40.
call	The call which produced the object.

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

plot, summary, update methods for class "BayesFBHborrow" objects

Examples

```
n_cc_1 <- 200
n_cc_0 <- 100
n_hst <- 100
int_cc <- int_hst <- -log(3)
```

```
B_x_cc <- B_x_hst <- c(-0.3,0.5,0.25,-0.5)
B_trt <- log(0.55)

dat_lst <-
    genBFBHBdat(n_cc_1=200, n_cc_0=100, n_hst=100,
                B_trt=B_trt, B_x_cc=B_x_cc, B_x_hst=B_x_hst,
                int_cc=int_cc, int_hst=int_hst, shape=2,
                t_er=0.5, t_fin=1.5, X_fact_levs=3)

DAT_cc <- dat_lst$DAT_cc
DAT_hst <- dat_lst$DAT_hst

## using default settings for hyperparameters and tuning parameters
## formula interface
## cntls only; no cov's
  ## Not run:
    test_f0 <- BayesFBHborrow(Surv(tte, event)~1, data = DAT_hst,
                              CntlOnly=TRUE, iter = 200, warmup_iter = 50,
                              refresh = 0, verbose = FALSE)

    ## cntls only; with cov's
    test_f1 <- BayesFBHborrow(Surv(tte, event) ~ X_01 + X_02 + X_03,
                              data = DAT_hst, CntlOnly=TRUE,
                              iter = 200, warmup_iter = 50, refresh = 0,
                              verbose = FALSE)

    ##  trtd+cntls; w/o borrow; no cov's:
    test_f2 <- BayesFBHborrow(Surv(tte, event) ~ X_trt, data = DAT_cc,
                              iter = 200, warmup_iter = 50, refresh = 0,
                              verbose = FALSE)

    ## trtd+cntls; w borrow, no cov's:
    test_f3 <- BayesFBHborrow(Surv(tte, event) ~ X_trt, data = DAT_cc,
                              data_hist = DAT_hst, model_choice = 'mix',
                              iter = 200, warmup_iter = 50, refresh = 0,
                              verbose = FALSE)

    ##  trtd+cntls; w/o borrow; w cov's:
    test_f4 <- BayesFBHborrow(Surv(tte, event) ~ X_trt + X_01 + X_02 + X_03,
                              data = DAT_cc, model_choice = 'mix',
                              iter = 200, warmup_iter = 50, refresh = 0,
                              verbose = FALSE)

    ## trtd+cntls; w borrow, w cov's:
    test_f5 <- BayesFBHborrow(Surv(tte, event) ~ X_trt + X_01 + X_02 + X_03,
                              data = DAT_cc, data_hist = DAT_hst,
                              model_choice = 'mix', iter = 10, warmup_iter = 5,
                              refresh = 0, verbose = FALSE)

## End(Not run)
```

`coef.BayesFBHborrow` *The coefficients extractor method for the* `BayesFBHborrow` *class*

Description

The coefficients extractor method for the `BayesFBHborrow` class with functionality dependent upon whether you select the conditional estimand or marginal contrast.

Usage

```
coef.BayesFBHborrow(object, ...)
```

Arguments

`object`	An object of class `BayesFBHborrow`
`...`	Not used

Details

Every call to the function runs the sampler and then produces the conditional estimand and marginal contrast for the treatment/pretreatment variable effects. The argument `G_compute` in the `BayesFBHborrow` call tells the print, plot, summary and coef methods which version the user wants displayed.

Value

`G_compute=FALSE`, then `coef()` will extract the conditional logged hazard ratio coefficients.

If `G_compute=TRUE` then a table of showing the marginal treatment contrast e.g. the difference between the log-logged marginal survival fucntion at landmark information times, 0.25, 0.50, 0.75, 1.00, with each line showing median (MTE: marginal treatment effect) its exponentiated value and its 95 percent credicble interval.

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

`BayesFBHborrow`,

Examples

```
## Not run:
    my_coefs_cndl <- coef(my_bfhb)
    my_coefs_mgnl <- coef(update(my_bfhb, G_compute=TRUE))

## End(Not run)
```

`Combine` *An Method for Easily Combining Two Similar BayesFBHborrow Plots*

Description

Combines two survival/hazard plots side by side or two TrtEff density plots atop one another.

Usage

```
Combine(p1, p2, lgnd = NULL)
```

Arguments

`p1`	First plot
`p2`	Second plot
`lgnd`	For the side by side hazard/survival plots the default is that one is conditional and one is marginal. If your use case is different, then put a legend consisting of two character strings to label the plots from left to right. See examples.

Details

Experimental at this stage.

Value

A ggplot2 object

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

`plot.BayesFBHborrow`, `BayesFBHborrow`

Examples

```
  ## Not run:
      p_haz_nb_wb <- Combine(p_haz_nb, p_haz_wb)
      p_gbcs_TrtEff <- Combine(p_gbcs_nb_TrtEff, p_gbcs_wb_TrtEff, lgnd=c("NB","WB"))

## End(Not run)
```

---

genBFBHBdat *Generate Current Trial/Historical Controls via Weibull Model*

Description

Data genereration to simultaneously generate from a proportional hazards Weibull model, two datasets, one to take the role as the current trial and the other to take the role as the historical controls.

Usage

```
genBFBHBdat(n_cc_1, n_cc_0, n_hst, B_trt, B_x_cc, int_cc, B_x_hst,
            int_hst, X_fact_levs = NULL, shape = 1, t_er, t_fin,
            dbg = FALSE)
```

Arguments

n_cc_1	Size of treated arm in current trial.
n_cc_0	Size of control arm in current trial.
n_hst	Size of historical controls dataset.
B_trt	Treatment effect (logged hazard ratio).
B_x_cc	Coefficients (logged hazard ratio per unit) for effect of pretreatment covariates in current trial. The leading end of the vector specifies continuous covariates and the tail end of the vector specifies coefficients for levels of factor variables. See X_fact_levs below.
int_cc	Intercept for current trial model.
B_x_hst	Coefficients (logged hazard ratio per unit) for effect of pretreatment covariates in historical coontrols. See X_fact_levs.
int_hst	Intercept for historical control model.
X_fact_levs	A numeric vector of length 'k' which specifies both the number, 'k', of factor variables among the list of pre-treatment covariates, and the number of levels of each factor variable in their components. For example if we desire 3 continous variables and two factor variables having 3 levels and 4 levels, then the coefficient vectors described above B_x_ must be of length 8 (3 + 2 + 3), and X_fact_levs=c(3,4). Any combination from 0/0, n/0, 0/m of continuous and factor variables is possible.
shape	The shape parameter for the Weibull distribution–currently the same for the current trial and historical controls.

t_er	The time at which randomization ends for use in administrative censoring for both the current trial and historical controls.
t_fin	The time of maximum follow-up for use in administrative censoring for both the current trial and historical controls.
dbg	If run at the command line, set dbg=TRUE to run the command line debugger to step through the function line at a time.

Value

A list of two component data.frames, DAT_cc and DAT_hst, the current trial and the historical controls. Both current trial and historical controls set have time to event and event indicator and any pretreatment covariates specified via the arguments B_x_ and X_fact_levs. In addition the current trial, DAT_cc, has a treatment indicator. Variables in the data.frames are named as follows.

tte	Time to event, both data.frames.
event	Event indicator, both data.frames.
X_trt	Treatment indicator, current trial only.
X_01...X_m	Pre-treatment covariates both data.frames.

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

BayesFBHborrow,

Examples

```
n_cc_1 <- 200
n_cc_0 <- 100
n_hst <- 100
int_cc <- int_hst <- -log(3)
B_x_cc <- B_x_hst <- c(-0.3,0.5,0.25,-0.5)
B_trt <- log(0.55)

dat_lst <-
    genBFBHBdat(n_cc_1=200, n_cc_0=100, n_hst=100,
                B_trt=B_trt, B_x_cc=B_x_cc, B_x_hst=B_x_hst,
                int_cc=int_cc, int_hst=int_hst, shape=2,
                t_er=0.5, t_fin=1.5, X_fact_levs=3)
```

```
DAT_cc <- dat_lst$DAT_cc
DAT_hst <- dat_lst$DAT_hst
```

`group_summary` *Create group level data*

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

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

`BayesFBHborrow`,

Examples

```
set.seed(111)

## simulate an example data and set your initial values and hyper parameters
n_cc_1 <- 200
n_cc_0 <- 100
n_hst <- 100
int_cc <- int_hst <- -log(3)
B_x_cc <- B_x_hst <- c(-0.3,0.5,0.25,-0.5)
B_trt <- log(0.55)

dat_lst <-
    genBFBHBdat(n_cc_1=200, n_cc_0=100, n_hst=100,
                B_trt=B_trt, B_x_cc=B_x_cc, B_x_hst=B_x_hst,
                int_cc=int_cc, int_hst=int_hst, shape=2,
                t_er=0.5, t_fin=1.5, X_fact_levs=3)

DAT_cc <- dat_lst$DAT_cc
DAT_hst <- dat_lst$DAT_hst

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

with(DAT_cc, group_summary(tte, event, X_trt, 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

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

BayesFBHborrow,

Examples

```
set.seed(111)

## simulate an example data and set your initial values and hyper parameters
n_cc_1 <- 200
n_cc_0 <- 100
n_hst <- 100
int_cc <- int_hst <- -log(3)
B_x_cc <- B_x_hst <- c(-0.3,0.5,0.25,-0.5)
B_trt <- log(0.55)

dat_lst <-
    genBFBHBdat(n_cc_1=200, n_cc_0=100, n_hst=100,
                B_trt=B_trt, B_x_cc=B_x_cc, B_x_hst=B_x_hst,
                int_cc=int_cc, int_hst=int_hst, shape=2,
                t_er=0.5, t_fin=1.5, X_fact_levs=3)

DAT_cc <- dat_lst$DAT_cc
DAT_hst <- dat_lst$DAT_hst

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

grpd_data <-
  with(DAT_cc, group_summary(tte, event, NULL, s))

init_lambda_hyperparameters(grpd_data, s)
```

---

plot.BayesFBHborrow *Plot Method for the BayesFBHborrow Class*

Description

The plot method for the BayesFBHborrow class which allows quick convenient plots of important model summaries.

Usage

```
## S3 method for class 'BayesFBHborrow'
plot(x, type = c("survival", "hazard", "trace", "TrtEff"),
                              col = NULL, InfFrac = NULL, ylim = NULL, ...)
```

Arguments

x	An object of class BayesFBHborrow.
type	The type of plot desired. Can be one of the following "survival", "hazard", "trace", "TrtEff".
col	When type="trace" is specified you must name a column of the samples data.frame, which is a component of the output.
InfFrac	When type="TrtEff" is specified and the fitted object has been cast to its marginal estimand form, e.g. update(x, G_compute=TRUE), then you must specify 0.25, 0.50, 0.75 or 1 being the information fraction time at which you are deriving the marginal treatment effect. Defaults to 1.
ylim	Sometimes in type="hazard" plots the credible interval ribbons become obnoxious. Hence, this argument. Set to c(0, Mx).
...	Additional arguments to generic plot function

Value

A ggplot2 object.

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

BayesFBHborrow, Combine

Examples

```
## Not run:
  p_haz_wb <- plot(fit_sim_wb, type="hazard")
  p_gbcs_wb_trace <- plot(fit_gbcs_wb, type="trace", col="tamoxifen")
  p_gbcs_wb_TrtEff <- plot(fit_gbcs_wb, type="TrtEff")
  p_gbcs_wb_TrtEff_mgnl <- plot(update(fit_gbcs_wb, G_compute=TRUE), type="TrtEff")
  p_gbcs_wb_TrtEff_mgnl_75 <- plot(update(fit_gbcs_wb, G_compute=TRUE),
                                   type="TrtEff", InfFrac=0.75)
```

```
## End(Not run)
```

`read_haz_mcmc_smpls` *Reads in Fine Mesh Grid Hazards MCMC Samples*

Description

Reads in fine mesh grid conditional baseline hazard and arm specific marginal hazards of MCMC samples from the posterior that were written out sample at a time during iteration.

Usage

```
read_haz_mcmc_smpls(obj)
```

Arguments

`obj`	An object of class `BayesFBHborrow`.

Details

MCMC samples of the baseline hazard are natively represented as number of split-points, location of split-points and piecewise hazards. However the gibbs/MH updating done internally invovles integrals over the time to event CDF is done with respect to a fine mesh grid. Thus all `iter` samples must be snapped to this common fine mesh grid of length `max_grid`. Row by row updates of this matrix within iterations of the sampler is impractical as multiple copies and persistence within a loop will quickly consume resources. For this reason the`max_grid` by `iter` matrix representations of the conditional baseline hazard, marginal control arm hazard and marginal treated arm hazard are written out to three corresponding binary files: `cnd_blh_*.bin`, `mgnl_haz0_*.bin`, and `mgnl_haz1_*.bin`. The files are written out sample by sample during iterations and then read back in at the end for summarizing. The files are given a unique random hex suffix for each call to the function and are left in the working directory so that the user may use them to calculate any desired functional of the posterior distribution. If you delete the *.bin files it will, of course, not work. The names of the binary files associated with a given result are returned with the object so if desired you can clean house.

Value

A list with components

`cnd_haz_0`	samples of the conditional baseline hazard posterior as `iter` by `max_grid` matrix
`mgnl_haz_0`	samples of the marginal control arm hazard posterior as `iter` by `max_grid` matrix
`mgnl_haz_1`	samples of the marginal treated arm hazard posterior as `iter` by `max_grid` matrix

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

BayesFBHborrow

Examples

```
  ## Not run:
      read_haz_mcmc_smpls(fit_my_bfbhb)

## End(Not run)
```

`summary.BayesFBHborrow`

Summary Method for the BayesFBHborrow Class

Description

Summary method for the BayesFBHborrow class

Usage

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

Arguments

`object`	An object of class `BayesFBHborrow`.
`...`	Additional arguments to generic summary

Details

Every call to the function runs the sampler and then produces the conditional estimand and marginal contrast for the treatment/pretreatment variable effects. The argument `G_compute` in the `BayesFBHborrow` call tells the print, plot, summary and coef methods which version the user wants displayed.

Value

The result of the summary method is an object of class BayesFBHborrow identical to the input with the addition of two new components – the ones shown by the print method.

coefficients	If the original model involved p pre-treatment covariates and a treatment indicator, this will be a 2p + 1 by 4 matrix showing median of the logged hazard ratio, its exponentiated value and its 95 percent credible interval.
surv_summary	Shows arm specific conditional or A 8 by 6 matrix showing arm label C/I, information fraction Description of 'comp2'

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

BayesFBHborrow,

Examples

```
    ## Not run:
        my_coefs_cndl <- coef(my_bfhb)
        my_coefs_mgnl <- coef(update(my_bfhb, G_compute=TRUE))

## End(Not run)
```

---

update.BayesFBHborrow *The Update Method for the* BayesFBHborrow *Class*

Description

The Update Method for the BayesFBHborrow Class

Usage

```
update.BayesFBHborrow(object, formula = NULL, data, data_hist = NULL,
                      subset, na.action, CntlOnly = FALSE, model_choice = "mix",
                    tuning_parameters = NULL, hyperparameters = NULL, iter = 1000,
                  warmup_iter = 100, refresh = 0, verbose = FALSE, max_grid = 2000,
                       standardise = TRUE, G_compute = FALSE, preprocess = TRUE,
                       fnm_cnd_blh = "cnd_blh", fnm_mgnl_haz0 =  "mgnl_haz0",
                       fnm_mgnl_haz1 = "mgnl_haz1", dbg = FALSE, ...)
```

Arguments

object	An object of class BayesFBHborrow
formula	Optional but most likely preferred. When using the formula/data interface, specify the formula in the form typically used in other survival models e.g. Surv(TOS, Event) ~ Trt + Oth + Covs + etc The first listed covariate must be the treatment variable. The rest can be continuous or factor.
data	Required. The current trial/study data.frame with a treated and a control arm. For the formula/data interface, there is no naming convention for variables as the user specifies these with the formula. For the data only interface, you must name the time to event variable 'tte', and the event variable 'event'. All covariates including the treatment indicator must have the 'X_' prefix.
data_hist	When fitting the full model with borrowing, the historical controls data.frame with variables named to agree with the current trial data.frame specified in the 'data' argument. Comments above regarding the formula/data versus data only interface apply here as well.
subset	When using the formula/data interface, you may also use subset and na.action as you do in other statistical routines in R.
na.action	When using the formula/data interface, you may also use subset and na.action as you do in other statistical routines in R.
CntlOnly	Set to TRUE when running the model with on the historical controls dataset only. The default value is FALSE.
model_choice	Borrowing method. Determine the borrowing per split point by specifying the option "mix" (default) for a mixture of inverse gamma densities or "uni" for a single inverse gamma density. Otherwise, determine the borrowing once for all split points by specifying the option "all".
tuning_parameters	list with components cprop_beta (cprop_beta_0 for historical data), a_lambda, b_lambda, pi_b and alpha. Default is list(cprop_beta=1.1, cprop_beta_0=1.1, a_lambda=0.01, b_lambda=0.01, pi_b=0.5, alpha=0.4). The most important for the user are cprop_beta and cprop_beta_0. Starting at the default values, the user must adjust these values up or down in a series of test runs (iter=200) so that beta_acc_ratio and beta_0_acc_ratio (in the output list) are between 0.3 and 0.4. The relationship between cprop_beta parameters and the acceptance ratios is inverse.
hyperparameters	list with components beta_prior, beta_0_prior, a_tau, b_tau, c_tau, d_tau, type, p_0, a_sigma, b_sigma, phi, clam_smooth, Jmax. Default is list(beta_prior=10^2, beta_0_prior=10^2, a_tau=1, b_tau=0.001, c_tau=1, d_tau=5, type="mix", p_0=0.8, a_sigma=1, b_sigma=1, phi=3, clam_smooth=0.7, Jmax=5).
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	Whether or not to print the progress to the console every refresh iterations. Defaults to FALSE.

max_grid	Grid size for the smoothed baseline hazard. Default value is 2000.
standardise	Whether or not to normalize the current trial baseline hazard to unity and apply the same normalization constant to the historical data. Default is TRUE.
G_compute	If set to TRUE when treatment effect and pretreatment covariates are entered into the model (current trial only or current trial with borrowing), results are displayed as a marginal estimand computed via g-computation. This setting affects the behavior of the 'coef' and 'summary' methods and thus the 'print' method. The default is FALSE which results in display of a conditional estimand.
preprocess	Controls the interpretation of the 'baseline' hazard consequent to recoding of the input dataset(s). When set to TRUE, all continuous variables will be centered at their mean over the dataset in the data argument, and factor variables will be centered to their mean under a hypothetical design having balanced levels for each factor. This defaults to TRUE and works with either the formula/data interface or the data only interface. If complete control over recoding is desired, one must use the data only interface together with preprocess=FALSE. This is the only way to include interactions.
fnm_cnd_blh	Binary files generated during run time which are given a default name prefix with a random hex suffix. The collection of "snapped to common grid" samples from the posterior distribution of the baseline hazards is a matrix of dimension max_grid by iter. Adding updated columns to this very large matrix would result in memory caching and for this reason, these are written out to binary files during the run of the MCMC, and then read back in during the final sumarization. This file is for the conditional baseline hazard. These files are available to the user for computing any functional of the posterior distribution. See the documentation for the read_haz_mcmc_smpls function.
fnm_mgnl_haz0	Binary files generated during run time which are given a default name prefix with a random hex suffix. The collection of "snapped to common grid" samples from the posterior distribution of the baseline hazards is a matrix of dimension max_grid by iter. Adding updated columns to this very large matrix would result in memory caching and for this reason, these are written out to binary files during the run of the MCMC, and then read back in during the final sumarization. This file is for the control arm log-log marginal hazard. These files are available to the user for computing any functional of the posterior distribution. See the documentation for the read_haz_mcmc_smpls function.
fnm_mgnl_haz1	Binary files generated during run time which are given a default name prefix with a random hex suffix. The collection of "snapped to common grid" samples from the posterior distribution of the baseline hazards is a matrix of dimension max_grid by iter. Adding updated columns to this very large matrix would result in memory caching and for this reason, these are written out to binary files during the run of the MCMC, and then read back in during the final sumarization. This file is for the treated arm log-log marginal hazard. These files are available to the user for computing any functional of the posterior distribution. See the documentation for the read_haz_mcmc_smpls function.
dbg	When running in command line mode, set to TRUE in order to enable line by line debugging.
...	Other arguments as needed.

Details

Note that the marginal contrast is always computed in addition to the conditional estimand. If `G_compute=FALSE`, (the default) in the original call, the print, coef, summary and plot methods will produce results reflecting the conditional estimand, whereas these will reflect the marginal contrast otherwise. NOTE: calling `update(my_bfbhb, G_compute=TRUE)` doesn't require rerunning the sampler as the results are already there.

Value

An object of class `BayesFBHborrow`. See the documentation.

Author(s)

Darren A. V. Scott, Sophia Axillus and Grant Izmirlian

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

`plot`, `summary`, `update` methods for class `"BayesFBHborrow"` objects

Examples

```
    ## Not run:
       update(my_bfbhb, G_compute=TRUE)

## End(Not run)
```

`xifinder` *Find the root of the p_0 mixture probability equation*

Description

Finds the value of the root (in the interval `[0, 2]`) for the function `p0tp` involving mixture probability `p_0` and hyperparameters `b_tau` and `d_tau`.

Usage

```
xifinder(b_tau, d_tau, p_0)
```

Arguments

b_tau	Shape (or scale) parameter for the first mixture component.
d_tau	Shape (or scale) parameter for the second mixture component.
p_0	Mixture proportion; probability for the first component, in (0, 1).

Details

Uses uniroot() to numerically solve for the root of the function p0tp on the interval [0, 2]. The function p0tp should accept arguments x, b_tau, d_tau, and p_0. This is typically used for calibrating the mixture prior or solving for a relevant quantile in hierarchical Bayesian models.

Note: The auxiliary function p0tp must be defined in the environment.

Value

Numeric value; the root of the p0tp equation within the interval.

References

Scott DAV and Lewin A (2026). Borrowing from historical control data in a Bayesian time-to-event model with flexible baseline hazard function. Biostatistics 27(1)

Scott DAV, Axillus S, Lewin A and Izmirlian G. BayesFBHborrow: An R Package for Bayesian borrowing for time-to-event data from a flexible baseline hazard function (2026) <doi:10.48550/arXiv.2408.04327>

See Also

plot, summary, update methods for class "BayesFBHborrow" objects

Examples

```
## Suppose p0tp is defined elsewhere
## Find a root for specific parameters:
  ## Not run:
    xifinder(b_tau = 0.1, d_tau = 1, p_0 = 0.75)

## End(Not run)
```

Index

∗ **Bayesian borrowing**
BayesFBHborrow, 2
coef.BayesFBHborrow, 7
Combine, 8
genBFBHBdat, 9
plot.BayesFBHborrow, 13
read_haz_mcmc_smpls, 15
summary.BayesFBHborrow, 16
update.BayesFBHborrow, 17
xifinder, 20
∗ **G-computation**
BayesFBHborrow, 2
coef.BayesFBHborrow, 7
Combine, 8
genBFBHBdat, 9
plot.BayesFBHborrow, 13
read_haz_mcmc_smpls, 15
summary.BayesFBHborrow, 16
update.BayesFBHborrow, 17
xifinder, 20
∗ **covariate adjustment**
BayesFBHborrow, 2
coef.BayesFBHborrow, 7
Combine, 8
genBFBHBdat, 9
plot.BayesFBHborrow, 13
read_haz_mcmc_smpls, 15
summary.BayesFBHborrow, 16
update.BayesFBHborrow, 17
xifinder, 20
∗ **flexible baseline hazard**
BayesFBHborrow, 2
coef.BayesFBHborrow, 7
Combine, 8
genBFBHBdat, 9
plot.BayesFBHborrow, 13
read_haz_mcmc_smpls, 15
summary.BayesFBHborrow, 16
update.BayesFBHborrow, 17
xifinder, 20
∗ **plot methods**
plot.BayesFBHborrow, 13
∗ **time-to-event**
BayesFBHborrow, 2
coef.BayesFBHborrow, 7
Combine, 8
genBFBHBdat, 9
plot.BayesFBHborrow, 13
read_haz_mcmc_smpls, 15
summary.BayesFBHborrow, 16
update.BayesFBHborrow, 17
xifinder, 20

BayesFBHborrow, 2, *7*, *8*, *10*, *11*, *13*, *14*, *16*, *17*

coef.BayesFBHborrow, 7
coefficients *(*coef.BayesFBHborrow*)*, 7
Combine, 8, *14*

genBFBHBdat, 9
group_summary, 11

init_lambda_hyperparameters, 12

plot.BayesFBHborrow, *8*, 13

read_haz_mcmc_smpls, 15

summary.BayesFBHborrow, 16

update.BayesFBHborrow, 17

xifinder, 20