

Package: BDIB (via r-universe)

October 18, 2026

Type Package

Title Bayesian Dynamic Information Borrowing for Longitudinal Data
with Informative Dropout

Version 0.1.1

Description Implements 'BDIB' (Bayesian dynamic information borrowing)
for longitudinal outcomes with informative dropout. The package
provides the mixture prior for longitudinal data borrowing
(MLB) and the self-adapting mixture prior for longitudinal data
information borrowing (SLB). Both methods use a
shared-parameter model for outcomes and dropout.

License GPL-3

Encoding UTF-8

Depends R (>= 4.0.0)

Imports RBest, jagsUI, stats

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

Config/roxygen2/version 8.0.0

Author Saijun Zhao [aut, cre]

Maintainer Saijun Zhao <saijzhao@iu.edu>

Repository <https://cran.r-universe.dev>

Date/Publication 2026-10-18 18:12:27 UTC

RemoteUrl <https://github.com/cran/BDIB>

RemoteRef HEAD

RemoteSha b633d19021a870ef31ab86561cab4b1a8135ce96

Contents

fit_spm_jags	2
gaussian_kde	4

generate_spm	5
Mixprior	7
MLB_SLB_anlaysis	8
SLB_weight	11
unit_information_prior	12

Index 14

fit_spm_jags	<i>Fit SPM with MNAR monotone dropout in JAGS (continuous or binary outcomes)</i>
--------------	---

Description

Unified JAGS interface for the shared-parameter model (SPM) with MNAR dropout:

- family="gaussian": Continuous outcome.
- family="bernoulli": Binary outcome.

Usage

```
fit_spm_jags(
  df,
  family = c("gaussian", "bernoulli"),
  prior_theta = NULL,
  params_to_save = NULL,
  n.chains = 3,
  n.iter = 10000,
  n.burnin = 5000,
  n.thin = 2,
  parallel = FALSE
)
```

Arguments

df	Long-format data.frame with columns id, time, R, Y. R=1 means observed, R=0 means missing.
family	Either "gaussian" or "bernoulli" (probit).
prior_theta	Optional prior for θ . • family="gaussian": RBest::normMix object (mixture Normal on θ). • family="bernoulli": a "betaMix" object (mixture Beta on θ). If NULL, defaults to a very weak one-component prior.
params_to_save	Character vector of parameter names to monitor. If NULL, sensible defaults are used for each family.
n.chains, n.iter, n.burnin, n.thin	MCMC settings passed to jagsUI::jags.
parallel	Logical; whether to run chains in parallel (via jagsUI).

Value

Numeric vector of posterior draws of θ .

Examples

```
# ---- Example 1: Continuous outcome with weak prior ----
set.seed(1000)

# 1) Generate longitudinal data with MNAR monotone dropout
t_vec <- seq(4, 48, 4)
gen <- generate_spm(
  n = 80, t_vec = t_vec, family = "gaussian",
  alpha0 = -4, alpha1 = 0.05, rho = 1, sigma_b = 1,
  theta = -3.2, # total change at the last visit (= slope * max(t))
  sigma_e = 1
)
df <- gen$dat # long-format data: id, time, R, Y

# 2) Define a weakly informative prior for theta (one Normal component with large variance)
prior <- RBesT::mixnorm(c(1, 0, 1000)) # weight=1, mean=0, sd=1000

# 3) Fit the SPM (MNAR) and obtain posterior draws of theta

# Full MCMC fitting takes longer than a brief example check.
draws_theta <- fit_spm_jags(
  df = df, family = "gaussian",
  prior_theta = prior,
  params_to_save = c("theta", "slope", "alpha0", "alpha1", "rho", "sigma_e", "sigma_b"),
  n.chains = 3, n.iter = 10000, n.burnin = 5000, n.thin = 2, parallel = FALSE
)

# Summarize posterior results
summary(draws_theta) # posterior mean, median, quantiles
mean(draws_theta)    # posterior mean of theta

# ---- Example 2: Binary outcome (probit link) with weak prior ----
set.seed(1000)

# 1) Generate longitudinal binary data with MNAR monotone dropout
t_vec <- seq(4, 48, 4)
gen <- generate_spm(
  n      = 200,
  t_vec  = t_vec,
  family = "bernoulli",
  alpha0 = -4, # dropout logit-intercept
  alpha1 = 0.05, # dropout logit-slope in time
  rho    = -1, # association between random effect and dropout
  sigma_b = 1, # SD of random intercept b_i
  theta  = 0.4, # target marginal Pr(Y=1) at final visit
  beta0  = -2 # outcome probit-intercept
)
df <- gen$dat # long-format data: id, time, R, Y
```

```

# 2) Define a weakly informative prior for theta:
#   Beta(1,1) (Uniform on (0,1)) as a one-component mixture
prior <- RBesT::mixbeta(c(1, 1, 1)) # weight=1, a=1, b=1

# 3) Fit the SPM (MNAR) with probit link for the binary outcome
#   and obtain posterior draws of theta (final-visit response rate)

# Full MCMC fitting takes longer than a brief example check.
draws_theta <- fit_spm_jags(
  df                = df,
  family            = "bernoulli",
  prior_theta       = prior,
  params_to_save    = c("theta", "slope", "beta0", "alpha0", "alpha1", "rho", "sigma_b"),
  n.chains          = 3,
  n.iter            = 5000,
  n.burnin          = 3000,
  n.thin            = 2,
  parallel          = FALSE
)

# 4) Summarize posterior results
summary(draws_theta) # posterior mean, median, quantiles of theta
mean(draws_theta)    # posterior mean of theta

```

gaussian_kde

Gaussian Kernel Density Estimation

Description

Gaussian Kernel Density Estimation

Usage

```
gaussian_kde(samples, eval_points, bandwidth = NULL)
```

Arguments

<code>samples</code>	Numeric vector of samples.
<code>eval_points</code>	Numeric vector of locations to evaluate.
<code>bandwidth</code>	Optional bandwidth; Silverman's rule if NULL.

Value

Numeric vector of density estimates.

Examples

```
set.seed(1000)
xs <- rnorm(1000, mean = -3, sd = 0.5)
pts <- seq(-4.5, -1.5, length.out = 5)
dens <- gaussian_kde(xs, pts)      # KDE values at 'pts'
cbind(pts, round(dens, 4))
```

generate_spm	<i>Generate longitudinal data from a shared-parameter model (SPM) with MNAR monotone dropout (continuous or binary outcomes)</i>
--------------	--

Description

Generate longitudinal data from a shared-parameter model (SPM) with MNAR monotone dropout (continuous or binary outcomes)

Usage

```
generate_spm(
  n,
  t_vec,
  family = c("gaussian", "bernoulli"),
  alpha0,
  alpha1,
  rho,
  sigma_b,
  theta,
  beta0 = NA_real_,
  sigma_e = NA_real_
)
```

Arguments

n	Integer. Sample size (number of subjects).
t_vec	Numeric vector of visit times.
family	Character. Either "gaussian" for a continuous outcome or "bernoulli" for a binary outcome.
alpha0, alpha1	Numerics. Intercept and time slope in the dropout model (logit link).
rho	Numeric. Coupling between the shared random effect b_i and the dropout model; $\rho \neq 0$ induces MNAR.
sigma_b	Numeric (>0). Standard deviation of the subject-specific random intercept $b_i \sim \mathcal{N}(0, \sigma_b^2)$.
theta	Numeric. Target effect: family="gaussian": change at final visit K: $\theta = \beta_1 t_K$ (so the slope is $\beta_1 = \theta/t_K$).

	family="bernoulli": marginal response probability at the final visit in $(0, 1)$ (probit link).
beta0	Numeric. For family="bernoulli" only: probit intercept in $\Phi(\beta_0 + \beta_1 t_k + b_i)$. Ignored for "gaussian".
sigma_e	Numeric (>0). For family="gaussian" only: residual SD.

Details

Outcome model (shared-parameter).

- Gaussian*: $Y_{ik} \mid b_i \sim \mathcal{N}(\beta_1 t_k + b_i, \sigma_e^2)$, with $\beta_1 = \theta/t_K$.
- Bernoulli (probit)*: $Y_{ik} \mid b_i \sim \text{Bernoulli}(\Phi(\beta_0 + \beta_1 t_k + b_i))$, with $\beta_1 = \{\sqrt{1 + \sigma_b^2} \Phi^{-1}(\theta) - \beta_0\}/t_K$.

Dropout model (MNAR, monotone).

$$\text{logit } \Pr(R_{ik} = 0 \mid R_{i,k-1} = 1, b_i) = \alpha_0 + \alpha_1 t_k + \rho b_i,$$

and once dropout occurs ($R_{ik} = 0$), all subsequent $R_{i,k'} = 0$ for $k' > k$.

Value

A list with:

Ymat	$n \times K$ matrix of outcomes (NA for missing).
Rmat	$n \times K$ matrix of response indicators (1=observed, 0=missing).
dat	Long-format data.frame with columns id, time, R, Y.

Examples

```
set.seed(1000)
t_vec <- seq(4, 48, 4)
# Continuous outcome
out_c <- generate_spm(
  n = 50, t_vec = t_vec, family = "gaussian",
  alpha0 = -4, alpha1 = 0.05, rho = -1, sigma_b = 1,
  theta = -3.2, sigma_e = 1
)
# Binary outcome
out_b <- generate_spm(
  n = 200, t_vec = t_vec, family = "bernoulli",
  alpha0 = -4, alpha1 = 0.05, rho = -1, sigma_b = 1,
  theta = 0.4, beta0 = -2
)
```

Mixprior	<i>Constructing a mixture prior for longitudinal data with informative dropout</i>
----------	--

Description

The `Mixprior` function constructs a mixture prior for longitudinal data with informative dropout by mixing an informative prior (built from the historical arm/posterior draws) and a non-informative (e.g., unit-information) prior. It supports both continuous (`normMix`) and binary (`betaMix`) outcomes and simply delegates to `RBesT::mixcombine`.

Usage

```
Mixprior(informative_prior, noninformative_prior, weight)
```

Arguments

<code>informative_prior</code>	Informative prior for θ derived from historical data, represented as <code>RBesT::normMix</code> (continuous) or <code>"betaMix"</code> (binary).
<code>noninformative_prior</code>	Non-informative prior (e.g., unit-information for continuous outcome or <code>Uniform(0,1)</code> for binary outcome) of the same class as <code>informative_prior</code> : • Continuous: <code>normMix</code>. See also <code>unit_information_prior()</code>. • Binary: <code>"betaMix"</code>; commonly <code>RBesT::mixbeta(c(1,1,1))</code>.
<code>weight</code>	Mixture weight assigned to the informative component ($0 \leq \text{weight} \leq 1$); may be a scalar w or a vector $c(w, 1-w)$.

Value

A prior of the same class as `informative_prior`: `normMix` for continuous endpoints or `"betaMix"` for binary endpoints.

Examples

```
# --- Continuous endpoint (normMix) ---
set.seed(1000)
hist_draws <- rnorm(1000, mean = -3.2, sd = 0.35)
inf_prior_c <- RBesT::mixfit(hist_draws, type = "norm", Nc = 3) # informative
nf_prior_c <- unit_information_prior(inf_prior_c, n_hist = 200) # unit-info
w_c <- 0.6 # (e.g., from SLB_weight)
prior_c <- Mixprior(informative_prior = inf_prior_c,
                    noninformative_prior = nf_prior_c,
                    weight = w_c)

prior_c

# --- Binary endpoint (betaMix) ---
```

```

inf_prior_b <- RBest::mixbeta(c(1, 20, 30)) # Beta(20,30) as one-component mix
nf_prior_b  <- RBest::mixbeta(c(1, 1, 1))   # Uniform(0,1)
w_b <- 0.5
prior_b <- Mixprior(informative_prior = inf_prior_b,
                    noninformative_prior = nf_prior_b,
                    weight = w_b)

prior_b

```

MLB_SLB_anlaysia	<i>The mixture prior for longitudinal data borrowing (MLB) and self-adapting mixture prior for longitudinal data information borrowing (SLB) Analysis under SPM with MNAR dropout</i>
------------------	---

Description

Arms and notation (H/C/T):

- H — Historical control arm. External/previous-study control, used to build an *informative prior* for the concurrent control.
- C — Concurrent control arm. In-trial control; first fitted under a non-informative prior to assess prior–data conflict and compute an adaptive weight; then re-fitted under an MLB/SLB prior.
- T — Treatment arm. In-trial treatment; typically fitted under a non-informative prior, then compared against the (re)fitted control.

Usage

```

MLB_SLB_anlaysia(
  historical_df,
  concurrent_df,
  treatment_df,
  family = c("gaussian", "bernoulli"),
  delta,
  n_hist = NULL,
  fixed_weight = 0.5,
  mcmc_settings = list(n.chains = 3, n.iter = 10000, n.burnin = 5000, n.thin = 2,
    parallel = FALSE),
  decision_MLB,
  direction_MLB = c("lower", "higher"),
  decision_SLB,
  direction_SLB = c("lower", "higher")
)

```

Arguments

`historical_df` Long-format data.frame for H with columns `id`, `time`, `R`, `Y`.

`concurrent_df` Long-format data.frame for C with columns `id`, `time`, `R`, `Y`.

treatment_df	Long-format data.frame for T with columns id, time, R, Y.
family	Character, "gaussian" or "bernoulli" (probit link), passed to SPM.
delta	Clinically significant difference (CSD) used in SLB weight.
n_hist	Positive integer: historical sample size for unit-information prior (continuous only).
fixed_weight	MLB mixing weight ω (default 0.5).
mcmc_settings	JAGS settings list with fields n.chains, n.iter, n.burnin, n.thin, parallel.
decision_MLB	A REQUIRED decision function for MLB prior with threshold p that takes two numeric vectors of posterior samples (θ_T, θ_C) and returns logical/0-1 indicating treatment superiority. Direction of test (how probabilities are computed/decisions typically defined): • Larger-is-better: <code>function(theta_t, theta_c, p=0.95) mean(theta_t > theta_c) > p</code> • Smaller-is-better: <code>function(theta_t, theta_c, p=0.95) mean(theta_t < theta_c) > p</code>
direction_MLB	Character scalar specifying the clinical direction of superiority for MLB prior: • "lower": smaller is better; report $\Pr(\theta_T < \theta_C)$. • "higher": larger is better; report $\Pr(\theta_T > \theta_C)$.
decision_SLB	A REQUIRED decision function for SLB prior with threshold p that takes two numeric vectors of posterior samples (θ_T, θ_C) and returns logical/0-1 indicating treatment superiority. Direction of test (how probabilities are computed/decisions typically defined): • Larger-is-better: <code>function(theta_t, theta_c, p=0.95) mean(theta_t > theta_c) > p</code> • Smaller-is-better: <code>function(theta_t, theta_c, p=0.95) mean(theta_t < theta_c) > p</code>
direction_SLB	Character scalar specifying the clinical direction of superiority for SLB prior: • "lower": smaller is better; report $\Pr(\theta_T < \theta_C)$. • "higher": larger is better; report $\Pr(\theta_T > \theta_C)$.

Details

Target parameters $\theta_H, \theta_C, \theta_T$:

- family = "gaussian" (continuous outcome): θ is the total change at the final visit t_K , i.e., $\theta = \beta_1 t_K$ (thus $\beta_1 = \theta/t_K$).
- family = "bernoulli" (binary, probit link): θ is the marginal response probability at the final visit, $\Pr(Y = 1 \text{ at } t_K) \in (0, 1)$.

We write $\theta_H, \theta_C, \theta_T$ for the historical, concurrent-control, and treatment arms, respectively.

Workflow (continuous or binary endpoints):

1. Fit **H** under SPM with a vague prior on θ to obtain posterior draws.
2. Build an *informative prior* g_0 for θ_C via `RBest::mixfit` on the θ_H draws.
3. Build a *non-informative prior* g_1 : Gaussian: unit-information prior from g_0 (inflate SD by $\sqrt{n_{\text{hist}}}$); Bernoulli: `Beta(1, 1)`.
4. Fit **C** under g_1 to get posterior samples.
5. Compute SLB weight via posterior-probability-ratio KDE (see [SLB_weight](#)).
6. Construct MLB prior (fixed weight) and SLB prior (data-adaptive weight) via `Mixprior`.
7. Fit **C** under MLB/SLB priors; fit **T** under g_1 .
8. Posterior comparisons θ_T vs θ_C and decisions per direction.

Value

An object of class "mlbslb_result":

- `estimates`: posterior means of θ for each arm/prior (MLB/SLB).
- `weights`: list with `MLB_weight` and `SLB_weight`.
- `probabilities`: posterior superiority probabilities (per direction) under MLB/SLB.
- `decisions`: 0/1 decisions under MLB/SLB according to your `decision()`. (1 indicates test superiority is established).
- `posterior_samples`: posterior draws used in the analysis.

Examples

```
set.seed(1000)
t_vec <- seq(4, 48, 4)
# --- Continuous outcome ---
data_H <- generate_spm(n=60, t_vec, family="gaussian",
                      alpha0=-4, alpha1=0.05, rho=-1, sigma_b=1,
                      theta= -3.2, sigma_e=1)$dat
data_C <- generate_spm(n=30, t_vec, family="gaussian",
                      alpha0=-4, alpha1=0.05, rho=-1, sigma_b=1,
                      theta= -3.2, sigma_e=1)$dat
data_T <- generate_spm(n=60, t_vec, family="gaussian",
                      alpha0=-5.3, alpha1=0.05, rho=-1.5, sigma_b=1,
                      theta= -3.7, sigma_e=1)$dat

# Full MCMC fitting takes several minutes.
ans_1 <- MLB_SLB_anlaysia(
  historical_df = data_H, concurrent_df = data_C, treatment_df = data_T,
  family="gaussian", delta=0.5, n_hist=length(unique(data_H$id)), fixed_weight=0.5,
  mcmc_settings = list(n.chains=3, n.iter=10000, n.burnin=5000, n.thin=2, parallel=FALSE),
  decision_MLB = function(theta_t, theta_c, p = 0.95) mean(theta_t < theta_c) > 0.95,
  # Smaller-is-better (treatment < control), p = 0.95
  direction_MLB = "lower",
  decision_SLB = function(theta_t, theta_c, p = 0.95) mean(theta_t < theta_c) > 0.95,
  # Smaller-is-better (treatment < control), p = 0.95
  direction_SLB = "lower"
```

```

)
ans_1$decisions; ans_1$probabilities

# --- Binary outcome ---
set.seed(1000)
data_H <- generate_spm(n=200, t_vec, family="bernoulli",
                      alpha0=-4, alpha1=0.05, rho=-1, sigma_b=1,
                      theta=0.40, beta0=-2)$dat
data_C <- generate_spm(n=100, t_vec, family="bernoulli",
                      alpha0=-4, alpha1=0.05, rho=-1, sigma_b=1,
                      theta=0.40, beta0=-2)$dat
data_T <- generate_spm(n=200, t_vec, family="bernoulli",
                      alpha0=-5.3, alpha1=0.05, rho=-1.5, sigma_b=1,
                      theta=0.50, beta0=-1.5)$dat

# Full MCMC fitting takes several minutes.
ans_2 <- MLB_SLB_anlaysia(historical_df = data_H, concurrent_df = data_C, treatment_df = data_T,
                          family="bernoulli", delta=0.1, n_hist=length(unique(data_H$id)), fixed_weight=0.5,
                          mcmc_settings = list(n.chains=3, n.iter=10000, n.burnin=5000, n.thin=2, parallel=FALSE),
                          decision_MLB = function(theta_t, theta_c, p = 0.95) mean(theta_t > theta_c) > 0.95,
                          # Larger-is-better (treatment > control), p = 0.95
                          direction_MLB = "higher",
                          decision_SLB = function(theta_t, theta_c, p = 0.95) mean(theta_t > theta_c) > 0.95,
                          # Larger-is-better (treatment > control), p = 0.95
                          direction_SLB = "higher"
)
ans_2$decisions; ans_2$probabilities

```

SLB_weight

*Self-adapting mixture weight for longitudinal borrowing (SLB)***Description**

Given posterior samples of the concurrent control parameter (under a non-informative prior) and a historical point estimate, compute the SLB weight via a kernel-density posterior probability ratio:

$$R = \frac{\pi(\theta = \theta_h \mid \mathcal{D}_C)}{\max\{\pi(\theta = \theta_h + \delta \mid \mathcal{D}_C), \pi(\theta = \theta_h - \delta \mid \mathcal{D}_C)\}}, \quad w = \frac{R}{1 + R}.$$

Usage

```
SLB_weight(theta_cc_np_samples, theta_h, delta)
```

Arguments

```
theta_cc_np_samples
```

numeric vector. Posterior draws of the concurrent control parameter under a non-informative prior.

theta_h numeric scalar. Historical estimate.
 delta positive numeric. Clinically significant difference (CSD).

Value

numeric scalar in $[0, 1]$.

Examples

```
set.seed(1000)
# Suppose these are posterior theta samples from concurrent control (NP fit)
theta_cc_np_samples <- rnorm(2000, mean = -3.2, sd = 0.25)

# Historical estimate of theta and clinical delta
theta_h <- -3.2
delta <- 0.5

SLB_weight(theta_cc_np_samples, theta_h = theta_h, delta = delta)
```

unit_information_prior

Unit-Information Prior for continuous outcomes

Description

Constructs a unit-information (weak) prior from an informative normMix by inflating each component's standard deviation by $\sqrt{n_h}$.

Usage

```
unit_information_prior(informative_prior, n_hist)
```

Arguments

informative_prior A normMix (from RBest) built from historical data.
 n_hist Positive integer: historical sample size n_h .

Value

A normMix with inflated standard deviations.

Examples

```
# Start with an informative prior from historical samples via RBest::mixfit
set.seed(1000)
fake_hist_draws <- rnorm(300, mean = -3.2, sd = 0.4)
inf_prior <- RBest::mixfit(fake_hist_draws, type = "norm", Nc = 3)

nf_prior <- unit_information_prior(inf_prior, n_hist = 300)
# Compare SDs before/after
rbind(
  informative_sd = as.numeric(inf_prior[3, ]),
  unit_info_sd   = as.numeric(nf_prior[3, ])
)
```

Index

`fit_spm_jags`, [2](#)

`gaussian_kde`, [4](#)

`generate_spm`, [5](#)

`Mixprior`, [7](#), [10](#)

`MLB_SLB_anlaysia`, [8](#)

`SLB_weight`, [10](#), [11](#)

`unit_information_prior`, [12](#)