

Package ‘BDIB’

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Type Package

Title Bayesian Dynamic Information Borrowing for Longitudinal Data
with Informative Dropout

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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.

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Author Saijun Zhao [aut, cre]

Maintainer Saijun Zhao <saijzhao@iu.edu>

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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

Constructing a mixture prior for longitudinal data with informative dropout

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

informative_prior
Informative prior for θ derived from historical data, represented as `RBesT::normMix` (continuous) or `"betaMix"` (binary).

noninformative_prior
Non-informative prior (e.g., unit-information for continuous outcome or `Uniform(0,1)` for binary outcome) of the same class as `informative_prior`:

- Continuous: `normMix`. See also `unit_information_prior()`.
- Binary: `"betaMix"`; commonly `RBesT::mixbeta(c(1,1,1))`.

weight
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_anlaysis	<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_anlaysis(
  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 <code>n.chains</code> , <code>n.iter</code> , <code>n.burnin</code> , <code>n.thin</code> , <code>parallel</code> .
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_anlalysis(
  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_anlaysis(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, ])
)

```

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