Package ‘bayesCT’

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Author Thevaa Chandereng [aut, cre, cph]
          (https://orcid.org/0000-0003-4078-9176),
          Donald Musgrove [aut, cph],
          Tarek Haddad [aut, cph],
          Graeme Hickey [aut, cph],
          Timothy Hanson [aut, cph],
          Theodore Lystig [aut, cph]
Maintainer  Thevaa Chandereng <chandereng@wisc.edu>

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Analysis wrapper function

Description
Wrapper function to analyze bayesian trials.

Usage
```r
analysis(input, type = "binomial", .data = NULL)
```

Arguments
- `input` list. Input function for all the analysis.
- `type` character. Type of analysis to be ran (binomial (default), normal. etc.).
- `.data` NULL. stores the all the details, please do not fill it in.

Value
- a list with results of the analysis of bayesian trial.
  - `prob_of_accepting_alternative` scalar. The input parameter of probability of accepting the alternative.
  - `margin` scalar. The margin input value of difference between mean estimate of treatment and mean estimate of the control.
  - `alternative` character. The input parameter of alternative hypothesis.
  - `N_treatment` scalar. The number of patients enrolled in the experimental group for each simulation.
  - `N_control` scalar. The number of patients enrolled in the control group for each simulation.
  - `N_enrolled` vector. The number of patients enrolled in the trial (sum of control and experimental group for each simulation.)
  - `N_complete` scalar. The number of patients who completed the trial and had no loss to follow-up.
  - `post_prob_accept_alternative` vector. The final probability of accepting the alternative hypothesis after the analysis is done.
  - `est_final` scalar. The final estimate of the difference in posterior estimate of treatment and posterior estimate of the control group.
  - `stop_futility` scalar. Did the trial stop for futility during imputation of patient who had loss to follow up? 1 for yes and 0 for no.
  - `stop_expected_success` scalar. Did the trial stop for early success during imputation of patient who had loss to follow up? 1 for yes and 0 for no.
**beta_prior**  
*Beta prior for control and treatment group*

**Description**

Wrapper function for beta prior $\beta(a_0, b_0)$.

**Usage**

beta_prior(a0 = 1, b0 = 1, .data = NULL)

**Arguments**

- **a0**: numeric. The first shape parameter in the beta distribution ($\beta(a_0, b_0)$).
- **b0**: numeric. The second shape parameter in the beta distribution ($\beta(a_0, b_0)$).
- **.data**: NULL. stores the beta prior rate, please do not fill it in.

**Value**

a list with vector of beta rate for the beta prior for treatment and control group.

**Examples**

beta_prior(a0 = 1, b0 = 1)

---

**binomialBACT**  
*Binomial counts for Bayesian Adaptive Trials*

**Description**

Simulation for binomial counts for Bayesian Adaptive trial with different inputs to control for power, sample size, type 1 error rate, etc.

**Usage**

binomialBACT(
  p_treatment,
  p_control = NULL,
  y0_treatment = NULL,
  N0_treatment = NULL,
  y0_control = NULL,
  N0_control = NULL,
  N_total,
  lambda = 0.3,
  lambda_time = NULL,
interim_look = NULL,
EndofStudy,
prior = c(1, 1),
block = 2,
rand_ratio = c(1, 1),
prop_loss_to_followup = 0.1,
alternative = "greater",
h0 = 0,
futility_prob = 0.05,
expected_success_prob = 0.9,
prob_ha = 0.95,
N_impute = 10,
number_mcmc = 10000,
discount_function = "identity",
alpha_max = 1,
fix_alpha = FALSE,
weibull_scale = 0.135,
weibull_shape = 3,
method = "fixed"
)

Arguments

- `p_treatment` scalar. Proportion of events under the treatment arm.
- `p_control` scalar. Proportion of events under the control arm.
- `y0_treatment` scalar. Number of events for the historical treatment arm.
- `N0_treatment` scalar. Sample size of the historical treatment arm.
- `y0_control` scalar. Number of events for the historical control arm.
- `N0_control` scalar. Sample size of the historical control arm.
- `N_total` scalar. Total sample size.
- `lambda` vector. Enrollment rates across simulated enrollment times. See `enrollment` for more details.
- `lambda_time` vector. Enrollment time(s) at which the enrollment rates change. Must be same length as lambda. See `enrollment` for more details.
- `interim_look` vector. Sample size for each interim look. Note: the maximum sample size should not be included.
- `EndofStudy` scalar. Length of the study.
- `prior` vector. Prior values of beta rate, Beta(a0, b0). The default is set to Beta(1, 1).
- `block` scalar. Block size for generating the randomization schedule.
- `rand_ratio` vector. Randomization allocation for the ratio of control to treatment. Integer values mapping the size of the block. See `randomization` for more details.
- `prop_loss_to_followup` scalar. Overall proportion of subjects lost to follow-up.
- `alternative` character. The string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided".
h0 scalar. Threshold for comparing two mean values. Default is h0=0.
futility_prob scalar. Probability of stopping early for futility.
prob_ha scalar. Probability of alternative hypothesis.
N_impute scalar. Number of imputations for Monte Carlo simulation of missing data.
number_mcmc scalar. Number of Monte Carlo Markov Chain draws in sampling posterior.
discount_function character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled-Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.
alpha_max scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.
fix_alpha logical. Fix alpha at alpha_max? Default value is FALSE.
weibull_scale scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
weibull_shape scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
method character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the the bdpsurvival vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.

Value

a list of output for a single trial simulation.

p_treatment scalar. The input parameter of proportion of events in the treatment group.
p_control scalar. The input parameter of proportion of events in the control group.
prob_of_accepting_alternative scalar. The input parameter of probability threshold of accepting the alternative.
Description

A dataset containing the results of 300 patients with binomial outcome, the dataset is filled with loss to follow up.

Usage

data(binomialdata)

Format

A data frame with 300 rows and 4 variables:

- id  Patient ID in the trial
- treatment  treatment assignment for patients, 1 for treatment group 0 for control group
- outcome  binomial outcome of the trial, 1 for response (success or failure), 0 for no response
- complete  1 for complete outcome, 0 for loss to follow up

Examples

data(binomialdata)
**binomial_analysis**  Analyzing Bayesian trial for binomial counts

**Description**

Function to analyze Bayesian trial for binomial count data which allows early stopping and incorporation of historical data using the discount function approach.

**Usage**

```r
binomial_analysis(
  treatment,
  outcome,
  complete = NULL,
  y0_treatment = NULL,
  N0_treatment = NULL,
  y0_control = NULL,
  N0_control = NULL,
  alternative = "greater",
  N_impute = 10,
  h0 = 0,
  number_mcmc = 10000,
  prob_ha = 0.95,
  futility_prob = 0.1,
  expected_success_prob = 0.9,
  prior = c(1, 1),
  discount_function = "identity",
  fix_alpha = FALSE,
  alpha_max = 1,
  weibull_scale = 0.135,
  weibull_shape = 3,
  method = "fixed"
)
```

**Arguments**

- `treatment`  
  vector. treatment assignment for patients, 1 for treatment group and 0 for control group.
- `outcome`  
  vector. binomial outcome of the trial, 1 for response (success or failure), 0 for no response.
- `complete`  
  vector. similar length as treatment and outcome variable, 1 for complete outcome, 0 for loss to follow up. If complete is not provided, the dataset is assumed to be complete.
- `y0_treatment`  
  scalar. Number of events for the historical treatment arm.
- `N0_treatment`  
  scalar. Number of observations of the historical treatment group.
binomial_analysis

y0_control  scalar. Number of events for the historical control arm.
N0_control  scalar. Number of observations of the historical control group.
alternative  character. The string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided".
N_impute  scalar. Number of imputations for Monte Carlo simulation of missing data.
h0  scalar. Threshold for comparing two mean values. Default is h0=0.
number_mcmc  scalar. Number of Monte Carlo Markov Chain draws in sampling posterior.
prob_ha  scalar. Probability of alternative hypothesis.
futility_prob  scalar. Probability of stopping early for futility.
prior  vector. Prior values of beta rate, Beta(a0, b0). The default is set to Beta(1, 1).
discount_function  character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled-Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.
fix_alpha  logical. Fix alpha at alpha_max? Default value is FALSE.
alpha_max  scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.
weibull_scale  scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
weibull_shape  scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
method  character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the the bdpsurvival vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.
Value

a list of output for the Bayesian trial for binomial count.

prob_of_accepting_alternative scalar. The input parameter of probability of accepting the alternative.

margin scalar. The margin input value of difference between mean estimate of treatment and mean estimate of the control.

alternative character. The input parameter of alternative hypothesis.

N_treatment scalar. The number of patients enrolled in the experimental group for each simulation.

N_control scalar. The number of patients enrolled in the control group for each simulation.

N_enrolled vector. The number of patients enrolled in the trial (sum of control and experimental group for each simulation.)

N_complete scalar. The number of patients who completed the trial and had no loss to follow-up.

post_prob_accept_alternative vector. The final probability of accepting the alternative hypothesis after the analysis is done.

est_final scalar. The final estimate of the difference in posterior estimate of treatment and posterior estimate of the control group.

stop_futility scalar. Did the trial stop for futility during imputation of patient who had loss to follow up? 1 for yes and 0 for no.

stop_expected_success scalar. Did the trial stop for early success during imputation of patient who had loss to follow up? 1 for yes and 0 for no.

**Description**

*Wrapper function for proportion of an event in control and treatment group with binomial outcome.*

**Usage**

```r
binomial_outcome(p_treatment = NULL, p_control = NULL, .data = NULL)
```

**Arguments**

- **p_treatment** numeric. The proportion of an event in the treatment group, $0 < p_{treatment} < 1$.
- **p_control** numeric. The proportion of an event in the control group, $0 < p_{control} < 1$.
- **.data** NULL. stores the proportion of control and treatment, please do not fill it in.

**Value**

a list with proportion of control and treatment group.
**Examples**

```r
binomial_outcome(p_control = 0.12, p_treatment = 0.08)
```

**Description**

Wrapper function for data file in binomial analysis.

**Usage**

```r
data_binomial(treatment, outcome, complete, .data = NULL)
```

**Arguments**

- `treatment`: vector. treatment assignment for patients, 1 for treatment group and 0 for control group
- `outcome`: vector. binomial outcome of the trial, 1 for response (success or failure), 0 for no response.
- `complete`: vector. similar length as treatment and outcome variable, 1 for complete outcome, 0 for loss to follow up. If complete is not provided, the dataset is assumed to be complete.
- `data`: NULL. stores the binomial data for analysis, please do not fill it in.

**Value**

a list with treatment, outcome and loss to follow up vector with binomial outcome.

**Examples**

```r
data_binomial(treatment = c(0, 1), outcome = c(1, 1), complete = c(1, 1))
```

---

**data_normal**

**Description**

Wrapper function for data file in normal analysis.

**Usage**

```r
data_normal(treatment, outcome, complete, .data = NULL)
```

**Value**

- NULL. stores the normal data for analysis, please do not fill it in.
Arguments

- **treatment**: vector. treatment assignment for patients, 1 for treatment group and 0 for control group.
- **outcome**: vector. normal outcome of the trial.
- **complete**: vector. similar length as treatment and outcome variable, 1 for complete outcome, 0 for loss to follow up. If complete is not provided, the dataset is assumed to be complete.
- **.data**: NULL. stores the normal data for analysis, please do not fill it in.

Value

a list with treatment, outcome and loss to follow up vector with normal outcome.

data_survival Data file for survival analysis

Description

Wrapper function for data file in survival analysis.

Usage

data_survival(time, treatment, event, .data = NULL)

Arguments

- **time**: vector. exposure time for the subjects. It must be the same length as the treatment variable.
- **treatment**: vector. treatment assignment for patients, 1 for treatment group and 0 for control group.
- **event**: vector. The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For censored data, the status indicator is 0=right censored, 1 = event at time. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.
- **.data**: NULL. stores the survival data for analysis, please do not fill it in.

Value

a list with time, treatment, and event with time-to-event outcome.

Examples

```r
data_survival(time = c(6.2, 8.2, 8.0, 2.3),
              treatment = c(0, 1, 0, 1),
              event = c(1, 1, 1, 1))
```
**enrollment**

Simulating enrollment dates

**Description**

This function simulates enrollment dates using either poisson distribution

**Usage**

```
enrollment(param, N_total, time = NULL)
```

**Arguments**

- `param` a vector of lambda in poisson
- `N_total` a numeric value of total sample size
- `time` a vector of the `length(param) - 1` indicating end of time when a specific lambda is used

**Value**

a vector of enrollment dates

**Examples**

```
enrollment(param = c(0.003, 0.7), 100, time = 10)
enrollment(param = c(0.3, 0.5, 0.9, 1.2, 2.1), 200, c(20, 30, 40, 60))
```

---

**enrollment_rate**

Enrollment rate wrapper

**Description**

Wrapper function for enrollment rate.

**Usage**

```
enrollment_rate(lambda = 0.3, time = NULL, .data = NULL)
```

**Arguments**

- `lambda` vector. Vector with different enrollment rate parameters.
- `time` vector. Vector with different cut-off times for lambda.
- `.data` NULL. This should not be changed by the user.
Value

a list with enrollment rate information

Examples

enrollment_rate(lambda = c(0.3, 1), time = 25)

gamma_prior(a0 = 0.1, b0 = 0.1, .data = NULL)

Arguments

a0 numeric. The shape parameter in the gamma distribution (beta(a0, b0)).
b0 numeric. The scale parameter in the beta distribution (beta(a0, b0)).
.data NULL. stores the gamma prior rate, please do not fill it in.

Value

a list with vector of gamma rate for the gamma prior for treatment and control group.

Examples

gamma_prior(a0 = .1, b0 = .1)

historical_binomial Historical data for binomial distribution

Description

Wrapper function for historical data from binomial outcome.
historical_binomial

Usage

historical_binomial(
  y0_treatment = NULL,
  N0_treatment = NULL,
  discount_function = "identity",
  y0_control = NULL,
  N0_control = NULL,
  alpha_max = 1,
  fix_alpha = FALSE,
  weibull_scale = 0.135,
  weibull_shape = 3,
  method = "fixed",
  .data = NULL
)

Arguments

y0_treatment scalar. Number of events for the historical treatment arm.
N0_treatment scalar. Number of observations of the historical treatment group.
discount_function character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled-Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.
y0_control scalar. Number of events for the historical control arm.
N0_control scalar. Number of observations of the historical control group.
alpha_max scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.
fix_alpha logical. Fix alpha at alpha_max? Default value is FALSE.
weibull_scale scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
weibull_shape scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
historical_normal

method character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.

.data NULL. stores the proportion of control and treatment, please do not fill it in.

Value

a list with historical data for control and treatment group with the discount function.

Examples

historical_binomial(y0_treatment = 5, N0_treatment = 10, y0_control = 15, N0_control = 23)

historical_binomial(y0_treatment = 5, N0_treatment = 10, y0_control = 15, N0_control = 23,
  discount_function = "weibull", alpha_max = 1, fix_alpha = FALSE,
  weibull_scale = 0.135, weibull_shape = 3)

historical_normal

Historical data for normal distribution

Description

Wrapper function for historical data from normal outcome.

Usage

historical_normal(
  mu0_treatment = NULL,
  sd0_treatment = NULL,
  N0_treatment = NULL,
  mu0_control = NULL,
  sd0_control = NULL,
  N0_control = NULL,
  discount_function = "identity",
  alpha_max = 1,
  fix_alpha = FALSE,
  weibull_scale = 0.135,
  weibull_shape = 3,
  method = "fixed",
  .data = NULL
)
Arguments

- **mu0_treatment**: scalar. Mean of the historical treatment group.
- **sd0_treatment**: scalar. Standard deviation of the historical treatment group.
- **N0_treatment**: scalar. Number of observations of the historical treatment group.
- **mu0_control**: scalar. Mean of the historical control group.
- **sd0_control**: scalar. Standard deviation of the historical control group.
- **N0_control**: scalar. Number of observations of the historical control group.
- **discount_function**: character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled-Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.
- **alpha_max**: scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.
- **fix_alpha**: logical. Fix alpha at alpha_max? Default value is FALSE.
- **weibull_scale**: scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
- **weibull_shape**: scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
- **method**: character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the the bdpnormal vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.
- **.data**: NULL. stores the proportion of control and treatment, please do not fill it in.

Value

a list with historical data for control and treatment group with the discount function.
historical_survival

Examples

historical_normal(mu0_treatment = 15, sd0_treatment = 2, N0_treatment = 10,
                  mu0_control = 17, sd0_control = 3, N0_control = 20)

historical_survival  Historical data for survival analysis

Description

Wrapper function for historical data from time-to-event outcome.

Usage

historical_survival(
  time = NULL,
  treatment = NULL,
  event = NULL,
  discount_function = "identity",
  alpha_max = 1,
  fix_alpha = FALSE,
  weibull_scale = 0.135,
  weibull_shape = 3,
  method = "fixed",
  .data = NULL
)

Arguments

time  vector. exposure time for the subjects. It must be the same length as the treatment variable.
treatment  vector. treatment assignment for patients, 1 for treatment group and 0 for control group
event  vector. The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For censored data, the status indicator is 0=right censored, 1 = event at time. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.
discount_function  character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled-Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.
alpha_max scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.

fix_alpha logical. Fix alpha at alpha_max? Default value is FALSE.

weibull_scale scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".

weibull_shape scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".

method character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the the bdpsurvival vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.
.data NULL. stores the historical time, treatment and event, please do not fill it in.

Value

a list with historical data for time-to-event outcome with the discount function.

Examples

```r
historical_survival(time = rexp(10, 0.01),
                    treatment = rep(10, 1),
                    event = rep(10, 1))
```

---

**hypothesis**  

*Hypothesis wrapper*

Description

Wrapper function for the hypothesis in the trial.
Usage

hypothesis(
    delta = 0,
    futility_prob = 0.05,
    prob_accept_ha = 0.95,
    expected_success_prob = 0.9,
    alternative = "greater",
    .data = NULL
)

Arguments

delta numeric. Threshold set for margin in null hypothesis. The default is set to 0.
futility_prob numeric. Probability of futility. The default is 0.05.
prob_accept_ha numeric. Posterior probability of accepting alternative hypothesis. The default is 0.95.
expected_success_prob numeric. Probability of expected success.
alternative character. The string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided".
.data NULL. This should not be changed by the user.

Value

a list with information of hypothesis testing (threshold, futility probability, probability of accepting the alternative hypothesis, and probability of expected success).

Examples

hypothesis(delta = 0, futility_prob = 0.05, prob_accept_ha = 0.95,
          expected_success_prob = 0.90, alternative = "greater")
hypothesis(delta = 0.2, futility_prob = 0.1, prob_accept_ha = 0.975,
          expected_success_prob = 0.80, alternative = "less")

impute

Imputation wrapper

Description

Wrapper function for no_of_impute.

Usage

impute(no_of_impute = 10000, number_mcmc = 10000, .data = NULL)
normalBACT

Arguments

- `no_of_impute` integer. Number of Monte Carlo imputation for missing data.
- `number_mcmc` scalar. Number of Monte Carlo Markov Chain draws from posterior distribution.
- `.data` NULL. This should not be changed by the user.

Value

a list with number of imputation

Examples

```r
impute(no_of_impute = 100, number_mcmc = 1000)
```

Description

Simulation of normally distributed data for Bayesian adaptive trials with various inputs to control for power, sample size, type I error rate, etc.

Usage

```r
normalBACT(
  mu_treatment,
  sd_treatment,
  mu_control = NULL,
  sd_control = NULL,
  mu0_treatment = NULL,
  sd0_treatment = NULL,
  N0_treatment = NULL,
  mu0_control = NULL,
  sd0_control = NULL,
  N0_control = NULL,
  N_total,
  lambda = 0.3,
  lambda_time = NULL,
  interim_look = NULL,
  EndofStudy,
  block = 2,
  rand_ratio = c(1, 1),
  discount_function = "identity",
  alternative = "greater",
  prop_loss_to_followup = 0.15,
  h0 = 0,
  futility_prob = 0.05,
)```
expected_success_prob = 0.9,
prob_ha = 0.95,
N_impute = 10,
number_mcmc = 10000,
alpha_max = 1,
fix_alpha = FALSE,
weibull_scale = 0.135,
weibull_shape = 3,
method = "fixed"
)

Arguments

mu_treatment  scalar. Mean outcome in the treatment arm.

sd_treatment  scalar. Standard deviation of outcome in the treatment

mu_control  scalar. Mean outcome in the control arm.

sd_control  scalar. Standard deviation of outcome in the control arm.

mu0_treatment  scalar. Mean of the historical treatment group.

sd0_treatment  scalar. Standard deviation of the historical treatment group.

N0_treatment  scalar. Number of observations of the historical treatment group.

mu0_control  scalar. Mean of the historical control group.

sd0_control  scalar. Standard deviation of the historical control group.

N0_control  scalar. Number of observations of the historical control group.

N_total  scalar. Total sample size.

lambda  vector. Enrollment rates across simulated enrollment times. See enrollment for more details.

lambda_time  vector. Enrollment time(s) at which the enrollment rates change. Must be same length as lambda. See enrollment for more details.

interim_look  vector. Sample size for each interim look. Note: the maximum sample size should not be included.

EndofStudy  scalar. Length of the study.

block  scalar. Block size for generating the randomization schedule.

rand_ratio  vector. Randomization allocation for the ratio of control to treatment. Integer values mapping the size of the block. See randomization for more details.

discount_function  character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled-Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.

alternative  character. The string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided".
prop_loss_to_followup
scalar. Overall proportion of subjects lost to follow-up.

h0
scalar. Threshold for comparing two mean values. Default is h0=0.

futility_prob
scalar. Probability of stopping early for futility.

expected_success_prob
scalar. Probability of stopping early for success.

prob_ha
scalar. Probability of alternative hypothesis.

N_impute
scalar. Number of imputations for Monte Carlo simulation of missing data.

number_mcmc
scalar. Number of Monte Carlo Markov Chain draws in sampling posterior.

alpha_max
scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.

fix_alpha
logical. Fix alpha at alpha_max? Default value is FALSE.

weibull_scale
scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".

weibull_shape
scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".

method
character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the the bdpsurvival vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.

Value

a list of output for a single trial simulation.

mu_treatment scalar. The input parameter of mean value of the outcome in the treatment group.

mu_control scalar. The input parameter of mean value of the outcome in the control group.

sd_treatment scalar. The input parameter of standard deviation of the outcome in the control group.

sd_control scalar. The input parameter of standard deviation of the outcome in the control group.

prob_of_accepting_alternative scalar. The input parameter of probability threshold of accepting the alternative.

margin scalar. The margin input value of difference between mean estimate of treatment and mean estimate of the control.
alternative character. The input parameter of alternative hypothesis.
interim_look vector. The sample size for each interim look.
N_treatment scalar. The number of patients enrolled in the experimental group for each simulation.
N_control scalar. The number of patients enrolled in the control group for each simulation.
N_enrolled vector. The number of patients enrolled in the trial (sum of control and experimental group for each simulation.)
N_complete scalar. The number of patients who completed the trial and had no loss to follow-up.
post_prob_accept_alternative vector. The final probability of accepting the alternative hypothesis after the analysis is done.
est_final scalar. The final estimate of the difference in posterior estimate of treatment and posterior estimate of the control group.
stop_futility scalar. Did the trial stop for futility during imputation of patient who had loss to follow up? 1 for yes and 0 for no.
stop_expected_success scalar. Did the trial stop for early success during imputation of patient who had loss to follow up? 1 for yes and 0 for no.
est_interim scalar. The interim estimate of the difference in posterior estimate of treatment and posterior estimate of the control group.

normaldata Gaussian dataset for analyzing adaptive Bayesian trials

Description
A dataset containing the results of 300 patients with continuous (normal) outcome, the dataset is filled with loss to follow up.

Usage
data(normaldata)

Format
A data frame with 300 rows and 4 variables:
id Patient ID in the trial
treatment treatment assignment for patients, 1 for treatment group 0 for control group
outcome continuous outcome of the trial (gaussian distribution)
complete 1 for complete outcome, 0 for loss to follow up

Examples
data(normaldata)
**normal_analysis**  
*Analyzing Bayesian trial for normal mean data*

**Description**

Function to analyze Bayesian trial for normal mean data which allows early stopping and incorporation of historical data using the discount function approach.

**Usage**

```r
normal_analysis(
  treatment,
  outcome,
  complete = NULL,
  mu0_treatment = NULL,
  sd0_treatment = NULL,
  N0_treatment = NULL,
  mu0_control = NULL,
  sd0_control = NULL,
  N0_control = NULL,
  alternative = "greater",
  N_impute = 100,
  h0 = 0,
  number_mcmc = 10000,
  prob_ha = 0.95,
  futility_prob = 0.1,
  expected_success_prob = 0.9,
  discount_function = "identity",
  fix_alpha = FALSE,
  alpha_max = 1,
  weibull_scale = 0.135,
  weibull_shape = 3,
  method = "fixed"
)
```

**Arguments**

- `treatment`: vector. Treatment assignment for patients, 1 for treatment group and 0 for control group.
- `outcome`: vector. Normal outcome of the trial.
- `complete`: vector. Similar length as treatment and outcome variable, 1 for complete outcome, 0 for loss to follow up. If complete is not provided, the dataset is assumed to be complete.
- `mu0_treatment`: scalar. Mean of the historical treatment group.
- `sd0_treatment`: scalar. Standard deviation of the historical treatment group.
normal_analysis

N0_treatment  scalar. Number of observations of the historical treatment group.
mu0_control  scalar. Mean of the historical control group.
sd0_control  scalar. Standard deviation of the historical control group.
N0_control  scalar. Number of observations of the historical control group.
alternative  character. The string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided".
N_impute  scalar. Number of imputations for Monte Carlo simulation of missing data.
h0  scalar. Threshold for comparing two mean values. Default is h0=0.
number_mcmc  scalar. Number of Monte Carlo Markov Chain draws in sampling posterior.
prob_ha  scalar. Probability of alternative hypothesis.
futility_prob  scalar. Probability of stopping early for futility.
discount_function  character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled-Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.
fix_alpha  logical. Fix alpha at alpha_max? Default value is FALSE.
alpha_max  scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.
weibull_scale  scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
weibull_shape  scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
method  character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the the bdpsurvival vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.
Value

a list of output for the analysis of Bayesian trial for normal mean.

prob_of_accepting_alternative scalar. The input parameter of probability of accepting the alternative.

margin scalar. The margin input value of difference between mean estimate of treatment and mean estimate of the control.

alternative character. The input parameter of alternative hypothesis.

N_treatment scalar. The number of patients enrolled in the experimental group for each simulation.

N_control scalar. The number of patients enrolled in the control group for each simulation.

N_enrolled vector. The number of patients enrolled in the trial (sum of control and experimental group for each simulation.)

N_complete scalar. The number of patients who completed the trial and had no loss to follow-up.

post_prob_accept_alternative vector. The final probability of accepting the alternative hypothesis after the analysis is done.

est_final scalar. The final estimate of the difference in posterior estimate of treatment and posterior estimate of the control group.

stop_futility scalar. Did the trial stop for futility during imputation of patient who had loss to follow up? 1 for yes and 0 for no.

stop_expected_success scalar. Did the trial stop for early success during imputation of patient who had loss to follow up? 1 for yes and 0 for no.

---

normal_outcome Parameters for treatment and control in normal case

Description

Wrapper function for mean and standard deviation with normal outcome.

Usage

normal_outcome(
    mu_control = NULL,
    sd_control = NULL,
    mu_treatment = NULL,
    sd_treatment = NULL,
    data = NULL
)
pw_exp_impute

Arguments

- mu_control: numeric. The mean for the control group.
- sd_control: numeric. The standard deviation for the control group.
- mu_treatment: numeric. The mean for the treatment group.
- sd_treatment: numeric. The standard deviation for the treatment group.
- data: NULL. stores the proportion of control and treatment, please do not fill it in.

Value

a list with proportion of control and treatment group.

Examples

- normal_outcome(mu_control = 12, mu_treatment = 8, sd_treatment = 2.2, sd_control = 1.6)

pw_exp_impute

Imputes time-to-event outcomes.

Description

Imputation of time-to-event outcomes using the piecewise constant hazard exponential function.

Usage

pw_exp_impute(time, hazard, maxtime = NULL, cutpoint = NULL)

Arguments

- time: vector. The observed time for patient that have had no event or passed maxtime.
- hazard: vector. The constant hazard rates for exponential failures.
- maxtime: scalar. maximum time before end of study.
- cutpoint: vector. The change-point vector indicating time when the hazard rates change.

Value

a dataset with simulated follow-up time (time) and respective event indicator (1 = event, 0 = censoring)

Examples

- pw_exp_impute(time = c(120), c(0.005, 0.001), 110, 40)
- pw_exp_impute(time = c(10, 20, 30), c(0.005, 0.01, 0.02), 100, c(40, 80))
- pw_exp_impute(time = c(40, 30), c(0.005, 0.01), 120, c(50))
**pw_exp_sim**

Simulates time-to-event outcomes.

**Description**

Simulation of time-to-event outcomes using the piecewise constant hazard exponential function.

**Usage**

```r
pw_exp_sim(hazard, n, maxtime = NULL, cutpoint = NULL)
```

**Arguments**

- `hazard`: vector. The constant hazard rates for exponential failures.
- `n`: scalar. The number of outcomes for simulation.
- `maxtime`: scalar. Maximum time before end of study.
- `cutpoint`: vector. The change-point vector indicating time when the hazard rates change.

**Value**

A dataset with simulated follow-up time (time) and respective event indicator (1 = event, 0 = censoring)

**Examples**

```r
pw_exp_sim(c(0.02, 0.01, 0.005), 100, 100, c(10, 20))
pw_exp_sim(0.015, 100, 100)
```

---

**randomization**

Randomization allocation

**Description**

Implements a randomization allocation for control and treatment arms with different randomization ratios and block sizes.

**Usage**

```r
randomization(N_total, block = 2, allocation = c(1, 1))
```
randomize

Randomization scheme wrapper

Description
Wrapper function for the randomization scheme in the trial.

Usage
randomize(block_size = 2, randomization_ratio = c(1, 1), .data = NULL)

Arguments

block_size       integer. Block size for the complete randomization in a block.
randomization_ratio vector. The randomization allocation for control to treatment.
.data            NULL. This should not be changed by the user.

Value
a list with randomization details (block size and ratio).
Examples

```r
randomize(block_size = 100, randomization_ratio = c(2, 3))
randomize(block_size = 10, randomization_ratio = c(1, 4))
```

Description

Wrapper function for complete binomial and normal function to compute power and type I error.

Usage

```r
simulate(input, no_of_sim = 10000, .data = NULL)
```

Arguments

- **input**: list. Input function for all inputs in binomial and normal.
- **no_of_sim**: numeric. Number of simulations to run.
- **.data**: NULL. stores the proportion of control and treatment, please do not fill it in.

Value

A list with results of the simulation (power and type I error) and the input.

- **input**: A list of input values used in the trial simulation.
- **power**: data_frame. A data frame with the interim look and power at each look.
- **type1_error**: scalar. The type I error or the number of times the trial rejects the null when the parameters are simulated under the null hypothesis.
- **est_final**: vector. The final estimate of the difference in posterior estimate of treatment and posterior estimate of the control group for all the simulation.
- **post_prob_accept_alternative**: vector. The final probability of accepting the alternative for the simulations.
- **N_enrolled**: vector. The number of patients enrolled in the trial (sum of control and experimental group for each simulation.)
- **stop_futility**: vector. Did the trial stop for futility during imputation of patient who had loss to follow up? 1 for yes and 0 for no.
- **stop_expected_success**: vector. Did the trial stop for early success during imputation of patient who had loss to follow up? 1 for yes and 0 for no.
study_details  Details of the clinical study

Description
Wrapper function for details of the clinical trial simulation.

Usage
study_details(
  total_sample_size,
  study_period,
  interim_look = NULL,
  prop_loss_to_followup = 0.1,
  .data = NULL
)

Arguments
- total_sample_size: integer. The number of sample size needed.
- study_period: integer. The length of the study.
- interim_look: vector. Vector with interim looks.
- prop_loss_to_followup: integer. The proportion of loss to follow up.
- .data: NULL. This should not be changed by the user.

Value
a list with sample size, length of the study, interim looks and proportion loss to follow up

Examples
study_details(total_sample_size = 300, study_period = 50, interim_look = c(210, 240, 270))

survivalBACT  Time-to-event outcome for Bayesian Adaptive Trials

Description
Simulation for time-to-event outcome for Bayesian Adaptive trial with different inputs to control for power, sample size, type 1 error rate, etc.
Usage

survivalBACT(
    hazard_treatment,
    cutpoint = NULL,
    hazard_control = NULL,
    N_total,
    breaks = NULL,
    time0 = NULL,
    treatment0 = NULL,
    event0 = NULL,
    lambda = 0.3,
    lambda_time = NULL,
    interim_look = NULL,
    EndofStudy,
    prior = c(0.1, 0.1),
    block = 2,
    rand_ratio = c(1, 1),
    prop_loss_to_followup = 0.1,
    alternative = "greater",
    h0 = 0,
    futility_prob = 0.05,
    expected_success_prob = 0.9,
    prob_ha = 0.95,
    N_impute = 10,
    number_mcmc = 10000,
    discount_function = "identity",
    alpha_max = 1,
    fix_alpha = FALSE,
    weibull_scale = 0.135,
    weibull_shape = 3,
    method = "fixed"
)

Arguments

hazard_treatment
    vector. Constant hazard rates under the treatment arm.
cutpoint
    vector. The change-point vector indicating time when the hazard rates change.
hazard_control
    vector. Constant hazard rates under the control arm.
N_total
    scalar. Total sample size.
breaks
    vector. Breaks (interval starts) used to compose the breaks of the piecewise exponential model. Do not include zero. Default breaks are the quantiles of the input times.
time0
    vector. Historical exposure time for the subjects. It must be the same length as the treatment variable.
treatment0
    vector. The historical treatment assignment for patients, 1 for treatment group and 0 for control group.
event0 vector. Historical status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For censored data, the status indicator is 0=right censored, 1 = event at time. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.

lambda vector. Enrollment rates across simulated enrollment times. See enrollment for more details.

lambda_time vector. Enrollment time(s) at which the enrollment rates change. Must be same length as lambda. See enrollment for more details.

interim_look vector. Sample size for each interim look. Note: the maximum sample size should not be included.

EndofStudy scalar. Length of the study.

prior vector. Prior values of the gamma rate, Gamma(a0, b0). The default is set to Gamma(.1,.1).

block scalar. Block size for generating the randomization schedule.

rand_ratio vector. Randomization allocation for the ratio of control to treatment. Integer values mapping the size of the block. See randomization for more details.

prop_loss_to_followup scalar. Overall proportion of subjects lost to follow-up.

alternative character. The string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided".

h0 scalar. Threshold for comparing two mean values. Default is h0=0.

futility_prob scalar. Probability of stopping early for futility.


prob_ha scalar. Probability of alternative hypothesis.

N_impute scalar. Number of imputations for Monte Carlo simulation of missing data.

number_mcmc scalar. Number of Monte Carlo Markov Chain draws in sampling posterior.

discount_function character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled-Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.

alpha_max scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.

fix_alpha logical. Fix alpha at alpha_max? Default value is FALSE.
weibull_scale  scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".

weibull_shape  scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".

method  character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the the bdpsurvival vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.

Value

a list of output for a single trial simulation.

lambda_treatment  vector. The input parameter of constant hazard rates in the treatment group.

cutpoint_treatment  vector. The change-point vector when the constant hazard rate(s) changes for the treatment group.

lambda_control  vector. The input parameter of constant hazard rates in the control group.

cutpoint_control  vector. The change-point vector when the constant hazard rate(s) changes for the control group.

prob_of_accepting_alternative  scalar. The input parameter of probability threshold of accepting the alternative.

margin  scalar. The margin input value of difference between mean estimate of treatment and mean estimate of the control.

alternative  character. The input parameter of alternative hypothesis.

interim_look  vector. The sample size for each interim look.

N_treatment  scalar. The number of patients enrolled in the treatment group for each simulation.

event_treatment  scalar. The number of events in the treatment group for each simulation.

N_control  scalar. The number of patients enrolled in the control group for each simulation.

event_control  scalar. The number of events in the control group for each simulation.

N_enrolled  vector. The number of patients enrolled in the trial (sum of control and experimental group for each simulation.)

N_complete  scalar. The number of patients who completed the trial and had no loss to follow-up.

post_prob_accept_alternative  vector. The final probability of accepting the alternative hypothesis after the analysis is done.
est_final scalar. The final estimate of the difference in posterior estimate of treatment and posterior estimate of the control group.

stop_futility scalar. Did the trial stop for futility during imputation of patient who had loss to follow up? 1 for yes and 0 for no.

stop_expected_success scalar. Did the trial stop for early success during imputation of patient who had loss to follow up? 1 for yes and 0 for no.

est_interim scalar. The interim estimate of the difference in posterior estimate of treatment and posterior estimate of the control group.

---

**survivaldata**  
*Time-to-event dataset for analyzing adaptive Bayesian trials*

**Description**

A dataset containing the results of 100 patients with time-to-event outcome, the dataset is filled with treatment assignment and status (0 = censored, 1 = not censored).

**Usage**

```r
data(survivaldata)
```

**Format**

A data frame with 100 rows and 4 variables:

- **id** Patient ID in the trial
- **treatment** treatment assignment for patients, 1 for treatment group 0 for control group
- **time** the follow up time for patients
- **event** The status indicator, normally 0=alive, 1=dead or 0 = no event, 1 = event occurred

**Examples**

```r
data(survivaldata)
```
survival_analysis

Analyzing Bayesian trial for time-to-event data

Description

Function to analyze Bayesian trial for time-to-event data which allows early stopping and incorporation of historical data using the discount function approach

Usage

survival_analysis(
  time,
  treatment,
  event = NULL,
  time0 = NULL,
  treatment0 = NULL,
  event0 = NULL,
  surv_time = NULL,
  h0 = 0,
  breaks = NULL,
  alternative = "greater",
  N_impute = 10,
  number_mcmc = 10000,
  prob_ha = 0.95,
  futility_prob = 0.1,
  expected_success_prob = 0.9,
  prior = c(0.1, 0.1),
  discount_function = "identity",
  fix_alpha = FALSE,
  alpha_max = 1,
  weibull_scale = 0.135,
  weibull_shape = 3,
  method = "fixed"
)

Arguments

time: vector. exposure time for the subjects. It must be the same length as the treatment variable.
treatment: vector. treatment assignment for patients, 1 for treatment group and 0 for control group
event: vector. The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For censored data, the status indicator is 0=right censored, 1 = event at time. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.
time0 vector. Historical exposure time for the subjects. It must be the same length as the treatment variable.

treatment0 vector. the historical treatment assignment for patients, 1 for treatment group and 0 for control group.

event0 vector. Historical status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For censored data, the status indicator is 0=right censored, 1 = event at time. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.

surv_time scalar. scalar. Survival time of interest for computing the probability of survival for a single arm (OPC) trial. Default is overall, i.e., current+historical, median survival time.

h0 scalar. Threshold for comparing two mean values. Default is h0=0.

breaks vector. Breaks (interval starts) used to compose the breaks of the piecewise exponential model. Do not include zero. Default breaks are the quantiles of the input times.

alternative character. The string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided".

N_impute scalar. Number of imputations for Monte Carlo simulation of missing data.

number_mcmc scalar. Number of Monte Carlo Markov Chain draws in sampling posterior.

prob_ha scalar. Probability of alternative hypothesis.

futility_prob scalar. Probability of stopping early for futility.


prior vector. Prior values of the gamma rate, Gamma(a0, b0). The default is set to Gamma(.1,.1).

discount_function character. If incorporating historical data, specify the discount function. Currently supports the Weibull function (discount_function="weibull"), the scaled- Weibull function (discount_function="scaledweibull"), and the identity function (discount_function="identity"). The scaled-Weibull discount function scales the output of the Weibull CDF to have a max value of 1. The identity discount function uses the posterior probability directly as the discount weight. Default value is "identity". See bdpnormal for more details.

fix_alpha logical. Fix alpha at alpha_max? Default value is FALSE.

alpha_max scalar. Maximum weight the discount function can apply. Default is 1. For a two-arm trial, users may specify a vector of two values where the first value is used to weight the historical treatment group and the second value is used to weight the historical control group.

weibull_scale scalar. Scale parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 0.135. For a two- arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".
weibull_shape scalar. Shape parameter of the Weibull discount function used to compute alpha, the weight parameter of the historical data. Default value is 3. For a two-arm trial, users may specify a vector of two values where the first value is used to estimate the weight of the historical treatment group and the second value is used to estimate the weight of the historical control group. Not used when discount_function = "identity".

method character. Analysis method with respect to estimation of the weight parameter alpha. Default method "mc" estimates alpha for each Monte Carlo iteration. Alternate value "fixed" estimates alpha once and holds it fixed throughout the analysis. See the the bdpsurvival vignette vignette("bdpsurvival-vignette", package="bayesDP") for more details.

Value

a list of output for the Bayesian trial for time-to-event.

prob_of_accepting_alternative scalar. The input parameter of probability of accepting the alternative.

margin scalar. The margin input value of difference between mean estimate of treatment and mean estimate of the control.

alternative character. The input parameter of alternative hypothesis.

alpha_max scalar. The alpha_max input.

N_treatment scalar. The number of patients enrolled in the experimental group for each simulation.

event_treatment scalar. The number of events in the experimental group for each simulation.

N_control scalar. The number of patients enrolled in the control group for each simulation.

event_control scalar. The number of events in the control group for each simulation.

N_enrolled scalar. The number of patients enrolled in the trial (sum of control and experimental group for each simulation. )

N_complete scalar. The number of patients whose time passes the surv_time.

alpha_discount vector. The alpha discount funtion used for control and treatment.

post_prob_accept_alternative vector. The final probability of accepting the alternative hypothesis after the analysis is done.

est_final scalar. The final estimate of the difference in posterior estimate of treatment and posterior estimate of the control group.

stop_futility scalar. Did the trial stop for futility during imputation of patient who had loss to follow up? 1 for yes and 0 for no.

stop_expected_success scalar. Did the trial stop for early success during imputation of patient who had loss to follow up? 1 for yes and 0 for no.
survival_outcome  Piecewise constant hazard rates and the cutpoint for control and treatment group

Description

Wrapper function for the piecewise constant hazard rates and the cutpoint for control and treatment group.

Usage

```r
survival_outcome(
  hazard_treatment = NULL,
  cutpoint = NULL,
  hazard_control = NULL,
  .data = NULL
)
```

Arguments

- `hazard_treatment`  
  vector. Constant hazard rates under the treatment arm.
- `cutpoint`  
  vector. The change-point vector indicating time when the hazard rates change.
- `hazard_control`  
  vector. Constant hazard rates under the control arm.
- `.data`  
  NULL. stores the hazard rates and cutpoint, please do not fill it in.

Value

a list with hazard rates and cutpoint for control and treatment group.

Examples

```r
survival_outcome(hazard_treatment = 0.06,
  hazard_control = 0.08,
  cutpoint = NULL )
```
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