

Package ‘brar’

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Title Null Hypothesis Bayesian Response-Adaptive Randomization

Description Implements Bayesian response-adaptive randomization methods based on Bayesian hypothesis testing for multi-arm settings (Pawel and Held, 2025, <[doi:10.48550/arXiv.2510.01734](https://doi.org/10.48550/arXiv.2510.01734)>).

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Encoding UTF-8

Imports mvtnorm

Suggests roxygen2, tinytest

NeedsCompilation no

URL <https://github.com/SamCH93/brar>

BugReports <https://github.com/SamCH93/brar/issues>

Config/roxygen2/version 8.0.0

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brar_binomial

*Bayesian response-adaptive randomization for binomial outcomes***Description**

This function computes Bayes factors, posterior probabilities, and response-adaptive randomization probabilities for binomial outcomes.

Usage

```
brar_binomial(
  y,
  n,
  a0 = 1,
  b0 = 1,
  a = rep(1, length(y)),
  b = rep(1, length(y)),
  pH0 = 0.5,
  ...
)
```

Arguments

y	Vector with the number of successes in each group. The first element corresponds to the control group, and the remaining elements correspond to the treatment groups
n	Vector with the number of observations in each group. The first element corresponds to the control group, and the remaining elements correspond to the treatment groups
a0	First shape parameter of the beta prior for the common success probability under the null hypothesis. Can be interpreted as prior number of successes. Defaults to 1
b0	Second shape parameter of the beta prior for the common success probability under the null hypothesis. Can be interpreted as prior number of failures. Defaults to 1
a	Vector of first shape parameters of the beta priors for the success probabilities under the alternative hypothesis. Can be interpreted as prior numbers of successes. The first element corresponds to the control group, and the remaining elements correspond to the treatment groups. Defaults to <code>rep(1, length(y))</code>
b	Vector of second shape parameters of the beta priors for the success probabilities under the alternative hypothesis. Can be interpreted as prior numbers of failures. The first element corresponds to the control group, and the remaining elements correspond to the treatment groups. Defaults to <code>rep(1, length(y))</code>
pH0	Prior probability of the null hypothesis (i.e., a common probability in the control and all treatment groups). Defaults to 0.5. Set to 0 to obtain Thompson sampling and to 1 to obtain equal randomization

... Other arguments passed to `stats::integrate`

Value

An object of class "brar". This is a list with the following elements:

`data` The input data.

`prior` Prior probabilities of the null hypothesis and of each group being superior to all other groups.

`BF_ij` Matrix of Bayes factors. Entry (i, j) is the Bayes factor of hypothesis i against hypothesis j.

`posterior` Posterior probabilities of the null hypothesis and of each group being superior to all other groups.

`prand` Response-adaptive randomization probabilities

Author(s)

Samuel Pawel

Examples

```
## 1 control and 1 treatment group
y <- c(15, 12)
n <- c(20, 15)
brar_binomial(y = y, n = n, pH0 = 0.5)

## 1 control and 5 treatment groups
y <- c(10, 10, 10, 10, 10, 10)
n <- c(15, 15, 20, 17, 13, 25)
brar_binomial(y = y, n = n, pH0 = 0.5)
```

brar_normal	<i>Bayesian response-adaptive randomization for approximately normal effect estimates</i>
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Description

This function computes Bayes factors, posterior probabilities, and response-adaptive randomization probabilities for data summarized by approximately normal effect estimates.

Usage

```
brar_normal(estimate, sigma, pm = rep(0, length(estimate)), psigma, pH0 = 0.5)
```

Arguments

estimate	Vector of effect estimates (e.g., a vector of mean differences or log odds/hazard/rate ratios). Each estimate quantifies the effect of a treatment relative to control
sigma	Covariance matrix of the effect estimate vector. If there is only one effect estimate, this is the squared standard error of the estimate
pm	Mean vector of the normal prior assigned to the effects under the alternative hypothesis. Defaults to <code>rep(0, length(estimate))</code>
psigma	Covariance matrix of the normal prior assigned to the effects under the alternative hypothesis. If there is only one effect estimate, this is the prior variance
pH0	Prior probability of the point null hypothesis (i.e., all treatment effects equal to 0). Defaults to 0.5. Set to 0 to obtain Thompson sampling and to 1 to obtain equal randomization

Value

An object of class "brar". This is a list with the following elements:

`data` The input data.
`prior` Prior probabilities of the null hypothesis and of each group being superior to all other groups.
`BF_ij` Matrix of Bayes factors. Entry (i, j) is the Bayes factor of hypothesis i against hypothesis j.
`posterior` Posterior probabilities of the null hypothesis and of each group being superior to all other groups.
`prand` Response-adaptive randomization probabilities

Author(s)

Samuel Pawel

Examples

```
## simulate normal data from a control group and four treatment groups
set.seed(42)
n <- 10
muc <- 0
datc <- data.frame(y = rnorm(n, muc), group = "Control")
mu <- c(1, -0.5, 0, 0.25)
K <- length(mu)
datt <- do.call("rbind", lapply(seq(1, K), function(k) {
  data.frame(y = rnorm(n, mu[k]), group = paste("Treatment", k))
}))
dat <- rbind(datc, datt)
fit <- lm(y ~ group, data = dat)
estimate <- fit$coef[-1]
sigma <- vcov(fit)[-1,-1]
pm <- rep(0, K)

## prior correlation 0.5 gives the control and each treatment the same prior
## probability of being the best group
```

```
rho <- 0.5
psigma <- matrix(rho, nrow = K, ncol = K)
diag(psigma) <- 1
brar_normal(estimate = estimate, sigma = sigma, pm = pm, psigma = psigma,
            pH0 = 0.5)

## brar for the first treatment group only
est <- summary(fit)$coefficients[2,1]
se <- summary(fit)$coefficients[2,2]
brar_normal(est, sigma = se^2, pm = 0, psigma = 1, pH0 = 0.5)
```

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