

# Package: BayesAT (via r-universe)

March 7, 2025

**Type** Package

**Title** Bayesian Adaptive Trial

**Version** 0.1.0

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**Description** Bayesian adaptive trial algorithm implements multiple-stage interim analysis. Package includes data generating function, and Bayesian hypothesis testing function.

**License** GPL-3

**Encoding** UTF-8

**RoxygenNote** 7.2.3

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2025-02-05 18:20:09 UTC

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 BayesAT

*Bayesian adaptive trial interim analysis*


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## Description

BayesAT conducts Bayesian adaptive trials through multiple-stage interim analysis.

## Usage

```
BayesAT(
  data,
  D,
  stage,
  threshold,
  start,
  objective,
  alpha,
  beta,
  boundary = NULL
)
```

## Arguments

<code>data</code>	Matrix. The data contains both survival time and event status.
<code>D</code>	Numerical. The duration of interim analysis, matching the length of enrollment time.
<code>stage</code>	Integer. Numbers of interim analysis stages.
<code>threshold</code>	Numerical. The value tested against hypothesis or evidence.
<code>start</code>	Numerical. The time point when the interim analysis starts.
<code>objective</code>	Numerical. The time point for predicted survival rate, for example, 2 years, or 5 years survival probability.
<code>alpha</code>	Numerical. Gamma distribution alpha parameter.
<code>beta</code>	Numerical. Gamma distribution beta parameter (rate = 1/scale).
<code>boundary</code>	The stopping criterion for interim analysis, and the default sets at 5% significance level and calculate quantiles by <code>qnorm()</code> for each stages.

## Value

Interim analysis reporting Bayesian adaptive trial results.

If there is one data set applied to BayesAT, the result will provide a table containing:

Upper bound can be used as stopping criterion for efficacy;

Lower bound can be used as stopping criterion for futility;

Z score Z statistic is calculated based on the predicted survival probability:

$$\frac{\hat{S} - S_0}{SD(\hat{S})}$$

with predicted mean survival rate  $\hat{S}$  and test evidence or threshold  $S_0$ .

Efficacy Prob and Futility Prob Predictive probability measures the efficacy or futility, such as  $P(\hat{S} > \text{Efficacy})$  and  $P(\hat{S} < \text{Futility})$ .

Efficacy and Futility indicate the interim analysis results: + means the trial reach the stopping criterion, otherwise it is -.

### Examples

```
data <- Simulate_Enroll(n = c(30,20,20,15,30), lambda = 0.03,
                      event = 0.1, M = 3, group = 5, maxt = 5,
                      accrual = 3, censor = 0.9, followup = 2,
                      partition = "Uneven")
## assign patients in each group analyzed at each stage of time points
IA <- BayesAT(data,D = 3,stage = 5,threshold = 0.9, start = 1.5,
              objective = 2, alpha = 3, beta = 82)
summary(IA)
plot(IA)
```

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Bayes\_test

*Bayesian inference for survival analysis*

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### Description

Bayes\_test conduct hypothesis test through Bayesian survival model

### Usage

```
Bayes_test(data, alpha, beta, test, threshold, type, pred, diagnosis = FALSE)
```

### Arguments

data	Matrix. The data contains both survival time and event status.
alpha	Numerical. Gamma distribution alpha parameter.
beta	Numerical. Gamma distribution beta parameter (rate = 1/scale).
test	Categorical. Three types of hypothesis includes "greater", "less", or "two_sided".
threshold	Numerical. The value tested against hypothesis or evidence.
type	Categorical. The types of Bayesian inference include "Posterior" for estimation of parameters or "Predictive" for predicted survival rate.
pred	Numerical. The time point for predicted survival rate, for example, 2 years, or 5 years survival probability.
diagnosis	Logical. If diagnosis == TRUE, the Bayes factor is calculated, and the formulation of Bayesian factors is given in details.

**Value**

Bayesian test provide mean, sd, CI, z\_score, prob, and bf.

mean Posterior mean is estimated by calculating the mean of MCMC outputs.

sd Posterior standard deviation is estimated as the standard deviation of MCMC outputs.

CI Summary statistics provides the credible intervals and specific quantile.

z\_score Standardized test of statistics is calculated based on MCMC outputs. For example,

$$\frac{\hat{\lambda} - \lambda_0}{SD(\hat{\lambda})} \text{ or } \frac{\hat{S} - S_0}{SD(\hat{S})},$$

where  $\hat{\lambda}$  is the estimated posterior mean of hazard rate, and  $\hat{S}$  is the predicted survival probability. Both  $\lambda_0$  and  $S_0$  are threshold used for test against hypothesis or evidence.

prob Posterior probability:  $P(\hat{\lambda} > \lambda_0)$  if test is "greater",  $P(\hat{\lambda} \leq \lambda_0)$  if test is "less", and  $2\min(P(\hat{\lambda} > \lambda_0), P(\hat{\lambda} \leq \lambda_0))$  if test is "two-sided".

bf Bayes Factor is calculated if diagnosis = TRUE, and the comparison model is non-informative prior, Jeffreys prior,  $\pi \propto 1/\lambda$ .

**References**

Jeffreys, H. (1946). An invariant form for the prior probability in estimation problems. Proceedings of the Royal Society of London. Series A. Mathematical and Physical Sciences, 186(1007), 453-461.

Kass, R. E., & Raftery, A. E. (1995). Bayes factors. Journal of the american statistical association, 90(430), 773-795.

**Examples**

```
data <- Simulate_Enroll(n = c(50,20,20), lambda = 0.03,
                      event = 0.1, M = 1, group = 3,
                      maxt = 5, accrual = 3, censor = 0.9,
                      followup = 2,partition = "Uneven")
test <- Bayes_test(data, alpha = 3, beta = 82, test = "greater",
                  pred = 2, threshold = 0.9, type = "Predictive",
                  diagnosis = TRUE)

print(test)
```

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 Simulate\_Enroll

*Survival data simulation*


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**Description**

Simulate\_Enroll generates multiple streams of data sets with survival time, censoring status, and enrollment time.

**Usage**

```

Simulate_Enroll(
  n,
  lambda,
  event,
  M,
  group,
  maxt,
  accrual,
  censor,
  followup,
  partition = "Even"
)

```

**Arguments**

n	Integer. Sample size of patients
lambda	Numerical range 0 and 1. Hazard rate of exponential distribution
event	Numerical range 0 and 1. Event rate
M	Integer. Number of trials generated for multiple streams of MCMC
group	Integer. Number of subgroup for patient enrollment
maxt	Numerical. The maximum time length of entire trial
accrual	Numerical. The duration of patient enrolment
censor	Numerical range 0 and 1. The censoring rate of patients leaving before trial ends.
followup	Integer. The time length of follow up.
partition	Logical. If partition == "Even", the trial recruits equal numbers of patients in each stage. If partition == "Uneven", the trial recruits unequal numbers of patients in each stage.

**Value**

Simulated survival data contain both survival time, censoring status, and enrollment time.

**Examples**

```

data <- Simulate_Enroll(n = c(50,20,20), lambda = 0.03,
  event = 0.1, M = 3, group = 3, maxt = 5,
  accrual = 3, censor = 0.9, followup = 2,
  partition = "Uneven")

head(data[[1]])
head(data[[2]])
head(data[[3]])

```

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