# Package: BayesAT (via r-universe)

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**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** https://hermitz9.r-universe.dev

**RemoteUrl** https://github.com/cran/BayesAT

**RemoteRef** HEAD

**RemoteSha** ced020e3fb8a053f8816248245cdecc00cae33d1

## Contents

BayesAT *Bayesian adaptive trial interim analysis*

## Description

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

## Usage

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

## Arguments

| | |
|---|---|
| data | Matrix. The data contains both survival time and event status. |
| D | Numerical. The duration of interim analysis, matching the length of enrollment time. |
| stage | Integer. Numbers of interim analysis stages. |
| threshold | Numerical. The value tested against hypothesis or evidence. |
| start | Numerical. The time point when the interim analysis starts. |
| objective | Numerical. The time point for predicted survival rate, for example, 2 years, or 5 years survival probability. |
| alpha | Numerical. Gamma distribution alpha parameter. |
| beta | Numerical. Gamma distribution beta parameter (rate = 1/scale). |
| boundary | The stopping criterion for interim analysis, and the default sets at 5% significance level and calculate quantiles by qnorm() 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 $P(\hat{S} >$ Efficacy$)$ and $P(\hat{S} <$ 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 $2min(P(\hat{\lambda} > \lambda_0), P(\hat{\lambda} \leq \lambda_0))$ 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 expoential 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 tition == "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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