

Package ‘bayesAB’

July 3, 2019

Type Package

Title Fast Bayesian Methods for AB Testing

Version 1.1.2

Date 2019-07-02

Description A suite of functions that allow the user to analyze A/B test data in a Bayesian framework. Intended to be a drop-in replacement for common frequentist hypothesis test such as the t-test and chi-sq test.

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Imports Rcpp (>= 0.12.4), ggplot2 (>= 3.2.0), methods, rlang (>= 0.4.0)

LinkingTo Rcpp

RoxygenNote 6.1.0

Encoding UTF-8

URL <https://github.com/FrankPortman/bayesAB>

BugReports <https://github.com/FrankPortman/bayesAB/issues>

Suggests testthat, knitr, rmarkdown, magrittr, plumber (>= 0.3.0)

VignetteBuilder knitr

NeedsCompilation yes

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Repository CRAN

Date/Publication 2019-07-02 23:11:08 UTC

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banditize	<i>Create a multi-armed Bayesian bandit object.</i>
-----------	---

Description

Fit a multi-armed bandit object based on a bayesTest which can serve recommendations and adapt to new data.

Usage

```
banditize(bT, param, higher_is_better = TRUE)
```

Arguments

bT	a bayesTest object
param	which model parameter (posterior) to evaluate; defaults to first param
higher_is_better	is a higher value of ‘param’ equivalent to a better choice?

Details

banditize is an ‘object-oriented’ implementation of multi-armed bandits in bayesAB. It is useful in conjunction with a Shiny app or Plumber deployment. The object itself is mutable and can adapt/learn from new data without having to re-assign the variable.

Comes with 5 methods:

- `serveRecipe()`: serves a recipe to show your user based on samples from both posteriors.
- `setResults(results)`: set results for one or more recipes for one or more instances of feed-back. Used to update bandit.

- `getBayesTest()`: returns most updated `bayesTest` object.
- `getOriginalTest()`: returns original `bayesTest` object without any updates.
- `getUpdates()`: returns a summarized version of all updates this bandit has processed.

Value

A `bayesBandit` object.

Examples

```
A_binom <- rbinom(100, 1, .5)
B_binom <- rbinom(100, 1, .6)
```

```
AB1 <- bayesTest(A_binom, B_binom, priors = c('alpha' = 1, 'beta' = 1), distribution = 'bernoulli')
```

```
binomialBandit <- banditize(AB1)
binomialBandit$serveRecipe()
binomialBandit$setResults(list('A' = c(1, 0, 1, 0, 0), 'B' = c(0, 0, 0, 0, 1)))
```

bayesAB

bayesAB: Fast Bayesian Methods for A/B Testing

Description

`bayesAB` provides a suite of functions that allow the user to analyze A/B test data in a Bayesian framework. `bayesAB` is intended to be a drop-in replacement for common frequentist hypothesis test such as the t-test and chi-sq test.

Details

Bayesian methods provide several benefits over frequentist methods in the context of A/B tests - namely in interpretability. Instead of p-values you get direct probabilities on whether A is better than B (and by how much). Instead of point estimates your posterior distributions are parametrized random variables which can be summarized any number of ways. Bayesian tests are also immune to 'peeking' and are thus valid whenever a test is stopped.

The general `bayesAB` workflow is as follows:

- Decide how you want to parametrize your data (Poisson for counts of email submissions, Bernoulli for CTR on an ad, etc.)
- Use our helper functions to decide on priors for your data ([bayesTest](#), [plotDistributions](#))
- Fit a `bayesTest` object
 - Optional: Use [combine](#) to munge together several `bayesTest` objects together for an arbitrary / non-analytical target distribution
- print, [plot.bayesTest](#), and [summary.bayesTest](#) to interpret your results

- Determine whether to stop your test early given the Posterior Expected Loss in summary output

Optionally, use [banditize](#) and/or [deployBandit](#) to turn a pre-calculated (or empty) bayesTest into a multi-armed bandit that can serve recipe recommendations and adapt as new data comes in.

Note, while bayesAB was designed to exploit data related to A/B/etc tests, you can use the package to conduct Bayesian analysis on virtually any vector of data, as long as it can be parametrized by the available functions.

To learn more about bayesAB, start with the vignettes: `browseVignettes(package = "bayesAB")`

bayesTest

Fit a Bayesian model to A/B test data.

Description

This function fits a Bayesian model to your A/B testing sample data. See **Details** for more information on usage.

Usage

```
bayesTest(A_data, B_data, priors, n_samples = 1e+05,
          distribution = c("bernoulli", "normal", "lognormal", "poisson",
                          "exponential", "uniform", "bernoulliC", "poissonC"))
```

Arguments

A_data	Vector of collected samples from recipe A
B_data	Vector of collected samples from recipe B
priors	Named vector or named list providing priors as required by the specified distribution: <ul style="list-style-type: none"> • For 'bernoulli' distribution <code>list("alpha" = val1, "beta" = val2)</code> • For 'normal' distribution <code>c("mu" = val1, "lambda" = val2, "alpha" = val3, "beta" = val4)</code> • For 'lognormal' distribution <code>c("mu" = val1, "lambda" = val2, "alpha" = val3, "beta" = val4)</code> • For 'poisson' distribution <code>c("shape" = val1, "rate" = val2)</code> • For 'exponential' distribution <code>list("shape" = val1, "rate" = val2)</code> • For 'uniform' distribution <code>c("xm" = val1, "alpha" = val2)</code> • For 'bernoulliC' distribution: same prior definitions as 'bernoulli' • For 'poissonC' distribution: same prior definitions as 'poisson' See plotDistributions or the <i>Note</i> section of this help document for more info.
n_samples	Number of posterior samples to draw. Should be large enough for the distribution to converge. 1e5 is a good rule of thumb. Not used for closed form tests.
distribution	Distribution of underlying A/B test data.

Details

bayesTest is the main driver function of the **bayesAB** package. The input takes two vectors of data, corresponding to recipe A and recipe B of an A/B test. Order does not matter, except for interpretability of the final plots and intervals/point estimates. The Bayesian model for each distribution uses conjugate priors which must be specified at the time of invoking the function. Currently, there are *eight* supported distributions for the underlying data:

- Bernoulli: If your data is well modeled by 1s and 0s, according to a specific probability p of a 1 occurring
 - For example, click-through-rate /conversions for a page
 - Data **must** be in a $\{0, 1\}$ format where 1 corresponds to a 'success' as per the Bernoulli distribution
 - Uses a conjugate Beta distribution for the parameter p in the Bernoulli distribution
 - alpha and beta must be set for a prior distribution over p
 - * $\alpha = 1, \beta = 1$ can be used as a diffuse or uniform prior
- Normal: If your data is well modeled by the normal distribution, with parameters μ, σ^2 controlling mean and variance of the underlying distribution
 - Data *can* be negative if it makes sense for your experiment
 - Uses a conjugate NormalInverseGamma distribution for the parameters μ and σ^2 in the Normal Distribution.
 - mu, lambda, alpha, and beta must be set for prior distributions over μ, σ^2 in accordance with the parameters of the conjugate prior distributions:
 - * $\mu, \sigma^2 \sim \text{NormalInverseGamma}(\text{mu}, \text{lambda}, \text{alpha}, \text{beta})$
 - This is a bivariate distribution (commonly used to model mean and variance of the normal distribution). You may want to experiment with both this distribution and the plotNormal and plotInvGamma outputs separately before arriving at a suitable set of priors for the Normal and LogNormal bayesTest
- LogNormal: If your data is well modeled by the log-normal distribution, with parameters μ, σ^2 as the **parameters** of the corresponding log-normal distribution (log of data is $\sim N(\mu, \sigma^2)$)
 - Support for a log-normal distribution is strictly positive
 - The Bayesian model requires same conjugate priors on μ, σ^2 as for the Normal Distribution priors
 - Note: The μ and σ^2 are not the mean/variance of lognormal numbers themselves but are rather the corresponding parameters of the lognormal distribution. Thus, posteriors for the statistics 'Mean' and 'Variance' are returned alongside 'Mu' and 'Sig_Sq' for interpretability.
- Poisson: If your data is well modeled by the Poisson distribution, with parameter λ controlling the average number of events per interval.
 - For example, pageviews per session
 - Data *must* be strictly integral or 0.
 - Uses a conjugate Gamma distribution for the parameter λ in the Poisson Distribution
 - shape and rate must be set for prior distribution over λ

- Exponential: If your data is well modeled by the Exponential distribution, with parameter λ controlling the rate of decay.
 - For example, time spent on a page or customers' LTV
 - Data *must* be strictly ≥ 0
 - Uses a conjugate Gamma distribution for the parameter λ in the Exponential Distribution
 - shape and rate must be set for prior distribution over λ
- Uniform: If your data is well modeled by the Uniform distribution, with parameter θ controlling the *max* value.
 - bayesAB has only implemented Uniform(0, θ) forms
 - For example, estimating max/total inventory size from individually numbered snapshots
 - Data *must* be strictly > 0
 - Uses a conjugate Pareto distribution for the parameter θ in the Uniform(0, θ) Distribution
 - xm and alpha must be set for prior distribution over θ
- BernoulliC: Closed form (computational) calculation of the 'bernoulli' bayesTest. Same priors are required.
- PoissonC: Closed form (computational) calculation of the 'poisson' bayesTest. Same priors are required.

Value

A bayesTest object of the appropriate distribution class.

Note

For 'closed form' tests, you do not get a distribution over the posterior, but simply $P(A > B)$ for the parameter in question.

Choosing priors correctly is very important. Please see <http://fportman.com/writing/bayesab-0-dot-7-0-plus-a-primer-on-priors/> for a detailed example of choosing priors within bayesAB. Here are some ways to leverage objective/diffuse (assigning equal probability to all values) priors:

- Beta(1, 1)
- Gamma(eps, eps) ~ Gamma(.00005, .00005) will be effectively diffuse
- InvGamma(eps, eps) ~ InvGamma(.00005, .00005) will be effectively diffuse
- Pareto(eps, eps) ~ Pareto(.005, .005) will be effectively diffuse

Keep in mind that the Prior Plots for bayesTest's run with diffuse priors may not plot correctly as they will not be truncated as they approach infinity. See [plot.bayesTest](#) for how to turn off the Prior Plots.

Examples

```
A_binom <- rbinom(100, 1, .5)
B_binom <- rbinom(100, 1, .6)

A_norm <- rnorm(100, 6, 1.5)
B_norm <- rnorm(100, 5, 2.5)
```

```

AB1 <- bayesTest(A_binom, B_binom,
                priors = c('alpha' = 1, 'beta' = 1),
                distribution = 'bernoulli')
AB2 <- bayesTest(A_norm, B_norm,
                priors = c('mu' = 5, 'lambda' = 1, 'alpha' = 3, 'beta' = 1),
                distribution = 'normal')

print(AB1)
summary(AB1)
plot(AB1)

summary(AB2)

# Create a new variable that is the probability multiplied
# by the normally distributed variable (expected value of something)
AB3 <- combine(AB1, AB2, f = `*`, params = c('Probability', 'Mu'), newName = 'Expectation')

print(AB3)
summary(AB3)
plot(AB3)

```

c.bayesTest

Concatenate bayesTest objects

Description

Concatenate method for objects of class "bayesTest".

Usage

```
## S3 method for class 'bayesTest'
c(..., errorCheck = TRUE)
```

Arguments

...	bayesTest objects
errorCheck	check that objects can be concatenated? Setting this to FALSE can have unintended effects if the bayesTest objects have different params but can have some speedups if you are sure the objects are of the same type.

Value

A bayesTest object with concatenated posteriors.

Examples

```
A_pois <- rpois(100, 5)
B_pois <- rpois(100, 4.7)

AB1 <- bayesTest(A_pois, B_pois, priors = c('shape' = 25, 'rate' = 5), distribution = 'poisson')
AB2 <- bayesTest(A_pois, B_pois, priors = c('shape' = 25, 'rate' = 5), distribution = 'poisson')
c(AB1, AB2)
```

 combine

Combine two bayesAB objects given a binary function.

Description

Combine two (or any number, in succession) bayesTest objects into a new arbitrary posterior distribution. The resulting object is of the same class.

Usage

```
combine(bT1, bT2, f = `+`, params, newName)
```

Arguments

bT1	a bayesTest object
bT2	a bayesTest object
f	a binary function (f(x, y)) used to combine posteriors from bT1 to bT2
params	a character vector of length 2, corresponding to names of the posterior parameters you want to combine; defaults to first posterior parameter if not supplied
newName	a string indicating the name of the new 'posterior' in the resulting object; defaults to string representation of f(params[1], params[2])

Value

a bayesTest object with the newly combined posterior samples.

Note

The generics '+.bayesTest', '*.bayesTest', '-.bayesTest', and '/.bayesTest' are shorthand for combine(f = '+'), combine(f = '*'), combine(f = '-'), and combine(f = '/').

See Also

[grab](#)

Examples

```
A_binom <- rbinom(100, 1, .5)
B_binom <- rbinom(100, 1, .6)

A_norm <- rnorm(100, 6, 1.5)
B_norm <- rnorm(100, 5, 2.5)

AB1 <- bayesTest(A_binom, B_binom,
  priors = c('alpha' = 1, 'beta' = 1),
  distribution = 'bernoulli')

AB2 <- bayesTest(A_norm, B_norm,
  priors = c('mu' = 5, 'lambda' = 1, 'alpha' = 3, 'beta' = 1),
  distribution = 'normal')

AB3 <- combine(AB1, AB2, f = `*`, params = c('Probability', 'Mu'), newName = 'Expectation')
# Equivalent to
AB3 <- AB1 * grab(AB2, 'Mu')

# To get the same posterior name as well
AB3 <- rename(AB3, 'Expectation')

# Dummy example
weirdVariable <- (AB1 + AB2) * (AB2 / AB1)
weirdVariable <- rename(weirdVariable, 'confusingParam')

print(AB3)
summary(AB3)
plot(AB3)
```

deployBandit

Deploy a bayesBandit object as a JSON API.

Description

Turn your bayesBandit object into an API and serve/update requests through HTTP.

Usage

```
deployBandit(bandit, port = 8000)
```

Arguments

bandit	a bayesBandit object
port	port to deploy on

Details

deployBandit turns a Bayesian bandit into a JSON API that accepts curl requests. Two of the five methods of bayesBandit classes are exposed: serveRecipe and setResults. Assuming the API is deployed on localhost this is an example of how it would be hit:

```
curlhttp : //localhost : 8000/serveRecipe
```

```
curl --data'" A" : [1,0,1,1], " B" : [0,0,0,1]'http : //localhost : 8000/setResults
```

Value

An active http process on some port.

Examples

```
A_binom <- rbinom(100, 1, .5)
B_binom <- rbinom(100, 1, .6)

AB1 <- bayesTest(A_binom, B_binom, priors = c('alpha' = 1, 'beta' = 1), distribution = 'bernoulli')

binomialBandit <- banditize(AB1)
## Not run: deployBandit(binomialBandit)
```

grab

Grab the supplied posterior from a bayesTest object

Description

Grab the supplied posterior from a bayesTest object, returning another bayesTest object.

Usage

```
grab(bT, posterior)
```

Arguments

bT	a bayesTest object
posterior	the name of a posterior in that object (string)

Value

a bayesTest object with the posterior parameter isolated

See Also

[combine](#)

plot.bayesTest *Plot bayesTest objects*

Description

Plot method for objects of class "bayesTest".

Usage

```
## S3 method for class 'bayesTest'
plot(x, percentLift = rep(0, length(x$posteriors)),
     priors = TRUE, posteriors = TRUE, samples = TRUE, ...)
```

Arguments

x	an object of class "bayesTest"
percentLift	a vector of length(x\$posteriors). Each entry corresponds to the percent lift $((A - B) / B)$ to plot for the respective posterior in x. Note this is on a 'point' scale. percentLift = 5 implies you want to test for a 5% lift.
priors	logical indicating whether prior plots should be generated.
posteriors	logical indicating whether posterior plots should be generated.
samples	logical indicating whether sample plots should be generated.
...	graphics parameters to be passed to the plotting routines. (For example p, in prior plots)

Note

You can either directly plot a bayesTest object (in which case it will plot interactively), or you can save the plot object to a variable and extract what you need separately. If extracted, you can treat it like any ggplot2 object and modify it accordingly.

Plots are slightly truncated on the extremes to solve the general case of potentially long tail-ends.

Examples

```
A_pois <- rpois(100, 5)
B_pois <- rpois(100, 4.7)

AB1 <- bayesTest(A_pois, B_pois, priors = c('shape' = 25, 'rate' = 5), distribution = 'poisson')

plot(AB1)
plot(AB1, percentLift = 5)

p <- plot(AB1)
p$posteriors$Lambda

## Not run: p$posteriors$Lambda + ggtitle('yolo') # modify ggplot2 object directly
```

plotBeta

Plot the PDF of the Beta distribution.

Description

Plot the PDF of the Beta distribution.

Usage

```
plotBeta(alpha, beta)
```

Arguments

alpha α parameter of the Beta distribution.
beta β parameter of the Beta distribution.

Value

The PDF of Beta(α , β).

Note

The output can be treated like any ggplot2 object and modified accordingly.

Examples

```
plotBeta(1, 1)
plotBeta(2, 5)
## Not run: plotBeta(2, 5) + ggtitle('I hate the default title!')
```

plotDistributions*Plot distributions to explore data and/or choose priors.*

Description

These are helper functions to help explore data and/or choose priors. Click further for more details.

- [plotBeta](#)
- [plotGamma](#)
- [plotInvGamma](#)
- [plotLogNormal](#)
- [plotNormal](#)
- [plotPareto](#)
- [plotPoisson](#)

Note

Choosing priors correctly is very important. Please see <http://fportman.com/writing/bayesab-0-dot-7-0-plus-a-primer-on-priors/> for a detailed example of choosing priors within bayesAB. Here are some ways to leverage objective/diffuse (assigning equal probability to all values) priors:

- $\text{Beta}(1, 1)$
- $\text{Gamma}(\text{eps}, \text{eps}) \sim \text{Gamma}(.00005, .00005)$ will be effectively diffuse
- $\text{InvGamma}(\text{eps}, \text{eps}) \sim \text{InvGamma}(.00005, .00005)$ will be effectively diffuse
- $\text{Pareto}(\text{eps}, \text{eps}) \sim \text{Pareto}(.005, .005)$ will be effectively diffuse

Keep in mind that the Prior Plots for bayesTest's run with diffuse priors may not plot correctly as they will not be truncated as they approach infinity. See [plot.bayesTest](#) for how to turn off the Prior Plots.

plot... functions are generated programmatically so the function calls in their body will be substituted directly

plotGamma

Plot the PDF of the Gamma distribution.

Description

Plot the PDF of the Gamma distribution.

Usage

```
plotGamma(shape, rate)
```

Arguments

shape	shape (α) parameter of the Gamma distribution.
rate	rate (β) parameter of the Gamma distribution.

Details

Note: We use the shape/rate parametrization of Gamma. See https://en.wikipedia.org/wiki/Gamma_distribution for details.

Value

The PDF of Gamma(shape, rate).

Note

The output can be treated like any ggplot2 object and modified accordingly.

Examples

```
plotGamma(1, 1)
plotGamma(2, 5)
## Not run: plotGamma(2, 5) + ggtitle('I hate the default title!')
```

plotInvGamma

Plot the PDF of the Inverse Gamma distribution.

Description

Plot the PDF of the Inverse Gamma distribution.

Usage

```
plotInvGamma(shape, scale)
```

Arguments

shape	shape parameter of the Inverse Gamma distribution.
scale	scale parameter of the Inverse Gamma distribution.

Value

The PDF of `InvGamma(shape, scale)`.

Note

The output can be treated like any `ggplot2` object and modified accordingly. Also note that the scale parameter of the Inverse Gamma distribution is analogous to the beta (or rate) parameter of the regular Gamma distribution. The beta parameter of the [plotNormalInvGamma](#) distribution is analogous to the scale parameter here.

Examples

```
plotInvGamma(2, 4)
plotInvGamma(1, 17)
## Not run: plotInvGamma(1, 17) + ggtitle('I hate the default title!')
```

plotLogNormal	<i>Plot the PDF of the Log Normal distribution.</i>
---------------	---

Description

Plot the PDF of the Log Normal distribution.

Usage

```
plotLogNormal(mu, sigma)
```

Arguments

mu	μ parameter of the Log Normal distribution.
sigma	σ parameter of the Log Normal distribution.

Value

The PDF of Log Normal(μ, σ^2).

Note

The output can be treated like any ggplot2 object and modified accordingly.

Examples

```
plotLogNormal(1, 1)
plotLogNormal(2, .5)
## Not run: plotLogNormal(2, .5) + ggtitle('I hate the default title!')
```

plotNormal	<i>Plot the PDF of the Normal distribution.</i>
------------	---

Description

Plot the PDF of the Normal distribution.

Usage

```
plotNormal(mu, sd)
```

Arguments

mu	μ parameter of the Normal distribution.
sd	σ parameter of the Normal distribution.

Value

The PDF of $\text{Normal}(\mu, \sigma^2)$.

Note

The output can be treated like any ggplot2 object and modified accordingly.

Examples

```
plotNormal(1, 1)
plotNormal(2, 5)
## Not run: plotNormal(2, 5) + ggtitle('I hate the default title!')
```

plotNormalInvGamma *Plot the bivariate PDF of the Normal Inverse Gamma Distribution.*

Description

Plot the bivariate PDF of the Normal Inverse Gamma Distribution.

Usage

```
plotNormalInvGamma(mu, lambda, alpha, beta)
```

Arguments

mu	μ parameter of the Normal Inverse Gamma distribution.
lambda	λ parameter of the Normal Inverse Gamma distribution.
alpha	α parameter of the Normal Inverse Gamma distribution.
beta	β parameter of the Normal Inverse Gamma distribution.

Value

The PDF of $\text{NormalInverseGamma}(\mu, \lambda, \alpha, \beta)$

Note

This is a bivariate distribution (commonly used to model mean and variance of the normal distribution) and returns a 2d contour plot instead of a typical one dimensional PDF. You may want to experiment with both this distribution and the plotNormal and plotInvGamma outputs separately before arriving at a suitable set of priors for the Normal and LogNormal bayesTest.

Examples

```
plotNormalInvGamma(3, 1, 1, 1)
```

plotPareto	<i>Plot the PDF of the Pareto distribution.</i>
------------	---

Description

Plot the PDF of the Pareto distribution.

Usage

```
plotPareto(xm, alpha)
```

Arguments

xm	xm parameter of the Pareto distribution.
alpha	alpha parameter of the Pareto distribution.

Value

The PDF of Pareto(xm, alpha).

Note

The output can be treated like any ggplot2 object and modified accordingly.

Examples

```
plotPareto(1, 1)
plotPareto(5, 3)
## Not run: plotPareto(5, 3) + ggtitle('I hate the default title!')
```

plotPoisson	<i>Plot the PDF of the Poisson distribution.</i>
-------------	--

Description

Plot the PDF of the Poisson distribution.

Usage

```
plotPoisson(lambda)
```

Arguments

lambda	λ parameter of the Poisson distribution.
--------	--

Value

The PDF of $\text{Poisson}(\lambda)$.

Note

The output can be treated like any `ggplot2` object and modified accordingly.

Examples

```
plotPoisson(1)
plotPoisson(5)
## Not run: plotPoisson(5) + ggtitle('I hate the default title!')
```

rename

Rename the posterior for a bayesTest object

Description

Rename the posterior param for a `bayesTest` object.

Usage

```
rename(bT, newName)
```

Arguments

bT	a <code>bayesTest</code> object
newName	the new name you want for the posterior param (string)

Value

a `bayesTest` object with the posterior parameter renamed

See Also

[combine](#)

```
summary.bayesTest      Summarize bayesTest objects
```

Description

Summary method for objects of class "bayesTest".

Usage

```
## S3 method for class 'bayesTest'
summary(object, percentLift = rep(0,
  length(object$posteriors)), credInt = rep(0.9,
  length(object$posteriors)), ...)
```

Arguments

object	an object of class "bayesTest"
percentLift	a vector of length(x\$posteriors). Each entry corresponds to the percent lift $((A - B) / B)$ to summarize for for the respective posterior in x. Note this is on a 'point' scale. percentLift = 5 implies you want to test for a 5% lift.
credInt	a vector of length(x\$posteriors). Each entry corresponds to the width of credible interval of $(A - B) / B$ to calculate for the respective posterior in x. Also on a 'point' scale.
...	additional arguments affecting the summary produced.

Value

A summaryBayesTest object which contains summaries of the Posterior distributions, direct probabilities that $A > B$ (by percentLift), credible intervals on $(A - B) / B$, and the Posterior Expected Loss on all estimated parameters.

Note

The Posterior Expected Loss (https://en.wikipedia.org/wiki/Bayes_estimator) is a good indicator of when to end a Bayesian AB test. If the PEL is lower than the absolute delta of the minimum effect you wish to detect, the test can be reasonably be stopped.

Examples

```
A_pois <- rpois(100, 5)
B_pois <- rpois(100, 4.7)

AB1 <- bayesTest(A_pois, B_pois, priors = c('shape' = 25, 'rate' = 5), distribution = 'poisson')

summary(AB1)
summary(AB1, percentLift = 10, credInt = .95)
```

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