Package 'BAEssd'

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Type Package

Title Bayesian Average Error approach to Sample Size Determination

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Description Implements sample size calculations following the approach
described in ``Bayesian Average Error Based Approach to
Hypothesis Testing and Sample Size Determination."

Depends mvtnorm

License GPL-2

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BAEssd-package   *Bayesian Average Error approach to Sample Size Determination*

Description

Employes a Bayesian average error based approach to sample size determination. Several functions are included for sample size calculation for common designs in clinical trials including one- and two-sample binary and normal responses. These functions are grouped in "suites" that pertain to each type of example.

Details

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Before any calculations can be made, first identify the example of interest and the corresponding suite of functions:

binom1.1sided	One sample, binary response, one-sided hypothesis.
binom1.2sided	One sample, binary response, two-sided hypothesis.
binom2.1sided	Two indepednent samples, binary response, one-sided hypothesis.
binom2.2sided	Two independent samples, binary response, two-sided hypothesis.
norm1KV.1sided	One sample, normal response, known variance, one-sided hypothesis.
norm1KV.2sided	One sample, normal response, known variance, two-sided hypothesis.
norm1UV.2sided	One sample, normal response, unknown variance, two-sided hypothesis.
norm2KV.2sided	Two independent samples, normal response, known variance, two-sided hypothesis.

After selecting the suite of functions of interest, the suite must be generated with appropriate parameters. Then, the corresponding ssd function can be used to calculate the sample size. The two primary constraints for choosing a sample size are the bound on the Total Error to maintain and the weight given to controlling the Average Type-I Error (as opposed to the Average Type-II Error).

Examples

```
###########################################################
# Calculate the sample size required for a one-sample
# normal experiment with known variance (sigma2=25) with
# the hypothesis of interest being
```

```
#     H0: theta==0   vs.   H1: theta!=0
#
# where theta is the mean of the normal distribution. For
# details on the prior used, see documentation for
# norm1KV.2sided().

# generate suite of functions
f1 <- norm1KV.2sided(sigma=5,theta0=0,prob=0.5,mu=2,tau=1)

# attach suite
attach(f1)

# calculate sample size for TE bound of 0.25 and weight 0.5
ssd.norm1KV.2sided(alpha=0.25,w=0.5)

# detach suite
detach(f1)


#############################################################
# Calculate the sample size required for a two-sample
# experiment with a binary response in which the hypothesis
# of interest is
#     H0: p1==p2   vs.   H1: p1!=p2
#
# where p1 is the response rate for group 1 and p2 is the
# response rate for group 2, independent samples. For
# details on the prior used, see documentation for
# binom2.2sided().

# generate suite of functions
f2 <- binom2.2sided(prob=0.5,a0=1,b0=1,a1=1,b1=1,a2=1,b2=1)

# attach suite
attach(f2)

# calculate sample size for TE bound of 0.25 and weight 0.5
#  - here the log marginal distribution (logm) is part of the suite.
ssd.binom(alpha=0.25,w=0.5,logm=logm,two.sample=TRUE)

# detach suite
detach(f2)
```

---

binom1.1sided	*Binomial Suite: One Sample, One Sided*

Description

Generates the suite of functions related to the one sample binomial experiment with a one-sided alternative hypothesis of interest.

Usage

```
binom1.1sided(p0, a, b)
```

Arguments

p0	Scalar. The upper bound of p under null hypothesis Ho: p<=p0.
a	Scalar. Shape1 parameter for prior Beta distribution. See documentation for [dbeta]().
b	Scalar. Shape2 parameter for prior Beta distribution. See documentation for [dbeta]().

Details

binom1.1sided is used to generate a suite of functions for a one-sample binomial experiment with a one-sided alternative hypothesis. That is, when

$$X \sim Binomial(n, p)$$

$$H_0 : p \leq p_0 \quad vs. \quad H_1 : p > p_0$$

using the following prior on p

$$p \sim Beta(a, b)$$

The functions that are generated are useful in examining the prior and posterior densities of the parameter p, as well as constructing the Bayes Factor and determining the sample size via an average error based approach.

The arguments of binom1.1sided are passed to each of the additional functions upon their creation as default values. That is, if p0 is set to 0.5 in the call to binom1.1sided, each of the functions returned will have the defaualt value of 0.5 for p0. If an argument is not specified in the call to binom1.1sided, then it remains a required parameter in all functions created.

Value

binom1.1sided returns a list of 4 functions. These functions are useful for either visualizing the problem, or computing the required sample size:

logm	The function returns a list of three vectors: the log marginal density under the null hypothesis (logm0), the log marginal density under the alternative hypothesis (logm1), and the log marginal density (logm). Each are evaluated at the observed data provided. This function is also passed to [ssd.binom]() to calculate required sample sizes. This function has the following usage:

logm(x, n, p0, a, b)

- x: Vector. Number of successes observed, out of n independent Bernoulli trials.
- n: Scalar. Sample size, the number of independent Bernoulli trials.
- Remaining parameters are specified above for binom1.1sided.

logbf	Returns a vector: the value of the log Bayes Factor given the observed data provided and the prior parameters specified. This function has the following usage:

`logbf(x, n, p0, a, b)`

For details on the parameters for this function, see the above description for `logm`.

prior	Returns a vector: the value of the prior density at the specified value of p with parameters a and b. This function has the following usage:

`prior(p, a, b)`

- p: Vector. Quantiles at which to evaluate the prior distribution.
- Remaining parameters are specified above for `binom1.1sided`.

post	Returns a vector: the value of the posterior density. This function has the following usage:

`post(p, x, n, a, b)`

- p: Vector. Quantiles at which to evaluate the posterior distribution.
- x: Scalar. Number of successes observed, out of n independent Bernoulli trials.
- n: Scalar: The number of independent Bernoulli trials.
- Remaining parameters are specified above for `binom1.1sided`.

See Also

[binom1.2sided](),[binom2.1sided](), [binom2.2sided](),[norm1KV.1sided](), [norm1KV.2sided](),[norm2KV.2sided]() [norm1UV.2sided](),[ssd](),[BAEssd]()

Examples

```
############################################################
# Generate the suite of functions for a one-sample binomial
# with a one-sided test. Consider the hypothesis
#      H0: p<=0.5   vs.  H1: p>0.5
#
# with a uniform prior on p.

# generate suite
f1 <- binom1.1sided(p0=0.5,a=1,b=1)

# attach suite
attach(f1)

# plot prior and posterior given x = 25, n = 30
ps <- seq(0.01,0.99,0.01)
p1 <- prior(ps)
p2 <- post(ps,x=25,n=30)

plot(c(p1,p2)~rep(ps,2),type="n",ylab="Density",xlab="p",main="")
lines(p1~ps,lty=1,lwd=2)
```

```
lines(p2~ps,lty=2,lwd=2)

# perform sample size calculation with TE bound of 0.25 and weight 0.5
ssd.binom(alpha=0.25,w=0.5,logm=logm)

# detain suite
detach(f1)
```

---

binom1.2sided   *Binomial Suite: One Sample, Two Sided*

Description

Generates the suite of functions related to the one sample binomial experiment with a two-sided alternative hypothesis of interest.

Usage

```
binom1.2sided(p0, prob, a, b)
```

Arguments

p0	Scalar. The value of p under null hypothesis Ho: p==p0. Must be a value between 0 and 1.
prob	Scalar. The prior probability that the null hypothesis is true. Must be a value between 0 and 1.
a	Scalar. Shape1 parameter for prior Beta distribution. See documentation for [dbeta]().
b	Scalar. Shape2 parameter for prior Beta distribution. See documentation for [dbeta]().

Details

binom1.2sided is used to generate a suite of functions for a one-sample binomial experiment with a two-sided alternative hypothesis. That is, when

$$X \sim Binomial(n, p)$$

$$H_0 : p = p_0 \quad vs. \quad H_1 : p \neq p_0$$

using the following prior on p

$$\pi(p) = u * I(p = p_0) + (1 - u) * I(p \neq p_0)Beta(a, b)$$

where Beta(a,b) is Beta density with parameters a and b and u is the prior probability of the null hypothesis (prob).

The functions that are generated are useful in examining the prior and posterior densities of the parameter p, as well as constructing the Bayes Factor and determining the sample size via an average error based approach.

The arguments of `binom1.2sided` are passed to each of the additional functions upon their creation as default values. That is, if `p0` is set to 0.5 in the call to `binom1.2sided`, each of the functions returned will have the defaualt value of 0.5 for `p0`. If an argument is not specified in the call to `binom1.2sided`, then it remains a required parameter in all functions created.

Value

`binom1.2sided` returns a list of 4 functions:

`logm`   Returns a list of three vectors: the log marginal density under the null hypothesis (`logm0`), the log marginal density under the alternative hypothesis (`logm1`), the log marginal density (`logm`). Each are evaluated at the observed data provided. This function is passed to [ssd.binom](#) to calculate required sample sizes. The function has the following usage:

> `logm(x, n, p0, prob, a, b)`

> - x: Vector. Number of successes observed, out of n independent Bernoulli trials.
> - n: Scalar. Sample size, the number of independent Bernoulli trials.
> - Remaining parameters specified above for `binom1.1sided`.

`logbf`   Returns a vector: the value of the log Bayes Factor given the observed data provided and the prior parameters specified. The function has the following usage:

> `logbf(x, n, p0, prob, a, b)`

> For details on the parameters, see above function `logm`

`prior`   Returns a vector: the value of the prior density. The function has the following usage:

> `prior(p, p0, prob, a, b)`

> - p: Scalar. Quantiles for the prior distribution.
> - Remaining parameters specified above for `binom1.1sided`.

`post`   Returns a vector: the value of the posterior density. The function has the following usage:

> `post(p, x, n, p0, prob, a, b)`

> - p: Scalar. Quantiles for the posterior distribution.
> - x: Scalar. Number of successes observed, out of n independent Bernoulli trials.
> - Remaining parameters specified above for `binom1.1sided`.

See Also

[binom1.1sided](#),[binom2.1sided](#), [binom2.2sided](#),[norm1KV.1sided](#), [norm1KV.2sided](#),[norm2KV.2sided](#)
[norm1UV.2sided](#),[ssd](#),[BAEssd](#)

Examples

```
#############################################################
# Generate the suite of functions for a one-sample binomial
# with a two-sided test. Consider the hypothesis
#      H0: p==0.5   vs.  H1: p!=0.5
#
# with a uniform prior on p under the alternative and a
# prior probability of the null hypothesis equal to 0.5.

# generate suite
f2 <- binom1.2sided(p0=0.5,prob=0.5,a=1,b=1)

# attach suite
attach(f2)

# plot prior and posterior given x = 25, n = 30
# - don't forget that point mass is not shown on plot
ps <- seq(0.01,0.99,0.01)
p1 <- prior(ps)
p2 <- post(ps,x=25,n=30)

plot(c(p1,p2)~rep(ps,2),type="n",ylab="Density",xlab="p",main="")
lines(p1~ps,lty=1,lwd=2)
lines(p2~ps,lty=2,lwd=2)

# perform sample size calculation with TE bound of 0.25 and weight 0.5
ssd.binom(alpha=0.25,w=0.5,logm=logm)

# detain suite
detach(f2)
```

---

binom2.1sided   *Binomial Suite: Two Sample, One Sided*

Description

Generates the suite of functions related to the two sample binomial experiment with a one-sided alternative hypothesis of interest.

Usage

```
binom2.1sided(a1, b1, a2, b2)
```

Arguments

a1   Scalar. Shape1 parameter for prior Beta distribution for the parameter governing
                sample 1. See documentation for dbeta.

b1   Scalar. Shape2 parameter for prior Beta distribution for the parameter governing
                sample 1. See documentation for dbeta.

a2	Scalar. Shape1 parameter for prior Beta distribution for the parameter governing sample 2. See documentation for [dbeta]().
b2	Scalar. Shape2 parameter for prior Beta distribution for the parameter governing sample 2. See documentation for [dbeta]().

Details

binom2.1sided is used to generate a suite of functions for a two-sample binomial experiment with a one-sided alternative hypothesis. That is, when

$$X_j|p_j \sim Binomial(n, p_j), \quad independent$$

$$H_0 : p_1 \leq p_2 \quad vs. \quad H_1 : p_1 > p_2$$

using the following prior on p[1] and p[2]

$$\pi(p) = Beta(a_1, b_1)Beta(a_2, b_2)$$

where Beta(a,b) is Beta density with parameters a and b.

The functions that are generated are useful in examining the prior and posterior densities of the parameter p, as well as constructing the Bayes Factor and determining the sample size via an average error based approach.

The arguments of binom2.1sided are passed to each of the additional functions upon their creation as default values. That is, if a1 is set to 1 in the call to binom2.1sided, each of the functions returned will have the defaualt value of 1 for a1. If an argument is not specified in the call to binom2.1sided, then it remains a required parameter in all functions created.

Value

binom2.1sided returns a list of 4 functions:

logm	Returns a list of three vectors: the log marginal density under the null hypothesis (logm0), the log marginal density under the alternative hypothesis (logm1), the log marginal density (logm). Each are evaluated at the observed data provided. This function is passed to [ssd.binom]() to calculate required sample sizes. This function takes the following usage: logm(x, n, a1, b1, a2, b2) • x: Matrix with two columns. Each row represents the number of successes in sample 1 and sample 2, respectively, observed out of n independent Bernoulli trials. • n: Scalar. The number of independent Bernoulli trials. • Remaining parameters described above for bionom2.1sided.
logbf	Returns a vector. The value of the log Bayes Factor given the observed data provided and the prior parameters specified. The function has the following usage: logbf(x, n, a1, b1, a2, b2) For details on the parameters, see logm above.

prior   Returns a vector. The value of the prior density. The function takes the following
                   usage:

                   prior(p, a1, b1, a2, b2)

                     • p: Matrix with 2 columns. Each row is a vector of length 2 correspond-
                       ing to a 2-dimensional quantile at which to compute the density. The first
                       column represents the parameter for sample 1, and the second column, the
                       parameter for sample 2.
                     • Remaining parameters described above for binom2.1sided.

post   Returns a vector. The value of the posterior density. The function takes the
                   following usage:

                   post(p, x, n, a1, b1, a2, b2)

                     • p: Matrix with 2 columns. Each row is a vector of length 2 correspond-
                       ing to a 2-dimensional quantile at which to compute the density. The first
                       column represents the parameter for sample 1, and the second column, the
                       parameter for sample 2.
                     • x: Vector of length 2. Element 1 represents the number of successes for
                       sample 1 and element 2 the number of successes in sample 2.
                     • Remaining parameters described above for binom2.1sided.

See Also

[binom1.1sided](),[binom1.2sided](), [binom2.2sided](),[norm1KV.1sided](), [norm1KV.2sided](),[norm2KV.2sided]()
[norm1UV.2sided](),[ssd](),[BAEssd]()

Examples

```
#############################################################
# Generate the suite of functions for a one-sample binomial
# with a two-sided test. Consider the hypothesis
#      H0: p[1]<=p[2]   vs.  H1: p[1]>p[2]
#
# with a uniform prior on p[1] and a uniform prior on p[2].

# generate suite
f3 <- binom2.1sided(a1=1,b1=1,a2=1,b2=1)

# attach suite
attach(f3)

# calculate the Bayes factor when the observed data are
#   n = 30, x[1] = 10, x[2] = 20
logbf(x=matrix(c(10,20),ncol=2,nrow=1),n=30)

# perform sample size calculation with TE bound of 0.25 and weight 0.5
ssd.binom(alpha=0.25,w=0.5,logm=logm,two.sample=TRUE)

# detain suite
detach(f3)
```

---

binom2.2sided	*Binomial Suite: Two Sample, Two Sided*

Description

Generates the suite of functions related to the two sample binomial experiment with a two-sided alternative hypothesis of interest.

Usage

```
binom2.2sided(prob, a0, b0, a1, b1, a2, b2)
```

Arguments

prob	Scalar. The prior probability that the null hypothesis is true. Must be a value between 0 and 1.
a0	Scalar. Shape1 parameter for prior Beta distribution under the null hypothesis that the two parameters are equal. See documentation for dbeta.
b0	Scalar. Shape2 parameter for prior Beta distribution under the null hypothesis that the two parameters are equal. See documentation for dbeta.
a1	Scalar. Shape1 parameter for prior Beta distribution for the parameter governing sample 1 under the alternative hypothesis. See documentation for dbeta.
b1	Scalar. Shape2 parameter for prior Beta distribution for the parameter governing sample 1 under the alternative hypothesis. See documentation for dbeta.
a2	Scalar. Shape1 parameter for prior Beta distribution for the parameter governing sample 2 under the alternative hypothesis. See documentation for dbeta.
b2	Scalar. Shape2 parameter for prior Beta distribution for the parameter governing sample 2 under the alternative hypothesis. See documentation for dbeta.

Details

binom2.2sided is used to generate a suite of functions for a two-sample binomial experiment with a two-sided alternative hypothesis. That is, when

$$X_j|p_j \sim Binomial(n, p_j), \quad independent$$

$$H_0 : p_1 = p_2 \quad vs. \quad H_1 : p_1 \neq p_2$$

using the following prior on p[1] and p[2]

$$\pi(p) = u * I(p_1 = p_2)Beta(a_0, b_0) + (1 - u) * I(p_1 \neq p_2)Beta(a_1, b_1)Beta(a_2, b_2)$$

where Beta(a,b) is Beta density with parameters a and b and u is the prior probability of the null hypothesis (prob).

The functions that are generated are useful in examining the prior and posterior densities of the parameter p, as well as constructing the Bayes Factor and determining the sample size via an average error based approach.

The arguments of `binom2.2sided` are passed to each of the additional functions upon their creation as default values. That is, if a0 is set to 1 in the call to `binom2.2sided`, each of the functions returned will have the defaualt value of 1 for a0. If an argument is not specified in the call to `binom2.2sided`, then it remains a required parameter in all functions created.

Value

`binom2.2sided` returns a list of 4 functions:

logm   Returns a list of three vectors: the log marginal density under the null hypothesis
                  (logm0), the log marginal density under the alternative hypothesis (logm1), the
                  log marginal density (logm). Each are evaluated at the observed data provided.
                  This function is passed to [ssd.binom](#) to calculate required sample sizes. This
                  function takes the following usage:

                  `logm(x, n, prob, a0, b0, a1, b1, a2, b2)`
                  - x: Matrix with two columns. Each row represents the number of successes
                    in sample 1 and sample 2, respectively, observed out of n independent
                    Bernoulli trials.
                  - n: Scalar. The number of independent Bernoulli trials.
                  - Remaining parameters described above for `bionom2.2sided`.

logbf   Returns a vector. The value of the log Bayes Factor given the observed data
                  provided and the prior parameters specified. The function has the following
                  usage:

                  `logbf(x, n, prob, a0, b0, a1, b1, a2, b2)`

                  For details on the parameters, see `logm` above.

prior   Returns a vector. The value of the prior density. The function takes the following
                  usage:

                  `prior(p, prob, a0, b0, a1, b1, a2, b2)`
                  - p: Matrix with 2 columns. Each row is a vector of length 2 correspond-
                    ing to a 2-dimensional quantile at which to compute the density. The first
                    column represents the parameter for sample 1, and the second column, the
                    parameter for sample 2.
                  - Remaining parameters described above for `binom2.2sided`.

post   Returns a vector. The value of the posterior density. The function takes the
                  following usage:

                  `post(p, x, n, prob, a0, b0, a1, b1, a2, b2)`
                  - p: Matrix with 2 columns. Each row is a vector of length 2 correspond-
                    ing to a 2-dimensional quantile at which to compute the density. The first
                    column represents the parameter for sample 1, and the second column, the
                    parameter for sample 2.
                  - x: Vector of length 2. Element 1 represents the number of successes for
                    sample 1 and element 2 the number of successes in sample 2.
                  - Remaining parameters described above for `binom2.2sided`.

See Also

binom1.1sided,binom1.2sided, binom2.1sided,norm1KV.1sided, norm1KV.2sided,norm2KV.2sided
norm1UV.2sided,ssd,BAEssd

Examples

```
###########################################################
# Generate the suite of functions for a one-sample binomial
# with a two-sided test. Consider the hypothesis
#     H0: p[1]==p[2]   vs.  H1: p[1]!=p[2]
#
# with a uniform prior on p under the null and a uniform
# prior on p[1] and p[2] under the alternative with a 0.5
# probability of the null hypothesis being true.

# generate suite
f4 <- binom2.2sided(prob=0.5,a0=1,b0=1,a1=1,b1=1,a2=1,b2=1)

# attach suite
attach(f4)

# calculate the Bayes factor when the observed data are
#   n = 30, x[1] = 10, x[2] = 20
logbf(x=matrix(c(10,20),ncol=2,nrow=1),n=30)

# perform sample size calculation with TE bound of 0.25 and weight 0.5
ssd.binom(alpha=0.25,w=0.5,logm=logm,two.sample=TRUE)

# detain suite
detach(f4)
```

GammaGamma	*The Gamma-Gamma Distribution*

Description

Density and random generation for the Gamma-Gamma distribution with parameters shape1, rate1, and shape2.

Usage

```
dggamma(x, shape1, rate1, shape2)
rggamma(n, shape1, rate1, shape2)
```

Arguments

x	Vector. Quantiles.
n	Scalar. Number of random variates to generate (sample size).

shape1, rate1   Vector. Shape and rate parameters for y-distribution. Must be strictly positive.

shape2   Vector. Shape parameter for conditional x-distribution. Must be a positive integer.

Details

A Gamma-Gamma distribution with parameters shape1 = a, rate1 = r and shape2 = b has density

$$f(x) = \frac{r^a}{\Gamma(a)} \frac{\Gamma(a+b)}{\Gamma(b)} \frac{x^{b-1}}{(r+x)^{(a+b)}}$$

for $x > 0$ where $a, r > 0$ and $b = 1, 2, \ldots$.

The distribution is generated using the following scheme:

1. Generate Y ~ Gamma(shape=shape1,rate=rate1).
2. Generate X ~ Gamma(shape=shape2,rate=Y).

Then, X follows a Gamma-Gamma distribution.

Value

dggamma gives the density, and rggamma gives random variates.

References

Bernardo JM, Smith AFM. (1994) *Bayesian Theory*. Wiley, New York.

See Also

dgamma

Examples

```
###########################################################
# Construct a plot of the density function with median and
# quantiles marked.

# define parameters
shape1 <- 4
rate1 <- 4
shape2 <- 20

# construct density plot
x <- seq(0.1,150,0.1)
plot(dggamma(x,shape1,rate1,shape2)~x,
     type="l",lwd=2,main="",xlab="x",ylab="Density f(x)")

# determine median and quantiles
set.seed(123)
X <- rggamma(5000,shape1,rate1,shape2)
```

```
quants <- quantile(X,prob=c(0.25,0.5,0.75))

# add quantities to plot
abline(v=quants,lty=c(3,2,3),lwd=2)


############################################################
# Consider the following set-up:
#   Let x ~ N(theta,sigma2), sigma2 is unknown variance.
#   Consider a prior on theta and sigma2 defined by
#       theta|sigma2 ~ N(mu,(r*sigma)^2)
#       sigma2 ~ InverseGamma(a/2,b/2), (b/2) = rate.
#
#   We want to generate random variables from the marginal
#   (prior predictive) distribution of the sufficient
#   statistic T = (xbar,s2) where the sample size n = 25.

# define parameters
a <- 4
b <- 4
mu <- 1
r <- 3
n <- 25


# generate random variables from Gamma-Gamma
set.seed(123)
shape1 <- a/2
rate1 <- b
shape2 <- 0.5*(n-1)

Y <- rggamma(5000,shape1,rate1,shape2)

# generate variables from a non-central t given Y
df <- n+a-1
scale <- (Y+b)*(1/n + r^2)/(n+a-1)

X <- rt(5000,df=df)*sqrt(scale) + mu

# the pair (X,Y) comes from the correct marginal density

# mean of xbar and s2, and xbar*s2
mean(X)
mean(Y)
mean(X*Y)
```

---

norm1KV.1sided   *Normal Suite: One Sample, One Sided, Known Variance*

Description

Generates the suite of functions related to the one sample normal experiment with a one-sided alternative hypothesis of interest when the variance is known.

Usage

```
norm1KV.1sided(sigma, theta0, mu, tau)
```

Arguments

sigma	Scalar. The known standard deviation of the population of interest.
theta0	Scalar. The critical value of the mean under the null hypothesis: theta<=theta0.
mu	Scalar. The mean of the normal prior density on theta. See documentation for [dnorm]().
tau	Scalar. The standard deviation for the normal prior density on theta. See documentation for [dnorm]().

Details

norm1KV.1sided is used to generate a suite of functions for a one-sample normal experiment with a one-sided alternative hypothesis when the variance is known. That is, when

$$X \sim Normal(\theta, \sigma^2)$$

$$H_0 : \theta \leq \theta_0 \quad vs. \quad H_1 : \theta > \theta_0$$

using the following prior on theta

$$\pi(\theta) = Normal(\mu, \tau^2)$$

where Normal(mu,tau2) is Normal density with mean mu and variance tau2.

The functions that are generated are useful in examining the prior and posterior densities of the parameter theta, as well as constructing the Bayes Factor and determining the sample size via an average error based approach.

The arguments of norm1KV.1sided are passed to each of the additional functions upon their creation as default values. That is, if mu is set to 1 in the call to norm1KV.1sided, each of the functions returned will have the defaualt value of 1 for mu. If an argument is not specified in the call to norm1KV.1sided, then it remains a required parameter in all functions created.

Value

norm1KV.1sided returns a list of 4 functions:

logm	Returns a list of three vectors: the log marginal density under the null hypothesis (logm0), the log marginal density under the alternative hypothesis (logm1), the log marginal density (logm). Each are evaluated at the observed data provided. The function takes the following usage:

```
logm(xbar, n, sigma, theta0, mu, tau)
```

- xbar: Vector. Observed sample mean from the experiment.
- n: Scalar. Sample Size.
- Remaining parameters described above for `norm1KV.1sided`.

logbf   Returns a vector. The value of the log Bayes Factor given the observed data provided and the prior parameters specified. The function has the following usage:

`logbf(xbar, n, sigma, theta0, mu, tau)`

See `logm` above for details on the parameters of the function.

prior   Returns a vector. The value of the prior density. The function has the following usage:

`prior(theta, mu, tau)`

- theta: Vector. The quantiles at which to evaluate the prior.
- Remaining parameters described above for `norm1KV.1sided`.

post   Returns a vector. The value of the posterior density. The function has the following usage:

`post(theta, xbar, n, sigma, mu, tau)`

- theta: Vector. The quantiles at which to evaluate the prior.
- xbar: Vector. Observed sample mean from the experiment.
- n: Scalar. Sample Size.
- Remaining parameters described above for `norm1KV.1sided`.

See Also

[binom1.1sided,binom1.2sided](#), [binom2.1sided,binom2.2sided](#), [norm1KV.2sided,norm2KV.2sided](#) [norm1UV.2sided,ssd,BAEssd](#)

Examples

```
#############################################################
# Generate the suite of functions for a one-sample normal
# with a one-sided test. Consider the hypothesis
#      H0: theta<=0  vs.  H1: theta>0
#
# with a normal prior for theta with prior mean 2 and
# prior standard deviation 1. The known standard
# deviation for the population is 5.

# generate suite
f5 <- norm1KV.1sided(sigma=5,theta0=0,mu=2,tau=1)

# attach suite
attach(f5)

# plot the prior and posterior density when the observed data is
#  n = 30, xbar = 1.
mus <- seq(-5,5,0.01)
```

```
mu1 <- prior(mus)
mu2 <- post(mus,xbar=1,n=30)

plot(c(mu1,mu2)~rep(mus,2),type="n",ylab="Density",xlab="mu",main="")
lines(mu1~mus,lty=1,lwd=2)
lines(mu2~mus,lty=2,lwd=2)

# perform sample size calculation with TE bound of 0.25 and weight 0.5
ssd.norm1KV(alpha=0.25,w=0.5,logm=logm)

# detain suite
detach(f5)
```

---

norm1KV.2sided   *Normal Suite: One Sample, Two Sided, Known Variance*

Description

Generates the suite of functions related to the one sample normal experiment with a two-sided alternative hypothesis of interest when the variance is known.

Usage

```
norm1KV.2sided(sigma, theta0, prob, mu, tau)
```

Arguments

sigma	Scalar. The known standard deviation of the population of interest.
theta0	Scalar. The critical value of the mean under the null hypothesis: theta==theta0.
prob	Scalar. The prior probability of the null hypothesis. Must be a value between 0 and 1.
mu	Scalar. The mean of the normal prior density on theta under the alternative hypothesis. See documentation for dnorm.
tau	Scalar. The standard deviation for the normal prior density on theta under the alternative hypothesis. See documentation for dnorm.

Details

norm1KV.2sided is used to generate a suite of functions for a one-sample normal experiment with a two-sided alternative hypothesis when the variance is known. That is, when

$$X \sim Normal(\theta, \sigma^2)$$

$$H_0 : \theta = \theta_0 \quad vs. \quad H_1 : \theta \neq \theta_0$$

using the following prior on theta

$$\pi(\theta) = u * I(\theta = \theta_0) + (1 - u) * I(\theta \neq \theta_0)Normal(\mu, \tau^2)$$

where Normal(mu,tau2) is Normal density with mean `mu` and variance `tau2` and u is the prior probability of the null hypothesis (`prob`).

The functions that are generated are useful in examining the prior and posterior densities of the parameter `theta`, as well as constructing the Bayes Factor and determining the sample size via an average error based approach.

The arguments of `norm1KV.2sided` are passed to each of the additional functions upon their creation as default values. That is, if mu is set to 1 in the call to `norm1KV.2sided`, each of the functions returned will have the defaualt value of 1 for `mu`. If an argument is not specified in the call to `norm1KV.2sided`, then it remains a required parameter in all functions created.

Value

norm1KV.2sided returns a list of 5 functions:

logm   Returns a list of three vectors: the log marginal density under the null hypothesis (`logm0`), the log marginal density under the alternative hypothesis (`logm1`), the log marginal density (`logm`). Each are evaluated at the observed data provided. The function takes the following usage:

                  `logm(xbar, n, sigma, theta0, prob, mu, tau)`

- xbar: Vector. Observed sample mean from the experiment.
- n: Scalar. Sample Size.
- Remaining parameters described above for `norm1KV.2sided`.

logbf   Returns a vector. The value of the log Bayes Factor given the observed data provided and the prior parameters specified. The function has the following usage:

                  `logbf(xbar, n, sigma, theta0, prob, mu, tau)`

See `logm` above for details on the parameters of the function.

prior   Returns a vector. The value of the prior density. The function has the following usage:

                  `prior(theta, theta0, prob, mu, tau)`

- theta: Vector. The quantiles at which to evaluate the prior.
- Remaining parameters described above for `norm1KV.2sided`.

post   Returns a vector. The value of the posterior density. The function has the following usage:

                  `post(theta, xbar, n, sigma, theta0, prob, mu, tau)`

- theta: Vector. The quantiles at which to evaluate the prior.
- xbar: Vector. Observed sample mean from the experiment.
- n: Scalar. Sample Size.
- Remaining parameters described above for `norm1KV.2sided`.

ssd.norm1KV.2sided

                Sample size calculations for this particular set-up. The function has the following usage:

```
ssd.norm1KV.2sided(alpha, w, sigma, theta0, prob, mu, tau,
    minn = 2, maxn = 1000, all = FALSE)
```

See ssd for more details. The suite-specific parameters are described above for
norm1KV.2sided.

See Also

binom1.1sided,binom1.2sided, binom2.1sided,binom2.2sided, norm1KV.1sided,norm2KV.2sided
norm1UV.2sided,ssd,BAEssd

Examples

```
############################################################
# Generate the suite of functions for a one-sample normal
# with a two-sided test. Consider the hypothesis
#      H0: theta==0  vs.  H1: theta!=0
#
# with a normal prior for theta with prior mean 2 and
# prior standard deviation 1. The known standard
# deviation for the population is 5. The prior proability
# of the null hypothesis is set to 0.5.

# generate suite
f6 <- norm1KV.2sided(sigma=5,theta0=0,prob=0.5,mu=2,tau=1)

# attach suite
attach(f6)

# plot the prior and posterior density when the observed data is
#  n = 30, xbar = 1.
mus <- seq(-5,5,0.01)
mu1 <- prior(mus)
mu2 <- post(mus,xbar=1,n=30)

plot(c(mu1,mu2)~rep(mus,2),type="n",ylab="Density",xlab="mu",main="")
lines(mu1~mus,lty=1,lwd=2)
lines(mu2~mus,lty=2,lwd=2)

# perform sample size calculation with TE bound of 0.25 and weight 0.5
#   using both the example-specific function as well as the general.
ssd.norm1KV(alpha=0.25,w=0.5,logm=logm)
ssd.norm1KV.2sided(alpha=0.25,w=0.5)

# detain suite
detach(f6)
```

---

norm1UV.2sided   *Normal Suite: One Sample, Two Sided, Unknown Variance*

Description

Generates the suite of functions related to the one sample normal experiment with a two-sided alternative hypothesis of interest when the variance is unknown.

Usage

```
norm1UV.2sided(theta0, prob, mu, scale, shape, rate)
```

Arguments

theta0	Scalar. The critical value of the mean under the null hypothesis: theta==theta0.
prob	Scalar. The prior probability of the null hypothesis. Must be a value between 0 and 1.
mu	Scalar. The mean of the normal prior density on theta under the alternative hypothesis. See documentation for dnorm.
scale	Scalar. Used to determine the standard deviation for the normal prior density on theta under the alternative hypothesis. The standard deviation is equal to scale*sigma. See documentation for dnorm.
shape	Scalar. The shape parameter for the gamma prior on the inverse of the unknown standard deviation sigma2. See documenation for dgamma.
rate	Scalar. The rate parameter for the gamma prior on the inverse of the unknown standard deviation sigma2. See documentation for dgamma.

Details

norm1UV.2sided is used to generate a suite of functions for a one-sample normal experiment with a two-sided alternative hypothesis when the variance is unknown. That is, when

$$X \sim Normal(\theta, \sigma^2)$$

$$H_0 : \theta = \theta_0 \quad vs. \quad H_1 : \theta \neq \theta_0$$

using the following prior on theta and sigma2

$$\pi(\theta|\sigma^2) = u * I(\theta = \theta_0) + (1 - u) * I(\theta \neq \theta_0)Normal(\mu, (scale\sigma)^2)$$

$$\pi(\sigma^2) = InverseGamma(shape, rate)$$

where Normal(mu,tau2) is Normal density with mean mu and variance tau2 and u is the prior probability of the null hypothesis (prob).

The functions that are generated are useful in examining the prior and posterior densities of the parameters theta and sigma2, as well as constructing the Bayes Factor and determining the sample size via an average error based approach.

The arguments of norm1UV.2sided are passed to each of the additional functions upon their creation as default values. That is, if mu is set to 1 in the call to norm1UV.2sided, each of the functions returned will have the defaualt value of 1 for mu. If an argument is not specified in the call to norm1UV.2sided, then it remains a required parameter in all functions created.

Value

norm1UV.2sided returns a list of 5 functions:

logm   Returns a list of three vectors: the log marginal density under the null hypothesis
              (logm0), the log marginal density under the alternative hypothesis (logm1), the
              log marginal density (logm). Each are evaluated at the observed data provided.
              The function takes the following usage:

              logm(xbar, s2, n, theta0, prob, mu, scale, shape, rate)

              - xbar: Vector. Observed sample mean from the experiment.
              - s2: Vector. Observed sample standard deviation from the experiment.
              - n: Scalar. Sample size.
              - Remaining parameters described above for norm1UV.2sided.

logbf   Returns a vector. The value of the log Bayes Factor given the observed data
              provided and the prior parameters specified. The function has the following
              usage:

              logbf(xbar, s2, n, theta0, prob, mu, scale, shape, rate)

              For details on the arguments, see logm above.

prior   Returns a vector. The value of the prior density. The function has the following
              usage:

              prior(theta, sigma2, theta0, prob, mu, scale, shape, rate)

              - theta: Vector. The quantiles of the mean at which to evaluate the prior.
              - sigma2: Vector. The quantiles of the standard deviation at which to evaluate
                the prior.
              - Remaining parameters described above for norm1UV.2sided

post   Returns a vector. The value of the posterior density. The function has the fol-
              lowing usage:

              post(theta, sigma2, xbar, s2, n, theta0, prob, mu, scale,
                 shape, rate)

              - theta: Vector. The quantiles of the mean at which to evaluate the posterior.
              - sigma2: Vector. The quantiles of the standard deviation at which to evaluate
                the psterior.
              - xbar: Vector. Observed sample mean from the experiment.
              - s2: Vector. Observed sample standard deviation from the experiment.
              - n: Scalar. Sample size.
              - Remaining parameters described above for norm1UV.2sided

ssd.norm1UV.2sided
              Sample size calculations for this particular set-up. The function has the follow-
              ing usage:

              ssd.norm1UV.2sided(alpha, w, theta0, prob, mu, scale, shape,
                 rate, m = 2500, minn = 3, maxn = 1000, all = FALSE)

              See [ssd](#) for more details. The suite-specific parameters are described above for
              norm1UV.2sided. Note that this example will not work with ssd.norm1KV.

See Also

binom1.1sided,binom1.2sided, binom2.1sided,binom2.2sided, norm1KV.1sided,norm1KV.2sided,
norm2KV.2sided,ssd,BAEssd

Examples

```
############################################################
# Generate the suite of functions for a one-sample normal
# with a two-sided test. Consider the hypothesis
#      H0: theta==0  vs.  H1: theta!=0
#
# with a normal prior for theta with prior mean 2 and
# scale of 1/3 for the standard deviation. The prior proability
# of the null hypothesis is set to 0.5. The prior density
# on sigma2 is taken to be InverseGamma with parameters
# 11 and 30 for the shape and rate.

# generate suite
f8 <- norm1UV.2sided(theta0=0,prob=0.5,mu=2,scale=(1/3),shape=11,rate=30)

# attach suite
attach(f8)

# calculate the Bayes Factor for the following observed data
#   n = 30, xbar = 1, s2 = 2
logbf(xbar=1,s2=2,n=30)

# perform sample size calculation with TE bound of 0.25 and weight 0.5
ssd.norm1UV.2sided(alpha=0.25,w=0.5)

# detain suite
detach(f8)
```

---

norm2KV.2sided   *Normal Suite: Two Sample, Two Sided, Known Variance*

Description

Generates the suite of functions related to the two sample normal experiment with a two-sided
alternative hypothesis of interest when the variance is known.

Usage

```
norm2KV.2sided(sigma, prob, mu0, tau0, mu1, tau1, mu2, tau2)
```

Arguments

sigma	Scalar. The known standard deviation of the population.
prob	Scalar. The prior probability of the null hypothesis. Must be a value between 0 and 1.
mu0	Scalar. The mean of the normal prior density on theta under the null hypothesis. See documentation for [dnorm]().
tau0	Scalar. The standard deviation of the normal prior density on theta under the null hypothesis. See documentation for [dnorm]().
mu1	Scalar. The mean of the normal prior density on mean for sample 1 under the alternative hypothesis. See documentation for [dnorm]().
tau1	Scalar. The standard deviation of the normal prior density on mean for sample 1 under the alternative hypothesis. See documentation for [dnorm]().
mu2	Scalar. The mean of the normal prior density on mean for sample 2 under the alternative hypothesis. See documentation for [dnorm]().
tau2	Scalar. The standard deviation of the normal prior density on mean for sample 2 under the alternative hypothesis. See documentation for [dnorm]().

Details

norm2KV.2sided is used to generate a suite of functions for a two-sample normal experiment with a two-sided alternative hypothesis when the variance is known and the samples are independent. That is, when

$$X_j \sim Normal(\theta_j, \sigma^2)$$

$$H_0 : \theta_1 = \theta_2 \quad vs. \quad H_1 : \theta_1 \neq \theta_2$$

using the following prior on theta[1] and theta[2]

$$\pi(\theta) = u * I(\theta_1 = \theta_2) Normal(\mu_0, \tau_0^2) + (1 - u) * I(\theta_1 \neq \theta_2) Normal(\mu_1, \tau_1^2) Normal(\mu_2, \tau_2^2)$$

where Normal(mu,tau^2) is Normal density with mean mu and variance tau^2 and u is the prior probability of the null hypothesis (prob).

The functions that are generated are useful in examining the prior and posterior densities of the parameter theta, as well as constructing the Bayes Factor and determining the sample size via an average error based approach.

The arguments of norm2KV.2sided are passed to each of the additional functions upon their creation as default values. That is, if mu0 is set to 1 in the call to norm2KVV.2sided, each of the functions returned will have the defaualt value of 1 for mu0. If an argument is not specified in the call to norm2KV.2sided, then it remains a required parameter in all functions created.

Value

norm2KV.2sided returns a list of 5 functions:

logm	Returns a list of three vectors: the log marginal density under the null hypothesis (logm0), the log marginal density under the alternative hypothesis (logm1), the log marginal density (logm). Each are evaluated at the observed data provided. The function takes the following usage:

```
logm(xbar, n, sigma, prob, mu0, tau0, mu1, tau1, mu2, tau2)
```

- xbar: Matrix with 2 columns. Each column represents the sample mean for each of the two samples.
- n: Scalar. The sample size.
- Remaining parameters are described above for norm2KV.2sided.

logbf   Returns a vector. The value of the log Bayes Factor given the observed data provided and the prior parameters specified. The function has the following usage:

```
logbf(xbar, n, sigma, prob, mu0, tau0, mu1, tau1, mu2, tau2)
```

For details on the arguments, see logm above.

prior   Returns a vector. The value of the prior density. The function takes the following usage:

```
prior(theta, prob, mu0, tau0, mu1, tau1, mu2, tau2)
```

- theta: Vector. The quantiles at which to evaluate the prior.
- Remaining paramters are described above for norm2KV.2sided.

post   Returns a vector. The value of the posterior density. The function takes the following usage:

```
post(theta, xbar, n, sigma, prob, mu0, tau0, mu1, tau1, mu2,
    tau2)
```

- theta: Vector. The quantiles at which to evaluate the posterior.
- xbar: Vector of length 2. Each element represents the sample mean for each of the two samples, respectively.
- n: Scalar. The sample size.
- Remaining paramters are described above for norm2KV.2sided.

ssd.norm2KV.2sided

   Sample size calculations for this particular set-up. The function has the following usage:

```
ssd.norm2KV.2sided(alpha, w, sigma, prob, mu0, tau0, mu1,
    tau1, mu2, tau2, m = 2500, minn = 2, maxn = 1000, all = FALSE)
```

See ssd for more details. The suite-specific parameters are described above for norm2KV.2sided.

See Also

binom1.1sided,binom1.2sided, binom2.1sided,binom2.2sided, norm1KV.1sided,norm1KV.2sided, norm1UV.2sided,ssd,BAEssd

Examples

```
###########################################################
# Generate the suite of functions for a two-sample normal
# with a two-sided test. Consider the hypothesis
#     H0: theta[1]==theta[2]  vs.  H1: theta[1]!=theta[2]
```

```
#
# with a known variance of 3.

# generate suite
f7 <- norm2KV.2sided(sigma=3,prob=0.5,mu0=0,tau0=1,mu1=2,tau1=1,mu2=2,tau2=1)

# attach suite
attach(f7)

# calculate the Bayes Factor for the following observed data
#   n = 30, xbar[1] = -1, xbar[2] = 1
logbf(xbar=matrix(c(-1,1),nrow=1,ncol=2),n=30)

# perform sample size calculation with TE bound of 0.5 and weight 0.9
# - due to a need for a Monte Carlo implementation of this procedure, this
#   problem can take significantly longer to solve, compared to other examples.
#   Thus, for this example, a large error bound and weight were chosen to
#   decrease computation time while illustrating the function.
ssd.norm2KV.2sided(alpha=0.5,w=0.9)

# detain suite
detach(f7)
```

---

plot.BAEssd   *Plotting Average Errors*

Description

Create plots of various average errors as a function of the sample size calculated via the Bayesian
Average Error based approach.

Usage

```
   ## S3 method for class 'BAEssd'
plot(x, y = "TE", alpha.line = TRUE, type = "l",
    xlab = "Sample Size (n)", ylab = NULL, main = NULL, ...)
```

Arguments

x	BAEssd object. Result from a Bayesian Average Error based sample size calculation.
y	Character string. Indicates what type of error should be plotted on the y-axis (default being Total Error). One of "TE","TWE","AE1", or "AE2".
alpha.line	Boolean. If TRUE, a horizontal line - indicating the bound on Total Error used in determining the sample size - is added to the plot.
type, xlab, ylab, main	
	Character string. See plot.default() for more details.
...	Additional parameters to be passed to plotting functions.

Details

Each `BAEssd` object contains a history of the Average Errors for each sample size considered. `plot.BAEssd` allows for examination of the trend in errors as the sample size changes.

See Also

ssd, plot.default

Examples

```
#############################################################
# Construct a plot of the Total Error as a function of
# sample size for a one-sample normal experiment with known
# variance.

# load suite of functions
f1 <- norm1KV.2sided(sigma=5,theta0=0,prob=0.5,mu=2,tau=1)

# get TE for many more sample sizes larger than the optimal
attach(f1)
ss1 <- ssd.norm1KV.2sided(alpha=0.25,w=0.5,minn=2,maxn=200,all=TRUE)
ss1
detach(f1)

# create plot of Total Error
plot(ss1)

# create plot of Average Type-I Error
plot(ss1,y="AE1",alpha.line=FALSE)
abline(h=0.05,lty=2)
```

---

ssdFcts   *Sample Size Calculations via Bayesian Average Errors*

Description

A Bayesian average error based approach to sample size determination. These functions compute the required sample size for various designs common to clinical trials. A specified Total Error rate is maintain and more emphasis can be placed on controlling Average Type-I Error or Type-II Error.

Usage

```
ssd.binom(alpha, w, logm, minn = 2, maxn = 1000, two.sample = FALSE,
        all = FALSE, ...)
ssd.norm1KV(alpha, w, logm, minn = 2, maxn = 1000, all = FALSE, ...)
```

Arguments

`alpha`	Scalar. The bound to maintain on the Total Error rate. Must be a decimal between 0 and 1.
`w`	Scalar. The weight to be given to Average Type-I Error. Larger values of w control Type-I error rates more. Must be a decimal between 0 and 1.
`logm`	Function. Computes the log marginal (prior predictive density) under H0 and H1. This function should return a list that contains two components:

> | `logm0` | vector giving marginal density under H0. |
> |---|---|
> | `logm1` | vector giving marginal density under H1. |

	The first parameter of this function should be the observed data. See details for necessary form. The second parameter should be the sample size.
`minn, maxn`	Scalar. The minimum and maximum sample size to consider.
`all`	Boolean. If `FALSE` (default), the function terminates when an acceptable sample size is found or when `maxn` is reached. If `TRUE`, the function will only terminate when `maxn` is reached. This is useful for tracing out the Average Error as a function of sample size.
`two.sample`	Boolean. If `FALSE` (default), one sample experiment is assumed. If `TRUE`, two sample experiment is assumed.
`...`	Additional parameters to be passed to `logm` if necessary.

Details

Sample size calculations are dependent upon the knowledge of the marginal density under each hypothesis. The function `logm` should provide these densities.

For a one-sample binomial experiment, the first argument of `logm` should be a vector in which each entry represents a different number of successes out of n independent binary trials. For a two-sample binomial experiment, the first argument of `logm` should be a matrix, in which each row represents the number of successes for each of the samples out of n indpendent trials. For an example see binom1.1sided.

For a one-sample normal experiment with known variance, the first argument shoul be a vector of different sample means. For an example see norm1KV.1sided.

In addition, there are a few functions specific to a given situation (or suite); these are

- ssd.norm1KV.2sided(alpha, w, sigma, theta0, prob, mu,
        tau, minn = 2, maxn = 1000, all = FALSE)
- ssd.norm2KV.2sided(alpha, w, sigma, prob, mu0, tau0,
        mu1, tau1, mu2, tau2, m = 2500, minn = 2, maxn = 1000, all = FALSE)
- ssd.norm1UV.2sided(alpha, w, theta0, prob, mu, scale,
        shape, rate, m = 2500, minn = 3, maxn = 1000, all = FALSE)

The only parameter unique to these functions is

- m: The number of Monte Carlo replicates to use in computing the average errors.

The logm function is not required as the function is specific to that suite. Instead, various parameters unique to that suite are required. See the corresponding suite for details.

Value

An object of class "BAEssd" which is a list containing the following elements:

call	The call to the function.
history	Dataframe. Contains one row for each sample size considered during the function evaluation. Each row records the sample size attempted, the average type-I and type-II errors, the total weighted error, and the total error.
n	Scalar. The chosen sample size with attributes related to the function call and total error.

See Also

summary.BAEssd, plot.BAEssd, binom1.1sided, binom1.2sided, binom2.1sided, binom2.2sided, norm1KV.1sided, norm1KV.2sided, norm2KV.2sided, norm1UV.2sided

Examples

```
############################################################
# Computing a sample size for a one-sample binomial
# experiment with a two-sided alternative.

# load suite of functions
f1 <- binom1.2sided(p0=0.5,prob=0.5,a=1,b=1)

# calculate sample size for total error bound of 0.25 and weight 0.5
attach(f1)
ss1 <- ssd.binom(alpha=0.25,w=0.5,logm=logm,two.sample=FALSE)
detach(f1)

# see results
ss1

# examine structure
str(ss1)


############################################################
# Computing a sample size for a one-sample normal
# experiment with a two-sided alternative using the
# functions internal to the suite.

# load suite of functions
f2 <- norm1KV.2sided(sigma=5,theta0=0,prob=0.5,mu=2,tau=1)

# calculate sample size for total error bound of 0.25 and weight 0.5
attach(f2)
ss2 <- ssd.norm1KV.2sided(alpha=0.25,w=0.5)
```

```
detach(f2)

# see results
ss2
```

---

summary.BAEssd   *Summarizing BAE Sample Size Calculations*

Description

summary method for class BAEssd.

Usage

```
   ## S3 method for class 'BAEssd'
summary(object, ...)
```

Arguments

object   BAEssd object. Result from a Bayesian Average Error based sample size calcu-
                lation.

...   Additional parameters passed to or from other methods.

Details

Creates a nice printout giving the Average Errors at the chosen sample size.

Value

Vector with 5 elements:

n   Selected sample size.

AE1   Average Bayes Type-I Error rate for the selected sample size.

AE2   Average Bayes Type-II Error rate for the selected sample size.

TWE   Total Weighted Error for the selected sample size.

TE   Total Error for the selected sample size.

See Also

[ssd](), [summary]()

Examples

```
############################################################
# One-sample normal experiment with known variance.

# load suite of functions
f1 <- norm1KV.2sided(sigma=5,theta0=0,prob=0.5,mu=2,tau=1)

# compare results of fast method with general method
attach(f1)
ss1 <- ssd.norm1KV(alpha=0.25,w=0.5,logm=logm)
ss2 <- ssd.norm1KV.2sided(alpha=0.25,w=0.5)
detach(f1)

# look at structure
str(summary(ss1))
```

Index