Package ‘SampleSizeMeans’

February 19, 2015

Type Package

Title Sample size calculations for normal means

Version 1.1

Date 2012-12-10

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Description A set of R functions for calculating sample size
requirements using three different Bayesian criteria in the
context of designing an experiment to estimate a normal mean or
the difference between two normal means. Functions for
calculation of required sample sizes for the Average Length
Criterion, the Average Coverage Criterion and the Worst Outcome
Criterion in the context of normal means are provided.
Functions for both the fully Bayesian and the mixed
Bayesian/likelihood approaches are provided.

License GPL (>= 2)

Repository CRAN

Date/Publication 2012-12-10 18:40:34

NeedsCompilation no

R topics documented:

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SampleSizeMeans-package

Bayesian sample sizes calculations based on highest posterior density intervals for normal means and differences between normal means

Description

Sample size determination based on highest posterior density intervals for normal means and difference between normal means using three different Bayesian approaches

Details

Package: SampleSizeMeans
Type: Package
Version: 1.1
Date: 2012-12-10
License: GLP (version 2 or later)

A set of R functions for calculating sample size requirements using three different Bayesian criteria in the context of designing an experiment to estimate normal means or the difference between two normal means. Criteria include the Average Length Criterion, the Average Coverage Criterion and the Modified Worst Outcome Criterion. Functions for both the fully Bayesian and the mixed Bayesian/likelihood approaches are provided.

See the related package SampleSizeProportions for Bayesian sample size determination for the difference between two binomial proportions
Bayesian sample size determination for estimating a single normal mean using the Average Coverage Criterion

The function `mu.acc` returns the required sample size to reach a given coverage probability on average for a posterior credible interval of fixed length for a normal mean.

**Usage**

`mu.acc(len, alpha, beta, n0, level=0.95)`

**Arguments**

- `len`: The desired fixed length of the posterior credible interval for the mean
- `alpha`: First parameter of the Gamma prior density for the precision (reciprocal of the variance)
- `beta`: Second parameter of the Gamma prior density for the precision (reciprocal of the variance)
- `n0`: Prior sample size equivalent for the mean
- `level`: The desired average coverage probability of the posterior credible interval (e.g., 0.95)
Details

Assume that a sample will be collected in order to estimate the mean of a normally distributed random variable. Assume that the precision (reciprocal of the variance) of this random variable is unknown, but has prior information in the form of a Gamma($\alpha$, $\beta$) density. Assume that the mean is unknown, but has prior information equivalent to $n_0$ previous observations. The function mu.acc returns the required sample size to attain the desired average coverage probability level for the posterior credible interval of fixed length $len$ for the unknown mean.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.

Value

The required sample size given the inputs to the function.

Note

The sample size returned by this function is exact.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

mu.alc, mu.modwoc, mu.varknown, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mbl.varknown, mu.freq, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.freq

Examples

mu.acc(len=0.2, alpha=2, beta=2, n0=10)
mu.alc

Bayesian sample size determination for estimating a single normal mean using the Average Length Criterion

Description

The function mu.alc returns the required sample size to reach a given posterior credible interval length on average for a fixed coverage probability for a normal mean.

Usage

mu.alc(len, alpha, beta, n0, level = 0.95)

Arguments

len The desired average length of the posterior credible interval for the mean
alpha First prior parameter of the Gamma density for the precision (reciprocal of the variance)
beta Second prior parameter of the Gamma density for the precision (reciprocal of the variance)
n0 Prior sample size equivalent for the mean
level The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)

Details

Assume that a sample will be collected in order to estimate the mean of a normally distributed random variable. Assume that the precision (reciprocal of the variance) of this random variable is unknown, but has prior information in the form of a Gamma(alpha, beta) density. Assume that the mean is unknown, but has prior information equivalent to n0 previous observations. The function mu.alc returns the required sample size to attain the desired average length len for the posterior credible interval of fixed coverage probability level for the unknown mean.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.

Value

The required sample size given the inputs to the function.

Note

The sample size returned by this function is exact.
Author(s)
Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References
Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also
mu.acc, mu.modwoc, mu.varknown, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mbl.varknown, mu.freq, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.freq

Examples
mu.alc(len=0.2, alpha=2, beta=2, n0=10)

### mu.freq

**Frequentist sample size determination for normal means**

Description
The function `mu.freq` returns the required sample size to obtain a confidence interval of given length and confidence level for a normal mean.

Usage
mu.freq(len, lambda, level = 0.95)

Arguments

- `len`: The desired total length of the confidence interval for the mean
- `lambda`: Known precision (reciprocal of variance)
- `level`: The desired confidence level (e.g., 0.95)

Details
Assume that a random sample will be collected in order to estimate the mean of a normally distributed random variable with known precision `lambda` (precision is the reciprocal of the variance). The function `mu.freq` returns the required sample size to attain the desired length `len` and confidence level `level` for a confidence interval for the mean from a frequentist point of view.
mu.mbl.varknown

Value

The required sample size given the inputs to the function.

Note

The sample size returned by this function is exact.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References


See Also

mu.acc, mu.alc, mu.modwoc, mu.varknown, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mbl.varknown, mudiff.freq, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown

Examples

# Suppose the variance = 4
mu.freq(len=P.R, lambda=1/T)

mu.mbl.varknown

Bayesian sample size determination for estimating a single normal mean with known variance using the Mixed Bayesian/Likelihood criteria

Description

The function mu.mbl.varknown returns the required sample size to reach a desired posterior credible interval length and coverage probability for a normal mean - using a mixed Bayesian/likelihood approach - when the variance is known.

Usage

mu.mbl.varknown(len, lambda, level = 0.95)
Arguments

len The desired total length of the posterior credible interval for the mean
lambda The known precision (reciprocal of variance)
level The desired coverage probability of the posterior credible interval (e.g., 0.95)

Details

Assume that a sample will be collected in order to estimate the mean of a normally distributed random variable with known precision \(\lambda\) (where the precision is the reciprocal of the variance). The function \(\text{mu.mbl.varknown}\) returns the required sample size to attain the desired length \(\text{len}\) and coverage probability \(\text{level}\) for the posterior credible interval for the unknown mean.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but use only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

Value

The required sample size given the inputs to the function.

Note

The sample size returned by this function is exact.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

\(\text{mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.varknown, mu.acc, mu.alc, mu.modwoc, mu.freq,}
\text{mudiff.mbl.varknown, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar,}
\text{mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.varknown, mudiff.acc, mudiff.alc,}
\text{mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.freq}\)

Examples

\(\text{mu.mbl.varknown(len=0.2, lambda=1/4)}\)
mu.mblacc

Bayesian sample size determination for estimating a single normal mean using the Mixed Bayesian/Likelihood Average Coverage Criterion

Description

The function mu.mblacc returns the required sample size to reach a given coverage probability on average - using a mixed Bayesian/likelihood approach - for a posterior credible interval of fixed length for a normal mean.

Usage

mu.mblacc(len, alpha, beta, level = 0.95, m = 10000, mcs = 3)

Arguments

- **len**: The desired fixed length of the posterior credible interval for the mean
- **alpha**: First prior parameter of the Gamma density for the precision (reciprocal of the variance)
- **beta**: Second prior parameter of the Gamma density for the precision (reciprocal of the variance)
- **level**: The desired average coverage probability of the posterior credible interval (e.g., 0.95)
- **m**: The number of points simulated from the preposterior distribution of the data. For each point, the probability coverage of the highest posterior density interval of fixed length len is estimated, in order to approximate the average coverage probability. Usually 10000 is sufficient, but one can increase this number at the expense of program running time.
- **mcs**: The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, mcs = 3 is a good choice.

Details

Assume that a sample will be collected in order to estimate the mean of a normally distributed random variable. Assume that the precision (reciprocal of the variance) of this random variable is unknown, but has prior information in the form of a Gamma(alpha, beta) density. The function mu.mblacc returns the required sample size to attain the desired average coverage probability level for the posterior credible interval of fixed length len for the unknown mean.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but use only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.
Value

The required sample size given the inputs to the function.

Note

The sample size is calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References


See Also

mu.mblalc, mu.mblmodwoc, mu.mbl.varknown, mu.acc, mu.alc, mu.modwoc, mu.varknown, mu.freq, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.freq

Examples

mu.mblacc(len=0.2, alpha=2, beta=2)
**mu.mblalc**

**Arguments**

- **len**  The desired average length of the posterior credible interval for the mean
- **alpha**  First prior parameter of the Gamma density for the precision (reciprocal of the variance)
- **beta**  Second prior parameter of the Gamma density for the precision (reciprocal of the variance)
- **level**  The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)

**Details**

Assume that a sample will be collected in order to estimate the mean of a normally distributed random variable. Assume that the precision (reciprocal of the variance) of this random variable is unknown, but has prior information in the form of a Gamma(\(\alpha, \beta\)) density. The function `mu.mblalc` returns the required sample size to attain the desired average length \(\text{len}\) for the posterior credible interval of fixed coverage probability \(\text{level}\) for the unknown mean.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but use only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

**Value**

The required sample size given the inputs to the function.

**Note**

The sample size returned by this function is exact.

**Author(s)**

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

**References**


**See Also**

`mu.mblacc, mu.mblmodwoc, mu.mbl.varknown, mu.acc, mu.alc, mu.modwoc, mu.varknown, mu.freq, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.freq`
mu.mblmodwoc

Examples

mu.mblalc(len=0.2, alpha=2, beta=2)

Bayesian sample size determination for estimating a single normal mean using the Mixed Bayesian/Likelihood Modified Worst Outcome Criterion

Description

The function mu.mblmodwoc uses a mixed Bayesian/likelihood approach to determine conservative sample sizes, in the sense that the desired posterior credible interval coverage and length for a normal mean are guaranteed over a given proportion of data sets that can arise according to the prior information.

Usage

mu.mblmodwoc(len, alpha, beta, level = 0.95, worst.level = 0.95, m = 50000, mcs = 3)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>len</td>
<td>The desired total length of the posterior credible interval for the mean</td>
</tr>
<tr>
<td>alpha</td>
<td>First prior parameter of the Gamma density for the precision (reciprocal of the variance)</td>
</tr>
<tr>
<td>beta</td>
<td>Second prior parameter of the Gamma density for the precision (reciprocal of the variance)</td>
</tr>
<tr>
<td>level</td>
<td>The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)</td>
</tr>
<tr>
<td>worst.level</td>
<td>The probability that the length of the posterior credible interval of fixed coverage probability level will be at most len</td>
</tr>
<tr>
<td>m</td>
<td>The number of points simulated from the preposterior distribution of the data. For each point, the length of the highest posterior density interval of fixed coverage probability level is estimated, in order to approximate the (100*worst.level)%-percentile of the posterior credible interval length. Usually 50000 is sufficient, but one can increase this number at the expense of program running time.</td>
</tr>
<tr>
<td>mcs</td>
<td>The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, mcs = 3 is a good choice.</td>
</tr>
</tbody>
</table>

Details

Assume that a sample will be collected in order to estimate the mean of a normally distributed random variable. Assume that the precision (reciprocal of the variance) of this random variable is unknown, but has prior information in the form of a Gamma(alpha, beta) density. The function mu.mblmodwoc returns the required sample size to attain the desired length len for the posterior...
credibility interval of fixed coverage probability \textit{level} for the unknown mean. The Modified Worst Outcome Criterion used is conservative, in the sense that the posterior credible interval length \textit{len} is guaranteed over the \textit{worst.level} proportion of all possible data sets that can arise according to the prior information, for a fixed coverage probability \textit{level}.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but uses only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

\textbf{Value}

The required sample size given the inputs to the function.

\textbf{Note}

The sample size is calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

It is also correct to state that the coverage probability of the posterior credible interval of fixed length \textit{len} will be at least \textit{level} with probability \textit{worst.level} with the sample size returned.

\textbf{Author(s)}

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

\textbf{References}


\textbf{See Also}

\texttt{mu.mblacc, mu.mblalc, mu.mbl.varknown, mu.acc, mu.alc, mu.modwoc, mu.varknown, mu.freq, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.freq}

\textbf{Examples}

\texttt{mu.mblmodwoc(len=0.2, alpha=2, beta=2)}
mu.modwoc

Bayesian sample size determination for estimating a single normal mean using the Modified Worst Outcome Criterion

Description

The function mu.modwoc calculates conservative sample sizes, in the sense that the desired posterior credible interval coverage and length for a normal mean are guaranteed over a given proportion of data sets that can arise according to the prior information.

Usage

mu.modwoc(len, alpha, beta, nP, level = 0.95, worst.level = 0.95)

Arguments

len The desired length of the posterior credible interval for the mean
alpha First prior parameter of the Gamma density for the precision (reciprocal of the variance)
beta Second prior parameter of the Gamma density for the precision (reciprocal of the variance)
nP Prior sample size equivalent for the mean
level The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
worst.level The probability that the length of the posterior credible interval of fixed coverage probability level will be at most len

Details

Assume that a sample will be collected in order to estimate the mean of a normally distributed random variable. Assume that the precision (reciprocal of the variance) of this random variable is unknown, but has prior information in the form of a Gamma(alpha, beta) density. Assume that the mean is unknown, but has prior information equivalent to nP previous observations. The function mu.modwoc returns the required sample size to attain the desired length len for the posterior credible interval of fixed coverage probability level for the unknown mean. The Modified Worst Outcome Criterion used is conservative, in the sense that the posterior credible interval length len is guaranteed over the worst.level proportion of all possible data sets that can arise according to the prior information, for a fixed coverage probability level.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.
**Value**

The required sample size given the inputs to the function.

**Note**

The sample size returned by this function is exact.

It is also correct to state that the coverage probability of the posterior credible interval of fixed length len will be at least level with probability worst.level with the sample size returned.

**Author(s)**

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

**References**


**See Also**


**Examples**

mu.modwoc(len=0.2, alpha=2, beta=2, n0=10)

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**mu.varknown**

Bayesian sample size determination for estimating a single normal mean with known variance

**Description**

The function mu.varknown returns the required sample size to reach a desired posterior credible interval length and coverage probability for a normal mean when the variance is known.

**Usage**

mu.varknown(len, lambda, n0, level = 0.95)
Arguments

- `len`: The desired total length of the posterior credible interval for the mean
- `lambda`: The known precision (reciprocal of variance)
- `nP`: Prior sample size equivalent for the mean
- `level`: The desired coverage probability of the posterior credible interval (e.g., 0.95)

Details

Assume that a sample will be collected in order to estimate the mean of a normally distributed random variable with known precision `lambda` (where the precision is the reciprocal of the variance). Assume that the mean is unknown, but has prior information equivalent to `nP` previous observations. The function `mu.varknown` returns the required sample size to attain the desired length `len` and coverage probability `level` for the posterior credible interval for the unknown mean.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.

Value

The required sample size given the inputs to the function.

Note

The sample size returned by this function is exact.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

`mu.acc`, `mu.alc`, `mu.modwoc`, `mu.mbl.varknown`, `mu.mblacc`, `mu.mblalc`, `mu.mblmodwoc`, `mu.freq`, `mudiff.varknown`, `mudiff.acc`, `mudiff.alc`, `mudiff.modwoc`, `mudiff.acc.equalvar`, `mudiff.alc.equalvar`, `mudiff.modwoc.equalvar`, `mudiff.mbl.varknown`, `mudiff.mblacc`, `mudiff.mblalc`, `mudiff.mblmodwoc`, `mudiff.mblacc.equalvar`, `mudiff.mblalc.equalvar`, `mudiff.mblmodwoc.equalvar`, `mudiff.freq`

Examples

`mu.varknown(len=0.2, lambda=1/4, nP=10)`
mudiff.acc  

*Bayesian sample size determination for differences in normal means using the Average Coverage Criterion*

**Description**

The function `mudiff.acc` returns the required sample sizes to reach a given coverage probability on average for a posterior credible interval of fixed length for the difference between two normal means.

**Usage**

\[
mudiff.acc(len, \alpha_1, \beta_1, \alpha_2, \beta_2, n_01, n_02, \text{level} = 0.95, \text{equal} = \text{TRUE}, m = 10000, mcs = 3)
\]

**Arguments**

- `len`: The desired fixed length of the posterior credible interval for the difference between the two unknown means.
- `alpha1`: First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population.
- `beta1`: Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population.
- `alpha2`: First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population.
- `beta2`: Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population.
- `n01`: Prior sample size equivalent for the mean for the first population.
- `n02`: Prior sample size equivalent for the mean for the second population.
- `level`: The desired average coverage probability of the posterior credible interval (e.g., 0.95).
- `equal`: logical. Whether or not the final group sizes \((n_1, n_2)\) are forced to be equal:
  - when `equal` = `TRUE`, final sample sizes \(n_1 = n_2\);
  - when `equal` = `FALSE`, final sample sizes \((n_1, n_2)\) minimize the expected posterior variance given a total of \(n_1+n_2\) observations.
- `m`: The number of points simulated from the preposterior distribution of the data. For each point, the probability coverage of the highest posterior density interval of fixed length \(len\) is estimated, in order to approximate the average coverage probability. Usually 10000 is sufficient, but one can increase this number at the expense of program running time.
- `mcs`: The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower
bound is cross-checked. In our experience, mcs = 3 is a good choice.

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precision within each of the two populations are unknown, but have prior information in the form of Gamma($\alpha_1$, $\beta_1$) and Gamma($\alpha_2$, $\beta_2$) densities, respectively. Assume that the means are unknown, but have prior information equivalent to $(n_{01}, n_{02})$ previous observations, respectively. The function `mudiff.acc` returns the required sample sizes to attain the average coverage probability $\text{level}$ for the posterior credible interval of fixed length $\text{len}$ for the difference between the two unknown means.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.

Value

The required sample sizes $(n_1, n_2)$ for each group given the inputs to the function.

Note

The sample sizes are calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

`mudiff.alc`, `mudiff.modwoc`, `mudiff.acc.equalvar`, `mudiff.alc.equalvar`, `mudiff.modwoc.equalvar`, `mudiff.varknown`, `mudiff.mblacc`, `mudiff.mblalc`, `mudiff.mblmodwoc`, `mudiff.mblacc.equalvar`, `mudiff.mblalc.equalvar`, `mudiff.mblmodwoc.equalvar`, `mudiff.mbl.varknown`, `mudiff.freq`, `mu.acc`, `mu.alc`, `mu.modwoc`, `mu.varknown`, `mu.mblacc`, `mu.mblalc`, `mu.mblmodwoc`, `mu.mbl.varknown`, `mu.freq`

Examples

mudiff.acc(len=0.2, alpha1=2, beta1=2, alpha2=3, beta2=3, n01=10, n02=25)
mudiff.acc.equalvar

Bayesian sample size determination for differences in normal means when variances are equal using the Average Coverage Criterion

Description

The function `mudiff.acc.equalvar` returns the required sample sizes to reach a given coverage probability on average for a posterior credible interval of fixed length for the difference between two normal means, when variances are equal.

Usage

```r
mudiff.acc.equalvar(len, alpha, beta, n01, n02, level = 0.95, equal = TRUE)
```

Arguments

- `len` The desired fixed length of the posterior credible interval for the difference between the two unknown means
- `alpha` First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `beta` Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `n01` Prior sample size equivalent for the mean for the first population
- `n02` Prior sample size equivalent for the mean for the second population
- `level` The desired average coverage probability of the posterior credible interval (e.g., 0.95)
- `equal` logical. Whether or not the final group sizes (n1, n2) are forced to be equal:
  - when `equal = TRUE`, final sample sizes n1 = n2;
  - when `equal = FALSE`, final sample sizes (n1, n2) minimize the expected posterior variance given a total of n1+n2 observations.

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precisions of the two normal sampling distributions are unknown but equal, with prior information in the form of a Gamma(alpha, beta) density. Assume that the means are unknown, but have prior information equivalent to (n01, n02) previous observations, respectively. The function `mudiff.acc.equalvar` returns the required sample sizes to attain the desired average coverage probability `level` for the posterior credible interval of fixed length `len` for the difference between the two unknown means.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used.
for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.

**Value**

The required sample sizes \((n_1, n_2)\) for each group given the inputs to the function.

**Note**

The sample sizes returned by this function are exact.

**Author(s)**

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

**References**

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

**See Also**

mudiff.alc.equalvar, mudiff.modalvar, mudiff.accc, mudiff.alc, mudiff.modwoc, mudiff.varknown, mudiff.mblacc.equalvar, mudiff.mblacc.equalvar,mudiff.mblmodalvar.equalvar, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblvarknown, mudiff.freq, mu.acc, mu.alc, mu.modalvar, mu.varknown, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mblvarknown, mu.freq

**Examples**

mudiff.acc.equalvar(len=0.2, alpha=2, beta=2, n01=10, n02=50)

---

**mudiff.alc**

Bayesian sample size determination for differences in normal means using the Average Length Criterion

**Description**

The function mudiff.alc returns the required sample sizes to reach a desired posterior credible interval length on average for a fixed coverage probability for the difference between two normal means.

**Usage**

mudiff.alc(len, alpha1, beta1, alpha2, beta2, n01, n02, level = 0.95, equal = TRUE, m = 10000, mcs = 3)
Arguments

- **len**: The desired average length of the posterior credible interval for the difference between the two unknown means.
- **alpha1**: First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population.
- **beta1**: Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population.
- **alpha2**: First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population.
- **beta2**: Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population.
- **n01**: Prior sample size equivalent for the mean for the first population.
- **n02**: Prior sample size equivalent for the mean for the second population.
- **level**: The desired fixed coverage probability of the posterior credible interval (e.g., 0.95).
- **equal**: logical. Whether or not the final group sizes (n1, n2) are forced to be equal:
  - when `equal = TRUE`, final sample sizes n1 = n2;
  - when `equal = FALSE`, final sample sizes (n1, n2) minimize the expected posterior variance given a total of n1+n2 observations.
- **m**: The number of points simulated from the preposterior distribution of the data. For each point, the length of the highest posterior density interval of fixed coverage probability `level` is estimated, in order to approximate the average length. Usually 10000 is sufficient, but one can increase this number at the expense of program running time.
- **mcs**: The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, mcs = 3 is a good choice.

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precision within each of the two populations are unknown, but have prior information in the form of Gamma(alpha1, beta1) and Gamma(alpha2, beta2) densities, respectively. Assume that the means are unknown, but have prior information equivalent to (n01, n02) previous observations, respectively. The function `mudiff.alc` returns the required sample sizes to attain the desired average length `len` for the posterior credible interval of fixed coverage probability `level` for the difference between the two unknown means.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.
Value

The required sample sizes \((n_1, n_2)\) for each group given the inputs to the function.

Note

The sample sizes are calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References


See Also

mudiff.acc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.freq, mu.acc, mu.alc, mu.modwoc, mu.varknown, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mbl.varknown, mu.freq

Examples

mudiff.alc(len=P.R, alpha1=R, beta1=R, alphaR=S, betaR=S, nP1=1P, nPR=RU)

mudiff.alc.equalvar

Bayesian sample size determination for differences in normal means when variances are equal using the Average Length Criterion

Description

The function mudiff.alc.equalvar returns the required sample sizes to reach a given posterior credible interval length on average for a fixed coverage probability for the difference between two normal means, when variances are equal.

Usage

mudiff.alc.equalvar(len, alpha, beta, n01, n02, level = 0.95, equal = TRUE)
Arguments

- `len`: The desired average length of the posterior credible interval for the difference between the two unknown means.
- `alpha`: First prior parameter of the Gamma density for the common precision (reciprocal of the variance).
- `beta`: Second prior parameter of the Gamma density for the common precision (reciprocal of the variance).
- `n01`: Prior sample size equivalent for the mean for the first population.
- `n02`: Prior sample size equivalent for the mean for the second population.
- `level`: The desired fixed coverage probability of the posterior credible interval (e.g., 0.95).
- `equal`: Logical. Whether or not the final group sizes (n1, n2) are forced to be equal:
  - when `equal = TRUE`, final sample sizes n1 = n2;
  - when `equal = FALSE`, final sample sizes (n1, n2) minimize the expected posterior variance given a total of n1+n2 observations.

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precisions of the two normal sampling distributions are unknown but equal, with prior information in the form of a Gamma(`alpha`, `beta`) density. Assume that the means are unknown, but have prior information equivalent to (n01, n02) previous observations, respectively. The function `mudiff.alc.equalvar` returns the required sample sizes to attain the desired average length `len` for the posterior credible interval of fixed coverage probability `level` for the difference between the two unknown means.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.

Value

The required sample sizes (n1, n2) for each group given the inputs to the function.

Note

The sample sizes returned by this function are exact.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle
References
Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also
mudiff.acc.equalvar, mudiff.modwoc.equalvar, mudiff.acc, mudiff.alc, mudiff.modwoc,
mudiff.varknown, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar,
mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mbl.varknown, mudiff.freq, mu.acc,
mu.alc, mu.modwoc, mu.varknown, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mbl.varknown,
mu.freq

Examples
mudiff.alc.equalvar(len=0.2, alpha=2, beta=2, n01=10, n02=50)

mudiff.freq
Frequentist sample size determination for differences in normal means

Description
The function mudiff.freq returns the required sample sizes to get a confidence interval of given
length and confidence level for the difference between two normal means.

Usage
mudiff.freq(len, lambda1, lambda2, level = 0.95, equal=TRUE)

Arguments
len The desired total length of the confidence interval for the difference between the
two unknown means
lambda1 Known precision (reciprocal of the variance) for the first population
lambda2 Known precision (reciprocal of the variance) for the second population
level The desired confidence level (e.g., 0.95)
equal logical. Whether or not the final group sizes (n1, n2) are forced to be equal:

when equal = TRUE, final sample sizes n1 = n2;
when equal = FALSE, final sample sizes (n1, n2) minimize the variance given a total of n1+n2 observations
Details
Assume that a random sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume further that the two precisions \( \lambda_1 \) and \( \lambda_2 \) are known (where precision is the reciprocal of the variance). The function `mudiff.freq` returns the required sample sizes to attain the desired length \( \text{len} \) and confidence level \( \text{level} \) for the confidence interval for the difference between the two unknown means from a frequentist point of view.

Value
The required sample sizes \((n_1, n_2)\) for each group given the inputs to the function.

Note
The sample sizes returned by this function are exact.

Author(s)
Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

See Also
`mudiff.acc`, `mudiff.alc`, `mudiff.modwoc`, `mudiff.acc.equalvar`, `mudiff.alc.equalvar`, `mudiff.modwoc.equalvar`, `mudiff.varknown`, `mudiff.mblacc`, `mudiff.mblalc`, `mudiff.mblmodwoc`, `mudiff.mblacc.equalvar`, `mudiff.mblalc.equalvar`, `mudiff.mblmodwoc.equalvar`, `mudiff.mbl.varknown`, `mu.freq`, `mu.acc`, `mu.alc`, `mu.modwoc`, `mu.varknown`, `mu.mblacc`, `mu.mblalc`, `mu.mblmodwoc`, `mu.mbl.varknown`

Examples
```r
# Suppose variance1 = 2, variance2 = 4
mudiff.freq(len=2, lambda1=1/2, lambda2=1/4)
```

Description
The function `mudiff.mbl.varknown` returns the required sample sizes to reach a given posterior credible interval length and coverage probability for the difference between two normal means - using a mixed Bayesian/likelihood approach - when variances are known.
mudiff.mbl.varknown

Usage

mudiff.mbl.varknown(len, lambda1, lambda2, level = 0.95, equal = TRUE)

Arguments

len
The desired total length of the posterior credible interval for the difference between the two unknown means

lambda1
The known precision (reciprocal of variance) for the first population

lambda2
The known precision (reciprocal of variance) for the second population

level
The desired coverage probability of the posterior credible interval (e.g., 0.95)

equal
logical. Whether or not the final group sizes (n1, n2) are forced to be equal:

when equal = TRUE, final sample sizes n1 = n2;
when equal = FALSE, final sample sizes (n1, n2) minimize the posterior variance given a total of n1+n2 observations

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means when the variances are known. The function mudiff.mbl.varknown returns the required sample sizes to attain the desired length len and coverage probability level for the posterior credible interval for the difference between the two unknown means.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but use only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

Value

The required sample sizes (n1, n2) for each group given the inputs to the function.

Note

The sample sizes returned by this function are exact.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means
See Also

`mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.varknown, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.freq, mu.mbl.varknown, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.varknown, mu.acc, mu.alc, mu.modwoc, mu.freq`

Examples

```r
mudiff.mbl.varknown(len=0.2, lambda1=1, lambdaR=1/1.5)
```

---

### mudiff.mblacc

**Bayesian sample size determination for differences in normal means using the mixed Bayesian/likelihood Average Coverage Criterion**

**Description**

The function `mudiff.mblacc` returns the required sample sizes to reach a given coverage probability on average for a posterior credible interval of fixed length - using a mixed Bayesian/likelihood approach - for the difference between two normal means.

**Usage**

```r
mudiff.mblacc(len, alpha1, beta1, alpha2, beta2, level = 0.95, m = 10000, mcs = 3)
```

**Arguments**

- `len` The desired fixed length of the posterior credible interval for the difference between the two unknown means
- `alpha1` First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
- `beta1` Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
- `alpha2` First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
- `beta2` Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
- `level` The desired average coverage probability of the posterior credible interval (e.g., 0.95)
- `m` The number of points simulated from the preposterior distribution of the data. For each point, the probability coverage of the highest posterior density interval of fixed length `len` is estimated, in order to approximate the average coverage probability. Usually 10000 is sufficient, but one can increase this number at the expense of program running time.
- `mcs` The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, `mcs = 3` is a good choice.
Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precision within each of the two the populations are unknown, but have prior information in the form of Gamma($\alpha_1$, $\beta_1$) and Gamma($\alpha_2$, $\beta_2$) densities, respectively. The function `mudiff.mblacc` returns the required sample sizes to attain the desired average coverage probability level for the posterior credible interval of fixed length $len$ for the difference between the two unknown means.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but use only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

Value

The required sample sizes ($n_1$, $n_2$) for each group given the inputs to the function.

Note

The sample sizes are calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

`mudiff.mblalc`, `mudiff.mblmodwoc`, `mudiff.mblacc.equalvar`, `mudiff.mblalc.equalvar`, `mudiff.mblmodwoc.equalvar`, `mudiff.mbl.varknown`, `mudiff.acc`, `mudiff.alc`, `mudiff.modwoc`, `mudiff.acc.equalvar`, `mudiff.alc.equalvar`, `mudiff.modwoc.equalvar`, `mudiff.varknown`, `mudiff.freq`, `mu.mblacc`, `mu.mblalc`, `mu.mblmodwoc`, `mu.mbl.varknown`, `mu.acc`, `mu.alc`, `mu.modwoc`, `mu.varknown`, `mu.freq`

Examples

`mudiff.mblacc(len=0.2, alpha1=2, beta1=2, alpha2=3, beta2=3)`
**mudiff.mblacc.equalvar**

*Bayesian sample size determination for differences in normal means when variances are equal using the Mixed Bayesian/Likelihood Average Coverage Criterion*

---

**Description**

The function `mudiff.mblacc.equalvar` returns the required sample sizes to reach a given coverage probability on average for a posterior credible interval of fixed length for the difference between two normal means using a mixed Bayesian/likelihood approach, when variances are equal.

**Usage**

```r
mudiff.mblacc.equalvar(len, alpha, beta, level = 0.95, m = 10000, mcs = 3)
```

**Arguments**

- `len` The desired fixed length of the posterior credible interval for the difference between the two unknown means
- `alpha` First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `beta` Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `level` The desired average coverage probability of the posterior credible interval (e.g., 0.95)
- `m` The number of points simulated from the preposterior distribution of the data. For each point, the probability coverage of the highest posterior density interval of fixed length `len` is estimated, in order to approximate the average coverage probability. Usually 10000 is sufficient, but one can increase this number at the expense of program running time.
- `mcs` The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, mcs = 3 is a good choice.

**Details**

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precision within each of the two the populations are unknown but equal, with prior information in the form of a Gamma(`alpha`, `beta`) density. The function `mudiff.mblacc.equalvar` returns the required sample sizes to attain the average coverage probability `level` for the posterior credible interval of fixed length `len` for the difference between the two unknown means.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior
information to derive the predictive distribution of the data, but use only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

Value
The required sample sizes \((n_1, n_2)\) for each group given the inputs to the function.

Note
The sample sizes are calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

Author(s)
Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References
Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

\texttt{mudiff.mblalc.equalvar}, \texttt{mudiff.mblmodwoc.equalvar}, \texttt{mudiff.mblacc}, \texttt{mudiff.mblalc}, \texttt{mudiff.mblmodwoc}, \texttt{mudiff.mbl.varknown}, \texttt{mudiff.acc.equalvar}, \texttt{mudiff.alc.equalvar}, \texttt{mudiff.modwoc.equalvar}, \texttt{mudiff.acc}, \texttt{mudiff.alc}, \texttt{mudiff.modwoc}, \texttt{mudiff.varknown}, \texttt{mudiff.freq}, \texttt{mu.mblacc}, \texttt{mu.mblalc}, \texttt{mu.mblmodwoc}, \texttt{mu.mbl.varknown}, \texttt{mu.acc}, \texttt{mu.alc}, \texttt{mu.modwoc}, \texttt{mu.varknown}, \texttt{mu.freq}

Examples

\begin{verbatim}
  mudiff.mblacc.equalvar(len=0.2, alpha=2, beta=2)
\end{verbatim}

\begin{verbatim}
  mudiff.mblalc
\end{verbatim}

\textbf{Bayesian sample size determination for differences in normal means using the Mixed Bayesian/Likelihood Average Length Criterion}

Description
The function \texttt{mudiff.mblalc} returns the required sample sizes to reach a given posterior credible interval length on average for a fixed coverage probability - using a mixed Bayesian/likelihood approach - for the difference between two normal means.

Usage

\begin{verbatim}
  mudiff.mblalc(len, alpha1, beta1, alpha2, beta2, level = 0.95, m = 10000, mcs = 3)
\end{verbatim}
mudiff.mblalc

Arguments

len    The desired average length of the posterior credible interval for the difference between the two unknown means
alpha1 First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
beta1  Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
alpha2 First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
beta2  Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
level  The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
m     The number of points simulated from the preposterior distribution of the data. For each point, the length of the highest posterior density interval of fixed coverage probability level is estimated, in order to approximate the average length. Usually 10000 is sufficient, but one can increase this number at the expense of program running time.

mcs   The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, mcs = 3 is a good choice.

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precision within each of the two populations are unknown, but have prior information in the form of Gamma(alpha1, beta1) and Gamma(alpha2, beta2) densities, respectively. The function mudiff.mblalc returns the required sample sizes to attain the desired average length len for the posterior credible interval of fixed coverage probability level for the difference between the two unknown means.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but use only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

Value

The required sample sizes (n1, n2) for each group given the inputs to the function.

Note

The sample sizes are calculated via Monte Carlo simulations, and therefore may vary from one call to the next.
**Author(s)**

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

**References**

Joseph L, Belisle P. Bayesian sample size determination for Normal means and differences between Normal means

**See Also**

mudiff.mblacc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.freq, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mbl.varknown, mu.acc, mu.alc, mu.modwoc, mu.varknown, mu.freq

**Examples**

mudiff.mblalc(len=P.R, alpha1=R, beta1=R, alphaR=S, betaR=S)

```r
mudiff.mblalc.equalvar(len=0.2, alpha=2, beta=2, alpha2=3, beta2=3)
```

**Description**

The function `mudiff.mblalc.equalvar` returns the required sample sizes to reach a given posterior credible interval length on average for a fixed coverage probability for the difference between two normal means - using a mixed Bayesian/likelihood approach - when variances are equal.

**Usage**

`mudiff.mblalc.equalvar(len, alpha, beta, level = 0.95)`

**Arguments**

- `len` The desired average length of the posterior credible interval for the difference between the two unknown means
- `alpha` First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `beta` Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `level` The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precisions of the two normal sampling distributions are unknown but equal, with prior information in the form of a Gamma\((alpha, beta)\) density. The function `mudiff.mblalc.equalvar` returns the required sample sizes to attain the desired average length \(len\) for the posterior credible interval of fixed coverage probability \(level\) for the difference between the two unknown means.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but use only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

Value

The required sample sizes \((n1, n2)\) for each group given the inputs to the function.

Note

The sample sizes returned by this function are exact.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

`mudiff.mblacc.equalvar`, `mudiff.mblmodwoc.equalvar`, `mudiff.mblacc`, `mudiff.mblalc`, `mudiff.mblmodwoc`, `mudiff.mbl.varknown`, `mudiff.acc.equalvar`, `mudiff.alc.equalvar`, `mudiff.modwoc.equalvar`, `mudiff.acc`, `mudiff.alc`, `mudiff.modwoc`, `mudiff.varknown`, `mudiff.freq`, `mu.mblacc`, `mu.mblalc`, `mu.mblmodwoc`, `mu.mbl.varknown`, `mu.acc`, `mu.alc`, `mu.modwoc`, `mu.varknown`, `mu.freq`

Examples

`mudiff.mblalc.equalvar(len=0.2, alpha=2, beta=2)`
**mudiff.mblmodwoc**

*Bayesian sample size determination for differences in normal means using the Mixed Bayesian/Likelihood Modified Worst Outcome Criterion*

**Description**

The function `mudiff.mblmodwoc` uses a mixed Bayesian/likelihood approach to determine conservative sample sizes, in the sense that the desired posterior credible interval coverage and length for the difference between two normal means are guaranteed over a given proportion of data sets that can arise according to the prior information.

**Usage**

```r
mudiff.mblmodwoc(len, alpha1, beta1, alpha2, beta2, level = 0.95, worst.level = 0.95, m = 50000, mcs = ...)
```

**Arguments**

- `len`  
The desired total length of the posterior credible interval for the difference between the two unknown means
- `alpha1`  
The first prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
- `beta1`  
The second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
- `alpha2`  
The first prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
- `beta2`  
The second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
- `level`  
The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
- `worst.level`  
The probability that the length of the posterior credible interval of fixed coverage probability `level` will be at most `len`
- `m`  
The number of points simulated from the preposterior distribution of the data. For each point, the length of the highest posterior density interval of fixed coverage probability `level` is estimated, in order to approximate the (100*`worst.level`%)-percentile of the posterior credible interval length. Usually 50000 is sufficient, but one can increase this number at the expense of program running time.
- `mcs`  
The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, `mcs = 3` is a good choice.
Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precision within each of the two populations are unknown, but have prior information in the form of $\text{Gamma}(\alpha_1, \beta_1)$ and $\text{Gamma}(\alpha_2, \beta_2)$ densities, respectively. The function `mudiff.mblmodwoc` returns the required sample sizes to attain the desired length $\text{len}$ for the posterior credible interval of fixed coverage probability $\text{level}$ for the difference between the two unknown means. The Modified Worst Outcome Criterion used is conservative, in the sense that the posterior credible interval length $\text{len}$ is guaranteed over the $\text{worst.level}$ proportion of all possible data sets that can arise according to the prior information, for a fixed coverage probability $\text{level}$.

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but uses only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

Value

The required sample sizes $(n_1, n_2)$ for each group given the inputs to the function.

Note

The sample sizes are calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

It is also correct to state that the coverage probability of the posterior credible interval of fixed length $\text{len}$ will be at least $\text{level}$ with probability $\text{worst.level}$ with the sample sizes returned.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

`mudiff.mblacc, mudiff.mblalc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.freq, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mbl.varknown, mu.acc, mu.alc, mu.modwoc, mu.varknown, mu.freq`

Examples

`mudiff.mblmodwoc(len=0.2, alpha1=2, beta1=2, alpha2=3, beta2=3, worst.level=0.95)`
Bayesian sample size determination for differences in normal means when variances are equal using the Mixed Bayesian/Likelihood Modified Worst Outcome Criterion

Description

The function `mudiff.mblmodwoc.equalvar` uses a mixed Bayesian/likelihood approach to determine conservative sample sizes, in the sense that the desired posterior credible interval coverage and length for the difference between two normal means are guaranteed over a given proportion of data sets that can arise according to the prior information, when variances are equal.

Usage

```r
mudiff.mblmodwoc.equalvar(len, alpha, beta, level = 0.95, worst.level = 0.95, m = 50000, mcs = 3)
```

Arguments

- `len`: The desired total length of the posterior credible interval for the difference between the two unknown means
- `alpha`: First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `beta`: Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `level`: The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
- `worst.level`: The probability that the length of the posterior credible interval of fixed coverage probability `level` will be at most `len`
- `m`: The number of points simulated from the preposterior distribution of the data. For each point, the length of the highest posterior density interval of fixed coverage probability `level` is estimated, in order to approximate the (100*`worst.level`)%-percentile of the posterior credible interval length. Usually 50000 is sufficient, but one can increase this number at the expense of program running time.
- `mcs`: The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, `mcs = 3` is a good choice.

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precisions of the two normal sampling distributions are unknown but equal, with prior information in the form of a Gamma(\(alpha, beta\)) density. The function `mudiff.mblmodwoc.equalvar` returns the required sample sizes to attain the desired length `len` for the posterior credible interval of fixed coverage probability `level`.
for the difference between the two unknown means. The Modified Worst Outcome Criterion used is conservative, in the sense that the posterior credible interval length \( \text{len} \) is guaranteed over the \( \text{worst.level} \) proportion of all possible data sets that can arise according to the prior information, for a fixed coverage probability \( \text{level} \).

This function uses a Mixed Bayesian/Likelihood (MBL) approach. MBL approaches use the prior information to derive the predictive distribution of the data, but uses only the likelihood function for final inferences. This approach is intended to satisfy investigators who recognize that prior information is important for planning purposes but prefer to base final inferences only on the data.

### Value

The required sample sizes \((n_1, n_2)\) for each group given the inputs to the function.

### Note

The sample sizes are calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

It is also correct to state that the coverage probability of the posterior credible interval of fixed length \( \text{len} \) will be at least \( \text{level} \) with probability \( \text{worst.level} \) with the sample sizes returned.

### Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

### References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

### See Also

mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mbl.varknown, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.varknown, mudiff.freq, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.mbl.varknown, mu.acc, mu.alc, mu.modwoc, mu.varknown, mu.freq

### Examples

mudiff.mblmodwoc.equalvar(len=0.2, alpha=2, beta=2)
**Description**

The function `mudiff.modwoc` calculates conservative sample sizes, in the sense that the desired posterior credible interval coverage and length for the difference between two normal means are guaranteed over a given proportion of data sets that can arise according to the prior information.

**Usage**

```r
mudiff.modwoc(len, alpha1, beta1, alpha2, beta2, n01, n02, level = 0.95, worst.level = 0.95, equal = TRUE, m = 50000, mcs = S)
```

**Arguments**

- `len` The desired total length of the posterior credible interval for the difference between the two unknown means.
- `alpha1` First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population.
- `beta1` Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population.
- `alpha2` First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population.
- `beta2` Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population.
- `n01` Prior sample size equivalent for the mean for the first population.
- `n02` Prior sample size equivalent for the mean for the second population.
- `level` The desired fixed coverage probability of the posterior credible interval (e.g., 0.95).
- `worst.level` The probability that the length of the posterior credible interval of fixed coverage probability `level` will be at most `len`.
- `equal` logical. Whether or not the final group sizes (n1, n2) are forced to be equal:
  - when `equal` = TRUE, final sample sizes n1 = n2;
  - when `equal` = FALSE, final sample sizes (n1, n2) minimize the expected posterior variance given a total of n1+n2 observations.
- `m` The number of points simulated from the preposterior distribution of the data. For each point, the length of the highest posterior density interval of fixed coverage probability `level` is estimated, in order to approximate the (100*`worst.level`)%-percentile of the posterior credible interval length. Usually 50000 is sufficient, but one can increase this number at the expense of program running time.
mudiff.modwoc

mcs

The Maximum number of Consecutive Steps allowed in the same direction in the march towards the optimal sample size, before the result for the next upper/lower bound is cross-checked. In our experience, mcs = 3 is a good choice.

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precision within each of the two the populations are unknown, but have prior information in the form of Gamma($alpha_1$, $beta_1$) and Gamma($alpha_2$, $beta_2$) densities, respectively. Assume that the means are unknown, but have prior information equivalent to ($n01$, $n02$) previous observations, respectively. The function mudiff.modwoc returns the required sample sizes to attain the desired length $len$ for the posterior credible interval of fixed coverage probability level for the difference between the two unknown means. The Modified Worst Outcome Criterion used is conservative, in the sense that the posterior credible interval length $len$ is guaranteed over the worst.level proportion of all possible data sets that can arise according to the prior information, for a fixed coverage probability level.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.

Value

The required sample sizes (n1, n2) for each group given the inputs to the function.

Note

The sample sizes are calculated via Monte Carlo simulations, and therefore may vary from one call to the next.

It is also correct to state that the coverage probability of the posterior credible interval of fixed length $len$ will be at least level with probability worst.level with the sample sizes returned.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

mudiff.acc, mudiff.alc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.varknown, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.mbl.varknown, mudiff.freq,
Bayesian sample size determination for differences in normal means when variances are equal using the Modified Worst Outcome Criterion

Description

The function `mudiff.modwoc.equalvar` calculates conservative sample sizes, in the sense that the desired posterior credible interval coverage and length for the difference between two normal means are guaranteed over a given proportion of data sets that can arise according to the prior information, when variances are equal.

Usage

`mudiff.modwoc.equalvar(len, alpha, beta, n01, n02, level = 0.95, worst.level = 0.95, equal = TRUE)`

Arguments

- `len`: The desired total length of the posterior credible interval for the difference between the two unknown means
- `alpha`: First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `beta`: Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
- `n01`: Prior sample size equivalent for the mean for the first population
- `n02`: Prior sample size equivalent for the mean for the second population
- `level`: The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
- `worst.level`: The probability that the length of the posterior credible interval of fixed coverage probability `level` will be at most `len`
- `equal`: logical. Whether or not the final group sizes (n1, n2) are forced to be equal:

  - when `equal` = TRUE, final sample sizes n1 = n2;
  - when `equal` = FALSE, final sample sizes (n1, n2) minimize the expected posterior variance given a total of n1+n2 observations.
Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means. Assume that the precisions of the two normal sampling distributions are unknown but equal, with prior information in the form of a Gamma($\alpha, \beta$) density. Assume that the means are unknown, but have prior information equivalent to ($n_01$, $n_02$) previous observations, respectively. The function `mudiff.modwoc.equalvar` returns the required sample sizes to attain the desired length $len$ for the posterior credible interval of fixed coverage probability $level$ for the difference between the two unknown means. The Modified Worst Outcome Criterion used is conservative, in the sense that the posterior credible interval length $len$ is guaranteed over the $worst.level$ proportion of all possible data sets that can arise according to the prior information, for a fixed coverage probability $level$.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.

Value

The required sample sizes ($n1$, $n2$) for each group given the inputs to the function.

Note

The sample sizes returned by this function are exact.

It is also correct to state that the coverage probability of the posterior credible interval of fixed length $len$ will be at least $level$ with probability $worst.level$ with the sample sizes returned.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

`mudiff.acc.equalvar`, `mudiff.alc.equalvar`, `mudiff.acc`, `mudiff.alc`, `mudiff.modwoc`, `mudiff.varknown`, `mudiff.mblacc.equalvar`, `mudiff.mblalc.equalvar`, `mudiff.mblmodwoc.equalvar`, `mudiff.mblacc`, `mudiff.mblalc`, `mudiff.mblmodwoc`, `mudiff.mbl.varknown`, `mudiff.freq`, `mu.acc`, `mu.alc`, `mu.modwoc`, `mu.varknown`, `mu.mblacc`, `mu.mblalc`, `mu.mblmodwoc`, `mu.mbl.varknown`, `mu.freq`

Examples

```r
mudiff.modwoc.equalvar(len=0.2, alpha=2, beta=2, n01=10, n02=50)
```
Description

The function `mudiff.varknown` returns the required sample sizes to reach a given posterior credible interval length and coverage probability for the difference between two normal means, when variances are known.

Usage

```r
mudiff.varknown(len, lambda1, n01, lambda2, n02, level = 0.95, equal = TRUE)
```

Arguments

- `len`: The desired total length of the posterior credible interval for the difference between the two unknown means
- `lambda1`: The known precision (reciprocal of variance) for the first population
- `n01`: Prior sample size equivalent for the mean for the first population
- `lambda2`: The known precision (reciprocal of variance) for the second population
- `n02`: Prior sample size equivalent for the mean for the second population
- `level`: The desired coverage probability of the posterior credible interval (e.g., 0.95)
- `equal`: logical. Whether or not the final group sizes \((n_1, n_2)\) are forced to be equal:
  - when `equal = TRUE`, final sample sizes \(n_1 = n_2\);
  - when `equal = FALSE`, final sample sizes \((n_1, n_2)\) minimize the posterior variance given a total of \(n_1+n_2\) observations

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent normal means when the variances are known. Assume that the means are unknown, but have prior information equivalent to \((n01, n02)\) previous observations, respectively. The function `mudiff.varknown` returns the required sample sizes to attain the desired length `len` and coverage probability `level` for the posterior credible interval for the difference between the two unknown means.

This function uses a fully Bayesian approach to sample size determination. Therefore, the desired coverages and lengths are only realized if the prior distributions input to the function are used for final inferences. Researchers preferring to use the data only for final inferences are encouraged to use the Mixed Bayesian/Likelihood version of the function.
Value

The required sample sizes (n1, n2) for each group given the inputs to the function.

Note

The sample sizes returned by this function are exact.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca> and Patrick Belisle

References

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means

See Also

mudiff.acc, mudiff.alc, mudiff.modwoc, mudiff.acc.equalvar, mudiff.alc.equalvar, mudiff.modwoc.equalvar, mudiff.mbl.varknown, mudiff.mblacc, mudiff.mblalc, mudiff.mblmodwoc, mudiff.mblacc.equalvar, mudiff.mblalc.equalvar, mudiff.mblmodwoc.equalvar, mudiff.freq, mu.varknown, mu.acc, mu.alc, mu.modwoc, mu.mbl.varknown, mu.mblacc, mu.mblalc, mu.mblmodwoc, mu.freq

Examples

mudiff.varknown(len=0.2, lambda1=1, n01=10, lambdaR=1/1.5, n02=25)
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