

Package ‘SampleSizeMeans’

July 2, 2014

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

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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: GPL (version 2 or later)

URL: <http://www.medicine.mcgill.ca/epidemiology/Joseph/Methodological-Publications-Bayesian-Samp1>

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

<http://cran.r-project.org/web/packages/SampleSizeProportions/index.html>

Author(s)

Lawrence Joseph and Patrick Belisle

Maintainer: Lawrence Joseph <lawrence.joseph@mcgill.ca>

References

Joseph L, Belisle P.

Bayesian sample size determination for Normal means and differences between Normal means
The Statistician 1997;46(2):209-226.

See Also

[mu.acc](#), [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](#)

mu.acc

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

Description

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

<code>len</code>	The desired fixed length of the posterior credible interval for the mean
<code>alpha</code>	First parameter of the Gamma prior density for the precision (reciprocal of the variance)
<code>beta</code>	Second parameter of the Gamma prior density for the precision (reciprocal of the variance)
<code>n0</code>	Prior sample size equivalent for the mean
<code>level</code>	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(α , β) 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
The Statistician 1997;46(2):209-226.

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	<i>Bayesian sample size determination for estimating a single normal mean using the Average Length Criterion</i>
--------	--

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

<code>len</code>	The desired average length of the posterior credible interval for the mean
<code>alpha</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance)
<code>beta</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance)
<code>n0</code>	Prior sample size equivalent for the mean
<code>level</code>	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
The Statistician 1997;46(2):209-226.

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

<code>len</code>	The desired total length of the confidence interval for the mean
<code>lambda</code>	Known precision (reciprocal of variance)
<code>level</code>	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.

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

Lemeshow S, Hosmer Jr DW, Klar J, Lwanga SK.
Adequacy of Sample Size in Health Studies. Wiley and Sons, New York, 1990.

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means
The Statistician 1997;46(2):209-226.

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=0.2, lambda=1/4)
```

mu.mbl.varknown	<i>Bayesian sample size determination for estimating a single normal mean with known variance using the Mixed Bayesian/Likelihood criteria</i>
-----------------	--

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 `mu.mbl.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 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
The Statistician 1997;46(2):209-226.

See Also

[mu.mblacc](#), [mu.mblalc](#), [mu.mblmodwoc](#), [mu.varknown](#), [mu.acc](#), [mu.alc](#), [mu.modwoc](#), [mu.freq](#),
[mudiff.mbl.varknown](#), [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](#)

Examples

```
mu.mbl.varknown(len=0.2, lambda=1/4)
```

mu.mblacc	<i>Bayesian sample size determination for estimating a single normal mean using the Mixed Bayesian/Likelihood Average Coverage Criterion</i>
-----------	--

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

<code>len</code>	The desired fixed length of the posterior credible interval for the mean
<code>alpha</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance)
<code>beta</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance)
<code>level</code>	The desired average coverage probability of the posterior credible interval (e.g., 0.95)
<code>m</code>	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 <i>len</i> 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.
<code>mcs</code>	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, <code>mcs = 3</code> 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 $\text{Gamma}(\alpha, \beta)$ 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

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means
The Statistician 1997;46(2):209-226.

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

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

Description

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

Usage

```
mu.mblalc(len, alpha, beta, 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)
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 $\text{Gamma}(\alpha, \beta)$ density. The function `mu.mblalc` 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 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
The Statistician 1997;46(2):209-226.

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](#)

Examples

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

mu.mblmodwoc	<i>Bayesian sample size determination for estimating a single normal mean using the Mixed Bayesian/Likelihood Modified Worst Outcome Criterion</i>
--------------	--

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

len	The desired total 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)
worst.level	The probability that the length of the posterior credible interval of fixed coverage probability <i>level</i> will be at most <i>len</i>
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 <i>level</i> is estimated, in order to approximate the $(100*\text{worst.level})\%$ -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, $\text{mcs} = 3$ 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 $\text{Gamma}(\alpha, \beta)$ density. The function `mu.mblmodwoc` 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 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 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.

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

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means
The Statistician 1997;46(2):209-226.

See Also

[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](#)

Examples

```
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, n0, level = 0.95, worst.level = 0.95)
```

Arguments

<code>len</code>	The desired length of the posterior credible interval for the mean
<code>alpha</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance)
<code>beta</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance)
<code>n0</code>	Prior sample size equivalent for the mean
<code>level</code>	The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
<code>worst.level</code>	The probability that the length of the posterior credible interval of fixed coverage probability <i>level</i> will be at most <i>len</i>

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(α , β) density. Assume that the mean is unknown, but has prior information equivalent to n_0 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

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means
The Statistician 1997;46(2):209-226.

See Also

[mu.acc](#), [mu.alc](#), [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.modwoc(len=0.2, alpha=2, beta=2, n0=10)
```

mu.varknown	<i>Bayesian sample size determination for estimating a single normal mean with known variance</i>
-------------	---

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)
n0	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 *n0* 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
The Statistician 1997;46(2):209-226.

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, n0=10)
```

mudiff.acc	<i>Bayesian sample size determination for differences in normal means using the Average Coverage Criterion</i>
------------	--

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, alpha1, beta1, alpha2, beta2, n01, n02, level = 0.95, equal = TRUE, m = 10000, mcs = 3)
```

Arguments

<code>len</code>	The desired fixed length of the posterior credible interval for the difference between the two unknown means
<code>alpha1</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
<code>beta1</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
<code>alpha2</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
<code>beta2</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
<code>n01</code>	Prior sample size equivalent for the mean for the first population
<code>n02</code>	Prior sample size equivalent for the mean for the second population
<code>level</code>	The desired average coverage probability of the posterior credible interval (e.g., 0.95)
<code>equal</code>	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.

<code>m</code>	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 <code>len</code> 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.
<code>mcs</code>	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. 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 *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 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
The Statistician 1997;46(2):209-226.

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

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

Arguments

<code>len</code>	The desired fixed length of the posterior credible interval for the difference between the two unknown means
<code>alpha</code>	First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>beta</code>	Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>n01</code>	Prior sample size equivalent for the mean for the first population
<code>n02</code>	Prior sample size equivalent for the mean for the second population
<code>level</code>	The desired average coverage probability of the posterior credible interval (e.g., 0.95)
<code>equal</code>	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.

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 $\text{Gamma}(\alpha, \beta)$ density. Assume that the means are unknown, but have prior information equivalent to (n_01, n_02) previous observations, respectively. The function `mudiff.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 (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
The Statistician 1997;46(2):209-226.

See Also

[mudiff.alc.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.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 <i>level</i> 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 $\text{Gamma}(\alpha1, \beta1)$ and $\text{Gamma}(\alpha2, \beta2)$ 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 (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
The Statistician 1997;46(2):209-226.

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=0.2, alpha1=2, beta1=2, alpha2=3, beta2=3, n01=10, n02=25)
```

mudiff.alc.equalvar	<i>Bayesian sample size determination for differences in normal means when variances are equal using the Average Length Criterion</i>
---------------------	---

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
 The Statistician 1997;46(2):209-226.

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

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

when `equal = TRUE`, final sample sizes $n_1 = n_2$;
 when `equal = FALSE`, final sample sizes (n1, n2) minimize the variance given a total of n_1+n_2 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 λ_1 and λ_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 len and confidence level $level$ 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

Joseph L, Belisle P.
Bayesian sample size determination for Normal means and differences between Normal means
The Statistician 1997;46(2):209-226.

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

```
# Suppose variance1 = 2, variance2 = 4
mudiff.freq(len=0.2, lambda1=1/2, lambda2=1/4)
```

<code>mudiff.mbl.varknown</code>	<i>Bayesian sample size determination for differences in normal means when variances are known using the Mixed Bayesian/Likelihood criteria</i>
----------------------------------	---

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.

Usage

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

Arguments

<code>len</code>	The desired total length of the posterior credible interval for the difference between the two unknown means
<code>lambda1</code>	The known precision (reciprocal of variance) for the first population
<code>lambda2</code>	The known precision (reciprocal of variance) for the second population
<code>level</code>	The desired coverage probability of the posterior credible interval (e.g., 0.95)
<code>equal</code>	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. 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 (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
The Statistician 1997;46(2):209-226.

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

```
mudiff.mbl.varknown(len=0.2, lambda1=1, lambda2=1/1.5)
```

mudiff.mblacc	<i>Bayesian sample size determination for differences in normal means using the mixed Bayesian/likelihood Average Coverage Criterion</i>
---------------	--

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

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

Arguments

<code>len</code>	The desired fixed length of the posterior credible interval for the difference between the two unknown means
<code>alpha1</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
<code>beta1</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
<code>alpha2</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
<code>beta2</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
<code>level</code>	The desired average coverage probability of the posterior credible interval (e.g., 0.95)
<code>m</code>	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 <i>len</i> 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.
<code>mcs</code>	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, <code>mcs = 3</code> 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.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 (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
The Statistician 1997;46(2):209-226.

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

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

Arguments

<code>len</code>	The desired fixed length of the posterior credible interval for the difference between the two unknown means
<code>alpha</code>	First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>beta</code>	Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>level</code>	The desired average coverage probability of the posterior credible interval (e.g., 0.95)
<code>m</code>	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 <i>len</i> 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.
<code>mcs</code>	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, <code>mcs = 3</code> 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 (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
The Statistician 1997;46(2):209-226.

See Also

[mudiff.mblalc.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.mblacc.equalvar(len=0.2, alpha=2, beta=2)
```

mudiff.mblalc	<i>Bayesian sample size determination for differences in normal means using the Mixed Bayesian/Likelihood Average Length Criterion</i>
---------------	--

Description

The function `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

```
mudiff.mblalc(len, alpha1, beta1, alpha2, beta2, level = 0.95, 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
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 <i>level</i> 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 the 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.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 (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
The Statistician 1997;46(2):209-226.

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=0.2, alpha1=2, beta1=2, alpha2=3, beta2=3)
```

```
mudiff.mblalc.equalvar
```

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

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

<code>len</code>	The desired average length of the posterior credible interval for the difference between the two unknown means
<code>alpha</code>	First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>beta</code>	Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>level</code>	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(α , β) 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 (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
The Statistician 1997;46(2):209-226.

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	<i>Bayesian sample size determination for differences in normal means using the Mixed Bayesian/Likelihood Modified Worst Outcome Criterion</i>
------------------	--

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

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

Arguments

<code>len</code>	The desired total length of the posterior credible interval for the difference between the two unknown means
<code>alpha1</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
<code>beta1</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
<code>alpha2</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
<code>beta2</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
<code>level</code>	The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
<code>worst.level</code>	The probability that the length of the posterior credible interval of fixed coverage probability <i>level</i> will be at most <i>len</i>
<code>m</code>	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 <i>level</i> is estimated, in order to approximate the $(100 * \text{worst.level})\%$ -percentile of the posterior credible interval length. Usually 50000 is sufficient, but one can increase this number at the expense of program running time.
<code>mcs</code>	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, <code>mcs = 3</code> 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 $\text{Gamma}(\alpha_1, \beta_1)$ and $\text{Gamma}(\alpha_2, \beta_2)$ densities, respectively. The function `mudiff.mblmodwoc` returns the required sample sizes to attain the desired length *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 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 (*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
The Statistician 1997;46(2):209-226.

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.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.mblmodwoc(len=0.2, alpha1=2, beta1=2, alpha2=3, beta2=3, worst.level=0.95)
```

mudiff.mblmodwoc.equalvar

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

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

Arguments

<code>len</code>	The desired total length of the posterior credible interval for the difference between the two unknown means
<code>alpha</code>	First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>beta</code>	Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>level</code>	The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
<code>worst.level</code>	The probability that the length of the posterior credible interval of fixed coverage probability <i>level</i> will be at most <i>len</i>
<code>m</code>	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 <i>level</i> is estimated, in order to approximate the $(100*\text{worst.level})\%$ -percentile of the posterior credible interval length. Usually 50000 is sufficient, but one can increase this number at the expense of program running time.
<code>mcs</code>	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, <code>mcs = 3</code> 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 *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 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 (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
The Statistician 1997;46(2):209-226.

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)
```

mudiff.modwoc	<i>Bayesian sample size determination for differences in normal means using the Modified Worst Outcome Criterion</i>
---------------	--

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

```
mudiff.modwoc(len, alpha1, beta1, alpha2, beta2, n01, n02, level = 0.95, worst.level = 0.95, equal = T)
```

Arguments

<code>len</code>	The desired total length of the posterior credible interval for the difference between the two unknown means
<code>alpha1</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
<code>beta1</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the first population
<code>alpha2</code>	First prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
<code>beta2</code>	Second prior parameter of the Gamma density for the precision (reciprocal of the variance) for the second population
<code>n01</code>	Prior sample size equivalent for the mean for the first population
<code>n02</code>	Prior sample size equivalent for the mean for the second population
<code>level</code>	The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
<code>worst.level</code>	The probability that the length of the posterior credible interval of fixed coverage probability <i>level</i> will be at most <i>len</i>
<code>equal</code>	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.

<code>m</code>	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 <i>level</i> is estimated, in order to approximate the $(100*\text{worst.level})\%$ -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 the populations are unknown, but have prior information in the form of Gamma(α_1 , β_1) and Gamma(α_2 , β_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.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 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
The Statistician 1997;46(2):209-226.

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`,

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

Examples

```
mudiff.modwoc(len=0.2, alpha1=2, beta1=2, alpha2=3, beta2=3, n01=10, n02=50)
```

```
mudiff.modwoc.equalvar
```

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

<code>len</code>	The desired total length of the posterior credible interval for the difference between the two unknown means
<code>alpha</code>	First prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>beta</code>	Second prior parameter of the Gamma density for the common precision (reciprocal of the variance)
<code>n01</code>	Prior sample size equivalent for the mean for the first population
<code>n02</code>	Prior sample size equivalent for the mean for the second population
<code>level</code>	The desired fixed coverage probability of the posterior credible interval (e.g., 0.95)
<code>worst.level</code>	The probability that the length of the posterior credible interval of fixed coverage probability <i>level</i> will be at most <i>len</i>
<code>equal</code>	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 obs

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(α , β) density. Assume that the means are unknown, but have prior information equivalent to ($n01$, $n02$) 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
The Statistician 1997;46(2):209-226.

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

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

mudiff.varknown	<i>Bayesian sample size determination for differences in normal means when variances are known</i>
-----------------	--

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

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

Arguments

<code>len</code>	The desired total length of the posterior credible interval for the difference between the two unknown means
<code>lambda1</code>	The known precision (reciprocal of variance) for the first population
<code>n01</code>	Prior sample size equivalent for the mean for the first population
<code>lambda2</code>	The known precision (reciprocal of variance) for the second population
<code>n02</code>	Prior sample size equivalent for the mean for the second population
<code>level</code>	The desired coverage probability of the posterior credible interval (e.g., 0.95)
<code>equal</code>	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 (n_{01}, n_{02}) 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
The Statistician 1997;46(2):209-226.

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, lambda2=1/1.5, n02=25)
```

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