Package 'SampleSizeProportions'

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Type Package

Title Calculating Sample Size Requirements when Estimating the Difference Between Two Binomial Proportions

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Description Sample size requirements calculation using three different Bayesian criteria in the context of designing an experiment to estimate the difference between two binomial proportions. 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 binomial observations are provided. In all cases, estimation of the difference between two binomial proportions is considered. Functions for both the fully Bayesian and the mixed Bayesian/likelihood approaches are provided.
For reference see Joseph L., du Berger R. and Bélisle P. (1997) <doi:10.1002/(sici)1097-0258(19970415)16:7%3C769::aid-sim495%3E3.0.co;2-v>.

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Bayesian Sample Size Determination for the Difference between Two Binomial Proportions

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Description

Calculate sample sizes based on highest posterior density intervals when comparing two binomial proportions using three different Bayesian approaches.

Details

Package:	SampleSizeProportions
Type:	Package
Version:	1.1.3
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A set of R functions for calculating sample size requirements using three different Bayesian criteria in the context of designing an experiment to estimate the difference between two binomial proportions. 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 binomial observations are provided. In all cases, estimation of the difference between two binomial proportions is considered. Functions for both the fully Bayesian and the mixed Bayesian/likelihood approaches are provided.

See the related package **SampleSizeMeans** for Bayesian sample sizes calculations based on highest posterior density intervals for normal means
https://CRAN.R-project.org/package=SampleSizeMeans

Author(s)

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References

Joseph L, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

[propdiff.acc](), [propdiff.alc](), [propdiff.modwoc](), [propdiff.woc](), [propdiff.mblacc](), [propdiff.mblalc](),
[propdiff.mblmodwoc](), [propdiff.mblwoc]()

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propdiff.acc	*Bayesian sample size determination for the difference between two binomial proportions using the Average Coverage Criterion*

Description

The function `propdiff.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 binomial proportions.

Usage

```
propdiff.acc(len, c1, d1, c2, d2, level = 0.95, equal = TRUE, m = 10000, mcs = 3)
```

Arguments

len	The fixed length of the posterior credible interval for the difference between the two unknown proportions
c1	First prior parameter of the Beta density for the binomial proportion for the first population
d1	Second prior parameter of the Beta density for the binomial proportion for the first population
c2	First prior parameter of the Beta density for the binomial proportion for the second population
d2	Second prior parameter of the Beta density for the binomial proportion 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 obse

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 binomial proportions. Assume that the proportions have prior information in the form of Beta(*c1*, *d1*) and Beta(*c2*, *d2*) densities in each population, respectively. The function propdiff.acc 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 proportions.

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>, Patrick Belisle and Roxane du Berger

References

Joseph L, du Berger R, and Belisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

propdiff.alc, propdiff.modwoc, propdiff.woc, propdiff.mblacc, propdiff.mblalc, propdiff.mblmodwoc, propdiff.mblwoc

Examples

```
propdiff.acc(len=0.05, c1=3, d1=11, c2=11, d2=54)
```

---

propdiff.alc	*Bayesian sample size determination for the difference between two binomial proportions using the Average Length Criterion*

Description

The function `propdiff.alc` 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 binomial proportions.

Usage

```
propdiff.alc(len, c1, d1, c2, d2, 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 proportions
c1	First prior parameter of the Beta density for the binomial proportion for the first population
d1	Second prior parameter of the Beta density for the binomial proportion for the first population
c2	First prior parameter of the Beta density for the binomial proportion for the second population
d2	Second prior parameter of the Beta density for the binomial proportion for the second population
level	The 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 obse

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 binomial proportions. Assume that the proportions have prior information in the form of Beta(*c1*, *d1*) and Beta(*c2*, *d2*) densities in each population, respectively. The function propdiff.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 proportions.

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>, Patrick Bélisle and Roxane du Berger

References

Joseph L, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

propdiff.acc, propdiff.modwoc, propdiff.woc, propdiff.mblacc, propdiff.mblalc, propdiff.mblmodwoc, propdiff.mblwoc

Examples

```
propdiff.alc(len=0.05, c1=3, d1=11, c2=11, d2=54)
```

---

propdiff.freq	*Frequentist sample size determination for the difference between two binomial proportions*

Description

The function `propdiff.freq` returns the required sample sizes to obtain a confidence interval of given length and confidence level for the difference between two binomial proportions.

Usage

```
propdiff.freq(len, p1.estimate, p2.estimate, level = 0.95)
```

Arguments

`len`	The desired total length of the confidence interval for the proportion
`p1.estimate`	A point estimate for the binomial proportion for the first population
`p2.estimate`	A point estimate for the binomial proportion for the second population
`level`	The desired level of the confidence interval (e.g., 0.95)

Details

Assume that a random sample from each of two populations will be collected in order to estimate the difference between two independent binomial proportions. Assume that the best point estimates for the unknown binomial proportions in the two populations are *(p1.estimate, p2.estimate)*, respectively. The function `propdiff.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 proportions from a **frequentist** point of view, using a normal approximation.

Value

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

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca>, Patrick Bélisle and Roxane du Berger

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, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

propdiff.acc, propdiff.modwoc, propdiff.woc, propdiff.mblacc, propdiff.mblalc, propdiff.mblmodwoc, propdiff.mblwoc

Examples

```
propdiff.freq(len=0.01, p1.estimate=0.15, p2.estimate=0.20)
```

---

propdiff.mblacc	*Bayesian sample size determination for the difference between two binomial proportions using the Mixed Bayesian/Likelihood Average Coverage Criterion*

Description

The function propdiff.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 binomial proportions.

Usage

```
propdiff.mblacc(len, c1, d1, c2, d2, level = 0.95, m = 10000, mcs = 3)
```

Arguments

len	The fixed length of the posterior credible interval for the difference between the two unknown proportions
c1	First prior parameter of the Beta density for the binomial proportion for the first population
d1	Second prior parameter of the Beta density for the binomial proportion for the first population
c2	First prior parameter of the Beta density for the binomial proportion for the second population
d2	Second prior parameter of the Beta density for the binomial proportion 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 binomial proportions. Assume that the proportions have prior information in the form of Beta($c1$, $d1$) and Beta($c2$, $d2$) densities in each population, respectively. The function propdiff.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 proportions.

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>, Patrick Bélisle and Roxane du Berger

References

Joseph L, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

[propdiff.mblalc](#), [propdiff.mblmodwoc](#), [propdiff.mblwoc](#), [propdiff.acc](#), [propdiff.alc](#), [propdiff.modwoc](#), [propdiff.woc](#)

Examples

```
propdiff.mblacc(len=0.05, c1=3, d1=11, c2=11, d2=54)
```

---

propdiff.mblalc	*Bayesian sample size determination for the difference between two binomial proportions using the Mixed Bayesian/Likelihood Average Length Criterion*

Description

The function `propdiff.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 binomial proportions.

Usage

```
propdiff.mblalc(len, c1, d1, c2, d2, 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 proportions
c1	First prior parameter of the Beta density for the binomial proportion for the first population
d1	Second prior parameter of the Beta density for the binomial proportion for the first population
c2	First prior parameter of the Beta density for the binomial proportion for the second population
d2	Second prior parameter of the Beta density for the binomial proportion for the second population
level	The 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 binomial proportions. Assume that the proportions have prior information in the form of Beta(*c1*, *d1*) and Beta(*c2*, *d2*) densities in each population, respectively. The function `propdiff.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 proportions.

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>, Patrick Bélisle and Roxane du Berger

References

Joseph L, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

propdiff.mblacc, propdiff.mblmodwoc, propdiff.mblwoc, propdiff.acc, propdiff.alc, propdiff.modwoc, propdiff.woc

Examples

```
propdiff.mblalc(len=0.05, c1=3, d1=11, c2=11, d2=54)
```

---

propdiff.mblmodwoc	*Bayesian sample size determination for the difference between two binomial proportions using the Mixed Bayesian/Likelihood Modified Worst Outcome Criterion*

Description

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

Usage

```
propdiff.mblmodwoc(len, c1, d1, c2, d2, level = 0.95, worst.level = 0.95)
```

Arguments

`len`	The desired total length of the posterior credible interval for the difference between the two unknown proportions
`c1`	First prior parameter of the Beta density for the binomial proportion for the first population
`d1`	Second prior parameter of the Beta density for the binomial proportion for the first population
`c2`	First prior parameter of the Beta density for the binomial proportion for the second population
`d2`	Second prior parameter of the Beta density for the binomial proportion for the second population
`level`	The 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 from each of two populations will be collected in order to estimate the difference between two independent binomial proportions. Assume that the proportions have prior information in the form of Beta(*c1*, *d1*) and Beta(*c2*, *d2*) densities in each population, respectively. The function `propdiff.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 proportions. 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 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>, Patrick Bélisle and Roxane du Berger

References

Joseph L, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

propdiff.mblacc, propdiff.mblalc, propdiff.mblwoc, propdiff.acc, propdiff.alc, propdiff.modwoc, propdiff.woc

Examples

```
propdiff.mblmodwoc(len=0.05, c1=3, d1=11, c2=11, d2=54, worst.level=0.95)
```

---

propdiff.mblwoc	*Bayesian sample size determination for the difference between two binomial proportions using the Mixed Bayesian/Likelihood Worst Outcome Criterion*

Description

The function propdiff.mblwoc uses a mixed Bayesian/likelihood approach to determine conservative sample sizes for the difference between two binomial proportions, in the sense that the desired posterior credible interval coverage and length are guaranteed over all possible data sets.

Usage

```
propdiff.mblwoc(len, c1, d1, c2, d2, level = 0.95)
```

Arguments

len	The desired length of the posterior credible interval for the difference between the two unknown proportions
c1	First prior parameter of the Beta density for the binomial proportion for the first population
d1	Second prior parameter of the Beta density for the binomial proportion for the first population
c2	First prior parameter of the Beta density for the binomial proportion for the second population
d2	Second prior parameter of the Beta density for the binomial proportion for the second population
level	The 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 binomial proportions. Assume that the proportions have prior information in the form of Beta(*c1*, *d1*) and Beta(*c2*, *d2*) densities in each population, respectively. The function propdiff.mblwoc 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 proportions. The Worst Outcome Criterion used is conservative, in the sense that the posterior credible interval length *len* is guaranteed over all possible data sets that can arise, 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 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 the sample sizes returned.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca>, Patrick Bélisle and Roxane du Berger

References

Joseph L, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

propdiff.mblacc, propdiff.mblalc, propdiff.mblmodwoc, propdiff.acc, propdiff.alc, propdiff.modwoc, propdiff.woc

Examples

```
propdiff.mblwoc(len=0.05, c1=3, d1=11, c2=11, d2=54)
```

---

propdiff.modwoc	*Bayesian sample size determination for the difference between two bi-nomial proportions using the Modified Worst Outcome Criterion*

Description

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

Usage

```
propdiff.modwoc(len, c1, d1, c2, d2, level = 0.95, worst.level = 0.95, equal = TRUE)
```

Arguments

len	The desired length of the posterior credible interval for the difference between the two unknown proportions
c1	First parameter of the Beta prior density for the binomial proportion for the first population
d1	Second parameter of the Beta prior density for the binomial proportion for the first population
c2	First parameter of the Beta prior density for the binomial proportion for the second population
d2	Second parameter of the Beta prior density for the binomial proportion for the second population
level	The 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 obse

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent binomial proportions. Assume that the proportions have prior information in the form of Beta(*c1*, *d1*) and Beta(*c2*, *d2*) densities in each population, respectively. The function `propdiff.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 proportions. 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>, Patrick Bélisle and Roxane du Berger

References

Joseph L, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

propdiff.acc, propdiff.alc, propdiff.woc, propdiff.mblacc, propdiff.mblalc, propdiff.mblmodwoc, propdiff.mblwoc

Examples

```
propdiff.modwoc(len=0.05, c1=3, d1=11, c2=11, d2=54, worst.level=0.95)
```

| propdiff.woc | *Bayesian sample size determination for the difference between two binomial proportions using the Worst Outcome Criterion* |

Description

The function propdiff.woc calculates conservative sample sizes for the difference between two binomial proportions, in the sense that the desired posterior credible interval coverage and length are guaranteed over all possible data sets.

Usage

```
propdiff.woc(len, c1, d1, c2, d2, level = 0.95, equal = TRUE)
```

Arguments

len	The desired total length of the posterior credible interval for the difference between the two unknown proportions
c1	First parameter of the Beta prior density for the binomial proportion for the first population
d1	Second parameter of the Beta prior density for the binomial proportion for the first population
c2	First parameter of the Beta prior density for the binomial proportion for the second population
d2	Second parameter of the Beta prior density for the binomial proportion for the second population
level	The 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 obse

Details

Assume that a sample from each of two populations will be collected in order to estimate the difference between two independent binomial proportions. Assume that the proportions have prior information in the form of Beta(*c1*, *d1*) and Beta(*c2*, *d2*) densities in each population, respectively. The function propdiff.woc 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 proportions. The Worst Outcome Criterion used is conservative, in the sense that the posterior credible interval length *len* is guaranteed over all possible data sets that can arise, 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 the sample sizes returned.

Author(s)

Lawrence Joseph <lawrence.joseph@mcgill.ca>, Patrick Bélisle and Roxane du Berger

References

Joseph L, du Berger R, and Bélisle P.
Bayesian and mixed Bayesian/likelihood criteria for sample size determination
Statistics in Medicine 1997;16(7):769-781.

See Also

propdiff.acc, propdiff.alc, propdiff.modwoc, propdiff.mblacc, propdiff.mblalc, propdiff.mblmodwoc,
propdiff.mblwoc

Examples

```
propdiff.woc(len=0.05, c1=3, d1=11, c2=11, d2=54)
```

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