

Package ‘PriorGen’

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Type Package

Title Generates Prior Distributions for Proportions

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Description Translates beliefs into prior information in the form of Beta and Gamma distributions. It can be mainly used for the generation of priors on the prevalence of disease and the sensitivity/specificity of diagnostic tests.

License GPL-3

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LazyData true

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findbeta*The findbeta function***Description**

A function to estimate the parameters alpha and beta of a Beta distribution based on the existing prior beliefs (data and/or expert opinion). Information is provided about the mean (or the median or the mode) and whether it is lower or greater than a certain value with a pre-specified certainty (usually set at 95%).

Usage

```
findbeta(themean=NULL, themedian=NULL, themode=NULL,
percentile=0.95,lower.v=F, percentile.value)
```

Arguments

themean	specify your prior belief about the mean. It takes a value between 0 and 1. Not to be specified if a value has been given for the median or the mode.
themedian	specify your prior belief about the median. It takes a value between 0 and 1. Not to be specified if a value has been given for the mean or the mode.
themode	specify your prior belief about the mode. It takes a value between 0 and 1. Not to be specified if a value has been given for the mean or the median.
percentile	specify the level of confidence that the true value of the mean (or the median or the mode) is greater or lower than the percentile.value. It takes a value between 0 and 1 and the default =0.95.
lower.v	logical, if TRUE the specified percentile.value is the upper limit for the mean (or the median or the mode) at the specified confidence level (percentile). If FALSE the specified percentile.value is the lower limit for the mean (or the median or the mode) at the specified confidence level (percentile). The default is FALSE.
percentile.value	specify the upper or lower limit for the mean (or the median or the mode) at the specified level of confidence (percentile). It takes a value between 0 and 1.

References

Branscum, A. J., Gardner, I. A., & Johnson, W. O. (2005): Estimation of diagnostic test sensitivity and specificity through Bayesian modeling. Preventive veterinary medicine, **68**, 145–163.

Examples

```
##Example 1
##Based on the available literature the mean value for the sensitivity of a test
##is expected to be 0.90 and we can be 95% sure that it is higher than 0.80.

findbeta(themean=0.90, percentile=0.95,lower.v=FALSE, percentile.value=0.80)
```

```
## The output is:  
##[1] "The desired Beta distribution that satisfies the specified conditions is:  
##Beta( 27.79 3.09 )"  
##[1] "Here is a plot of the specified distribution."  
##[1] "Descriptive statistics for this distribution are:"  
## Min. 1st Qu. Median Mean 3rd Qu. Max.  
## 0.6192 0.8688 0.9077 0.8996 0.9391 0.9974  
##[1] "Verification: The percentile value 0.8 corresponds to the 0.05th  
##percentile"  
  
##Example 2  
##Based on the available literature the median value for the specificity of a  
##test is expected to be 0.99 and we can be 95% sure that it is higher than  
##0.90.  
  
findbeta(themedian=0.99, percentile=0.95,lower.v=FALSE, percentile.value=0.90)  
  
## The output is:  
##[1] "The desired Beta distribution that satisfies the specified conditions is:  
##Beta( 18.97 0.52 )"  
##[1] "Here is a plot of the specified distribution."  
##[1] "Descriptive statistics for this distribution are:"  
## Min. 1st Qu. Median Mean 3rd Qu. Max.  
## 0.5634 0.9637 0.9871 0.9735 0.9970 1.0000  
##[1] "Verification: The percentile value 0.9 corresponds to the 0.05th  
##percentile"  
  
##Example 3  
##The most probable value (mode) for the prevalence of a disease/infection in a  
##population is expected to be 0.15 and we are 90% sure that it is less than  
##0.40.  
  
findbeta(themode=0.15, percentile=0.90,lower.v=TRUE, percentile.value=0.40)  
  
## The output is:  
##[1] "The desired Beta distribution that satisfies the specified conditions is:  
##Beta( 2.15 7.52 )"  
##[1] "Here is a plot of the specified distribution."  
##[1] "Descriptive statistics for this distribution are:"  
## Min. 1st Qu. Median Mean 3rd Qu. Max.  
## 0.001939 0.125475 0.204776 0.223724 0.300515 0.785156  
##[1] "Verification: The percentile value 0.4 corresponds to the 0.9th  
##percentile"
```

findbetamupsi *The findbetamupsi function*

Description

A function to estimate (a) the parameters of a Beta distribution for the expected mean of a proportion - usually the prevalence of disease/infection for the units in an area/region and (b) the parameters of a Gamma distribution expressing our prior belief about the variability of the prevalence estimates across the units of the area/region under consideration.

Usage

```
findbetamupsi(themean, percentile=0.95, lower.v=T,
percentile.value, psi.percentile=0.90, percentile.median,
percentile95value)
```

Arguments

themean	specify your prior belief about the mean. It takes a value between 0 and 1.
percentile	specify the level of confidence that the true value of the mean is greater or lower than the percentile.value. It takes a value between 0 and 1 and the default is 0.95.
lower.v	logical, if TRUE the specified percentile.value is the upper limit for the mean at the specified confidence level (percentile). If FALSE the specified percentile.value is the lower limit for the mean at the specified confidence level (percentile). The default is TRUE.
percentile.value	specify the upper or lower limit for the mean at the specified level of confidence (percentile). It takes a value between 0 and 1.
psi.percentile	specify the level of confidence that a certain fraction of the units under study has a prevalence less than the percentile.median. It takes a value between 0 and 1 and the default is 0.90.
percentile.median	specify the median value that corresponds to the defined psi.percentile. It takes a value between 0 and 1 and has to be higher than both themean and the percentile.
percentile95value	specify the value that the percentile.median does not exceed with 95% confidence. It takes a value between 0 and 1 and has to be higher than the percentile.median.

References

Branscum, A. J., Gardner, I. A., & Johnson, W. O. (2004): Bayesian modeling of animal- and herd-level prevalences. Preventive Veterinary Medicine, **66**, 101–112.

Examples

```
##Example 1
##The mean prevalence of a disease/infection for the units within an area/region
##is thought to be 0.20 and we are 99% confident that it is not more than 0.40.
##Within this area, we are also confident that 90% of all units have a prevalence
##less or equal to 0.50 and we are 95% certain that it does not exceed 0.60

findbetamupsi(the mean=0.20, percentile=0.99, lower.v=TRUE,
percentile.value=0.30, psi.percentile=0.90,
percentile.median=0.50, percentile95value=0.60)

##The output is:
##[1] "The desired Beta distribution that satisfies the specified conditions
##about the mean of the prevalence 'mu' is: Beta( 20.27 81.07 )"
##[1] "The desired Gamma distribution that satisfies the specified conditions
##about the variability 'psi' of the prevalence is: Gamma( 8.97 2.79 )"
##[1] "The plot gives the specified prior belief on the prevalence distribution."
##[1] "Descriptive statistics for this distribution are:"
## Min. 1st Qu. Median Mean 3rd Qu. Max.
##0.00000 0.03589 0.13164 0.20156 0.30799 0.99971
```

findbetaqq

The findbetaqq function

Description

A function to estimate the parameters alpha and beta of a Beta distribution based on the existing prior belief (data and/or expert opinion) about the values of two distinct percentiles.

Usage

```
findbetaqq(percentile.value1,percentile1,percentile.value2,percentile2)
```

Arguments

percentile.value1	specify the value for the first percentile. It takes a value between 0 and 1.
percentile1	specify which is the percentile that corresponds to percentile.value1. It takes a value between 0 and 1.
percentile.value2	specify the value for the second percentile. It takes a value between 0 and 1.
percentile2	specify which is the percentile that corresponds to percentile.value2. It takes a value between 0 and 1.

References

Kostoulas, P., Nielsen, S. S., Branscum, A. J., Johnson, W. O., Dendukuri, N., Dhand, N. K., Toft, N., Gardner, I. A. (2017): Reporting guidelines for diagnostic accuracy studies that use Bayesian latent class models (STARD–BLCM). *Statistics in medicine*, **23**, 3603–3604.

Examples

```
##Example 1
##We believe that 20% of the units in an area/region have a prevalence of
##disease/infection less than or equal to 0.30 while at the same time we are 90%
##certain that the prevalence is less than 0.60

findbetaqq(percentile.value1=0.30,percentile1=0.20,percentile.value2=0.60,percentile2=0.90)

##The output is:
##[1] "The desired Beta distribution that satisfies the specified conditions is:
##Beta( 5.19 7.17 )"
##[1] "Here is a plot of the specified distribution."
##[1] "Descriptive statistics for this distribution are:"
##   Min. 1st Qu. Median 3rd Qu. Max.
##0.02999 0.31999 0.41419 0.41974 0.51413 0.85487
##[1] "Verification: The first percentile value 0.3 corresponds to the 0.2 th
##percentile"
##[1] "Verification: The second percentile value 0.6 corresponds to the 0.9 th
##percentile"
```

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