Package 'bimodalitytest'

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Type Package

Title Testing for bimodality in a normal mixture

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Description The package implements a Likelihoodratiotest to test wheter a normal mixture is bimodal.

License GPL-2

LazyLoad Yes

Depends methods, graphics, boot, mclust

R topics documented:

`bimodalitytest-package`

Package Overview: Testing for bimodality in a normal mixture

Description

The package implements a likelihood ratio test to test whether a normal mixture is bimodal. The function `bimodality.test` performs the test. The returned value is an object of the `Bimodalitytest-class`, which can be plotted by the function plot(). The function `dmixnor` returns the density of a normal mixture for a given parameter and the function `rmixnor` creates random numbers of a normal mixture also for a given parameter. Finally `is.unimodal` returns whether the density of a two component normal mixture is bimodal or unimodal and `plot_bimodalityregion` plots the region of bimodality.

Details

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Type:	Package
Version:	1.0
Date:	2013-07-26
License:	GPL-2
LazyLoad:	yes

Author(s)

Florian Schwaiger, Hajo Holzmann, Sebastian Vollmer

References

Holzmann, H.; Vollmer, S. (2008) *A likelihood ratio test for bimodality in two-component mixtures.*

Chen, J.; Li, P. (2009). *Hypothesis test for normal mixture models: The EM approach.*

Examples

```
# first example (unimodal)
m1  = 0
m2  = 2
s1  = 1
s2  = 1
p   = 0.5
par = c(p,m1,m2,s1,s2)

ran  = rmixnor(1000,p,m1,m2,s1,s2)
test = bimodality.test(ran,equal_sigmas=TRUE)
plot(test)
test
```

```
#second example (bimodal)
m1   = 0
m2   = 3
s1   = 0.7
s2   = 1.2
p    = 0.5
par = c(p,m1,m2,s1,s2)

ran   = rmixnor(500,p,m1,m2,s1,s2)
test2 = bimodality.test(ran,equal_sigmas=FALSE)
plot(test2)
test2
```

`bimodality.test` *Performing the likelihood ratio test*

Description

This function performs the likelihood ratio test for a given dataset. It tests the null hypothesis, whether a two componente normal mixture is bimodal. Therefor it calculates the maximum likelihood estimators for the restricted and non restricted parameter space and returns for example the likelihoodratio and the p-value.

Usage

```
bimodality.test(data, start_vec = NA, equal_sigmas = F, N = 10, move_data = T, p
```

Arguments

`data`	a given dataset
`start_vec`	if you have an idea what the parameter of the normal mixture might be you can enter it here. The iterative optimisation will then start at this parameter.
`equal_sigmas`	if you know, that both normal components have the same standard deviation you can enter ist here.
`N`	if you don't enter a `start_vec`, the function will start N optimisations with randomly choosen parameters. Therefore entering a start_vec accelerates the computation.
`move_data`	this option shifts the data for the calculation to zero. Especially for a dataset in a big range this makes the computation numerically much more stable.
`penalty`	this option activates the penalisation of small sigma-values in the likelihood-function and causes better estimaton of the parameters (see Chen and Li).

Value

An object of the class Bimodalitytest (see: `Bimodalitytest-class`).

References

Holzmann, H.; Vollmer, S. (2008) *A likelihood ratio test for bimodality in two-component mixtures.*

Chen,J.; Li, P. (2009). *Hypothesis test for normal mixture models: The EM approach.*

Examples

```
m1<-0
m2<-2
s1<-1
s2= 1
p=0.5

par=c(p,m1,m2,s1,s2)

ran<-rmixnor(1000,p,m1,m2,s1,s2)
plot.density(density(ran,bw="SJ"))

test= bimodality.test(ran,equal_sigmas=TRUE)
test
```

`Bimodalitytest-class` *Class "Bimodalitytest"*

Description

Objects of this class are the returned value of a `bimodality.test`.

Slots

`data`**:** the given dataset of a test

`p_value`**:** p-value of the test (reject H0 for p-value less significance level)

`LR`**:** the likelihood ratio value

`loglikelihood_unrest`**:** value of the likelihoodfunction for the unrestricted estimation

`loglikelihood_rest`**:** value of the likelihoodfunction for the restricted estimation

`mle_unrest`**:** vector of parameters of unrestricted maximumlikelihood estimation: first component is the mixing proportion p, second and third are the estimated means and the last two are the estimated standard deviations of the normal mixture

`mle_rest`**:** same as mle_unrest, but for the restricted case

Methods

We provide the following methods for a Bimadalitytest object:

see `plot-methods`

plot **show** the visualisation of an object

`dmixnor` *Density of a normal mixture*

Description

For a given parameter `(p,mu1,mu2,sigma1,sigma2)` of a normal mixture this function calculates the density at the point `x`.

Usage

```
dmixnor(x, p, mu1, mu2, sig1, sig2)
```

Arguments

`x`	point where the density is to be evaluated
`p`	mixing proportion
`mu1`	expected value of the first normal distribution
`mu2`	expected value of the second normal distribution
`sig1`	standard deviation of the first normal distribution
`sig2`	standard deviation of the second normal distribution

Value

Density of a normal mixture given by `(p,mu1,mu2,sigma1,sigma2)` at the point `x`.

See Also

`rmixnor`

`is.unimodal` *Investigation of the number of modes of a given two component normal mixture.*

Description

For a normal mixture given by `par=(p,mu1,mu2,sigma1,sigma2)` this function calculates if it is unimodal.

Usage

```
is.unimodal(par)
```

Arguments

`par`	parameter of the form (p,mu1,mu2,sigma1,sigma2) like in `dmixnor`.

Value

Boolean whether the normal mixture is unimodal.

Examples

```
#the normal mixture given by the following parameter is unimodal
m1<-0
m2<-2
s1<-1
s2= 1
p=0.5
par=c(p,m1,m2,s1,s2)

is.unimodal(par)
```

`plot-methods` *Plot method for Bimodalitytest objects*

Description

This method allows you to use the plot function for an object of the `Bimodalitytest-class`.

Methods

x = "Bimodalitytest" The function plots three densities: the empirical, the density of the unrestricted estimation and the the density of the restricted estimation.

Examples

```
m1<-0
m2<-2
s1<-1
s2= 1
p=0.5

par=c(p,m1,m2,s1,s2)

ran<-rmixnor(1000,p,m1,m2,s1,s2)
plot.density(density(ran,bw="SJ"))

test= bimodality.test(ran,equal_sigmas=TRUE)
plot(test)
```

`plot_bimodalityregion` *Plotting the region of bimodality*

Description

The function plots the parameter region where the density is bimodal. On the x-axis is the paramter mu = (mu2-mu1)/sigma1, where mu1 <= mu2. The argument of the function is sigma = sigma1/sigma2.

Usage

```
plot_bimodalityregion(sig)
```

Arguments

`sig`	ratio of the standard deviations

Value

The function returns a plot and the left starting point of the bimodality region.

References

Robertson, C. A. and Fryer, J. G. (1969). Some descriptive properties of normal mixtures. Skand. Aktuarietidskr. 1969 137-146.

Examples

```
plot_bimodalityregion(1)
```

`rmixnor` *Random numbers of a normal mixture*

Description

For a given parameter `(p,mu1,mu2,sigma1,sigma2)` of a normal mixture this function calculates `n` random numbers.

Usage

```
rmixnor(n, p, mu1, mu2, sig1, sig2)
```

Arguments

`n`	quantity of random numbers
`p`	mixing proportion
`mu1`	expected value of the first normal distribution
`mu2`	expected value of the second normal distribution
`sig1`	standard deviation of the first normal distribution
`sig2`	standard deviation of the second normal distribution

Value

`n` random numbers of a normal mixture given by `(p,mu1,mu2,sigma1,sigma2)`.

See Also

`dmixnor`

Examples

```
ran = rmixnor(100,0.5,0,3,1,1)
```

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