

Package ‘multimode’

October 19, 2017

Encoding UTF-8

Type Package

Title Mode Testing and Exploring

Version 1.0

Date 2017-10-17

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The R Core Team 1996-2012 [ctb,cph] (C function 'BinDist2' obtained from package 'stats'),
The R Foundation 2005 [ctb,cph] (C function 'BinDist2' obtained from package 'stats')

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Description Different examples and methods for testing (including different proposals described in Ameijeiras-Alonso et al., 2016 <arXiv:1609.05188>) and exploring (including the mode tree, mode forest and SiZer) the number of modes using nonparametric techniques.

Depends R (>= 2.0.1)

License GPL-3

NeedsCompilation yes

LazyData TRUE

Imports diptest, ks, rootSolve

Suggests nor1mix

Repository CRAN

Date/Publication 2017-10-19 13:50:45 UTC

R topics documented:

multimode-package	2
acidity	3
bw.crit	4
chondrite	5
enzyme	6
excessmass	7

galaxy	8
geyser	9
locmodes	10
modeforest	12
modetest	14
modetree	16
nmodes	18
sizer	19
stamps	22

Index	24
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multimode-package	<i>Mode testing and exploring.</i>
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Description

Different examples and methods for testing (including different proposals described in Ameijeiras-Alonso et al., 2016 <arXiv:1609.05188>) and exploring (including the mode tree, mode forest and SiZer map) the number of modes using nonparametric techniques.

Details

Package:	multimode
Type:	Package
Version:	1.0
Date:	2017-10-17
License:	GPL-3
NeedsCompilation:	yes
LazyData:	yes

This package incorporates the function `modetest` which tests if the number of modes of a sample is equal to a given number (against if it is greater). Functions `bw.crit` and `excessmass` provide the critical bandwidth and the excess of mass statistic, respectively. Function `nmodes` computes the number of modes for a given bandwidth. Given a certain number of modes, function `locmodes` provides the estimation of the locations of modes and antimodes and their density value. Functions `modetree` and `modeforest` provide the mode tree and forest, respectively; they represent the estimated mode locations for different bandwidths. Function `sizer` can be used for determining where the smoothed curve is significantly increasing or decreasing. Registries with missing data are removed. For a complete list of functions, use `library(help="multimode")`.

Acknowledgements

This work has been supported by Projects MTM2016-76969-P (Spanish State Research Agency, AEI) and MTM2013-41383-P (Spanish Ministry of Economy, Industry and Competitiveness), both co-funded by the European Regional Development Fund (ERDF), IAP network (Developing cru-

cial Statistical methods for Understanding major complex Dynamic Systems in natural, biomedical and social sciences, StUDyS) from Belgian Science Policy. Work of J. Ameijeiras-Alonso has been supported by the PhD grant BES-2014-071006 from the Spanish Ministry of Economy and Competitiveness.

References

- Ameijeiras-Alonso, J., Crujeiras, R.M. and Rodríguez-Casal, A. (2016). Mode testing, critical bandwidth and excess mass, *arXiv preprint: 1609.05188*.
- Chaudhuri, P. and Marron, J. S. (1999). SiZer for exploration of structures in curves, *Journal of the American Statistical Association*, **94**, 807–823.
- Minnotte, M. C., Marchette, D. J. and Wegman, E. J. (1998). The bumpy road to the mode forest, *Journal of Computational and Graphical Statistics*, **7**, 239–251.

acidity

Acid-neutralizing capacity

Description

This dataset, analyzed by Crawford (1994), contains the Acid–Neutralizing Capacity (ANC) measured in a sample of 155 lakes in North–Central Wisconsin (USA). ANC describes the capability of a lake to absorb acid, where low ANC values may lead to a loss of biological resources.

Usage

`data(acidity)`

Format

`acidity` includes an acidity index of lakes in north–central Wisconsin on the log scale, in particular, it is provided the $\log(\text{ANC}+50)$ as in Crawford (1994).

Details

This is a classic example for determining the number of modes.

Source

Obtained from the Supplementary material of Richardson and Green (1997), available in <http://www.stats.bris.ac.uk/~peter/mixdata>.

References

- Crawford (1994). An application of the Laplace method to finite mixture distributions. *Journal of the American Statistical Association*, **89**, 259–267.
- Richardson, S. and Green, P. J. (1997). On Bayesian analysis of mixtures with unknown number of components (with discussion). *Journal of the Royal Statistical Society, Series B*, **59**, 731–792.

Examples

```
data("acidity")
# Kernel density estimation with two modes and SiZer
locmodes(acidity,mod0=2,display=TRUE,xlab="log(ANC+50)")
sizer(acidity,bws=c(0.1,1),xlab="log(ANC+50)")
```

`bw.crit`

Critical bandwidth

Description

This function computes the critical bandwidth for a specified number of modes.

Usage

```
bw.crit(data,mod0=1,lowsup=-Inf,uppsup=Inf,n=2^15,tol=10^(-5))
```

Arguments

<code>data</code>	Sample for computing the critical bandwidth.
<code>mod0</code>	Number of modes for which the critical bandwidth is calculated. Default <code>mod0=1</code> .
<code>lowsup</code>	Lower limit for the random variable support in the computation of the critical bandwidth. Default is <code>-Inf</code> .
<code>uppsup</code>	Upper limit for the random variable support in the computation of the critical bandwidth. Default is <code>Inf</code> .
<code>n</code>	The number of equally spaced points at which the density is estimated. When $n > 512$, it is rounded up to a power of 2 as in the density function. Default $n=2^{15}$.
<code>tol</code>	Accuracy requested in the computation of the critical bandwidth. Default value of <code>tol</code> is 10^{-5} .

Details

With `bw.crit` the critical bandwidth for the number of modes specified in `mod0` is calculated, e.g., the smallest bandwidth such that the kernel density estimator has at most `mod0` modes. If the compact support is unknown, the critical bandwidth introduced by Silverman (1981) is computed and if it is provided that one of Hall and York (2001) is calculated.

Since a dichotomy method is employed for computing the critical bandwidth, the parameter `tol` is used to determine a stopping time in such a way that the error committed in the computation of the critical bandwidth is less than `tol`.

The NAs will be automatically removed.

Value

Critical bandwidth of the sample for `mod0` modes.

Author(s)

Jose Ameijeiras-Alonso, Rosa M. Crujeiras and Alberto Rodríguez-Casal

References

- Hall, P. and York, M. (2001). On the calibration of Silverman's test for multimodality, *Statistica Sinica*, **11**, 515–536.
- Silverman, B. W. (1981). Using kernel density estimates to investigate multimodality, *Journal of the Royal Statistical Society. Series B*, **43**, 97–99.

Examples

```
# Critical bandwidth of Silverman (1981) for one mode.
set.seed(2016)
data=rnorm(50)
bw.crit(data)
# Critical bandwidth of Hall and York for two modes in the interval (-1.5,1.5).
set.seed(2016)
data=rnorm(50)
bw.crit(data,mod0=2,lowsup=-1.5,uppsup=1.5)
```

chondrite	<i>Percentage of silica in chondrite meteors</i>
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Description

This dataset contains the percentage silica (in %) in 22 chondrite meteors.

Usage

```
data(chondrite)
```

Format

chondrite and chondritegg include the data provided in Good and Gaskins (1980). In chondrite, the typo in the 9th observation was corrected while chondritegg includes the original dataset. In chondritel is included the scaled data used by Leonard (1978).

Details

This is a classic example for determining the number of modes.

Source

Obtained from the Table 2 of Good and Gaskins (1980).

References

Good, I. J. and Gaskins, R. A. (1980). Density estimation and bump-hunting by the penalized likelihood method exemplified by scattering and meteorite data. *Journal of the American Statistical Association*, **75**, 42–56.

Leonard, T. (1978). Density estimation, stochastic processes and prior information. *Journal of the Royal Statistical Society. Series B (Methodological)*, **40**, 113–146.

Examples

```
data("chondrite")
# SiZer between the critical bandwidths for one and six modes
sizer(chondrite,cbw1=1,cbw2=6)
```

enzyme

Blood enzymatic activity

Description

This dataset concerns the distribution of enzymatic activity in the blood, for an enzyme involved in the metabolism of carcinogenic substances.

Usage

```
data(enzyme)
```

Format

enzyme includes the values of the urinary metabolic ratio of 5-acetylamino-6-formylamino-3-methyluracil to 1-methylxanthine (AFMU/IX) after oral administration of caffeine.

Details

This is a classic example for determining the number of modes.

Source

Obtained from the Supplementary material of Richardson and Green (1997), available in <http://www.stats.bris.ac.uk/~peter/mixdata>.

References

Bechtel, Y. C., Bonaiti-Pellie, C., Poisson, N., Magnette, J. and Bechtel, P. R. (1993). A population and family study N-acetyltransferase using caffeine urinary metabolites. *Clinical Pharmacology and Therapeutics*, **54**, 134–141.

Richardson, S. and Green, P. J. (1997). On Bayesian analysis of mixtures with unknown number of components (with discussion). *Journal of the Royal Statistical Society, Series B*, **59**, 731–792.

Examples

```
data("enzyme")
# It can be seen that there are two groups in this dataset
# Via exploratory tools
sizer(enzyme,bws=c(0.03,1))
modetree(enzyme,bws=c(0.02,1),logbw=TRUE,addplot=TRUE,col.lines="white")
#Via mode testing
modetest(enzyme)
## Not run:
modetest(enzyme,mod0=2)

## End(Not run)
```

excessmass	<i>Excess of mass</i>
------------	-----------------------

Description

This function computes the excess of mass statistic.

Usage

```
excessmass(data,mod0=1)
```

Arguments

data	Sample for computing the excess of mass.
mod0	Number of modes for which the excess of mass is calculated. Default mod0=1.

Details

With `excessmass`, the excess of mass statistic, introduced by Müller and Sawitzki (1991), for the integer number of modes specified in `mod0` is computed.

If there are repeated data in the sample or the distance between different pairs of data points shows ties, a data perturbation is applied. This modification is made in order to avoid the discretization of the data which has important effects on the computation of the test statistic. The perturbed sample is obtained by adding a sample from the uniform distribution in minus/plus a half of the minimum of the positive distances between two sample points.

The NAs will be automatically removed.

Value

Excess of mass for `mod0` modes of the sample.

Author(s)

Jose Ameijeiras-Alonso, Rosa M. Crujeiras and Alberto Rodríguez-Casal

References

Müller, D. W. and Sawitzki, G. (1991). Excess mass estimates and tests for multimodality, *The Annals of Statistics*, **13**, 70–84.

Examples

```
# Excess of mass statistic for one mode
set.seed(2016)
data=rnorm(50)
excessmass(data)
```

galaxy

Velocities of galaxies diverging away from our own galaxy

Description

This dataset contains the velocities in km/sec of different galaxies from the unfilled survey of the Corona Borealis region.

Usage

```
data(galaxy)
```

Format

galaxy includes the original measures in Roeder (1990). galaxyrg includes the data provided in the Supplementary material of Richardson and Green (1997), where the velocities are divided by 1000 and the 78th observation was replaced by 26690 km/sec. galaxypr add a measurement of 5607 km/sec included in Postman *et al.* (1986).

Details

This is a classic example for determining the number of modes.

Source

Obtained from the Table 1 of Postman *et al.* (1986), Table 1 of Roeder (1990) and the Supplementary material of Richardson and Green (1997), available in <http://www.stats.bris.ac.uk/~peter/mixdata>.

References

Postman, M., Huchra, J. P. and Geller, M. J. (1986). Probes of large-scale structures in the Corona Borealis region. *Astronomical Journal*, **92**, 1238–1247.

Richardson, S. and Green, P. J. (1997). On Bayesian analysis of mixtures with unknown number of components (with discussion). *Journal of the Royal Statistical Society, Series B*, **59**, 731–792.

Roeder, K. (1990). Density estimation with confidence sets exemplified by superclusters and voids in the galaxies. *Journal of the American Statistical Association*, **85**, 617–624.

Examples

```
data("galaxy")
# Mode tree between the critical bandwidths for one and six modes
modetree(galaxy,cbw1=1,cbw2=6)
```

geyser

Waiting time between geyser eruptions

Description

This dataset contains the interval times between the starts of the geyser eruptions on the Old Faithful Geyser in Yellowstone National Park, Wyoming, USA.

Usage

```
data(geyser)
data(geyserab)
data(geyserh)
data(geyserw)
```

Format

geyser, geyserh and geyserw include data collected in October 1980. geyser and geyserh were obtained from Table 3 of Härdle (2012), in geyser some repeated data are removed. geyserw was obtained from the Supplementary material of Weisberg (2005). geyserab include data collected in August 1985 from Table 1 in Azzalini and Bowman (1990).

Details

This is a classic example for estimating the density.

Source

Obtained from the original tables in Azzalini and Bowman (1990), Härdle (2012) and Supplementary material of Weisberg (2005).

References

Azzalini, A. and Bowman, A. W. (1990). A look at some data on the Old Faithful geyser. *Applied Statistics*, **39**, 357-365.

Härdle, W. (1991). *Smoothing techniques: with implementation in S*. New York: Springer-Verlag.

Weisberg, S. (2005). *Applied Linear Regression*. New York: Wiley.

Examples

```
data("geyser")
# Kernel density estimation with two modes
locmodes(geyser, mod0=2, display=TRUE)
```

locmodes

*Location of modes and antimodes***Description**

Given a certain number of modes, this function provides the estimation of the location of modes and antimodes and their density value.

Usage

```
locmodes(data, mod0=1, lowsup=-Inf, uppsup=Inf, n=2^15, tol=10^(-5), display=F,
addplot=NULL, xlab=NULL, ylab=NULL, addLegend=NULL, posLegend=NULL)
```

Arguments

data	Sample in which the critical bandwidth is computed.
mod0	Number of modes for which the critical bandwidth is calculated. Default mod0=1.
lowsup	Lower limit for the random variable support in the computation of the critical bandwidth. Default is -Inf.
uppsup	Upper limit for the random variable support in the computation of the critical bandwidth. Default is Inf.
n	The number of equally spaced points at which the density is to be estimated. When $n > 512$, it is rounded up to a power of 2 as in the density function. Default $n=2^{15}$.
tol	Accuracy requested in the computation of the critical bandwidth. Default $tol=10^{-5}$.
display	Logical, if TRUE the kernel density estimation is plotted adding the estimated location of the modes and the antimodes. Default is FALSE.
addplot	Logical, if TRUE the plot is added to the current one. Default if display=TRUE is FALSE.
xlab	A title for the x axis. See title.
ylab	A title for the y axis. See title.
addLegend	Logical, if TRUE the legend is added in the plot. Default if display=TRUE is TRUE.
posLegend	The vector of two elements of coordinates to be used to position the legend. It can be specified by keyword as in the function legend. Default if display=TRUE is "topright".

Details

Given a certain number of modes, `mod0`, with `locmodes` the estimation of the location of modes and antimodes, their density value and the corresponding critical bandwidth is provided. To obtain these estimates, the kernel density estimation with gaussian kernel and the critical bandwidth for `mod0` modes is employed. If the compact support is unknown, the critical bandwidth of Silverman (1981) is computed and if such a support is provided, then the one proposed by Hall and York (2001) is calculated. Note that when the support is unknown the critical bandwidth may create artificial modes in the tails.

Since a dichotomy method is employed for computing the critical bandwidth, the parameter `tol` is used to determine a stopping time in such a way that the error committed in the computation of the critical bandwidth is less than `tol`.

If `display=TRUE`, then the kernel density estimation using the critical bandwidth for `mod0` modes is plotted. Additionally, the estimated location of modes (dashed lines), antimodes (point lines) and support (solid lines) can be also plotted. If `addLegend=TRUE`, a legend (in the position `posLegend`) with this information is included.

The NAs will be automatically removed.

Value

<code>locations</code>	Vector with the estimated locations of modes (odd positions of the vector) and antimodes (even positions).
<code>fvalue</code>	Vector with estimated density values at modes (odd positions of the vector) and antimodes (even positions).
<code>cbw</code>	Critical bandwidth of the sample for <code>mod0</code> modes.

Author(s)

Jose Ameijeiras–Alonso, Rosa M. Crujeiras and Alberto Rodríguez–Casal

References

- Ameijeiras–Alonso, J., Crujeiras, R.M. and Rodríguez–Casal, A. (2016). Mode testing, critical bandwidth and excess mass, *arXiv preprint: 1609.05188*.
- Hall, P. and York, M. (2001). On the calibration of Silverman’s test for multimodality, *Statistica Sinica*, **11**, 515–536.
- Silverman, B. W. (1981). Using kernel density estimates to investigate multimodality, *Journal of the Royal Statistical Society. Series B*, **43**, 97–99.

Examples

```
# Testing for unimodality
set.seed(2016)
data=rnorm(50)
modetest(data)
#There is no evidence to reject the null hypothesis of unimodality
#Estimated location of the mode and its density value
locmodes(data)
```

```
## Not run:
#Estimated locations of the five modes in the claw of Marron and Wand (1992)
library(nor1mix)
set.seed(2016)
n<-200
data<-nor1mix::rnorMix(n,MW.nm10)
#Adding the plot of the estimated locations
locmodes(data,5,display=T)
#Assuming that the compact support is [-1.5,1.5]
locmodes(data,5,-1.5,1.5,display=T)

## End(Not run)
```

modeforest

Mode forest

Description

This function provides the mode forest.

Usage

```
modeforest(data,bws=NULL,gridsize=NULL,B=99,n=512,cbw1=NULL,cbw2=NULL,
display=TRUE,logbw=FALSE,from=NULL,to=NULL,xlab=NULL,ylab=NULL)
```

Arguments

data	Sample in which the mode forest is computed.
bws	Vector or range of bandwidths. If it is a vector of size two, then it is used a grid of bandwidths between the given values. Default lower bandwidth is twice the distance between the grid points used for estimating the density and upper bandwidth equal to the range of the data. Unless it is specified a vector of size greater than two, the number of bandwidths employed is equal to the second element of gridsize.
gridsize	Number of grid points in the horizontal (values of the variable, first element) and vertical (bandwidths, second element) axis. Default is <code>c(100, 151)</code> .
B	Number of replicates used for generating the mode forest. Default <code>B=99</code> .
n	The number of equally spaced points at which the density is to be estimated. When <code>n > 512</code> , it is rounded up to a power of 2 as in the density function. Default <code>n=512</code> .
cbw1	Number of modes for which the first critical bandwidth is calculated. This is the first bandwidth used to compute the mode tree when <code>bws</code> is not specified.
cbw2	Number of modes for which the second critical bandwidth is calculated. This is the last bandwidth used to compute the mode tree when <code>bws</code> is not specified.
display	Logical, if <code>TRUE</code> the mode tree plot is plotted. Default <code>TRUE</code> .

logbw	Logical, if TRUE the plot displays and returns the log10 bandwidths. Default logbw=FALSE.
from	First plotted value of the variable. Default is below the data minimum.
to	Last plotted value of the variable. Default is above the data maximum.
xlab	A title for the x axis. See title.
ylab	A title for the y axis. See title.

Details

The mode forest for the sample given in data is computed. For this calculation, a kernel density estimator with Gaussian kernel and bandwidths `bws` is used. The mode forest is generated by looking simultaneously at a collection of mode trees generated by the original sample and `B` random resamples drawn with replacement from data. This tool represents the number of times an estimated mode falls in each location-bandwidth (horizontal-vertical axis) pixel. The pixels are then shaded proportionally to counts (large counts corresponding to darker pixels and low counts to lighter ones).

The NAs will be automatically removed.

Value

<code>modeforest</code>	Matrix including the percentage of times that a mode tree falls in each location-bandwidth pixel.
<code>range.x</code>	Employed location values to represent the mode forest.
<code>range.bws</code>	Employed bandwidths to compute the different mode trees.

Author(s)

Jose Ameijeiras-Alonso, Rosa M. Crujeiras and Alberto Rodríguez-Casal

References

Minnotte, M. C., Marchette, D. J. and Wegman, E. J. (1998). The bumpy road to the mode forest, *Journal of Computational and Graphical Statistics*, **7**, 239–251.

Examples

```
#Mode forest using a grid of bandwidths between 0.2 and 0.5 and 29 bootstrap replicas
set.seed(2016)
data=rnorm(50)
modeforest(data,bws=c(0.2,0.5),B=29)
#Original mode tree for this sample
modetree(data,bws=c(0.2,0.5),addplot=TRUE,col.lines="red")
```

modetest *Test for the number of modes*

Description

This function tests the number of modes.

Usage

```
modetest(data, mod0=1, method="NP", B=500, full.result=FALSE, lowsup=-Inf, uppsup=Inf,
n=NULL, tol=NULL, tol2=NULL, methodhy=NULL, alpha=NULL, nMC=NULL, BMC=NULL)
```

Arguments

data	Sample to be tested.
mod0	The maximum number of modes in the null hypothesis. Default mod0=1 (unimodality vs. multimodality test).
method	The method employed for testing the number of modes. Available methods are: SI (Silverman, 1981), HY (Hall and York, 2001), FM (Fisher and Marron, 2001), HH (Hartigan and Hartigan, 1985), CH (Cheng and Hall, 1998), NP (Ameijeiras-Alonso <i>et al.</i> , 2016). Default method="NP".
B	Number of replicates used in the test. Default B=500.
full.result	Logical. If TRUE, returns both the test statistic and the p-value. If FALSE, just the p-value is returned. Default is FALSE.
lowsup	Lower limit for the random variable support in the computation of the critical bandwidth. Default is -Inf.
uppsup	Upper limit for the random variable support in the computation of the critical bandwidth. Default is Inf.
n	The number of equally spaced points at which the density is to be estimated. When $n > 512$, it is rounded up to a power of 2 as for density function. Default is $n=2^{10}$ when method is SI, HY or FM and $n=2^{15}$ when the method is CH or NP. Argument not used for other methods.
tol	Accuracy for computing the critical bandwidth. Default $tol=10^{-5}$.
tol2	Accuracy for integration of the calibration function in the method NP when the support is known. Default $tol2=10^{-5}$.
methodhy	Different approaches when using Hall and York (2001) method. Default methodhy=1.
alpha	Significance level employed for testing unimodality when method 1 of Hall and York (2001) is used. Default $alpha=0.05$.
nMC	Number of Monte Carlo replicates used to approximate the p-value in the method 2 of Hall and York (2001). Default nMC=100.
BMC	Number of bootstrap replicas used for computing the p-value in each Monte Carlo replicate of the Hall and York (2001) method 2. Default BMC=100.

Details

The number of modes for the underlying density of a sample given by data can be tested with `modetest`. The null hypothesis states that the sample has `mod0` modes, and the alternative hypothesis is if it has more modes. The test used for calculating the p-value is specified in `method`. All the available proposals require bootstrap or Monte Carlo resamples (number specified in `B`).

Except when the support is employed, the typical usages are

```
modetest(data,mod0=1,...)
modetest(data,mod0=1,method="NP",B=500,full.result=FALSE,n=NULL,tol=NULL)
```

Since a dichotomy algorithm is employed for computing the critical bandwidth (methods `SI`, `HY`, `FM`, `NP`), the parameter `tol` is used to determine a stopping time in such a way that the error committed in the computation of the critical bandwidth is less than `tol`.

The sample data can be perturbed in the methods using the excess of mass or the dip statistic (`HH`, `CH` and `NP`) in order to avoid important effects on the computation of the test statistic. See `excessmass`.

If a compact support containing a mode is known, it can be used to compute the Hall and York (2001) critical bandwidth. Note that in the case of the test proposed by Hall and York (2001), this support must be known. For their proposal, two methods are implemented. Method 1 is an asymptotic correction of Silverman (1981) test based on the limiting distribution of the test statistic. When `methodhy=1`, the significance level must be previously determined with `alpha`. Method 2 is based on Monte Carlo techniques. For this reason, when `methodhy=2`, the number of replicates `nMC` and the number of bootstrap replicas used for computing the p-value in each Monte Carlo replicate `BMC` are needed.

Typical usages are

```
modetest(data,method="HY",lowsup=-1.5,uppsup=1.5,methodhy=1,alpha=NULL,...)
modetest(data,method="HY",B=500,full.result=FALSE,lowsup=-1.5,
uppsup=1.5,n=NULL,tol=NULL,methodhy=1,alpha=NULL)

modetest(data,method="HY",lowsup=-1.5,uppsup=1.5,methodhy=2,nMC=NULL,BMC=NULL,...)
modetest(data,method="HY",B=500,full.result=FALSE,lowsup=-1.5,
uppsup=1.5,n=NULL,tol=NULL,methodhy=2,nMC=NULL,BMC=NULL)
```

A modification of the proposal of Ameijeiras–Alonso *et al.* (2016) can be also applied, by setting `method=NP` and including a known compact support for detecting the modes. The parameter `tol2` is the accuracy required in the integration of the calibration function. For more information, see Ameijeiras–Alonso *et al.* (2016), the default approach, when the support is unknown, is given in Section 2.3 and, when it is provided, the approach shown in the Appendix B is employed.

Typical usages are

```
modetest(data,mod0=1,lowsup=-1.5,uppsup=1.5,...)
modetest(data,mod0=1,B=500,full.result=FALSE,lowsup=-1.5,uppsup=1.5,
n=NULL,tol=NULL,tol2=NULL)
```

The NAs will be automatically removed.

Value

p.value	P-value obtained after applying the test.
statistic	Value of the test statistic. Critical bandwidth if the method is SI or HY; Cramer-von Mises statistic if the method is FM; the dip statistic if the method is HH, and the excess of mass when the method is CH or NP.

Author(s)

Jose Ameijeiras–Alonso, Rosa M. Crujeiras and Alberto Rodríguez–Casal

References

- Jose Ameijeiras–Alonso, Rosa M. Crujeiras, Alberto Rodríguez–Casal (2016). Mode testing, critical bandwidth and excess mass, *arXiv preprint: 1609.05188*.
- Cheng, M. Y. and Hall, P. (1998). Calibrating the excess mass and dip tests of modality, *Journal of the Royal Statistical Society. Series B*, **60**, 579–589.
- Fisher, N.I. and Marron, J. S. (2001). Mode testing via the excess mass estimate, *Biometrika*, **88**, 419–517.
- Hall, P. and York, M. (2001). On the calibration of Silverman’s test for multimodality, *Statistica Sinica*, **11**, 515–536.
- Hartigan, J. A. and Hartigan, P. M. (1985). The Dip Test of Unimodality, *Journal of the American Statistical Association*, **86**, 738–746.
- Silverman, B. W. (1981). Using kernel density estimates to investigate multimodality, *Journal of the Royal Statistical Society. Series B*, **43**, 97–99.

Examples

```
# Testing for unimodality
data(geyser)
data=geyser
modetest(data)
## Not run:
# Testing bimodality using B=100 bootstrap replicas
modetest(data,mod0=2,B=100)
#There is no evidence to reject the null hypothesis of bimodality
locmodes(data,mod0=2,display=TRUE)

## End(Not run)
```

modetree

Mode tree

Description

This function provides the mode tree.

Usage

```
modetree(data,bws=NULL,gridsize=NULL,cbw1=NULL,cbw2=NULL,display=TRUE,
logbw=FALSE,addplot=FALSE,xlab=NULL,ylab=NULL,col.lines="black")
```

Arguments

<code>data</code>	Sample in which the mode tree is computed.
<code>bws</code>	Vector or range of bandwidths. If it is a vector of size two, then it is used a grid of bandwidths between the given values. Default lower bandwidth is twice the distance between the grid points used for estimating the density and upper bandwidth equal to the range of the data. Unless it is specified a vector of size greater than two, the number of bandwidths employed is equal to the second element of <code>gridsize</code> .
<code>gridsize</code>	Number of equally spaced points at which the density is to be estimated (first element) and bandwidths used to compute the mode tree (second element). Default is <code>gridsize=c(512,151)</code> .
<code>cbw1</code>	Number of modes for which the first critical bandwidth is calculated. This is the first bandwidth used to compute the mode tree when <code>bws</code> is not specified.
<code>cbw2</code>	Number of modes for which the second critical bandwidth is calculated. This is the last bandwidth used to compute the mode tree when <code>bws</code> is not specified.
<code>display</code>	Logical, if TRUE the mode tree plot is plotted. Default TRUE.
<code>logbw</code>	Logical, if TRUE the plot displays and returns the log10 bandwidths. Default <code>logbw=FALSE</code> .
<code>addplot</code>	Logical, if TRUE the plot is added to the current one. Default is FALSE.
<code>xlab</code>	A title for the x axis. See <code>title</code> .
<code>ylab</code>	A title for the y axis. See <code>title</code> .
<code>col.lines</code>	Color employed in the mode tree. If the length is two, the first color is employed for representing the location of the modes and the second one for the splitting of the modes. Default is <code>col.lines="black"</code> .

Details

The mode tree for the sample given in `data` is computed. For this calculation, a kernel density estimator with Gaussian kernel and bandwidths `bws` is used. This plot shows with the continuous lines the estimated mode locations at each bandwidth. The horizontal dashed lines indicate the splitting of a mode in more modes.

The NAs will be automatically removed.

Value

<code>locations</code>	Estimated mode locations for the bandwidths given in the row names.
<code>bandwidths</code>	Employed bandwidths to compute the mode tree.

Author(s)

Jose Ameijeiras-Alonso, Rosa M. Crujeiras and Alberto Rodríguez-Casal

References

Minnotte, M. C. and Scott, D. W. (1993). The mode tree: A tool for visualization of nonparametric density features, *Journal of Computational and Graphical Statistics*, **2**, 51–68.

Examples

```
#Mode tree using a grid of bandwidths between 0.2 and 0.5
set.seed(2016)
data=rnorm(50)
modetree(data,bws=c(0.2,0.5))
## Not run:
#Estimated locations of the five modes in the claw of Marron and Wand (1992)
library(nor1mix)
set.seed(2016)
n<-200
data<-nor1mix::rnormMix(n,MW.nm10)
#Mode tree between the critical bandwidths for 1 and 8 modes
modetree(data,cbw1=1,cbw2=8)
abline(v=1.5);abline(v=-1.5)

## End(Not run)
```

nmodes

Number of modes

Description

This function computes the number of modes in a kernel density estimator using the Gaussian kernel and a given bandwidth parameter.

Usage

```
nmodes(data,bw, lowsup=-Inf, uppsup=Inf, n=2^15)
```

Arguments

data	Sample for computing a kernel density estimator and determine the number of modes.
bw	Bandwidth parameter for kernel density estimation.
lowsup	Lower limit for the random variable support. Just the number of modes greater than lowsup are taken into account. Default is -Inf.
uppsup	Upper limit for the random variable support. Just the number of modes greater than lowsup are taken into account. Default is Inf.
n	The number of equally spaced points at which the density is to be estimated. When $n > 512$, it is rounded up to a power of 2 as in the density function. Default $n=2^{15}$.

Details

The number of modes in the interval provided by `lowsup` and `uppsup` is computed. For this calculation, a kernel density estimator with Gaussian kernel and bandwidth `bw` is used.

The NAs will be automatically removed.

Value

Number of modes for the bandwidth provided in `bw`.

Author(s)

Jose Ameijeiras–Alonso, Rosa M. Crujeiras and Alberto Rodríguez–Casal

Examples

```
# Number of modes in the interval (-1.5,1.5), using the bandwidth 0.5.
set.seed(2016)
data=rnorm(50)
nmodes(data,0.5,-1.5,1.5)
```

sizer

Significant ZERo crossing

Description

This function provides the SiZer map.

Usage

```
sizer(data,method=2,bws=NULL,gridsize=NULL,alpha=0.05,B=NULL,n0=NULL,
cbw1=NULL,cbw2=NULL,display=TRUE,logbw=TRUE,from=NULL,to=NULL,col.sizer=NULL,
xlab=NULL,ylab=NULL,addlegend=TRUE,poslegend="topright")
```

Arguments

<code>data</code>	Sample in which the SiZer map is computed.
<code>method</code>	The method employed for computing the SiZer map. Available methods are: 1 (q1, pointwise Gaussian quantiles), 2 (q2, approximate simultaneous over x Gaussian quantiles), 3 (q3, bootstrap quantile simultaneous over x) and 4 (q4, bootstrap quantile simultaneous over x and h). Default <code>method=2</code> .
<code>bws</code>	Vector or range of bandwidths. If it is a vector of size two, then it is used a grid of bandwidths between the given values. Default lower bandwidth is twice the grid size used for estimating the density and upper bandwidth equal to the range of the data. Unless it is specified a vector of size greater than two, the number of bandwidths employed is equal to the second element of <code>gridsize</code> .
<code>gridsize</code>	Number of grid points in the horizontal (values of the variable, first element) and vertical (bandwidths, second element) axis. Default is <code>c(512, 151)</code> .

alpha	Significance level employed for determining the significant features. Default alpha=0.05.
B	Number of replicates used for generating the SiZer map when method q3 or q4 are used. Default B=100.
n0	When the effective sample size is below this quantity, the pixel in the SiZer map is shaded grey. Default n0=5.
cbw1	Number of modes for which the first critical bandwidth is calculated. This is the first bandwidth used to compute the SiZer map when bws is not specified.
cbw2	Number of modes for which the second critical bandwidth is calculated. This is the last bandwidth used to compute the SiZer map when bws is not specified.
display	Logical, if TRUE the SiZer map is plotted. Default TRUE.
logbw	Logical, if TRUE the plot displays and returns the log10 bandwidths. Default logbw=FALSE.
from	First plotted value of the variable. Default is below the data minimum.
to	Last plotted value of the variable. Default is above the data maximum.
col.sizer	Colors employed in the SiZer map. The first color indicates where the smoothed curve is significantly increasing, the second where it is not significantly different from zero, the third where it is significantly negative and the fourth where the data are too sparse for meaningful inference. Default col.sizer=c("red", "orchid", "blue", "grey").
xlab	A title for the x axis. See title.
ylab	A title for the y axis. See title.
addlegend	Logical, if TRUE the legend is displayed. Default TRUE.
poslegend	Position where the legend should be displayed. Default posLegend="topright".

Details

With this function the assessment of Significant ZERO crossing of the derivative of the smoothed curve are computed for the sample given in data. For this calculation, a kernel density estimator with Gaussian kernel and bandwidths bws is used. At a given location (horizontal axis) and using a specified bandwidth parameter (vertical axis), the SiZer map represents where the curve is significantly increasing (blue color by default), decreasing (red by default) or not significantly different from zero (orchid, a light tone of purple, by default). Thus, for a given bandwidth, a region significantly increasing followed by a region significantly decreasing (blue-red pattern by default) indicates where there is a significant peak.

For methods q2, q3 and q4, it is calculated where the data are too sparse for meaningful inference (grey color by default). A location-bandwidth pixel is classified in this last category when the estimated Effective Sample Size is less than n0. For more information, see Chaudhuri and Marron (1999).

For methods q3 and q4, the bootstrap quantiles are computed generating B random samples drawn with replacement from data.

The NAs will be automatically removed.

Value

sizer	Matrix indicating the significant behavior of the smoothed curve in each location-bandwidth pixel. One indicates significantly decreasing; two, not significantly different from zero; three, significantly increasing and four where the data are too sparse for meaningful inference.
lower.CI	Matrix containing the lower limit of the confidence interval in each location-bandwidth pixel.
estimate	Matrix containing the derivative values of the kernel density estimation in each location-bandwidth pixel.
upper.CI	Matrix containing the upper limit of the confidence interval in each location-bandwidth pixel.
ESS	Matrix containing the Effective Sample Size in each location-bandwidth pixel.
range.x	Employed location values to represent the mode forest.
range.bws	Employed bandwidths to compute the different mode trees.

Author(s)

Jose Ameijeiras-Alonso, Rosa M. Crujeiras and Alberto Rodríguez-Casal

References

Chaudhuri, P. and Marron, J. S. (1999). SiZer for exploration of structures in curves, *Journal of the American Statistical Association*, **94**, 807–823.

Examples

```
#SiZer map using a grid of bandwidths between 1 and 10
data(geyser)
data=geyser
sizer(data,bws=c(1,10))

## Not run:
#Different methods for calculating the confidence limits

#Pointwise Gaussian quantiles
sizer(data,method=1,bws=c(1,10))

#Approximate simultaneous over x Gaussian quantiles
sizer(data,method=2,bws=c(1,10))

#Bootstrap quantile simultaneous over x
sizer(data,method=3,bws=c(1,10))

#Bootstrap quantile simultaneous over x and h
sizer(data,method=4,bws=c(1,10))

## End(Not run)

#Adding the original mode tree for this sample
```

```
modetree(data,bws=c(0.8,10),logbw=TRUE,addplot=TRUE,col.lines="white")
```

stamps

Stamps thickness

Description

This dataset, analysed in Izenman and Sommer (1988) and Ameijeiras–Alonso *et al.* (2017), consists of thickness measurements (in millimeters) of 485 unwatermarked used white wove stamps of the 1872 Hidalgo stamp issue of Mexico. All of them had an overprint with the year (1872 or either an 1873 or 1874) and some of them were watermarked (Papel Sellado or LA+-F).

Usage

```
data(stamps)
data(stamps1)
data(stamps2)
data(stampstable)
```

Format

stamps includes the thickness (in millimeters) of the different stamps in the 1872 Hidalgo stamp issue. stamps1 includes both the thickness and the overprinted year. stamps2 includes both the thickness and the watermark. stampstable reproduces the original frequency table in Izenman and Sommer (1988), including the thickness, the overprinted years (1872 or 1873–1874) and the watermarks (Papel Sellado or LA+-F).

Details

This is a classic example for determining the number of modes.

Source

Obtained from the original table in Izenman and Sommer (1988).

References

- Ameijeiras–Alonso, J., Crujeiras, R.M. and Rodríguez–Casal, A. (2016). Mode testing, critical bandwidth and excess mass, *arXiv preprint: 1609.05188*.
- Izenman, A. J., and Sommer, C. J. (1988). Philatelic mixtures and multimodal densities. *Journal of the American Statistical association*, **83**, 941–953.

Examples

```
data("stamps")
# Histogram of Wilson (bin width 0.008)
seqx=seq(0.0585,0.1385,by=0.008)
hist(stamps,breaks=seqx)
# Histogram of Figure 1, Izenman and Sommer (bin width 0.002)
seqx=seq(0.0585,0.1385,by=0.002)
hist(stamps,breaks=seqx)

# Kernel density estimation of Izenman and Sommer (number of modes: 7)
locmodes(stamps,mod0=7,lowsup=0.04,uppsup=0.15,display=TRUE)
# Kernel density estimation of Ameijeiras-Alonso et al. (number of modes: 4)
locmodes(stamps,mod0=4,lowsup=0.04,uppsup=0.15,display=TRUE)
```

Index

*Topic **datasets**

- acidity, [3](#)
- chondrite, [5](#)
- enzyme, [6](#)
- galaxy, [8](#)
- geyser, [9](#)
- stamps, [22](#)

*Topic **graphical tools**

- modeforest, [12](#)
- modetree, [16](#)
- sizer, [19](#)

*Topic **mode estimation**

- locmodes, [10](#)
- nmodes, [18](#)

*Topic **mode testing**

- bw.crit, [4](#)
- excessmass, [7](#)
- modetest, [14](#)

acidity, [3](#)

bw.crit, [4](#)

chondrite, [5](#)

chondritegg (chondrite), [5](#)

chondritel (chondrite), [5](#)

enzyme, [6](#)

excessmass, [7](#)

galaxy, [8](#)

galaxyp (galaxy), [8](#)

galaxyrg (galaxy), [8](#)

geyser, [9](#)

geyserab (geyser), [9](#)

geyserh (geyser), [9](#)

geyserw (geyser), [9](#)

locmodes, [10](#)

modeforest, [12](#)

modetest, [14](#)

modetree, [16](#)

multimode (multimode-package), [2](#)

multimode-package, [2](#)

nmodes, [18](#)

sizer, [19](#)

stamps, [22](#)

stamps1 (stamps), [22](#)

stamps2 (stamps), [22](#)

stampstable (stamps), [22](#)