Package ‘LogConcDEAD’

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Computes a log-concave (maximum likelihood) estimator for i.i.d. data in any number of dimensions

Description

This package contains a function to compute the maximum likelihood estimator of a log-concave density in any number of dimensions using Shor’s \( r \)-algorithm.

Functions to plot (for 1- and 2-d data), evaluate and draw samples from the maximum likelihood estimator are provided.

Details

This package contains a selection of functions for maximum likelihood estimation under the constraint of log-concavity.

\texttt{mlelcd} computes the maximum likelihood estimator (specified via its value at data points). Output is a list of class “LogConcDEAD” which is used as input to various auxiliary functions.

\texttt{hatA} calculates the difference between the sample covariance and the fitted covariance.

\texttt{dlcd} evaluates the estimated density at a particular point.
**LogConcDEAD-package**

- **dslcd** evaluates the smoothed version of estimated density at a particular point.
- **rlcd** draws samples from the estimated density.
- **rslcd** draws samples from the smoothed version of estimated density.
- **interplcd** interpolates the estimated density on a grid for plotting purposes.
- **dmarglcd** evaluates the estimated marginal density by integrating the estimated density over an appropriate subspace.
- **interpmarglcd** evaluates a marginal density estimate at equally spaced points along the axis for plotting purposes. This is done by integrating the estimated density over an appropriate subspace.
- **plot.LogConcDEAD** produces plots of the maximum likelihood estimator, optionally using the **rgl** package.
- **print** and **summary** methods are also available.

**Note**

The authors gratefully acknowledge the assistance of Lutz Duembgen at the University of Bern for his insight into the objective function in **mlelcd**.

For one dimensional data, the active set algorithm in **logcondens** is much faster.

**Author(s)**

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Madeleine Cule

Robert Gramacy

Richard Samworth

**References**


cov.LogConcDEAD

Compute the covariance matrix of a log-concave maximum likelihood estimator

Description

This function computes the covariance matrix of a log-concave maximum likelihood estimator.

Usage

cov.LogConcDEAD(lcd)
dlcd

Arguments

lcd Object of class "LogConcDEAD" (typically output from mlelcd)

Details

This function evaluates the covariance matrix of a given log-concave maximum likelihood estimator using the second order partial derivatives of the auxiliary function studied in Cule, M. L. and Dümbgen, L. (2008).

For examples, see mlelcd.

Value

A matrix equals the covariance matrix of the log-concave maximum likelihood density estimator.

Author(s)

Yining Chen
Madeleine Cule
Robert Gramacy
Richard Samworth

References


See Also

hatA

dlcd Evaluation of a log-concave maximum likelihood estimator at a point

Description

This function evaluates the density function of a log-concave maximum likelihood estimator at a point or points.

Usage

dlcd(x, lcd, use_log=FALSE, eps=10^-10)
Arguments

- **x**: Point (or matrix of points) at which the maximum likelihood estimator should be evaluated.
- **lcd**: Object of class "LogConcDEAD" (typically output from \texttt{mlelcd}).
- **uselog**: Scalar logical: should the estimator should be calculated on the log scale?
- **eps**: Tolerance for numerical stability.

Details

A log-concave maximum likelihood estimate \( \hat{f}_n \) satisfies \( \log \hat{f}_n = \bar{h}_y \) for some \( y \in R^n \), where

\[
\bar{h}_y(x) = \inf \{ h(x): h \text{ concave}, h(x_i) \geq y_i \text{ for } i = 1, \ldots, n \}.
\]

Functions of this form may equivalently be specified by dividing \( C_n \), the convex hull of the data, into simplices \( C_j \) for \( j \in J \) (triangles in 2d, tetrahedra in 3d etc), and setting

\[
f(x) = \exp \{ b_j^T x - \beta_j \}
\]

for \( x \in C_j \), and \( f(x) = 0 \) for \( x \notin C_n \). The estimated density is zero outside the convex hull of the data.

The estimate may therefore be evaluated by finding the appropriate simplex \( C_j \), then evaluating \( \exp \{ b_j^T x - \beta_j \} \) (if \( x \notin C_n \), set \( f(x) = 0 \)).

For examples, see \texttt{mlelcd}.

Value

A vector of maximum likelihood estimate (or log maximum likelihood estimate) values, as evaluated at the points \( x \).

Author(s)

- Madeleine Cule
- Robert Gramacy
- Richard Samworth

See Also

- \texttt{mlelcd}
**dmarglcd**

Evaluate the marginal of multivariate log-concave maximum likelihood estimators at a point

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**Description**

Integrates the log-concave maximum likelihood estimator of multivariate data to evaluate the marginal density at a point.

**Usage**

```r
dmarglcd(x=0, lcd, marg=1)
```

**Arguments**

- `x` Point (or vector of points) at which the marginal density is to be evaluated
- `lcd` Object of class "LogConcDEAD" (typically output from `mlelcd`)
- `marg` Which margin is required?

**Details**

Given a multivariate log-concave maximum likelihood estimator in the form of an object of class "LogConcDEAD", a margin `marg`, and a real-valued point `x`, this function evaluates the estimated marginal density $\hat{f}_{n,marg}(x)$, as obtained by integrating over all the other dimensions.

For examples, see `mlelcd`.

**Value**

A vector containing the values of the marginal density $\hat{f}_{n,marg}$ at the points `x`.

**Author(s)**

Madeleine Cule
Robert Gramacy
Richard Samworth

**See Also**

`mlelcd`
Evaluation of a smoothed log-concave maximum likelihood estimator at given points

Description

This function evaluates the density function of a smoothed log-concave maximum likelihood estimator at a point or points.

Usage

dslcd(x, lcd, A=hatA(lcd))

Arguments

x Point (or matrix of points) at which the smoothed log-concave maximum likelihood estimator should be evaluated
lcd Object of class "LogConcDEAD" (typically output from mlelcd)
A A positive definite matrix that determines the degree of smoothing, typically taken as the output of hatA(lcd)

Details

The smoothed log-concave maximum likelihood estimator is a fully automatic nonparametric density estimator, obtained as a canonical smoothing of the log-concave maximum likelihood estimator. More precisely, it equals the convolution $\hat{f} * \hat{\phi}_{d,\hat{A}}$, where $\hat{\phi}_{d,\hat{A}}$ is the density function of $d$-dimensional multivariate normal with covariance matrix $\hat{A}$. Typically, $\hat{A}$ is taken as the difference between the sample covariance and the covariance of fitted log-concave maximum likelihood density. Therefore, this estimator matches both the empirical mean and empirical covariance. The estimate is evaluated numerically either by Gaussian quadrature in two dimensions, or in higher dimensions, via a combinatorial method proposed by Grundmann and Moeller (1978). Details of the computational aspects can be found in Chen and Samworth (2011). In one dimension, explicit expression can be derived. See logcondens for more information.

For examples, see mlelcd

Value

A vector of smoothed log-concave maximum likelihood estimate values, as evaluated at the points x.

Author(s)

Yining Chen
Madeleine Cule
Robert Gramacy
Richard Samworth
EMmixlcd

References


See Also
dld, hatA, mlelcd

EMmixlcd

Estimate the mixture proportions and component densities using EM algorithm

Description

Uses EM algorithm to estimate the mixture proportions and the component densities. The output is an object of class "lcdmix" which contains mixture proportions at each observation and all the information of the estimated component densities.

Usage

EMmixlcd( x, k = 2, y, props, epsratio=10^-6, max.iter=50, epstheta=10^-8, verbose=-1 )

Arguments

x                     Data in $R^d$, in the form of an $n \times d$ numeric matrix
k                     The number of components, equals 2 by default
y                     An $n \times k$ numeric matrix giving the starting values for the EM algorithm. If none given, a hierachical Gaussian clustering model is used. To reduce the computational burden while allowing sufficient flexibility for the EM algorithm, it is recommended to leave this argument unspecified.
props                  Vector of length $k$ containing the starting value of proportions. If none given, a hierachical Gaussian clustering model is used. To reduce the computational burden while allowing sufficient flexibility for the EM algorithm, it is recommended to leave this argument unspecified.
epsratio               EM algorithm will terminate if the increase in the proportion of the likelihood is less than this specified ratio. Default value is $10^{-6}$.
max.iter               The maximum number of iterations for the EM algorithm
epstheta               $epstheta/n$ is the threshold of the weight below which data point is discarded from the cluster. This quantity is introduced to increase the computational efficiency and stability.
verbose                • -1: (default) prints nothing
                         • 0: prints warning messages
                         • > 0: prints summary information every $n$ iterations
Details

An introduction to the Em algorithm can be found in McLachlan and Krishnan (1997). Briefly, given the current estimates of the mixture proportions and component densities, we first update the estimates of the mixture proportions. We then update the estimates of the component densities by using mlelcd. In fact, the incorporation of the weights in the maximization process in mlelcd presents no additional complication.

In our case, because of the computational intensity of the method, we first cluster the points according to a hierarchical Gaussian clustering model and then iterate the EM algorithm until the increase in the proportion of the likelihood is less than a pre-specified quantity at each step.

More technical details can be found in Cule, Samworth and Stewart(2010).

Value

An object of class "lcdmix", with the following components:

- `x` Data copied from input (may be reordered)
- `logf` An $n \times k$ matrix of the log of the maximum likelihood estimate, evaluated at the observation points for each component.
- `props` Vector containing the estimated proportions of components
- `niter` Number of iterations of the EM algorithm
- `lcdloglik` The log-likelihood after the final iteration

Author(s)

Yining Chen
Madeleine Cule
Robert B. Gramacy
Richard Samworth

References


See Also

mclust, logcondens, plot.LogConcDEAD, mlelcd, dlcld

Examples

```r
## Simple bivariate normal data
set.seed( 1 )
n = 15
d = 2
props=c( 0.6, 0.4 )
shift=2
```
getinfolcd

Construct an object of class LogConcDEAD

Description

A function to construct an object of class LogConcDEAD from a dataset (given as a matrix) and the value of the log maximum likelihood estimator at datapoints.

Usage

getinfolcd(x, y, w = rep(1/length(y), length(y)), chtol = 10^-6, MinSigma = NA, NumberOfEvaluations = NA)

Arguments

x Data in $R^d$, in the form of an $n \times d$ numeric matrix
y Value of log of maximum likelihood estimator at data points
w Vector of weights $w_i$ such that the computed estimator maximizes

$$\sum_{i=1}^{n} w_i \log f(x_i)$$

subject to the restriction that $f$ is log-concave. The default is $\frac{1}{n}$ for all $i$, which corresponds to i.i.d. observations.

chtol Tolerance for computation of convex hull. Altering this is not recommended.
MinSigma Real-valued scalar giving minimum value of the objective function
NumberOfEvaluations Vector containing the number of steps, number of function evaluations, and number of subgradient evaluations. If the SolvOpt algorithm fails, the first component will be an error code ($<0$)

Details

This function is used in mlelcd

```r
x <- matrix( rnorm( n*d ), ncol = d )
shiftvec <- ifelse( runif( n ) > props[ 1 ], 0, shift )
x[,1] <- x[,1] + shiftvec
EMmixlcd( x, k = 2, max.iter = 2)
```
Value

An object of class "LogConcDEAD", with the following components:

- x: Data copied from input (may be reordered)
- w: weights copied from input (may be reordered)
- logMLE: vector of the log of the maximum likelihood estimate, evaluated at the observation points
- NumberOfEvaluations: Vector containing the number of steps, number of function evaluations, and number of subgradient evaluations. If the SolvOpt algorithm fails, the first component will be an error code (< 0).
- MinSigma: Real-valued scalar giving minimum value of the objective function
- b: matrix (see Details)
- beta: vector (see Details)
- triang: matrix containing final triangulation of the convex hull of the data
- verts: matrix containing details of triangulation for use in dlcd
- vertsoffset: matrix containing details of triangulation for use in dlcd
- chull: Vector containing vertices of faces of the convex hull of the data
- outnorm: matrix where each row is an outward pointing normal vectors for the faces of the convex hull of the data. The number of vectors depends on the number of faces of the convex hull.
- outoffset: matrix where each row is a point on a face of the convex hull of the data. The number of vectors depends on the number of faces of the convex hull.

Author(s)

Madeleine Cule
Robert B. Gramacy
Richard Samworth
Yining Chen

See Also

mlelcd
getweights

Find appropriate weights for likelihood calculations

Description

This function takes a matrix of (possibly binned) data and returns a matrix containing the distinct observations, and a vector of weights $w$ as described below.

Usage

geweights(x)

Arguments

x a data matrix

Details

Given an $n \times d$ matrix $x$ of points in $\mathbb{R}^d$, this function removes duplicated observations, and counts the number of times each observation occurs. This is used to compute a vector $w$ such that

$$w_i = \frac{\text{# of times value } i \text{ is observed}}{\text{# of observations}}.$$

This function is called by `mlelcd` in order to compute the maximum likelihood estimator when the observed data values are not distinct. In this case, the log likelihood function is of the form

$$\sum_{j=1}^{m} w_j \log f(X_j),$$

where the sum is over distinct observations.

Value

xout A matrix containing the distinct rows of the input matrix x

w A real-valued vector of weights as described above

Author(s)

Madeleine Cule
Robert Gramacy
Richard Samworth

See Also

`mlelcd`
Examples

```r
## simple normal example
x <- matrix(rnorm(200),nrow=2)
tmp <- getweights(x)
lcd <- mlelcd(tmp$x,tmp$w)
plot(lcd,type="ic")
```

hatA

`hatA()` computes the smoothing matrix of the smoothed log-concave maximum likelihood estimator.

**Description**

This function computes the matrix \( \hat{A} \) of the smoothed log-concave maximum likelihood estimator.

**Usage**

```r
hatA(lcd)
```

**Arguments**

- `lcd` Object of class "LogConcDEAD" (typically output from `mlelcd`)

**Details**

This function evaluates the the matrix \( \hat{A} \) of the smoothed log-concave maximum likelihood estimator, which is positive definite, and equals the difference between the sample covariance matrix and the covariance matrix of the fitted log-concave maximum likelihood density estimator.

For examples, see `mlelcd`

**Value**

A matrix equals \( \hat{A} \) of the smoothed log-concave maximum likelihood estimator.

**Note**

Details of the computational aspects can be found in *Chen and Samworth (2011)*.

**Author(s)**

Yining Chen
Madeleine Cule
Robert Gramacy
Richard Samworth
References


See Also
cov.LogConcDEAD

interactive2D A GUI for classification in two dimensions using smoothed log-concave

Description

Uses tkrplot to create a GUI for two-class classification in two dimensions using the smoothed log-concave maximum likelihood estimates

Usage

interactive2D(data, cl)

Arguments

data Data in $\mathbb{R}^2$, in the form of an $n \times 2$ numeric matrix
cl factor of true classifications of the data set

Details

This function uses tkrplot to create a GUI for two-class classification in two dimensions using the smoothed log-concave maximum likelihood estimates. The construction of the classifier is standard, and can be found in Chen and Samworth (2013). The slider controls the risk ratio of two classes (equals one by default), which provides a way of demonstrating how the decision boundaries change as the ratio varies. Observations from different classes are plotted in red and green respectively.

Value

A GUI with a slider

Author(s)

Yining Chen
Madeleine Cule
Robert B. Gramacy
Richard Samworth
References


See Also
dslcd,mlelcd

Examples

```r
## Simple bivariate normal data
## only works interactively, not run as a test example here
if(interactive()){  
  set.seed( 1 )
  n = 15
  d = 2
  props=c( 0.6, 0.4 )
  x <- matrix( rnorm( n*d ), ncol = d )
  shiftvec <- ifelse( runif( n ) > props[ 1 ], 0, 1)
  x[,1] <- x[,1] + shiftvec
  interactive2D( x, shiftvec )
}
```

interplcd Evaluate the log-concave maximum likelihood estimator of 2-d data on a grid for plotting

Description

Evaluates the logarithm of the log-concave maximum likelihood estimator on a grid for 2-d data, for use in plot.LogConcDEAD.

Usage

`interplcd(lcd, gridlen=100 )`

Arguments

- `lcd`: Object of class "LogConcDEAD" (typically output from mlelcd)
- `gridlen`: A scalar indicating the size of the grid

Details

Interpolates the MLE over a grid.
The output is of a form readily usable by plot.LogConcDEAD, image, contour, etc, as illustrated in the examples below.
For examples, please see mlelcd.
**Value**

- `x`: Vector of x-values of the grid
- `y`: Vector of y-values of the grid
- `z`: A matrix of the values of the log of the maximum likelihood estimator at points on the grid

**Author(s)**

Madeleine Cule
Robert Gramacy
Richard Samworth

**See Also**

`mlelcd`

---

**interpmarglcd**

Finds marginals of multivariate logconcave maximum likelihood estimators by integrating

**Description**

Integrates the maximum likelihood estimator of multivariate data over an appropriate subspace to produce axis-aligned marginals for use in `plot.LogConcDEAD`.

**Usage**

`interpmarglcd(lcd, marg=1, gridlen=100)`

**Arguments**

- `lcd`: Output from `mlelcd` (of class "LogConcDEAD")
- `marg`: An (integer) scalar indicating which margin is required
- `gridlen`: An (integer) scalar indicating the size of the grid

**Details**

Given a multivariate log-concave maximum likelihood estimator in the form of an object of class "LogConcDEAD" and a margin `marg`, this function will compute the marginal density estimate \( \hat{f}_{n,marg} \). The estimate is evaluated at `gridlen` equally spaced points in the range where the density estimate is nonzero. These points are given in the vector `xo`. 

\( \hat{f}_{n,marg} \) is evaluated by integrating the log-concave maximum likelihood estimator \( \hat{f}_n \) over the other components. The marginal density is zero outside the range of `xo`.

For examples, see `mlelcd`. 
mlelcd

Compute the maximum likelihood estimator of a log-concave density

Description

Uses Shor's r-algorithm to compute the maximum likelihood estimator of a log-concave density based on an i.i.d. sample. The estimator is uniquely determined by its value at the data points. The output is an object of class "LogConcDEAD" which contains all the information needed to plot the estimator using the plot method, or to evaluate it using the function dlcd.

Usage

mlelcd(x, w=rep(1/nrow(x), nrow(x)), y=initialy(x),
       verbose=-1, alpha=5, c=1, sigmatol=10^-8, integraltol=10^-4,
       ytol=10^-4, Jtol=0.001, chtol=10^-6)

Arguments

x       Data in $R^d$, in the form of an $n \times d$ numeric matrix
w       Vector of weights $w_i$ such that the computed estimator maximizes

$$\sum_{i=1}^{n} w_i \log f(x_i)$$

subject to the restriction that $f$ is log-concave. The default is $\frac{1}{n}$ for all $i$, which corresponds to i.i.d. observations.

y       Vector giving starting point for the r-algorithm. If none given, a kernel estimate is used.

verbose • -1: (default) prints nothing

Value

xo       Vector of values at which the marginal density is estimate is computed.
marg     Vector of values of the integrated maximum likelihood estimator at the locations xo

Author(s)

Madeleine Cule
Robert Gramacy
Richard Samworth

See Also

dmarglcd, mlelcd
• 0: prints warning messages
• $n > 0$: prints summary information every $n$ iterations

alpha  
Scalar parameter for SolvOpt

c  
Scalar giving starting step size

sigmatol  
Real-valued scalar giving one of the stopping criteria: Relative change in $\sigma$ must be below sigmatol for algorithm to terminate. (See Details)

ytol  
Real-valued scalar giving one of the stopping criteria: Relative change in $y$ must be below ytol for algorithm to terminate. (See Details)

integraltol  
Real-valued scalar giving one of the stopping criteria: $|1 - \exp(\bar{h}_y)|$ must be below integraltol for algorithm to terminate. (See Details)

Jtol  
Parameter controlling when Taylor expansion is used in computing the function $\sigma$

chtol  
Parameter controlling convex hull computations

Details
The log-concave maximum likelihood density estimator based on data $X_1, \ldots, X_n$ is the function that maximizes

$$\sum_{i=1}^{n} w_i \log f(X_i)$$

subject to the constraint that $f$ is log-concave. For i.i.d.-data, the weights $w_i$ should be $\frac{1}{n}$ for each $i$.

This is a function of the form $\bar{h}_y$ for some $y \in \mathbb{R}^n$, where

$$\bar{h}_y(x) = \inf \{ h(x): h \text{ concave}, h(x_i) \geq y_i \text{ for } i = 1, \ldots, n \}.$$

Functions of this form may equivalently be specified by dividing $C_n$, the convex hull of the data, into simplices $C_j$ for $j \in J$ (triangles in 2d, tetrahedra in 3d etc), and setting

$$f(x) = \exp \{ b_j^T x - \beta_j \}$$

for $x \in C_j$, and $f(x) = 0$ for $x \notin C_n$.

This function uses Shor’s $r$-algorithm (an iterative subgradient-based procedure) to minimize over vectors $y$ in $\mathbb{R}^n$ the function

$$\sigma(y) = -\frac{1}{n} \sum_{i=1}^{n} y_i + \int \exp(\bar{h}_y(x)) \, dx.$$

This is equivalent to finding the log-concave maximum likelihood estimator, as demonstrated in Cule, Samworth and Stewart (2008).

An implementation of Shor’s $r$-algorithm based on SolvOpt is used.

Computing $\sigma$ makes use of the qhull library. Code from this C-based library is copied here as it is not currently possible to use compiled code from another library. For points not in general position, this requires a Taylor expansion of $\sigma$, discussed in Cule and Durngen (2008).
Value

An object of class "LogConcDEAD", with the following components:

- \( x \)  Data copied from input (may be reordered)
- \( w \)  weights copied from input (may be reordered)
- \( \logMLE \)  vector of the log of the maximum likelihood estimate, evaluated at the observation points
- NumberOfEvaluations  Vector containing the number of steps, number of function evaluations, and number of subgradient evaluations. If the \texttt{SolvOpt} algorithm fails, the first component will be an error code \((-1)\).
- MinSigma  Real-valued scalar giving minimum value of the objective function
- \( b \)  matrix (see Details)
- \( \beta \)  vector (see Details)
- triang  matrix containing final triangulation of the convex hull of the data
- verts  matrix containing details of triangulation for use in \texttt{dlcd}
- vertsoffset  matrix containing details of triangulation for use in \texttt{dlcd}
- chull  Vector containing vertices of faces of the convex hull of the data
- outnorm  matrix where each row is an outward pointing normal vectors for the faces of the convex hull of the data. The number of vectors depends on the number of faces of the convex hull.
- outoffset  matrix where each row is a point on a face of the convex hull of the data. The number of vectors depends on the number of faces of the convex hull.

Note

For one-dimensional data, the active set algorithm of \texttt{logcondens} is faster, and may be preferred.

The authors gratefully acknowledge the assistance of Lutz Duembgen at the University of Bern for his insight into the objective function \( \sigma \).

Further references, including definitions and background material, may be found in Cule, Samworth and Stewart (2010).

Author(s)

Madeleine Cule
Robert B. Gramacy
Richard Samworth
Yining Chen
References


See Also

logcondens, interplcd, plot.LogConcDEAD, interpmarglcd, rlcd, dlcd, dmarglcd, cov.LogConcDEAD

Examples

## Some simple normal data, and a few plots

```r
x <- matrix(rnorm(200), ncol=2)
lcd <- mlelcd(x)
g <- interplcd(lcd)

oldpar <- par(mfrow = c(1,1))
par(mfrow=c(2,2), ask=TRUE)
plot(lcd, g=g, type="c")
plot(lcd, g=g, type="c", uselog=TRUE)
plot(lcd, g=g, type="i")
plot(lcd, g=g, type="i", uselog=TRUE)
par(oldpar)
```

## 2D interactive plot (need rgl package, not run here)

```r
if(interactive()) {plot(lcd, type="r")}
```

## Some plots of marginal estimates

```r
g.marg1 <- interpmarglcd(lcd, marg=1)
g.marg2 <- interpmarglcd(lcd, marg=2)
plot(lcd, marg=1, g.marg=g.marg1)
plot(lcd, marg=2, g.marg=g.marg2)
```

## generate some points from the fitted density
## via independent rejection sampling

```r
generated1 <- rlcd(100, lcd)
colMeans(generated1)
```

## via Metropolis-Hastings algorithm

```r
generated2 <- rlcd(100, lcd, "MH")
colMeans(generated2)
```
## evaluate the fitted density
mypoint <- c(0, 0)
dlcd(mypoint, lcd, uselog=FALSE)
mypoint <- c(1, 0)
dlcd(mypoint, lcd, uselog=FALSE)

## evaluate the marginal density
dmarglcd(0, lcd, marg=1)
dmarglcd(1, lcd, marg=2)

## evaluate the covariance matrix of the fitted density
covariance <- cov.LogConcDEAD(lcd)

## find the hat matrix for the smoothed log-concave that
## matches empirical mean and covariance
A <- hatA(lcd)

## evaluate the fitted smoothed log-concave density
mypoint <- c(0, 0)
dslcd(mypoint, lcd, A)
mypoint <- c(1, 0)
dslcd(mypoint, lcd, A)

## generate some points from the fitted smoothed log-concave density
generated <- rslcd(100, lcd, A)

---

plot.LogConcDEAD  

Plot a log-concave maximum likelihood estimator

### Description

`plot` method for class "LogConcDEAD". Plots of various types are available for 1- and 2-d data. For dimension greater than 1, plots of axis-aligned marginal density estimates are available.

### Usage

```r
## S3 method for class 'LogConcDEAD'
plot(x, uselog=FALSE, type="ic", addp=TRUE,
     drawlabels=TRUE, gridlen=400, g, marg, g.marg, main, xlab, ylab, ...)
```

### Arguments

- **x**: Object of class "LogConcDEAD" (typically output from `mlelcd`)
- **uselog**: Scalar logical: should the plot be on the log scale?
- **type**: Plot type: "p" perspective, "c" contour, "i" image, ic image and contour, r using rgl (the best!)
- **addp**: Scalar logical: should the data points be plotted? (as black dots on the surface for \(d \geq 2\); as circles for \(d = 1\))
drawlabels  Scalar logical: should labels be added to contour lines? (only relevant for types "ic" and "c")
gridlen  Integer scalar indicating the number of points at which the maximum likelihood estimator is evaluated in each dimension

g  (optional) a matrix of density estimate values (the result of a call to interplcd). If many plots of a single dataset are required, it may be quicker to compute the grid using interplcd(x) and pass the result to plot

marg  If non-NULL, this scalar integer determines which marginal should be plotted (should be between 1 and d)
g.marg  If g is non-NULL, can contain a vector of marginal density estimate values (the output of interpmarglcd). If many plots of a single dataset are required, it may be quicker to compute the marginal values to compute marginal values using interpmarglcd and pass the result to plot

main  Title
xlab  x-axis label
ylab  y-axis label
...  Other arguments to be passed to the generic plot method

Details

The density estimate is evaluated on a grid of points using the interplcd function. If several plots are required, this may be computed separately and passed to plot using the g argument.

For two dimensional data, the default plot type is "ic", corresponding to image and contour plots. These may be obtained separately using plot type "i" or "c" respectively. Where available, the use of plot type "r" is recommended. This uses the rgl package to produce a 3-d plot that may be rotated by the user. The option "p" produces perspective plots.

For data of dimension at least 2, axis-aligned marginals may be plotted by setting the marg argument. This integrates the estimated density over the remaining dimensions. If several plots are required, the estimate may be computed using the function interpmarglcd and passed using the argument g.marg.

Where relevant, the colors were obtained from the function heat_hcl in the colorspace package. Thanks to Achim Zeileis for this suggestion.

For examples, see mlelcd.

Value

No return value, plot will display

Author(s)

Madeleine Cule
Robert B. Gramacy
Richard Samworth
Yining Chen
print.LogConcDEAD

See Also

mlelcd, interplcd, interpmarglcd, heat_hcl

---

print.LogConcDEAD  Summarizing log-concave maximum likelihood estimator

Description

Generic print and summary method for objects of class "LogConcDEAD"

Usage

## S3 method for class 'LogConcDEAD'
print(x, ...)
## S3 method for class 'LogConcDEAD'
summary(object, ...)

Arguments

x  Object of class "LogConcDEAD" (typically output from mlelcd), as required by print
object  Object of class "LogConcDEAD" (typically output from mlelcd), as required by summary
...  Other arguments passed to print or summary

Details

print and summary currently perform the same function.
If there has been an error computing the maximum likelihood estimator, an error message is printed.
Otherwise, the value of the log maximum likelihood estimator at observation points is printed. The number of interactions required by the subgradient and the number of function evaluations are also printed.

Value

No return value, log MLE at observation points will be printed out on the screen.

Author(s)

Madeleine Cule
Robert B. Gramacy
Richard Samworth

See Also

mlelcd
rlcd

Sample from a log-concave maximum likelihood estimate

Description

Draws samples from a log-concave maximum likelihood estimate. The estimate should be specified in the form of an object of class "LogConcDEAD", the result of a call to mlelcd.

Usage

rlcd(n=1, lcd, method=c("Independent","MH"))

Arguments

n
A scalar integer indicating the number of samples required

lcd
Object of class "LogConcDEAD" (typically output from mlelcd)

method
Indicator of the method used to draw samples, either via independent rejection sampling (default choice) or via Metropolis-Hastings

Details

This function by default uses a simple rejection sampling scheme to draw independent random samples from a log-concave maximum likelihood estimator. One can also use the Metropolis-Hastings option to draw (dependent) samples with a higher acceptance rate.

For examples, see mlelcd.

Value

A numeric matrix with nsample rows, each row corresponding to a point in $\mathbb{R}^d$ drawn from the distribution with density defined by lcd.

Note

Details of the rejection sampling can be found in Appendix B.3 of Cule, Samworth and Stewart (2010). Details of the Metropolis-Hastings scheme can be found in Gopal and Casella (2010)

Author(s)

Yining Chen
Madeleine Cule
Robert Gramacy
Richard Samworth
rslcd

Sample from a smoothed log-concave maximum likelihood estimate

Description

Draws samples from a smoothed log-concave maximum likelihood estimate. The estimate should be specified in the form of an object of class "LogConcDEAD", the result of a call to mlelcd, and a positive definite matrix.

Usage

rslcd(n=1, lcd, A=hatA(lcd), method=c("Independent","MH"))

Arguments

n A scalar integer indicating the number of samples required
lcd Object of class "LogConcDEAD" (typically output from mlelcd)
A A positive definite matrix that determines the degree of smoothing, typically taken as the output of hatA(lcd)
method Indicator of the method used to draw samples, either via independent rejection sampling (default choice) or via Metropolis-Hastings

Details

This function by default uses a simple rejection sampling scheme to draw independent random samples from a smoothed log-concave maximum likelihood estimator. One can also use the Metropolis-Hastings option to draw (dependent) samples with a higher acceptance rate.

For examples, see mlelcd.

Value

A numeric matrix with n rows, each row corresponding to a point in $\mathbb{R}^d$ drawn from the distribution with density defined bylcd andA.
Author(s)
Yining Chen
Madeleine Cule
Robert Gramacy
Richard Samworth

References

See Also
mlelcd, rlcd, hatA
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