Package ‘frechet’

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Description Provides implementation of statistical methods for random objects lying in various metric spaces, which are not necessarily linear spaces. The core of this package is Fréchet regression for random objects with Euclidean predictors, which allows one to perform regression analysis for non-Euclidean responses under some mild conditions. Examples include distributions in \( L^2 \)-Wasserstein space, covariance matrices endowed with power metric (with Frobenius metric as a special case), Cholesky and log-Cholesky metrics.
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**R topics documented:**

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| color.bar | Generate color bar/scale. |

**Description**

Generate color bar/scale.

**Usage**

```r
color.bar(
  colVal = NULL,
  colBreaks = NULL,
  min = NULL,
  max = NULL,
  lut = NULL,
  nticks = 5,
  ticks = NULL,
  title = NULL
)
```

**Arguments**

- `colVal` A numeric vector giving the variable values to which each color is corresponding. It overrides `min` (and `max`) if `min > min(colVal)` (or `max < max(colVal)`).
- `colBreaks` A numeric vector giving the breaks dividing the range of variable into different colors. It overrides `min` and `max`. 
CovFMean

min  A scalar giving the minimum value of the variable represented by colors.
max  A scalar giving the maximum value of the variable represented by colors.
lut  Color vector. Default is colorRampPalette(colors = c("pink","royalblue"))(length(colBreaks)-1).
nticks  An integer giving the number of ticks used in the axis of color bar.
ticks  A numeric vector giving the locations of ticks used in the axis of color bar; it overrides nticks.
title  A character giving the label of the variable according to which the color bar is generated.

Value
No return value.

CovFMean | Fréchet mean of covariance matrices

Description
Fréchet mean computation for covariance matrices.

Usage
CovFMean(M = NULL, optns = list())

Arguments
M  A q by q by n array (resp. a list of q by q matrices) where M[,,i] (resp. M[[i]]) contains the i-th covariance matrix of dimension q by q.
optns  A list of options control parameters specified by list(name=value). See ‘Details’.

Details
Available control options are

metric  Metric type choice, "frobenius", "power", "log_cholesky", "cholesky" - default: "frobenius" which corresponds to the power metric with alpha equal to 1.
alpha  The power parameter for the power metric, which can be any non-negative number. Default is 1 which corresponds to Frobenius metric.

Value
A list containing the following fields:

Mout  A list containing the Fréchet mean of the covariance matrices in M.
optns  A list containing the optns parameters utilized.
CreateCovRegPlot

References


Examples

#Example M input
n=10 #sample size
m=5 # dimension of covariance matrices
M <- array(0,c(m,m,n))
for (i in 1:n){
y0=rnorm(m)
aux<-diag(m)+y0%*%t(y0)
M[,,i]<-aux
}
Fmean=CovFMean(M=M,optns=list(metric="frobenius"))

CreateCovRegPlot

Plots for Fréchet regression for covariance matrices.

Description

Plots for Fréchet regression for covariance matrices.

Usage

CreateCovRegPlot(x, optns = list())

Arguments

x
A covReg object obtained from CovFMean, GloCovReg or LocCovReg.

optns
A list of control options specified by list(name=value). See 'Details'.

Details

Available control options are

ind.xout A vector holding the indices of elements in x$Mout at which the plots will be made.
Default is

- 1:length(x$Mout) when x$Mout is of length no more than 3;
CreateCovRegPlot

- \( c(1, \text{round}(|\text{x$Mout}|/2), |\text{x$Mout}|) \) when \( \text{x$Mout} \) is of length greater than 3.

`nrow` An integer — default: 1; subsequent figures will be drawn in an `optns$nrow`-by-`ceiling(length(ind.xout)/optns$nrow)` array.

`plot.type` Character with two choices, "continuous" and "categorical". The former plots the correlations in a continuous scale of colors by magnitude while the latter categorizes the positive and negative entries into two different colors. Default is "continuous"

`plot.clust` Character, the ordering method of the correlation matrix. "original" for original order (default); "AOE" for the angular order of the eigenvectors; "FPC" for the first principal component order; "hclust" for the hierarchical clustering order, drawing 4 rectangles on the graph according to the hierarchical cluster; "alphabet" for alphabetical order.

`plot.method` Character, the visualization method of correlation matrix to be used. Currently, it supports seven methods, named "circle" (default), "square", "ellipse", "number", "pie", "shade" and "color".

`CorrOut` Logical, indicating if output is shown as correlation or covariance matrix. Default is `FALSE` and corresponds to a covariance matrix.

`plot.display` Character, "full" (default), "upper" or "lower", display full matrix, lower triangular or upper triangular matrix.

**Value**

No return value.

**Examples**

```r
# Example y input
n=20  # sample size
t=seq(0,1,length.out=100)  # length of data
x = matrix(runif(n),n)
theta1 = theta2 = array(0,n)
for(i in 1:n){
  theta1[i] = rnorm(1,x[i],x[i]^2)
  theta2[i] = rnorm(1,x[i]/2,(1-x[i])^2)
}
y = matrix(0,n,length(t))
phi1 = sqrt(3)*t
phi2 = sqrt(6/5)*(1-t/2)
y = theta1%*%t(phi1) + theta2 %*% t(phi2)
xout = matrix(c(0.25,0.5,0.75),3)
Cov_est=GloCovReg(x=x,y=y,xout=xout,optns=list(corrOut = FALSE, metric="power",alpha=3))
CreateCovRegPlot(Cov_est, optns = list(ind.xout = 2, plot.method = "shade"))
CreateCovRegPlot(Cov_est, optns = list(plot.method = "color"))
```
CreateDensity

Create density functions from raw data, histogram objects or frequency tables with bins

Description

Create kernel density estimate along the support of the raw data using the HADES method.

Usage

CreateDensity(
  y = NULL,
  histogram = NULL,
  freq = NULL,
  bin = NULL,
  optns = list()
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>A vector of raw readings.</td>
</tr>
<tr>
<td>histogram</td>
<td>A histogram object in R. Use this option when histogram object is only available, but not the raw data y. The default is NULL.</td>
</tr>
<tr>
<td>freq</td>
<td>A frequency vector. Use this option when frequency table is only available, but not the raw sample or the histogram object. The corresponding bin should be provided together. The default is NULL.</td>
</tr>
<tr>
<td>bin</td>
<td>A bin vector having its length with length(freq)+1. Use this option when frequency table is only available, but not the raw sample or the histogram object. The corresponding freq should be provided together. The default is NULL.</td>
</tr>
<tr>
<td>optns</td>
<td>A list of options control parameters specified by list(name=value). See ‘Details’.</td>
</tr>
</tbody>
</table>

Details

Available control options are

- **userBwMu** The bandwidth value for the smoothed mean function; positive numeric - default: determine automatically based on the data-driven bandwidth selector proposed by Sheather and Jones (1991)
- **nRegGrid** The number of support points the KDE; numeric - default: 101.
- **delta** The size of the bin to be used; numeric - default: diff(range(y))/1000. It only works when the raw sample is available.
- **kernel** smoothing kernel choice, "rect", "gauss", "epan", "gausvar", "quar" - default: "gauss".
- **infSupport** logical if we expect the distribution to have infinite support or not; logical - default: FALSE.
- **outputGrid** User defined output grid for the support of the KDE, it overrides nRegGrid; numeric - default: NULL.
CreateDensity

**Value**

A list containing the following fields:

- `bw` The bandwidth used for smoothing.
- `x` A vector of length `nRegGrid` with the values of the KDE's support points.
- `y` A vector of length `nRegGrid` with the values of the KDE at the support points.

**References**


**Examples**

```R
### compact support case

# input: raw sample
set.seed(100)
n <- 100
x0 <- seq(0,1,length.out=51)
Y <- rbeta(n,3,2)
f1 <- CreateDensity(y=Y,optns = list(outputGrid=x0))

# input: histogram
histY <- hist(Y)
f2 <- CreateDensity(histogram=histY,optns = list(outputGrid=x0))

# input: frequency table with unequally spaced (random) bins
binY <- c(0,sort(runif(9)),1)
freqY <- c()for (i in 1:(length(binY)-1)) {
    freqY[i] <- length(which(Y>binY[i] & Y<=binY[i+1]))
}
f3 <- CreateDensity(freq=freqY, bin=binY,optns = list(outputGrid=x0))

# plot
plot(f1$x,f1$y,type='l',col=2,lty=2,lwd=2,
     xlim=c(0,1),ylim=c(0,2),xlab='domain',ylab='density')
points(f2$x,f2$y,type='l',col=3,lty=3,lwd=2)
points(f3$x,f3$y,type='l',col=4,lty=4,lwd=2)
points(x0,dbeta(x0,3,2),type='l',lwd=2)
legend('topleft',
       c('true','raw sample','histogram','frequency table (unequal bin)'),
       col=1:4,lty=1:4,lwd=3,bty='n')
```
### infinite support case

# input: raw sample
set.seed(100)
n <- 200
x0 <- seq(-3,3,length.out=101)
Y <- rnorm(n)
f1 <- CreateDensity(y=Y,optns = list(outputGrid=x0))

# input: histogram
histY <- hist(Y)
f2 <- CreateDensity(histogram=histY,optns = list(outputGrid=x0))

# input: frequency table with unequally spaced (random) bins
binY <- c(-3,sort(runif(9,-3,3)),3)
freqY <- c()
for (i in 1:(length(binY)-1)) {
  freqY[i] <- length(which(Y>binY[i] & Y<=binY[i+1]))
}
f3 <- CreateDensity(freq=freqY, bin=binY,optns = list(outputGrid=x0))

# plot
plot(f1$x,f1$y,type='l',col=2,lty=2,lwd=2,
xlim=c(-3,3),ylim=c(0,0.5),xlab='domain',ylab='density')
points(f2$x,f2$y,type='l',col=3,lty=3,lwd=2)
points(f3$x,f3$y,type='l',col=4,lty=4,lwd=2)
points(x0,dnorm(x0),type='l',lwd=2)
legend('topright',
c('true','raw sample','histogram','frequency table (unequal bin)'),
col=1:4,lty=1:4,lwd=3,bty='n')

---

**DenFMean**

*Fréchet means of densities.*

---

**Description**

Obtain Fréchet means of densities with respect to \(L^2\)-Wasserstein distance.

**Usage**

DenFMean(yin = NULL, hin = NULL, qin = NULL, optns = list())

**Arguments**

- **yin**: A matrix or list holding the sample of measurements for the observed distributions. If yin is a matrix, each row holds the measurements for one distribution.

- **hin**: A list holding the histograms of an observed distribution.
**qin**
A matrix or list holding the quantile functions of the response. If qin is a matrix, each row holds the quantile function of an observed distribution taking values on optns\$qSup. Note that only one of the three yin, hin, and qin needs to be input. If more than one of them are specified, yin overwrites hin, and hin overwrites qin.

**optns**
A list of options control parameters specified by list(name=value).

**Details**
Available control options are qSup, nqSup, bwDen, ndSup, dSup, delta, kernelDen, infSupport, and denLowerThreshold. See LocDenReg for details.

**Value**
A list containing the following components:
- **dout**
  A numeric vector holding the density of the Fréchet mean.
- **dSup**
  A numeric vector giving the domain grid of dout when it is a matrix.
- **qout**
  A numeric vector holding the quantile function of the Fréchet mean.
- **qSup**
  A numeric vector giving the domain grid of qout.
- **optns**
  A list of control options used.

**Examples**
```r
xin = seq(0,1,0.05)
yin = lapply(xin, function(x) {
  rnorm(100, rnorm(1,x + x^2,0.005), 0.05)
})
res <- DenFMean(yin=yin)
plot(res)
```

---

**dist4cov**
*Distance between covariance matrices*

**Description**
Distance computation between two covariance matrices

**Usage**
dist4cov(A = NULL, B = NULL, optns = list())

**Arguments**
- **A**
an p by p matrix
- **B**
an p by p matrix
- **optns**
A list of options control parameters specified by list(name=value). See ‘Details’.
Details

Available control options are

- **metric**: Metric type choice, "frobenius", "power", "log_cholesky" and "cholesky" - default: "frobenius", which corresponds to the power metric with alpha equal to 1.

- **alpha**: The power parameter for the power metric, which can be any non-negative number. Default is 1 which corresponds to Frobenius metric.

Value

A list containing the following fields:

- **dist**: the distance between covariance matrices A and B.
- **optns**: A list containing the optns parameters utilized.

References


Examples

```r
# M input as array
m <- 5  # dimension of covariance matrices
M <- array(0,c(m,m,2))
for (i in 1:2) {
  y0 <- rnorm(m)
  aux <- diag(m) + y0 %*% t(y0)
  M[,i] <- aux
}
A <- M[,1]
B <- M[,2]
frobDist <- dist4cov(A=A, B=B, optns=list(metric="frobenius"))
```

Description

$L^2$ Wasserstein distance between two distributions.
Usage

dist4den(d1 = NULL, d2 = NULL, fctn_type = NULL, optns = list())

Arguments

d1, d2  Lists holding the density functions or quantile functions of the two distributions. Each list consists of two numeric vectors x and y of the same length, where x holds the support grid and y holds the values of the function. Note that the type of functions representing the distributions in d1 and d2 should be the same—either both are density functions, or both are quantile functions. If both are quantile functions, all elements in d1$x and d2$x must be between 0 and 1. d1$x and d2$x may have different lengths.

fctn_type  Character vector of length 1 holding the function type in d1 and d2 representing the distributions: "density" (default), "quantile".

optns  A list of control parameters specified by list(name=value).

Details

Available control options are:

**nqSup** A scalar giving the length of the support grid of quantile functions based on which the \(L^2\) Wasserstein distance (i.e., the \(L^2\) distance between the quantile functions) is computed. Default is 201.

Value

A scalar holding the \(L^2\) Wasserstein distance between d1 and d2.

Examples

d1 <- list(x = seq(-6,6,0.01))
d1$y <- dnorm(d1$x)
d2 <- list(x = d1$x + 1)
d2$y <- dnorm(d2$x, mean = 1)
dist <- dist4den(d1 = d1, d2 = d2)

frechet

frechet: Statistical Analysis for Random Objects and Non-Euclidean Data

Description

Provides implementation of statistical methods for random objects lying in various metric spaces, which are not necessarily linear spaces. The core of this package is Fréchet regression for random objects with Euclidean predictors, which allows one to perform regression analysis for non-Euclidean responses under some mild conditions. Examples include distributions in \(L^2\)-Wasserstein space, covariance matrices endowed with power metric (with Frobenius metric as a special case), Cholesky and log-Cholesky metrics. References: Petersen, A., & Müller, H.-G. (2019) <doi:10.1214/17-AOS1624>.
Global Fréchet regression of covariance matrices

Description

Global Fréchet regression of covariance matrices with Euclidean predictors.

Usage

```r
GloCovReg(x, y = NULL, M = NULL, xout, optns = list())
```

Arguments

- `x`: An n by p matrix of predictors.
- `y`: An n by l matrix, each row corresponds to an observation, l is the length of time points where the responses are observed. See 'metric' option in 'Details' for more details.
- `M`: A q by q by n array (resp. a list of q by q matrices) where M[,,i] (resp. M[[i]]) contains the i-th covariance matrix of dimension q by q. See 'metric' option in 'Details' for more details.
- `xout`: An m by p matrix of output predictor levels.
- `optns`: A list of options control parameters specified by list(name=value). See ‘Details’.

Details

Available control options are

- **corrOut**: Boolean indicating if output is shown as correlation or covariance matrix. Default is FALSE and corresponds to a covariance matrix.
- **metric**: Metric type choice, "frobenius", "power", "log_cholesky", "cholesky" - default: "frobenius" which corresponds to the power metric with alpha equal to 1. For power (and Frobenius) metrics, either y or M must be input; y would override M. For Cholesky and log-Cholesky metrics, M must be input and y does not apply.
- **alpha**: The power parameter for the power metric. Default is 1 which corresponds to Frobenius metric.

Value

A covReg object — a list containing the following fields:

- `xout`: An m by p matrix of output predictor levels.
- `Mout`: A list of estimated conditional covariance or correlation matrices at xout.
- `optns`: A list containing the optns parameters utilized.
GloDenReg

References


Examples

```r
#Example y input
n=50  # sample size
t=seq(0,1,length.out=100)  # length of data
x = matrix(runif(n),n)
theta1 = theta2 = array(0,n)
for(i in 1:n){
  theta1[i] = rnorm(1,x[i],x[i]^2)
  theta2[i] = rnorm(1,x[i]^2/(1-x[i]^2))
}
y = matrix(0,n,length(t))
phi1 = sqrt(3)*t
phi2 = sqrt(6/5)*(1-t/2)
y = theta1%*%t(phi1) + theta2%*%t(phi2)
xout = matrix(c(0.25,0.5,0.75),3)
Cov_est=GloCovReg(x=x,y=y,xout=xout,optns=list(corrOut=FALSE,metric="power",alpha=3))

#Example M input
n=10  #sample size
m=5  # dimension of covariance matrices
M <- array(0,c(m,m,n))
for (i in 1:n){
  y0=rnorm(m)
  aux<-diag(m)+y0%*%t(y0)
  M[,,i]<-aux
}
x=cbind(matrix(rnorm(n),n),matrix(rnorm(n),n))  #vector of predictor values
xout=cbind(runif(3),runif(3))  #output predictor levels
Cov_est=GloCovReg(x=x,M=M,xout=xout,optns=list(corrOut=FALSE,metric="power",alpha=3))
```

GloDenReg

Global density regression.

Description

Global Fréchet regression for densities with respect to $L^2$-Wasserstein distance.
Usage

GloDenReg(
    xin = NULL,
    yin = NULL,
    hin = NULL,
    qin = NULL,
    xout = NULL,
    optns = list()
)

Arguments

xin
An n by p matrix or a vector of length n (if p=1) with input measurements of the
predictors.

yin
A matrix or list holding the sample of observations of the response. If yin is a
matrix, each row holds the observations of the response corresponding to a row
in xin.

hin
A list holding the histograms of the response corresponding to each row in xin.

qin
A matrix or list holding the quantile functions of the response. If qin is a
matrix, each row holds the quantile function of the response taking values on
optns$qSup corresponding to a row in xin. Note that only one of the three yin,
hin, and qin needs to be input. If more than one of them are specified, yin
overwrites hin, and hin overwrites qin.

xout
A k by p matrix or a vector of length k (if p=1) with output measurements of the
predictors. Default is xin.

optns
A list of control parameters specified by list(name=value).

Details

Available control options are qSup, nqSup, lower, upper, Rsquared, bwDen, ndSup, dSup, delta,
kernelDen, infSupport, and denLowerThreshold. Rsquared is explained as follows and see
LocDenReg for the other options.

Rsquared A logical variable indicating whether R squared would be returned. Default is FALSE.

Value

A list containing the following components:

xout
Input xout.

dout
A matrix or list holding the output densities corresponding to xout. If dout is a
matrix, each row gives a density and the domain grid is given in dSup. If dout is
a list, each element is a list of two components, x and y, giving the domain grid
and density function values, respectively.

dSup
A numeric vector giving the domain grid of dout when it is a matrix.

qout
A matrix holding the quantile functions of the output densities. Each row corre-
ponds to a value in xout.
**LocCovReg**

**Local Fréchet regression of covariance matrices**

Description

Local Fréchet regression of covariance matrices with Euclidean predictors.

Usage

 LocCovReg(x, y = NULL, M = NULL, xout, optns = list())

Arguments

- **x**
  - An n by p matrix of predictors.

- **y**
  - An n by l matrix, each row corresponds to an observation, l is the length of time points where the responses are observed. See 'metric' option in 'Details' for more details.

References


Examples

```r
xin = seq(0,1,0.05)
yin = lapply(xin, function(x) {rnorm(100, rnorm(1,x,0.005), 0.05)})
qSup = seq(0,1,0.02)
xout = seq(0,1,0.25)
res1 <- GloDenReg(xin=xin, yin=yin, xout=xout, optns = list(qSup = qSup))
plot(res1)

hin = lapply(yin, function(y) hist(y, breaks = 50, plot=FALSE))
res2 <- GloDenReg(xin=xin, hin=hin, xout=xout, optns = list(qSup = qSup))
plot(res2)
```
\( \mathbf{M} \)  A \( q \times q \times n \) array (resp. a list of \( q \times q \) matrices) where \( \mathbf{M}[,,i] \) (resp. \( \mathbf{M}[i] \)) contains the \( i \)-th covariance matrix of dimension \( q \times q \). See 'metric' option in 'Details' for more details.

\( \mathbf{xout} \)  An \( m \times p \) matrix of output predictor levels.

\( \text{optns} \)  A list of options control parameters specified by \( \text{list}(\text{name}=\text{value}) \). See 'Details'.

Details

Available control options are

- \( \text{corrOut} \)  Boolean indicating if output is shown as correlation or covariance matrix. Default is FALSE and corresponds to a covariance matrix.

- \( \text{metric} \)  Metric type choice, "frobenius", "power", "log_cholesky", "cholesky" - default: "frobenius" which corresponds to the power metric with \( \alpha \) equal to 1. For power (and Frobenius) metrics, either \( y \) or \( \mathbf{M} \) must be input; \( y \) would override \( \mathbf{M} \). For Cholesky and log-Cholesky metrics, \( \mathbf{M} \) must be input and \( y \) does not apply.

- \( \alpha \)  The power parameter for the power metric. Default is 1 which corresponds to Frobenius metric.

- \( \text{bwMean} \)  A vector of length \( p \) holding the bandwidths for conditional mean estimation if \( y \) is provided. If \( \text{bwMean} \) is not provided, it is chosen by cross validation.

- \( \text{bwCov} \)  A vector of length \( p \) holding the bandwidths for conditional covariance estimation. If \( \text{bwCov} \) is not provided, it is chosen by cross validation.

- \( \text{kernel} \)  Name of the kernel function to be chosen from "rect", "gauss", "epan", "gausvar", "quar". Default is "gauss".

Value

A \( \text{covReg} \) object — a list containing the following fields:

- \( \mathbf{xout} \)  An \( m \times p \) matrix of output predictor levels.

- \( \mathbf{Mout} \)  A list of estimated conditional covariance or correlation matrices at \( \mathbf{xout} \).

- \( \text{optns} \)  A list containing the \( \text{optns} \) parameters utilized.

References


**Examples**

```r
#Example y input
n=30  # sample size
t=seq(0,1,length.out=100) # length of data
x = matrix(runif(n),n)
theta1 = theta2 = array(0,n)
for(i in 1:n){
  theta1[i] = rnorm(1,x[i],x[i]^2)
  theta2[i] = rnorm(1,x[i]/2,(1-x[i])^2)
}
y = matrix(0,n,length(t))
phi1 = sqrt(3)*t
phi2 = sqrt(6/5)*(1-t/2)
y = theta1%*%t(phi1) + theta2 %*% t(phi2)
xout = matrix(c(0.25,0.5,0.75),3)
Cov_est=LocCovReg(x=x,y=y,xout=xout,optns=list(corrOut=FALSE,metric="power",alpha=3))
```

```r
#Example M input
n=30  #sample size
m=30  #dimension of covariance matrices
M <- array(0,c(m,m,n))
for (i in 1:n){
y0=rnorm(m)
aux<-15*diag(m)+y0%*%t(y0)
M[,1,i]<-aux
}
x=matrix(rnorm(n),n)
xout = matrix(c(0.25,0.5,0.75),3) #output predictor levels
Cov_est=LocCovReg(x=x,M=M,xout=xout,optns=list(corrOut=FALSE,metric="power",alpha=0))
```

---

**LocDenReg**

*Local density regression.*

**Description**

Local Fréchet regression for densities with respect to $L^2$-Wasserstein distance.

**Usage**

```r
LocDenReg(
    xin = NULL,
    yin = NULL,
    hin = NULL,
    qin = NULL,
    xout = NULL,
    optns = list()
)
```
Arguments

xin  An n by p matrix or a vector of length n if p=1 holding the n observations of the predictor.

yin  A matrix or list holding the sample of observations of the response. If yin is a matrix, each row holds the observations of the response corresponding to a predictor value in the corresponding row of xin.

hin  A list holding the histograms of the response corresponding to each predictor value in the corresponding row of xin.

qin  A matrix or list holding the quantile functions of the response. If qin is a matrix, the support of the quantile functions should be the same (i.e., optns$qSup), and each row of qin holds the quantile function corresponding to a predictor value in the corresponding row of xin. If the quantile functions are evaluated on different grids, then qin should be a list, each element consisting of two components x and y holding the support grid and the corresponding values of the quantile functions, respectively. Note that only one of the three yin, hin, and qin needs to be input. If more than one of them are specified, yin overwrites hin, and hin overwrites qin.

xout An m by p matrix or a vector of length m if p=1 holding the m output predictor values. Default is xin.

optns A list of control parameters specified by list(name=value). See ‘Details’.

Details

Available control options are

bwReg A vector of length p used as the bandwidth for the Fréchet regression or "CV" (default), i.e., a data-adaptive selection done by cross-validation.

kernelReg A character holding the type of kernel functions for local Fréchet regression for densities; "rect", "gauss", "epan", "gausvar", "quar" - default: "gauss".

qSup A numeric vector holding the grid on [0,1] quantile functions take value on. Default is an equidistant grid.

nqSup A scalar giving the length of qSup. Default is 201.

lower A scalar with the lower bound of the distribution. Default is NULL.

upper A scalar with the upper bound of the distribution. Default is NULL.

bwRange A 2 by p matrix whose columns contain the bandwidth selection range for each corresponding dimension of the predictor xin for the case when bwReg equals "CV". Default is NULL and is automatically chosen by a data-adaptive method.

bwDen The bandwidth value used in CreateDensity() for density estimation; positive numeric - default: determine automatically based on the data-driven bandwidth selector proposed by Sheather and Jones (1991).

ndSup The number of support points the kernel density estimation uses in CreateDensity(); numeric - default: 101.

dSup User defined output grid for the support of kernel density estimation used in CreateDensity(), it overrides nRegGrid; numeric - default: NULL
**LocDenReg**

**delta**  The size of the bin to be used used in `CreateDensity()`; numeric - default: `diff(range(y))/1000`. It only works when the raw sample is available.

**kernelDen**  A character holding the type of kernel functions used in `CreateDensity()` for density estimation; "rect", "gauss", "epan", "gausvar", "quar" - default: "gauss".

**infSupport**  logical if we expect the distribution to have infinite support or not, used in `CreateDensity()` for density estimation; logical - default: FALSE

**denLowerThreshold**  FALSE or a positive value giving the lower threshold of the densities used in `CreateDensity()`; default: `0.001 * mean(qin[,ncol(qin)] - qin[,1])`.

**Value**

A list containing the following components:

- **xout**  Input `xout`.
- **dout**  A matrix or list holding the output densities corresponding to `xout`. If `dout` is a matrix, each row gives a density and the domain grid is given in `dSup`. If `dout` is a list, each element is a list of two components, `x` and `y`, giving the domain grid and density function values, respectively.
- **dSup**  A numeric vector giving the domain grid of `dout` when it is a matrix.
- **qout**  A matrix holding the quantile functions of the output densities. Each row corresponds to a value in `xout`.
- **qSup**  A numeric vector giving the domain grid of `qout`.
- **xin**  Input `xin`.
- **din**  Densities corresponding to the input `yin`, `hin` or `qin`.
- **qin**  Quantile functions corresponding to the input `yin`, `hin` or `qin`.
- **optns**  A list of control options used.

**References**


**Examples**

```r
xin = seq(0,1,0.05)
yin = lapply(xin, function(x) {
  rnorm(100, rnorm(1,x + x^2,0.005), 0.05)
})
qSup = seq(0,1,0.02)
xout = seq(0,1,0.1)
res1 <- LocDenReg(xin=xin, yin=yin, xout=xout, optns = list(bwReg = 0.12, qSup = qSup))
plot(res1)

xout <- xin
hin = lapply(yin, function(y) hist(y, breaks = 50))
res2 <- LocDenReg(xin=xin, hin=hin, xout=xout, optns = list(qSup = qSup))
plot(res2)
```
Description

Plots for Fréchet regression for univariate densities.

Usage

## S3 method for class 'denReg'
plot(
  x,
  obj = NULL,
  prob = NULL,
  xlab = NULL,
  ylab = NULL,
  main = NULL,
  ylim = NULL,
  xlim = NULL,
  col.bar = TRUE,
  widrt = 4,
  col.lab = NULL,
  nticks = 5,
  ticks = NULL,
  add = FALSE,
  pos.prob = 0.9,
  colPalette = NULL,
  ...
)

Arguments

x          A denReg object, result of DenFMean, GloDenReg or LocDenReg.
obj        An integer indicating which output to be plotted; 1, 2, 3, 4, and 5 for dout, qout, din, qin, and reference chart for qout, respectively - default: 1.
prob       A vector specifying the probability levels for reference chart if obj is set to 5. Default: c(0.05, 0.25, 0.5, 0.75, 0.95).
xlab       Character holding the label for x-axis; default: "Probability" when obj is 2 or 4, "" when obj is 1 or 3, "x" when obj is 5.
ylab       Character holding the label for y-axis; default: "Quantile" when obj is 2, 4, or 5, and "Density" when obj is 1 or 3.
main       Character holding the plot title; default: NULL.
ylim       A numeric vector of length 2 holding the range of the y-axis to be drawn; default: automatically determined by the input x.
plot.denReg

xlim A numeric vector of length 2 holding the range of the x-axis to be drawn; default: automatically determined by the input x.

col.bar A logical variable indicating whether a color bar is presented on the right of the plot - default: TRUE.

widrt A scalar giving the width ratio between the main plot and the color bar - default: 4.

col.lab A character giving the color bar label.

nticks An integer giving the number of ticks used in the axis of color bar.

ticks A numeric vector giving the locations of ticks used in the axis of color bar; it overrides nticks.

add Logical; only works when obj is 5. If TRUE add to an already existing plot. Taken as FALSE (with a warning if a different value is supplied) if no graphics device is open.

pos.prob FALSE or a scalar less than 0 or larger than 1. FALSE: no probability levels will be labeled on the quantile curves; a scalar between 0 and 1: indicating where to put the probability levels along the curves on growth charts: 0 and 1 correspond to left and right ends, respectively. Default: 0.9.

colPalette A function that takes an integer argument (the required number of colors) and returns a character vector of colors interpolating the given sequence (e.g., heat.colors, terrain.colors and functions created by colorRampPalette). Default is colorRampPalette(colors = c("pink","royalblue")) for more than one curves and "black" otherwise.

... Can set up lty, lwd, etc.

Value

No return value.

Note

see DenFMean, GloDenReg and LocDenReg for example code.
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