

# Package ‘edrGraphicalTools’

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**Title** Provides tools for dimension reduction methods

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**Description** This package comes to illustrate the articles “A graphical tool for selecting the number of slices and the dimension of the model in SIR and SAVE approaches” and “Comparison of sliced inverse regression approaches for underdetermined cases”

**License** GPL (>= 2.0)

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edrGraphicalTools-package

*Provides graphical tools for dimension reduction methods*

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## Description

This package illustrates the articles listed below. It estimates by bootstrap a squared trace correlation criterion which measures the quality of the estimation of the effective dimension reduction (EDR) space. It also contains functions to perform such an estimation when the sample size is smaller than the number of explanatory variables. Methods to select the relevant explanatory variables are also included.

## Details

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## Author(s)

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## References

Liquet, B. and Saracco, J. (2012). A graphical tool for selecting the number of slices and the dimension of the model in SIR and SAVE approaches. *Computational Statistics*, 27(1), 103-125.

Coudret, R., Liquet, B. and Saracco, J. Comparison of sliced inverse regression approaches for underdetermined cases. *Journal de la Société Française de Statistique*, in press.

## See Also

[criterionRkh](#), [edr](#), [plot.criterionRkh](#), [edrSelec](#), [edrUnderdet](#)

## Examples

```
## Sample generation
set.seed(10)
n <- 500
```

```

p <- 10
beta <- c(1,rep(0,p-1))
X <- rmvnorm(n,sigma=diag(p))
eps <- rnorm(n)
Y <- (X%*%beta)**3+eps*((X%*%beta)**2)

## Determining optimal values for H and K
grid.H <- c(2,5,10,15,20)
grid.K <- 1:p
res1 <- criterionRkh(Y,X,H=grid.H,K=grid.K,B=50,method="SIR-I")
plot(res1,choice.H=c(2,5),choice.K=c(1,2))
HK <- which(res1$Rkhbootmean[,1:(p-1)] == max(res1$Rkhbootmean[,1:(p-1)]),
arr.ind=TRUE)[1,]
H <- grid.H[HK[1]]
K <- grid.K[HK[2]]

## Selecting relevant variables in X
if (K==1) {
res2 <- edrSelec(Y, X, H, K, "CSS", pZero=p/2, NZero=200, zeta=0.05)
dev.new()
plot(res2)
if (1 %in% which(res2$scoreVar == max(res2$scoreVar))) {
message("The first variable is selected, as it should be.")
} else {
message("The variable selection failed.")
}
} else {
message("The choice of K failed.")
}
}

```

---

criterionRkh

*Estimation of the Rkh criterion by bootstrap method*


---

## Description

This is the main function in the `edrGraphicalTools` package. This function estimates the square trace correlation criterion  $R_{kh}$  by bootstrap in order to simultaneously choose the number  $H$  of slices and the dimension  $K$  of the EDR space reduction. It creates objects of class `criterionRkh`. Several helper functions that require a `criterionRkh` object can then be applied to the output from this function.

## Usage

```
criterionRkh(Y, X, H, K, indices, B = 50, method)
```

**Arguments**

Y	A numeric vector representing the dependent variable (a response vector).
X	A matrix representing the quantitative explanatory variables (bind by column).
H	An integer vector representing the different number of slices to be investigated. By default H takes integer values in 2, 3, . . . , round(n/4); n is the sample size.
K	An integer vector representing the different dimension K to be investigated. By default K takes integer values in 1, 2, . . . , min(p, 25); p is the number of explanatory variables.
indices	An optional integer vector specifying the indices of the bootstrap samples. By default, non-parametric resampling is performed. If used, an integer vector of length B*n will be specified; (n is the length of Y).
B	The number of bootstrap replicates. By default B equals 50.
method	This character string specifies the method of fitting. The options include "SIR-I", "SIR-II", and "SAVE".

**Details**

We are interested in the following semiparametric dimension reduction model proposed by Li (1991)

$$y = f(b_1'x, b_2'x, \dots, b_K'x, e)$$

where the univariate response variable  $y$  is associated with the  $p$ -dimensional regressor  $p$  only through the reduced  $K$ -dimensional variable  $(b_1'x, b_2'x, \dots, b_K'x)$  with  $K < p$ . The error term  $e$  is independent of  $x$ . The link function  $f$  and the  $b$ -vectors are unknown. We are interested in finding the linear subspace spanned by the  $K$  unknown  $b$ -vector, called the effective dimension reduction (EDR) space. We focus on the SIR (named SIR-I), SIR-II and SAVE methods to estimate the EDR space. The slicing step of these methods depends on the number  $H$  of slices. We propose a naive bootstrap estimation of the square trace correlation criterion to allow selection of an “optimal” number of slices and to simultaneously select the corresponding suitable dimension  $K$  (number of the linear combinations of  $x$ ).

**Value**

criterionRkh returns an object of class criterionRkh (the name of the type is the value of the method argument), with attributes:

Rkhbootmean	A matrix corresponding of the estimation by bootstrap of the square trace criterion Rkh (h in rows and k in columns).
Rkhboot	A list including the result of the estimation of the square trace criterion for each bootstrap replicate.
method	the dimension reduction method used.
n	Number of subject.
H	A vector representing the different numbers H of slices investigated.
K	A vector representing the different dimensions K investigated.
indices	An vector of integers representing the indices of the bootstrap sample used.

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**References**

Liquet, B. and Saracco, J. (2012). A graphical tool for selecting the number of slices and the dimension of the model in SIR and SAVE approaches. *Computational Statistics*, 27(1), 103-125.

Li, K.C. (1991). Sliced inverse regression for dimension reduction, with discussions. *Journal of the American Statistical Association* 86, 316-342.

Cook, R. D. and Weisberg, S. (1991). Discussion of “Sliced inverse regression”. *Journal of the American Statistical Association*, 86, 328-332.

**See Also**

[edr](#), [summary.criterionRkh](#), [plot.criterionRkh](#)

**Examples**

```
## simulated example 1
set.seed(10)
n <- 500
beta <- c(1,rep(0,9))
X <- rmvnorm(n,sigma=diag(10))
eps <- rnorm(n)
Y <- (X%*%beta)**3+eps*((X%*%beta)**2)
## Choice a grid of values for H
grid.H <- c(2,5,10,15,20,30)
res1 <- criterionRkh(Y,X,H=grid.H,B=50,method="SIR-I")
res1
plot(res1,choice.H=c(2,5),choice.K=c(1,2))
## Estimation for SIR-II method with the same bootstrap replicate than for SIR-I
res2 <- criterionRkh(Y,X,H=grid.H,indices=res1$indices,B=50,method="SIR-II")
res2
```

---

edr

*Main function for estimation of the EDR space*


---

**Description**

It creates objects of class `edr` to estimate the effective dimension regression (EDR) space. Several helper functions that require an `edr` object can then be applied to the output from this function.

**Usage**

```
edr(Y, X, H, K, method, submethod="SIR-QZ", ...)
```

**Arguments**

Y	A numeric vector representing the dependent variable (a response vector).
X	A matrix representing the quantitative explanatory variables (bind by column).
H	The chosen number of slices.
K	The chosen dimension K.
method	This character string specifies the method of fitting. The option includes "SIR-I", "SIR-II", and "SAVE".
submethod	This character string specifies the method of fitting when the number of lines of $X$ is greater than its number of columns. It should be either "SIR-QZ", "RSIR" or "SR-SIR".
...	Arguments to be passed to <code>edrUnderdet</code> when the number of lines of $X$ is greater than its number of columns.

**Details**

We are interested in the following semiparametric dimension reduction model proposed by Li (1991)

$$y = f(b_1'x, b_2'x, \dots, b_K'x, e)$$

where the univariate response variable  $y$  is associated with the  $p$ -dimensional regressor  $p$  only through the reduced  $K$ -dimensional variable  $(b_1'x, b_2'x, \dots, b_K'x)$  with  $K < p$ . The error term  $e$  is independent of  $x$ . The link function  $f$  and the  $b$ -vectors are unknown. We are interested in finding the linear subspace spanned by the  $K$  unknown  $b$ -vector, called the effective dimension reduction (EDR) space. We focus on the SIR, SIR-II and SAVE methods to estimate the EDR space. The slicing step of these methods depends on the number  $H$  of slices. We propose with the function `criterionRkh` a naive bootstrap estimation of the square trace correlation criterion to allow selection of an "optimal" number  $H$  of slices and simultaneously the corresponding suitable dimension  $K$  (number of the linear combination of  $x$ ). After choosing an optimal couple  $(H, K)$  for the best estimation method (the square trace correlation criterion closest to one), the EDR space could be estimate with this function. Each method consists in a spectral decomposition of a matrix of interest. The eigenvectors of this matrix associated of the  $K$  largest eigenvalues are EDR directions.

**Value**

`edr` returns an object of class `edr`, with attributes:

matEDR	A matrix corresponding of the eigenvectors of the interest matrix
eigvalEDR	The eigenvalues of the matrix of interest
K	The chosen dimension.
H	The chosen number of slices.
n	Sample size.
method	The dimension reduction method used.
X	The matrix of the quantitative explanatory variables (bind by column).
Y	The numeric vector of the dependent variable (a response vector).

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**References**

Liquet, B. and Saracco, J. (2012). A graphical tool for selecting the number of slices and the dimension of the model in SIR and SAVE approaches. *Computational Statistics*, 27(1), 103-125.

Li, K.C. (1991). Sliced inverse regression for dimension reduction, with discussions. *Journal of the American Statistical Association* 86, 316-342.

Cook, R. D. and Weisberg, S. (1991). Discussion of “Sliced inverse regression”. *Journal of the American Statistical Association*, 86, 328-332.

**See Also**

[criterionRkh](#), [summary.edr](#), [plot.edr](#)

**Examples**

```
set.seed(10)
n <- 500
beta1 <- c(1,1,rep(0,8))
beta2 <- c(0,0,1,1,rep(0,6))
X <- rmvnorm(n,sigma=diag(1,10))
eps <- rnorm(n)
Y <- (X%*%beta1)**2+(X%*%beta2)**2+eps

## Estimation of the trace square criterion
## grid.H <- c(2,5,10,15,20,30)
## res2 <- criterionRkh(Y,X,H=grid.H,B=50,method="SIR-II")
## summary(res2)
## plot(res2)

## Estimation of the EDR direction for K=2 and H=2 and SIR-II method
edr2 <- edr(Y,X,H=2,K=2,method="SIR-II")
summary(edr2)
plot(edr2)
```

---

edrSelec

---

*Variable selection based on sliced inverse regression*


---

**Description**

Gathers several procedures to determine which explanatory variables have an effect on a dependent variable. Works whether there are more explanatory variables than observations or not. Creates an object of class `edrSelec`.

**Usage**

```
edrSelec(Y, X, H, K, method, pZero=NULL, NZero=NULL, zeta=NULL,
         rho=NULL, baseEst=NULL, btspSamp=NULL, lassoParam=NULL)
```

**Arguments**

Y	A numeric vector representing the dependent variable (a response vector).
X	A matrix representing the quantitative explanatory variables (bind by column).
H	When method="SR-SIR" or method="RSIR", the chosen number of slices. When method="CSS", a vector with various numbers of slices.
K	The chosen dimension K.
method	This character string specifies the selection method. It should be either "CSS", "RSIR" or "SR-SIR".
pZero	When method="CSS", the number of variables to pick when creating a sub-model.
NZero	When method="CSS", the number of submodels to create.
zeta	When method="CSS", the proportion of 'best' submodels selected from the NZero submodels.
rho	When method="CSS", and if zeta is not provided, the threshold above which a submodel is considered as 'best'. It must be a real in ]0,1[.
baseEst	An initial estimate of the EDR space on which each method relies.
btspSamp	When method="RSIR", the bootstrap sample size for estimating the asymptotic distribution of the estimated EDR directions.
lassoParam	When method="SR-SIR", a vector of lasso parameters from which the optimal one is chosen, using the RIC criterion.

**Details**

The "CSS" method builds NZero submodels using only pZero explanatory variables. It estimates the indices for each of them. The squared correlation between these indices and those found with the whole set of explanatory variables is computed. Only the submodels with the highest squared correlation are kept. The method then counts how many times each explanatory variable appears in these 'best' submodels. The "RSIR" procedure uses an asymptotic test on each element of the estimated EDR directions. It was translated from a Matlab code made by Peng Zeng. The "SR-SIR" procedure relies on a lasso penalty. The underlying parameter is chosen using the residual information criterion (RIC). It was written using a R code made by Lexin Li. See also <http://www4.stat.ncsu.edu/~li/software.html>.

**Value**

edrSelec returns an object of class `edrSelec`, with some of the following attributes, depending on the value of method:

scoreVar	A numeric vector filled with a score for each explanatory variable. Variables that have a high score should be kept. For the "CSS" method, the score is the
----------	---

	presence of the variable in the 'best' submodels. For "RSIR", it is one minus the p-value of the test. For the "SR-SIR" procedure, it is a boolean that indicates if the variable should be kept when using the optimal lasso parameter.
K	The chosen dimension.
H	The chosen number(s) of slices.
n	The sample size.
method	The variable selection method used.
X	The matrix of the quantitative explanatory variables (bind by column).
Y	The numeric vector of the dependent variable (a response vector).
matModels	A NZero x pZero matrix that contains the variables of each created submodel, for the "CSS" method.
matModTop	A matrix with pZero columns made of the variables of each 'best' submodel, for the "CSS" method.
vectSqCor	A vector containing the squared correlation between indices for each submodel, for the "CSS" method.
aic	A vector made of values of the Akaike information criterion for every lasso parameter considered by the "SR-SIR" procedure.
bic	A vector made of values of the Bayesian information criterion for every lasso parameter considered by the "SR-SIR" procedure.
ric	A vector made of values of the residual information criterion for every lasso parameter considered by the "SR-SIR" procedure.
matEDR	A list which gives, for each lasso parameter studied with the "SR-SIR" procedure, a matrix spanning the estimated EDR space.

### Author(s)

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### References

- Coudret, R., Liquet, B. and Saracco, J. Comparison of sliced inverse regression approaches for underdetermined cases. *Journal de la Société Française de Statistique*, in press.
- Li, L. and Yin, X. (2008). Sliced inverse regression with regularizations. *Biometrics*, 64(1):124-131.
- Zhong, W., Zeng, P., Ma, P., Liu, J. S., and Zhu, Y. (2005). RSIR: regularized sliced inverse regression for motif discovery. *Bioinformatics*, 21(22):4169-4175.

### See Also

[edr](#), [edrUnderdet](#)

**Examples**

```

n <- 100
p <- 110
K <- 1
H <- 5:12
NZero <- 1000
pZero <- 10
zeta <- 0.1
beta <- c(1,1,1,1,rep(0,p-4))
U <- matrix(runif(p^2,-0.05,0.05),ncol=p)
X <- rmvnorm(n,sigma=diag(p) + U %*% t(U))
eps <- rnorm(n,sd=10)
Y <- (X%*%beta)^3+eps
result <- edrSelec(Y,X,H,K,"CSS",NZero=NZero, pZero=pZero, zeta=zeta)
summary(result)
plot(result)

```

---

edrUnderdet

*EDR space estimation for underdetermined cases.*


---

**Description**

Gathers several procedures to estimate the effective dimension regression (EDR) space when the number of explanatory variables is greater than the sample size. Creates an object of class `edr`.

**Usage**

```

edrUnderdet(Y, X, H, K, method, initEDR=NULL, maxIter=NULL,
  regulParam=NULL, sMin=1e-16, sChg=10, btspSamp=NULL)

```

**Arguments**

Y	A numeric vector representing the dependent variable (a response vector).
X	A matrix representing the quantitative explanatory variables (bind by column).
H	When <code>method="SR-SIR"</code> or <code>method="RSIR"</code> , the chosen number of slices. When <code>method="SIR-QZ"</code> , a vector with various numbers of slices.
K	The chosen dimension $K$ .
method	This character string specifies the method of fitting. It should be either "SIR-QZ", "RSIR" or "SR-SIR".
initEDR	When <code>method="SR-SIR"</code> , a $p \times K$ matrix which contains initial values for the iterative algorithm that estimates EDR directions.
maxIter	When <code>method="SR-SIR"</code> , a maximum number of iterations after which the algorithm stops.
regulParam	When <code>method="SR-SIR"</code> or <code>method="RSIR"</code> , a vector containing possible values of the regularization parameter, from which the optimal one will be chosen.

sMin	When method="SIR-QZ", the smallest regularization parameter to test.
sChg	When method="SIR-QZ", a positive real by which a regularization parameter is multiplied to produce the next one to consider.
btspSamp	When method="RSIR", the bootstrap sample size for estimating the mean squared error.

### Details

The "SIR-QZ" method estimates the indices rather than the EDR directions. It makes use of several estimations from several numbers of slices. It tries to find a minimal regularization of the covariance matrix of  $X$ . The "RSIR" procedure uses a bootstrap estimator of the mean squared error of regularized estimates of the EDR directions. It was translated from a Matlab code made by Peng Zeng. The "SR-SIR" procedure relies on a generalized cross-validation criterion and on an alternating least squares algorithm to find an optimal regularization parameter. It was written using a R code made by Lexin Li. See also <http://www4.stat.ncsu.edu/~li/software.html>.

### Value

edrUnderdet returns an object of class `edr`, with some of the following attributes, depending on the value of `method`:

matEDR	A matrix spanning the estimated EDR space.
indices	The estimated indices from the "SIR-QZ" method.
eigvalEDR	The eigenvalues of a matrix of interest.
K	The chosen dimension.
H	The chosen number(s) of slices.
n	The sample size.
method	The dimension reduction method used.
X	The matrix of the quantitative explanatory variables (bind by column).
Y	The numeric vector of the dependent variable (a response vector).
s	The optimal regularization parameter(s) found by the chosen method.
estMSE	For each tested regularization parameter, the estimated mean squared error from the "RSIR" method.
testedEDR	For each tested regularization parameter, a matrix spanning the estimated EDR space from the "SR-SIR" method.
iter	For each tested regularization parameter, the number of iterations needed for the alternating least squares algorithm from the "SR-SIR" method to converge.
gcv	For each tested regularization parameter, the corresponding generalized cross-validation criterion from the "SR-SIR" method.

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## References

- Coudret, R., Liquet, B. and Saracco, J. Comparison of sliced inverse regression approaches for underdetermined cases. *Journal de la Société Française de Statistique*, in press.
- Li, L. and Yin, X. (2008). Sliced inverse regression with regularizations. *Biometrics*, 64(1):124-131.
- Zhong, W., Zeng, P., Ma, P., Liu, J. S., and Zhu, Y. (2005). RSIR: regularized sliced inverse regression for motif discovery. *Bioinformatics*, 21(22):4169-4175.

## See Also

[edr](#), [sliceMat](#)

## Examples

```
n <- 100
p <- 200
K <- 2
H <- 3:8
beta1 <- c(1,1,1,1,rep(0,p-4))
beta2 <- c(rep(0,p-4), 1,1,1,1)
X <- rmvnorm(n,sigma=diag(p))
eps <- rnorm(n,sd=10)
Y <- (X%%beta1)^3 + (X%%beta2)^3+eps
result <- edrUnderdet(Y,X,H,K,"SIR-QZ")
summary(result)
plot(result)
```

---

plot.criterionRkh      *Graphical tools for the bootstrap criterion*

---

## Description

We propose a 3D-graphical tool which can be useful to select the suitable couple (H,K). We also add some boxplots of the distribution of the bootstrap criterion.

## Usage

```
## S3 method for class 'criterionRkh'
plot(x, choice.H, choice.K, ...)
```

**Arguments**

x	The name of an object of class <code>critereionRkh</code> .
choice.H	An optional integer vector specifying the values of H for which a boxplot of the distribution of the bootstrap criterion is plotted for all the values of K specified in the <code>critereionRkh</code> object. The values of <code>choice.H</code> must be included in the values of H specified in the <code>critereionRkh</code> object.
choice.K	An optional integer vector specifying the values of K for which a boxplot of the distribution of the bootstrap criterion is plotted for all the values of H specified in the <code>critereionRkh</code> object. The values of <code>choice.K</code> must be included in the values of K specified in the <code>critereionRkh</code> object.
...	Some methods for this generic require additional arguments. None are used in this method.

**Value**

Returns graphs.

**Author(s)**

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**References**

Liquet, B. and Saracco, J. (2012). A graphical tool for selecting the number of slices and the dimension of the model in SIR and SAVE approaches. *Computational Statistics*, 27(1), 103-125.

**See Also**

[critereionRkh](#)

**Examples**

```
## see example in function critereionRkh
```

---

plot.edr

*Basic plot of an edr object*

---

**Description**

For an edr object with attributes  $K \leq 2$ , this function plots the response  $y$  versus each new estimate indice with an estimation of the link function. For  $K = 2$ , a 3D plot of  $y$  versus the two estimate indices is represented. A smooth estimate of the link function is also represented. For  $K > 2$ , the `pairs` function is used.

**Usage**

```
## S3 method for class 'edr'
plot(x, ...)
```

**Arguments**

x	The name of an object of class <code>edr</code> .
...	Some methods for this generic require additional arguments. None are used in this method.

**Value**

Returns graphs.

**Author(s)**

Benoît Liquet, <benoit.liquet@isped.u-bordeaux2.fr> and Jérôme Saracco <jerome.saracco@math.u-bordeaux1.fr>

**See Also**

[summary.edr](#)

**Examples**

```
## simulated example
set.seed(10)
n <- 500
beta1 <- c(1,1,rep(0,8))
beta2 <- c(0,0,1,1,rep(0,6))
X <- rmvnorm(n,sigma=diag(1,10))
eps <- rnorm(n)
Y <- (X%*%beta1)**2+(X%*%beta2)**2+eps
edr2 <- edr(Y,X,H=2,K=2,method="SIR-II")
plot(edr2)
## edr4 <- edr(Y,X,H=2,K=4,method="SIR-II")
## plot(edr4)
```

---

plot.edrSelec

*Displaying methods for the class 'edrSelec'*

---

**Description**

Methods to present the results of a variable selection procedure based on slice inverse regression.

**Usage**

```
## S3 method for class 'edrSelec'
print(x, ...)
## S3 method for class 'edrSelec'
summary(object, nVar=5, ...)
## S3 method for class 'edrSelec'
plot(x, nVar=25, ...)
```

**Arguments**

x	An object of class <code>edrSelec</code> generated by the function <a href="#">edrSelec</a> .
object	An object of class <code>edrSelec</code> generated by the function <a href="#">edrSelec</a> .
nVar	If <code>nVar!=NULL</code> , the method will only show the <code>nVar</code> most important variables with respect to the criterion computed by the function <a href="#">edrSelec</a> . Not implemented for the summary method when executed with a "SR-SIR" procedure.
...	Other unused parameters.

**Value**

These methods display (with a text or a graphic) the score of each considered variable. The user should keep the variables with a high score.

**Author(s)**

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**See Also**

[edrSelec](#), [edrUnderdet](#), [edr](#)

**Examples**

```
## see the example of the function edrSelec.
```

---

print.criterionRkh      *Print a Summary of a criterionRkh Object*

---

**Description**

This is a method for the function `print` for objects of the class `criterionRkh`.

**Usage**

```
## S3 method for class 'criterionRkh'
print(x, ...)
```

**Arguments**

- x An object of class `criterionRkh` generated by the function `criterionRkh`.
- ... Further arguments passed to or from other methods.

**Value**

A summary of the `criterionRkh` Object is returned.

**Author(s)**

Benoît Liquet, <benoit.liquet@isped.u-bordeaux2.fr> and Jérôme Saracco <jerome.saracco@math.u-bordeaux1.fr>

**See Also**

[criterionRkh](#)

---

print.edr

*Print a Summary of an edr Object*

---

**Description**

This is a method for the function `print` for objects of the class `edr`.

**Usage**

```
## S3 method for class 'edr'  
print(x, ...)
```

**Arguments**

- x An object of class `edr` generated by the function `edr`.
- ... Further arguments to be passed to or from other methods. They are ignored in this function

**Value**

A summary of the `edr` Object is returned.

**Author(s)**

Benoît Liquet, <benoit.liquet@isped.u-bordeaux2.fr> and Jérôme Saracco <jerome.saracco@math.u-bordeaux1.fr>

**See Also**

[edr](#)

---

sliceMat	<i>Slicing matrix computation</i>
----------	-----------------------------------

---

**Description**

Returns the slicing matrix required for the "SIR-I" method.

**Usage**

```
sliceMat(Y, X, H, details=FALSE, rdSup=FALSE)
```

**Arguments**

Y	A numeric vector representing the dependent variable (a response vector).
X	A matrix representing the quantitative explanatory variables (bind by column).
H	The chosen number of slices.
details	A boolean that determines whether or not some matrices used to construct the slicing matrix should be sent back. See also 'Value'.
rdSup	When the number of slices is not a divisor of the sample size, this boolean determines whether or not the slices which contain an extra point are randomly chosen.

**Details**

This function divides the range of  $Y$  in  $H$  distinct intervals, or slices. It then puts every row of  $X$  into a slice with respect to the corresponding element of  $Y$ . It finally computes a matrix  $M = X'_h P_h X_h$  where each row of  $X_h$  is the mean vector over the vectors of  $X$  that belong to a given slice. The matrix  $P_h$  is diagonal and contains the number of rows of  $X$  placed in each sliced. The matrix  $M$  is required when trying to perform a sliced inverse regression.

**Value**

If `details=FALSE`, the  $p \times p$  slicing matrix  $M$ , where  $p$  is the number of columns of  $X$ .

If `details=TRUE`, a list made of  $M$ ,  $X_h$  and  $P_h$ .

**Author(s)**

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**See Also**

[edr](#), [edrUnderdet](#)

## Examples

```
#The "SIR-I" method without using 'edr'  
n <- 500  
p <- 5  
H <- 10  
beta <- c(1, 1, 1, 0, 0)  
X <- rmvnorm(n,rep(0,p),diag(p))  
eps <- rnorm(n, 0, 10)  
Y <- (X %*% beta)^3 + eps  
M <- sliceMat(Y,X,H)  
hatBeta <- eigen(solve(var(X)) %*% M)$vectors[,1]  
cor(hatBeta,beta)^2
```

---

summary.criterionRkh *Print a Summary of a criterionRkh Object*

---

## Description

This is a method for the function summary for objects of the class criterionRkh.

## Usage

```
## S3 method for class 'criterionRkh'  
summary(object, ...)
```

## Arguments

object            An object of class criterionRkh generated by the function [criterionRkh](#).  
...                Further arguments passed to or from other methods.

## Value

A summary of the criterionRkh Object is returned.

## Author(s)

Benoît Liquet, <benoit.liquet@isped.u-bordeaux2.fr> and Jérôme Saracco <jerome.saracco@math.u-bordeaux1.fr>

## See Also

[criterionRkh](#)

---

`summary.edr`*Print a Summary of an edr Object*

---

**Description**

This is a method for the function `summary` for objects of the class `edr`.

**Usage**

```
## S3 method for class 'edr'  
summary(object, ...)
```

**Arguments**

<code>object</code>	An object of class <code>edr</code> generated by the function <a href="#">edr</a> .
<code>...</code>	further arguments passed to or from other methods.

**Value**

A summary of the `edr` Object is returned.

**Author(s)**

Benoît Liquet, <benoit.liquet@isped.u-bordeaux2.fr> and Jérôme Saracco <jerome.saracco@math.u-bordeaux1.fr>

**See Also**

[edr](#)

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