

# Package ‘msir’

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**Title** Model-Based Sliced Inverse Regression

**Description** An R package for dimension reduction based on finite Gaussian mixture modeling of inverse regression.

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`msir-package`*Model-based Sliced Inverse Regression (MSIR)*

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**Description**

An R package that implements MSIR, a dimension reduction method based on Gaussian finite mixture models. The basis of the subspace is estimated by modeling the inverse distribution within slice using finite mixtures of Gaussians, with number of components and covariance matrix parameterization selected by BIC or defined by the user. The method provides an extension to sliced inverse regression (SIR) and allows to overcome the main limitation of SIR, i.e., the failure in the presence of regression symmetric relationships, without the need to impose further assumptions.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**References**

Scrucca, L. (2011) Model-based SIR for dimension reduction. *Computational Statistics & Data Analysis*, 55(11), 3010-3026.

**See Also**

[msir](#)

---

`loess.sd`*Local Polynomial Regression Fitting with Variability bands*

---

**Description**

Nonparametric estimation of mean function with variability bands.

**Usage**

```
loess.sd(x, y = NULL, nsigma = 1, ...)
```

```
panel.loess(x, y, col = par("col"), bg = NA, pch = par("pch"), cex = 1,  
            col.smooth = "red", span = 2/3, degree = 2, nsigma = 1, ...)
```

**Arguments**

<code>x</code>	a vector of values for the predictor variable $x$ .
<code>y</code>	a vector of values for the response variable $y$ .
<code>nsigma</code>	a multiplier for the standard deviation function.
<code>col, bg, pch, cex</code>	numeric or character codes for the color(s), point type and size of points; see also <a href="#">par</a> .
<code>col.smooth</code>	color to be used by lines for drawing the smooths.
<code>span</code>	smoothing parameter for <a href="#">loess</a> .
<code>degree</code>	the degree of the polynomials to be used, see <a href="#">loess</a> .
<code>...</code>	further argument passed to the function <a href="#">loess</a> .

**Value**

The function `loess.sd` computes the loess smooth for the mean function and the mean plus and minus  $k$  times the standard deviation function.

The function `panel.loess` can be used to add to a scatterplot matrix panel a smoothing of mean function using loess with variability bands at plus and minus  $nsigma$ s times the standard deviation.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**References**

Weisberg, S. (2005) Applied Linear Regression, 3rd ed., Wiley, New York, pp. 275-278.

**See Also**

[loess](#)

**Examples**

```
data(cars)
plot(cars, main = "lowess.sd(cars)")
lines(l <- loess.sd(cars))
lines(l$x, l$upper, lty=2)
lines(l$x, l$lower, lty=2)
```

msir

*Model-based Sliced Inverse Regression (MSIR)***Description**

A dimension reduction method based on Gaussian finite mixture models which provides an extension to sliced inverse regression (SIR). The basis of the subspace is estimated by modeling the inverse distribution within slice using Gaussian finite mixtures with number of components and covariance matrix parameterization selected by BIC or defined by the user.

**Usage**

```
msir(x, y, nslices = msir.nslices, slice.function = msir.slices,
     modelNames = NULL, G = NULL, cov = c("mle", "regularized"), ...)
```

**Arguments**

<code>x</code>	a $(n \times p)$ design matrix containing the predictors data values.									
<code>y</code>	a $(n \times 1)$ vector of data values for the response variable. It can be a numeric vector (regression) but also a factor (classification). In the latter case, the levels of the factor define the slices used.									
<code>nslices</code>	the number of slices used, unless <code>y</code> is a factor. By default the value returned by <code>msir.nslices</code> .									
<code>slice.function</code>	the slice functions to be used, by default <code>msir.slices</code> , but the user can provide a different slicing function.									
<code>modelNames</code>	a vector of character strings indicating the Gaussian mixture models to be fitted as described in <code>mclustModelNames</code> . If a vector of strings is given they are used for all the slices. If a list of vectors is provided then each vector refers to a single slice.									
<code>G</code>	an integer vector specifying the numbers of mixture components used in fitting Gaussian mixture models. If a list of vectors is provided then each vector refers to a single slice.									
<code>cov</code>	The predictors marginal covariance matrix. Possible choices are: <table> <tbody> <tr> <td><code>"mle"</code></td> <td>=</td> <td>maximum likelihood estimate</td> </tr> <tr> <td><code>"regularized"</code></td> <td>=</td> <td>regularized covariance matrix (see <code>msir.regularizedSigma</code>)</td> </tr> <tr> <td><code>R matrix</code></td> <td>=</td> <td>a <math>(p \times p)</math> user defined covariance matrix</td> </tr> </tbody> </table>	<code>"mle"</code>	=	maximum likelihood estimate	<code>"regularized"</code>	=	regularized covariance matrix (see <code>msir.regularizedSigma</code> )	<code>R matrix</code>	=	a $(p \times p)$ user defined covariance matrix
<code>"mle"</code>	=	maximum likelihood estimate								
<code>"regularized"</code>	=	regularized covariance matrix (see <code>msir.regularizedSigma</code> )								
<code>R matrix</code>	=	a $(p \times p)$ user defined covariance matrix								
<code>...</code>	other arguments passed to <code>msir.compute</code> .									

**Value**

Returns an object of class 'msir' with attributes:

<code>call</code>	the function call.
-------------------	--------------------

x	the design matrix.
y	the response vector.
slice.info	output from slicing function.
mixmod	a list of finite mixture model objects as described in <a href="#">mclustModel</a> .
loglik	the log-likelihood for the mixture models.
f	a vector of length equal to the total number of mixture components containing the fraction of observations in each fitted component within slices.
mu	a matrix of component within slices predictors means.
sigma	the marginal predictors covariance matrix.
M	the msir kernel matrix.
evalues	the eigenvalues from the generalized eigen-decomposition of M.
evector	the raw eigenvectors from the generalized eigen-decomposition of M ordered according to the eigenvalues.
basis	the normalized eigenvectors from the generalized eigen-decomposition of M ordered according to the eigenvalues.
std.basis	standardized basis vectors obtained by multiplying each coefficient of the eigenvectors by the standard deviation of the corresponding predictor. The resulting coefficients are scaled such that all predictors have unit standard deviation.
numdir	the maximal number of directions estimated.
dir	the estimated MSIR directions from mean-centered predictors.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**References**

Scrucca, L. (2011) Model-based SIR for dimension reduction. *Computational Statistics & Data Analysis*, 55(11), 3010-3026.

**See Also**

[summary.msir](#), [plot.msir](#), [dr](#)

**Examples**

```
# 1-dimensional simple regression
n = 200; p = 5
b = as.matrix(c(1,-1,rep(0,p-2)))
x = matrix(rnorm(n*p), nrow = n, ncol = p)
y = exp(0.5 * x%*%b) + 0.1*rnorm(n)
MSIR = msir(x, y)
summary(MSIR)
plot(MSIR, type = "2Dplot")

# 1-dimensional symmetric response curve
```

```

n = 200; p = 5
b = as.matrix(c(1,-1,rep(0,p-2)))
x = matrix(rnorm(n*p), nrow = n, ncol = p)
y = (0.5 * x%%b)^2 + 0.1*rnorm(n)
MSIR = msir(x, y)
summary(MSIR)
plot(MSIR, type = "2Dplot")
plot(MSIR, type = "coefficients")

# 2-dimensional response curve
n = 300; p = 5
b1 = c(1, 1, 1, rep(0, p-3))
b2 = c(1,-1,-1, rep(0, p-3))
b = cbind(b1,b2)
x = matrix(rnorm(n*p), nrow = n, ncol = p)
y = x %% b1 + (x %% b1)^3 + 4*(x %% b2)^2 + rnorm(n)
MSIR = msir(x, y)
summary(MSIR)
plot(MSIR, which = 1:2)
plot(MSIR, type = "spinplot")
plot(MSIR, which = 1, type = "2Dplot", span = 0.7)
plot(MSIR, which = 2, type = "2Dplot", span = 0.7)

```

---

msir.bic

*BIC-type criterion for dimensionality*


---

## Description

BIC-type criterion for selecting the dimensionality of a dimension reduction subspace.

## Usage

```
msir.bic(object, type = 1, plot = FALSE)
```

```
bicDimRed(M, x, nslices, type = 1, tol = sqrt(.Machine$double.eps))
```

## Arguments

object	a 'msir' object
plot	if TRUE a plot of the criterion is shown.
M	the kernel matrix. See details below.
x	the predictors data matrix. See details below.
type	See details below.
nslices	the number of slices. See details below.
tol	a tolerance value

## Details

This BIC-type criterion for the determination of the structural dimension selects  $d$  as the maximizer of

$$G(d) = l(d) - \text{Penalty}(p, d, n)$$

where  $l(d)$  is the log-likelihood for dimensions up to  $d$ ,  $p$  is the number of predictors, and  $n$  is the sample size. The term  $\text{Penalty}(p, d, n)$  is the type of penalty to be used:

```

type = 1   $\text{Penalty}(p, d, n) = -(p - d) \log(n)$ 
type = 2   $\text{Penalty}(p, d, n) = 0.5Cd(2p - d + 1)$ 
           where  $C = (0.5 \log(n) + 0.1n^{1/3})/2n\text{slices}/n$ 
type = 3   $\text{Penalty}(p, d, n) = 0.5Cd(2p - d + 1)$ 
           where  $C = \log(n)n\text{slices}/n$ 
type = 3   $\text{Penalty}(p, d, n) = 1/2d \log(n)$ 

```

## Value

Returns a list with components:

values	eigenvalues
l	log-likelihood
crit	BIC-type criterion
d	selected dimensionality

The `msir.bic` also assign the above information to the corresponding 'msir' object.

## Author(s)

Luca Scrucca <luca@stat.unipg.it>

## References

Zhu, Miao and Peng (2006) "Sliced Inverse Regression for CDR Space Estimation", JASA.  
 Zhu, Zhu (2007) "On kernel method for SAVE", Journal of Multivariate Analysis.

## See Also

[msir](#)

## Examples

```

# 1-dimensional symmetric response curve
n = 200; p = 5
b = as.matrix(c(1,-1,rep(0,p-2)))
x = matrix(rnorm(n*p), nrow = n, ncol = p)
y = (0.5 * x%*%b)^2 + 0.1*rnorm(n)
MSIR = msir(x, y)
msir.bic(MSIR, plot = TRUE)
summary(MSIR)
msir.bic(MSIR, type = 3, plot = TRUE)
summary(MSIR)

```

---

`msir.dir`*Model-based Sliced Inverse Regression directions*

---

**Description**

MSIR estimates a set of up to  $p$  orthogonal direction vectors each of length  $p$ , the first  $d$  of which are estimates of the basis of the dimensional reduction subspace.

**Usage**

```
msir.dir(object, numdir = object$numdir)
```

**Arguments**

<code>object</code>	a 'msir' object
<code>numdir</code>	the number of basis vectors to return.

**Value**

The function returns the estimated directions in the original  $n$  dimensional space for plotting.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**References**

Scrucca, L. (2011) Model-based SIR for dimension reduction. *Computational Statistics & Data Analysis*, 55(11), 3010-3026.

**See Also**

{msir}

**Examples**

```
# 1-dimensional simple regression
n = 200; p = 5
b = as.matrix(c(1,-1,rep(0,p-2)))
x = matrix(rnorm(n*p), nrow = n, ncol = p)
y = exp(0.5 * x%*%b) + 0.1*rnorm(n)
MSIR = msir(x, y)
msir.dir(MSIR, numdir = 1)
```



---

msir.nsllices	<i>Default number of slices</i>
---------------	---------------------------------

---

**Description**

This function computes a Sturges' type number of slices to be used as default in the `msir` function.

**Usage**

```
msir.nsllices(n, p)
```

**Arguments**

n	the number of observations in the sample.
p	the number of predictors in the sample.

**Value**

The function returns a single value, i.e. the number of slices.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**See Also**

[msir](#)

---

msir.permutation.test	<i>Permutation test for dimensionality</i>
-----------------------	--

---

**Description**

Approximates marginal dimension test significance levels by sampling from the permutation distribution.

**Usage**

```
msir.permutation.test(object, npermute = 99, numdir = object$numdir, verbose = TRUE)
```

**Arguments**

object	a 'msir' object.
npermute	number of permutations to compute.
numdir	maximum value of the dimension to test.
verbose	if TRUE a textual progress bar is shown during computation.

**Details**

The function approximates significance levels of the marginal dimension tests based on a permutation test.

**Value**

The function returns a list with components:

summary            a table containing the hypotheses, the test statistics, the permutation p-values.  
npermute           the number of permutations used.

Furthermore, it also assigns the above information to the corresponding 'msir' object.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**References**

Scrucca, L. (2011) Model-based SIR for dimension reduction. *Computational Statistics & Data Analysis*, 55(11), 3010-3026.

**See Also**

[dr](#)

**Examples**

```
## Not run:
# 1-dimensional simple regression
n = 200; p = 5
b = as.matrix(c(1,-1,rep(0,p-2)))
x = matrix(rnorm(n*p), nrow = n, ncol = p)
y = exp(0.5 * x%*%b) + 0.1*rnorm(n)
MSIR = msir(x, y)
msir.permutation.test(MSIR)
summary(MSIR)

## End(Not run)
```

---

msir.regularizedSigma *Regularized estimate of predictors covariance matrix.*

---

**Description**

This function computes a regularized version of the covariance matrix of the predictors. Among the possible models the one which maximizes BIC is returned.

**Usage**

```
msir.regularizedSigma(x, inv = FALSE, model = c("XII", "XXI", "XXX"))
```

**Arguments**

`x` the predictors data matrix.

`inv` if TRUE the inverse of the estimated covariance matrix is returned.

`model` available models:

XII	=	diagonal equal variances
XXI	=	diagonal unequal variances
XXX	=	full covariance matrix

**Value**

A  $(p \times p)$  covariance matrix estimate.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**See Also**

[msir](#)

---

<code>msir.slices</code>	<i>Slice a vector into slices of approximately equal size</i>
--------------------------	---

---

**Description**

Function used for slicing a continuous response variable.

**Usage**

```
msir.slices(y, nslices)
```

**Arguments**

`y` a vector of  $n$  values

`nslices` the number of slices, no larger than  $n$

**Value**

Returns a list with components:

`slice.indicator` an indicator variable for the slices.

`nslices` the actual number of slices produced.

`slice.sizes` the number of observations in each slice.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**See Also**

[msir](#)

---

plot.msir

*Plot method for 'msir' objects.*

---

**Description**

Plots directions and other information from MSIR estimation.

**Usage**

```
## S3 method for class 'msir'
plot(x, which,
     type = c("pairs", "2Dplot", "spinplot", "values", "coefficients"),
     span = NULL, std = TRUE, ylab, xlab, restore.par = TRUE, ...)
```

**Arguments**

x	a 'msir' object.
which	a vector of value(s) giving the directions for which the plot should be drawn.
type	the type of plot to be drawn.
span	the span of smoother (only for type = "pairs"   "2Dplot").
std	if TRUE coefficients are standardized (only for type = "coefficients").
ylab	a character string for the y-axis label.
xlab	a character string for the x-axis label.
restore.par	if TRUE the graphical parameters (see <a href="#">par</a> ) changed are restored to the previous state. If you want to manipulate the resulting plot you should set restore.par = FALSE.
...	additional arguments.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**References**

Scrucca, L. (2011) Model-based SIR for dimension reduction. *Computational Statistics & Data Analysis*, 55(11), 3010-3026.

**See Also**

[msir](#)

**Examples**

```
# 2-dimensional response curve
n = 300; p = 5
b1 = c(1, 1, 1, rep(0, p-3))
b2 = c(1,-1,-1, rep(0, p-3))
b = cbind(b1,b2)
x = matrix(rnorm(n*p), nrow = n, ncol = p)
y = x %>% b1 + (x %>% b1)^3 + 4*(x %>% b2)^2 + rnorm(n)
MSIR = msir(x, y)
summary(MSIR)
plot(MSIR)
plot(MSIR, which = 1:2)
plot(MSIR, type = "2Dplot", which = 1, span = 0.7)
plot(MSIR, type = "2Dplot", which = 2, span = 0.7)
## Not run: plot(MSIR, type = "spinplot")
plot(MSIR, type = "evalues")
plot(MSIR, type = "coefficients")
```

summary.msir

*Summary and print methods for 'msir' objects***Description**

Summary and print methods for 'msir' objects.

**Usage**

```
## S3 method for class 'msir'
summary(object, numdir = object$numdir, std = FALSE, verbose = TRUE, ...)
## S3 method for class 'summary.msir'
print(x, digits = max(5, getOption("digits") - 3), ... )
```

**Arguments**

object	a 'msir' object
numdir	the number of directions to be shown.
std	if TRUE the coefficients basis are scaled such that all predictors have unit standard deviation.
verbose	if FALSE the coefficients basis are omitted; by default verbose = TRUE.
x	a 'summary.msir' object.
digits	the significant digits to use.
...	additional arguments.

**Author(s)**

Luca Scrucca <luca@stat.unipg.it>

**See Also**

[msir](#)

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