

# Package ‘sSDR’

May 9, 2026

**Type** Package

**Title** Tools Developed for Structured Sufficient Dimension Reduction (sSDR)

**Version** 1.2.0

**Date** 2016-03-26

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**Description** Performs structured OLS (sOLS) and structured SIR (sSIR).

**License** GPL (>= 2)

**LazyData** TRUE

**Depends** R (>= 3.0.0), MASS, Matrix

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2016-03-26 22:02:24

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center *Center a vector*

---

**Description**

Center a vector

**Usage**

```
center(v)
```

**Arguments**

v                    A vector.

**Details**

This function centers any vector and returns a vector with mean zero.

**Value**

A vector with mean zero.

**Examples**

```
data <- gen.data(n=100)
y.centered <- center(data$y)
```

---

cov.x *Covariance matrix*

---

**Description**

Covariance matrix

**Usage**

```
cov.x(X)
```

**Arguments**

X                    a n x p matrix of n observations and p predictors.

**Details**

This function returns A p x p covariance matrix for any n x p matrix.

**Value**

A  $p \times p$  covariance matrix.

**Examples**

```
data <- gen.data(n=100)
x.cov <- cov.x(data$X)
```

---

disvm	<i>Subspace distance</i>
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---

**Description**

Subspace distance

**Usage**

```
disvm(v1, v2)
```

**Arguments**

v1                    A matrix, each column consists of a p-dimensional vector.  
v2                    A matrix, each column consists of a p-dimensional vector.

**Details**

This function computes the distances between two spaces using the formulation in Li, Zha, Chiaromonte (2005), which is the Frobenius norm of the difference between the two orthogonal projection matrices defined by v1 and v2.

**Value**

A scalar represents the distance between the two spaces spanned by v1 and v2 respectively.

**References**

Li, B., Zha, H., and Chiaromonte, F. (2005). Contour regression: a general approach to dimension reduction. *Annals of Statistics*, 33(4):1580-1616.

**Examples**

```
v1 <- c(1, 0, 0)
v2 <- c(0, 1, 0)
disvm(v1, v1)
disvm(v1, v2)
```

---

`gen.data`*Simulate data*

---

**Description**

Simulate data

**Usage**

```
gen.data(n, rho = 0.5, theta = 1, binary = FALSE)
```

**Arguments**

<code>n</code>	Sample size.
<code>rho</code>	Pairwise correlation between covariates.
<code>theta</code>	Standard deviation of the random error.
<code>binary</code>	If TRUE, generate binary responses; otherwise, by default, create continuous responses.

**Details**

This function simulates data as presented in Liu (2015).

**Value**

`gen.data` returns a list containing at least the following components: "X", a covariate matrix of  $n$  observations and  $p$  predictors; "y", a univariate response; "b.true", the actual coefficients for each predictor group.

**References**

Liu, Y. (2015). Approaches to reduce and integrate data in structured and high-dimensional regression problems in Genomics. Ph.D. Dissertation, The Pennsylvania State University, University Park, Department of Statistics.

**Examples**

```
data <- gen.data(n=100)
names(data)
```

---

gOLS *Groupwise OLS (gOLS)*

---

### Description

Groupwise OLS (gOLS)

### Usage

```
gOLS(X, Y, groups, dims)
```

### Arguments

X	A covariate matrix of n observations and p predictors.
Y	A univariate response.
groups	A vector with the number of predictors in each group.
dims	A vector with the dimension (at most 1) for each predictor group.

### Details

This function estimates directions for each predictor group using gOLS. Predictors need to be organized in groups within the "X" matrix, as the same order saved in "groups". We only allow continuous covariates in the "X" matrix; while categorical covariates can be handled outside of gOLS, e.g. structured OLS.

### Value

gOLS returns a list containing at least the following components: "b\_est", the estimated directions for each group with its own dimension using gOLS AFTER normalization; "B", the estimated directions for each group using gOLS BEFORE normalization.

### References

Liu, Y., Chiaromonte, F., and Li, B. (2015). Structured Ordinary Least Squares: a sufficient dimension reduction approach for regressions with partitioned predictors and heterogeneous units. Submitted.

### Examples

```
data <- gen.data(n=1000, binary=FALSE) # generate data
dim(data$X) # covariate matrix of 1000 observations and 15 predictors
dim(data$y) # univariate response
groups <- c(5, 10) # two predictor groups and their numbers of predictors
dims <- c(1,1) # dimension of each predictor group
est_gOLS <- gOLS(data$X,data$y,groups,dims)
names(est_gOLS)
```

---

gOLS.comp.d	<i>Groupwise OLS (gOLS) BIC criterion to estimate dimensions with eigen-decomposition</i>
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### Description

Groupwise OLS (gOLS) BIC criterion to estimate dimensions with eigen-decomposition

### Usage

```
gOLS.comp.d(X, y, groups)
```

### Arguments

X	A covariate matrix of n observations and p predictors.
y	A univariate response.
groups	A vector with the number of predictors in each group.

### Details

This function estimates dimension for each predictor group using eigen-decomposition. Predictors need to be organized in groups within the "X" matrix, as the same order saved in "groups". We only allow continuous covariates in the "X" matrix; while categorical covariates can be handled outside of gOLS, e.g. structured OLS.

### Value

gOLS.comp.d returns a list containing at least the following components: "d", the estimated dimension (at most 1) for each predictor group; "crit", the BIC criterion from each iteration.

### References

Liu, Y., Chiaromonte, F., and Li, B. (2015). Structured Ordinary Least Squares: a sufficient dimension reduction approach for regressions with partitioned predictors and heterogeneous units. Submitted.

### Examples

```
data <- gen.data(n=1000, binary=FALSE) # generate data
dim(data$X) # covariate matrix of 1000 observations and 15 predictors
dim(data$y) # univariate response
groups <- c(5, 10) # two predictor groups and their numbers of predictors
dim_gOLS<-gOLS.comp.d(data$X,data$y,groups)
names(dim_gOLS)
```

---

gSIR	<i>Groupwise SIR (gSIR) for binary response</i>
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---

## Description

Groupwise SIR (gSIR) for binary response

## Usage

```
gSIR(X, Y, groups, dims)
```

## Arguments

X	A covariate matrix of n observations and p predictors.
Y	A binary response.
groups	A vector with the number of predictors in each group.
dims	A vector with the dimension (at most 1) for each predictor group.

## Details

This function estimates directions for each predictor group using gSIR. Predictors need to be organized in groups within the "X" matrix, as the same order saved in "groups". We only allow continuous covariates in the "X" matrix; while categorical covariates can be handled outside of gSIR, e.g. structured SIR.

## Value

gSIR returns a list containing at least the following components: "b\_est", the estimated directions for each group with its own dimension using gSIR AFTER normalization; "B", the estimated directions for each group using gSIR BEFORE normalization.

## References

Guo, Z., Li, L., Lu, W., and Li, B. (2014). Groupwise dimension reduction via envelope method. Journal of the American Statistical Association, accepted.

## Examples

```
data <- gen.data(n=1000, binary=TRUE) # generate data
dim(data$X) # covariate matrix of 1000 observations and 15 predictors
length(data$y) # binary response
groups <- c(5, 10) # two predictor groups and their numbers of predictors
dims <- c(1,1) # dimension of each predictor group
est_gSIR<-gSIR(data$X,data$y,groups,dims)
names(est_gSIR)
```

---

gSIR.comp.d	<i>Groupwise SIR (gSIR) BIC criterion to estimate dimensions with eigen-decomposition (binary response)</i>
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---

## Description

Groupwise SIR (gSIR) BIC criterion to estimate dimensions with eigen-decomposition (binary response)

## Usage

```
gSIR.comp.d(X, y, groups)
```

## Arguments

X	A covariate matrix of n observations and p predictors.
y	A binary response.
groups	A vector with the number of predictors in each group.

## Details

This function estimates dimension for each predictor group using eigen-decomposition. Predictors need to be organized in groups within the "X" matrix, as the same order saved in "groups". We only allow continuous covariates in the "X" matrix; while categorical covariates can be handled outside of gSIR, e.g. structured SIR.

## Value

gSIR.comp.d returns a list containing at least the following components: "d", the estimated dimension (at most 1) for each predictor group; "crit", the BIC criterion from each iteration.

## References

Liu, Y. (2015). Approaches to reduce and integrate data in structured and high-dimensional regression problems in Genomics. Ph.D. Dissertation, The Pennsylvania State University, University Park, Department of Statistics.

## Examples

```
data <- gen.data(n=1000, binary=TRUE) # generate data
dim(data$X) # covariate matrix of 1000 observations and 15 predictors
length(data$y) # univariate response
groups <- c(5, 10) # two predictor groups and their numbers of predictors
dim_gSIR<-gSIR.comp.d(data$X,data$y,groups)
names(dim_gSIR)
```

---

matpower	<i>Power of a matrix</i>
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---

**Description**

Power of a matrix

**Usage**

```
matpower(X, alpha)
```

**Arguments**

X	A p x p square matrix.
alpha	A scalar determining the order of the power.

**Details**

This function calculates the power of a square matrix.

**Value**

A p x p square matrix.

**Examples**

```
data <- gen.data(n=100)
cov.squared <- matpower(cov.x(data$X), 2)
```

---

norm1	<i>Normalize a vector</i>
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---

**Description**

Normalize a vector

**Usage**

```
norm1(v)
```

**Arguments**

v	A vector.
---	-----------

**Details**

This function normalizes any non-zero vector and returns a vector with the norm equal to 1.

**Value**

A vector with norm 1.

**Examples**

```
data <- gen.data(n=100)
y.norm1 <- norm1(data$y)
```

---

orthnormal

*Gram-Schmidt orthonormalization*

---

**Description**

Gram-Schmidt orthonormalization

**Usage**

```
orthnormal(X)
```

**Arguments**

X                    a n x p matrix of n observations and p predictors.

**Details**

This function orthonormalizes any n x p matrix.

**Value**

A n x p matrix of n observations and p predictors.

**Examples**

```
data <- gen.data(n=100)
x.orth <- orthnormal(data$X)
```

---

sOLS.comp.d	<i>Structured OLS (sOLS) outer level BIC criterion to estimate dimension with eigen-decomposition</i>
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---

**Description**

Structured OLS (sOLS) outer level BIC criterion to estimate dimension with eigen-decomposition

**Usage**

```
sOLS.comp.d(X, sizes)
```

**Arguments**

X	A matrix containing directions estimated from all subpopulations.
sizes	A vector with the sample sizes of all subpopulation.

**Details**

This function estimates dimension across the subpopulations using eigen-decomposition. The order of the subpopulations in the "sizes" vector should match the one in the "X" matrix. Also, this function returns the linearly independent directions among all subpopulations.

**Value**

sOLS.comp.d returns a list containing at least the following components: "d", the dimension estimated across subpopulations; "u", the "d" linearly independent directions among the matrix X.

**References**

Liu, Y., Chiaromonte, F., and Li, B. (2015). Structured Ordinary Least Squares: a sufficient dimension reduction approach for regressions with partitioned predictors and heterogeneous units. Submitted.

**Examples**

```
v1 <- c(1, 1, 0, 0)
v2 <- c(0, 1, 1, 0)
v3 <- c(0, 0, 1, 1)
v4 <- c(1, 1, 1, 1)
m1 <- cbind(v1, v2)
sizes1 <- c(100, 200)
sOLS.comp.d(m1, sizes1)
m2 <- cbind(v1, v2, v3)
sizes2 <- c(100, 200, 500)
sOLS.comp.d(m2, sizes2)
m3 <- cbind(v1, v3, v4)
sizes3 <- c(100, 500, 1000)
sOLS.comp.d(m3, sizes3)
```

---

`standmat`*Matrix standardization*

---

**Description**

Matrix standardization

**Usage**

```
standmat(x)
```

**Arguments**

`x` A  $n \times p$  matrix of  $n$  observations and  $p$  predictors.

**Details**

This function standardizes a matrix treating each row as a random vector in an iid sample. It returns a  $n \times p$  matrix with column-mean zero and identity-covariance matrix.

**Value**

A  $n \times p$  matrix of  $n$  observations and  $p$  predictors.

**Examples**

```
data <- gen.data(n=100)
x.std <- standmat(data$X)
```

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