

# Package ‘sparseLDA’

January 2, 2012

**Version** 0.1-5

**Date** 2009-02-28

**Title** Sparse Discriminant Analysis

**Author** Line Clemmensen <lhc@imm.dtu.dk>, contributions by Max Kuhn

**Maintainer** Line Clemmensen <lhc@imm.dtu.dk>

**Depends** lars, elasticnet, MASS, mda

**Description**

Performs sparse linear discriminant analysis for gaussians and mixture of gaussians models.

**License** GPL (>= 2)

**URL** <http://www.imm.dtu.dk/~lhc>, <https://r-forge.r-project.org/projects/sparselda/>

**Revision** 8

**Repository** CRAN

**Date/Publication** 2009-03-03 08:11:48

## R topics documented:

normalize . . . . .	2
normalizetest . . . . .	3
penicilliumYES . . . . .	4
predict.sda . . . . .	5
sda . . . . .	6
smda . . . . .	8

<b>Index</b>	<b>11</b>
--------------	-----------

normalize

*Normalize training data*

---

**Description**

Normalize a vector or matrix to zero mean and unit length columns

**Usage**

```
normalize(X)
```

**Arguments**

**X** a matrix with the training data with observations down the rows and variables in the columns.

**Details**

The function can e.g. be used for the training data in `sda` or `smda`.

**Value**

Returns a list with the following attributes:

<code>Xc</code>	The normalized data.
<code>m<sub>x</sub></code>	Mean of columns of X.
<code>v<sub>x</sub></code>	Length of columns of X.
<code>Id</code>	Logical vector indicating which variables are included in X. If some of the columns have zero length they are omitted.

**Author(s)**

Line Clemmensen

**References**

Clemmensen, L., Hastie, T. and Ersboell, K. (2008) "Sparse discriminant analysis", Technical report, IMM, Technical University of Denmark

**See Also**

[normalizetest](#), [sda](#), [smda](#)

**Examples**

```
## Data
X<-matrix(sample(seq(3),12,replace=TRUE),nrow=3)

## Normalize data
Nm<-normalize(X)
print(Nm$Xc)

## See if any variables have been removed
which(!Nm$Id)
```

---

normalizetest	<i>Normalize test data</i>
---------------	----------------------------

---

**Description**

Normalize test data using output from the `normalize()` of the training data

**Usage**

```
normalizetest(Xtst,Xn)
```

**Arguments**

Xtst	a matrix with the test data with observations down the rows and variables in the columns.
Xn	List with the output from <code>normalize(Xtr)</code> of the training data.

**Details**

The function can e.g. be used to normalize the testing data in `sda` or `smda`.

**Value**

Returns the normalized test data

Xtst	The normalized data.
------	----------------------

**Author(s)**

Line Clemmensen

**References**

Clemmensen, L., Hastie, T. and Ersboell, K. (2007) "Sparse discriminant analysis", Technical report, IMM, Technical University of Denmark

**See Also**

[normalize](#), [sda](#), [smda](#)

**Examples**

```
## Data
Xtr<-matrix(sample(seq(3),12,replace=TRUE),nrow=3)
Xtst<-matrix(sample(seq(3),12,replace=TRUE),nrow=3)

## Normalize training data
Nm<-normalize(Xtr)

## Normalize test data
Xtst<-normalizetest(Xtst,Nm)
```

---

penicilliumYES

*Data set of three species of Penicillium fungi*

---

**Description**

The data set penicilliumYES has 36 rows and 3754 columns. The variables are 1st order statistics from multi-spectral images of three species of *Penicillium* fungi: *Melanoconidium*, *Polonicum*, and *Venetum*. These are the data used in the Clemmensen et al "Sparse Discriminant Analysis" paper.

**Usage**

```
data(penicilliumYES)
```

**Format**

This data set contains the following matrices:

**X** A matrix with 36 columns and 3754 rows. The training and test data. The first 12 rows are *P. Melanoconidium* species, rows 13-24 are *P. Polonicum* species, and the last 12 rows are *P. Venetum* species. The samples are ordered so that each pair of three is from the same isolate.

**Y** A matrix of dummy variables for the training data.

**Z** Z matrix of probabilities for the subclasses of the training data.

**Details**

The X matrix is not normalized.

**Source**

<http://www.imm.dtu.dk/~lhc>

## References

Clemmensen, Hansen, Frisvad, Ersboell (2007) "A method for comparison of growth media in objective identification of *Penicillium* based on multi-spectral imaging" *Journal of Microbiological Methods*

---

predict.sda	<i>Predict method for Sparse Discriminant Methods</i>
-------------	---

---

## Description

Prediction functions for `link{sda}` and `link{smda}`.

## Usage

```
## S3 method for class 'sda'
predict(object, newdata = NULL, ...)
## S3 method for class 'smda'
predict(object, newdata = NULL, ...)
```

## Arguments

object	an object of class <code>link{sda}</code> or <code>link{smda}</code>
newdata	a matrix or data frame of predictors
...	arguments passed to <code>link[MASS]{predict.lda}</code>

## Details

The current implementation for mixture discriminant models current predicts the subclass probabilities.

## Value

A list with components:

class	The classification (a factor)
posterior	posterior probabilities for the classes (or subclasses for <code>link{smda}</code> )
x	the scores

sda

*Sparse discriminant analysis***Description**

Performs sparse linear discriminant analysis. Using an alternating minimization algorithm to minimize the SDA criterion.

**Usage**

```
sda(x, ...)
```

## Default S3 method:  
sda(x, y, lambda = 1e-6, stop, maxIte = 100,  
trace = FALSE, tol = 1e-6, ...)

**Arguments**

x	A matrix of the training data with observations down the rows and variables in the columns.
y	A matrix initializing the dummy variables representing the groups.
lambda	The weight on the L2-norm for elastic net regression. Default: 1e-6.
stop	If STOP is negative, its absolute value corresponds to the desired number of variables. If STOP is positive, it corresponds to an upper bound on the L1-norm of the b coefficients. There is a one to one correspondence between stop and t.
maxIte	Maximum number of iterations. Default: 100.
trace	If TRUE, prints out its progress. Default: FALSE.
tol	Tolerance for the stopping criterion (change in RSS). Default is 1e-6.
...	additional arguments

**Details**

The function finds sparse directions for linear classification.

**Value**

Returns a list with the following attributes:

beta	The loadings of the sparse discriminative directions.
theta	The optimal scores.
rss	A vector of the Residual Sum of Squares at each iteration.

**Author(s)**

Line Clemmensen

## References

Clemmensen, L., Hastie, T. and Ersboell, K. (2007) "Sparse discriminant analysis", Technical report, IMM, Technical University of Denmark

## See Also

[normalize](#), [normalizetest](#), [smda](#)

## Examples

```
## load data
data(penicilliumYES)

X <- penicilliumYES$X
Y <- penicilliumYES$Y
colnames(Y) <- c("P. Melanoconidium",
                 "P. Polonicum",
                 "P. Venetum")

## test samples
Iout<-c(3,6,9,12)
Iout<-c(Iout,Iout+12,Iout+24)

## training data
Xtr<-X[-Iout,]
k<-3
n<-dim(Xtr)[1]

## Normalize data
Xc<-normalize(Xtr)
Xn<-Xc$Xc
p<-dim(Xn)[2]

## Perform SDA with one non-zero loading for each discriminative
## direction with Y as matrix input
out <- sda(Xn, Y,
           lambda = 1e-6,
           stop = -1,
           maxIte = 25,
           trace = TRUE)

## predict training samples
train <- predict(out, Xn)

## testing
Xtst<-X[Iout,]
Xtst<-normalizetest(Xtst,Xc)

test <- predict(out, Xtst)
print(test$class)
```

```
## Factor Y as input
Yvec <- factor(rep(colnames(Y), each = 8))
out2 <- sda(Xn, Yvec,
            lambda = 1e-6,
            stop = -1,
            maxIte = 25,
            trace = TRUE)
```

---

smda

*Sparse mixture discriminant analysis*


---

## Description

Performs sparse linear discriminant analysis for mixture of gaussians models.

## Usage

```
smda(x, ...)
```

```
## Default S3 method:
smda(x, y, Z = NULL, Rj = NULL,
     lambda = 1e-6, stop, maxIte = 50,
     trace = FALSE, tol = 1e-4, ...)
```

## Arguments

x	A matrix of the training data with observations down the rows and variables in the columns.
y	A matrix initializing the dummy variables representing the groups.
Z	Am optional matrix initializing the probabilities representing the groups.
Rj	K length vector containing the number of subclasses in each of the K classes.
lambda	The weight on the L2-norm for elastic net regression. Default: 1e-6.
stop	If STOP is negative, its absolute value corresponds to the desired number of variables. If STOP is positive, it corresponds to an upper bound on the L1-norm of the b coefficients. There is a one to one correspondence between stop and t.
maxIte	Maximum number of iterations. Default: 50.
trace	If TRUE, prints out its progress. Default: FALSE.
tol	Tolerance for the stopping criterion (change in RSS). Default: 1e-4
...	additional arguments

## Details

The function finds sparse directions for linear classification of mixture og gaussians models.

**Value**

Returns a list with the following attributes:

call	The call
beta	The loadings of the sparse discriminative directions.
theta	The optimal scores.
Z	Updated subclass probabilities.
Rj	a vector of the number of subclasses per class
rss	A vector of the Residual Sum of Squares at each iteration.

**Author(s)**

Line Clemmensen

**References**

Clemmensen, L., Hastie, T. and Ersboell, K. (2007) "Sparse discriminant analysis", Technical report, IMM, Technical University of Denmark

**See Also**

[normalize](#), [normalizetest](#), [sda](#)

**Examples**

```
# load data
data(penicilliumYES)
X <- penicilliumYES$X
Y <- penicilliumYES$Y
Z <- penicilliumYES$Z

## test samples
Iout <- c(3, 6, 9, 12)
Iout <- c(Iout, Iout+12, Iout+24)

## training data
Xtr <- X[-Iout,]
k <- 3
n <- dim(Xtr)[1]
Rj <- rep(4, 3)

## Normalize data
Xc <- normalize(Xtr)
Xn <- Xc$Xc
p <- dim(Xn)[2]

## perform SMDA with one non-zero loading for each discriminative
## direction
smdaFit <- smda(x = Xn,
                y = Y,
```

```
Z = Z,  
Rj = Rj,  
lambda = 1e-6,  
stop = -5,  
maxIte = 10,  
trace = TRUE,  
tol = 1e-2)  
  
# testing  
Xtst <- X[Iout,]  
Xtst <- normalizetest(Xtst, Xc)  
  
test <- predict(smdaFit, Xtst)
```

# Index

## \*Topic **classif**

penicilliumYES, 4  
sda, 6  
smda, 8

## \*Topic **datasets**

penicilliumYES, 4

## \*Topic **multivariate**

normalize, 2  
normalizetest, 3  
penicilliumYES, 4  
predict.sda, 5  
sda, 6  
smda, 8

normalize, 2, 4, 7, 9

normalizetest, 2, 3, 7, 9

penicilliumYES, 4

predict.sda, 5

predict.smda (predict.sda), 5

sda, 2, 4, 6, 9

smda, 2, 4, 7, 8