

# Package ‘SQDA’

February 19, 2015

**Type** Package

**Title** Sparse Quadratic Discriminant Analysis

**Version** 1.0

**Date** 2014-09-19

**Author** Jiehuan Sun

**Maintainer** Jiehuan Sun <jiehuan.sun@yale.edu>

**Depends** R (>= 2.10)

**Imports** limma (>= 3.18.13), PDSCE (>= 1.2), mvtnorm (>= 0.9.99992)

**Description** Sparse Quadratic Discriminant Analysis (SQDA) can be performed. In SQDA, the covariance matrix are assumed to be block-diagonal. And, for each block, sparsity assumption is imposed on the covariance matrix. It is useful in high-dimensional setting.

**License** GPL-3

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2014-10-01 07:22:24

## R topics documented:

SQDA-package . . . . .	2
cross . . . . .	2
exempledata . . . . .	3
sGda . . . . .	3
sGdaCV2 . . . . .	4
simpleAGG3 . . . . .	4
sortgene . . . . .	5
sQDA . . . . .	5
test.data . . . . .	6
train.data . . . . .	6

**Index**

7

SQDA-package

*Sparse Quadratic Discriminant Analysis***Description**

This package is used to perform Sparse Quadratic Discriminant Analysis (SQDA). In SQDA, the covariance matrix are assumed to be block-diagonal. And, for each block, sparsity assumption is imposed on the covariance matrix. It is useful in high-dimensional setting.

**Details**

Package:	SQDA
Type:	Package
Version:	1.0
Date:	2014-09-19
License:	GPL-3

The package has one function, sQDA(), which basically takes in several parameters and output the predictions on the new dataset based on the sparse quadratic discriminant analysis. More details on the algorithms see the reference below.

**Author(s)**

Jiehuan Sun Jiehuan Sun <jiehuan.sun@yale.edu>

**References**

The application of sparse estimation of covariance matrix to quadratic discriminant analysis. Jiehuan Sun and Hongyu Zhao.

**Examples**

```
data(exampledData)
res<-sQDA(train.data[1:100,],test.data[1:100,],lams=0.2,presel=FALSE)
sum(res$pred!=colnames(test.data))/ncol(test.data) ##prediction error
res$p ## number of blocks selected
res$pred ## predicted class labels on test.data
```

cross

*generate cross-validation ids***Description**

generate cross-validation ids

**Usage**

```
cross(data = NULL, cv = 5)
```

**Arguments**

- |      |   |
|------|---|
| data | data matrix with column names being the class labels and row names being the genes. |
| cv   | the cross-validation folds  |

**Value**

cross-validation ids that can be used to split data into training data and testing data.

---

exampeldata

*exampeldata*

---

**Description**

simulated example data

---

sGda

*Prediction function*

---

**Description**

Prediction function

**Usage**

```
sGda(data = NULL, data.new = NULL, lam = 0)
```

**Arguments**

- |          |   |
|----------|---|
| data     | data matrix with column names being the class labels and row names being the genes. |
| data.new | the new data needs to be predicted.   |
| lam      | optimal lambda from cross-validation.   |

**Value**

returns a list object with following items.

- |      |   |
|------|---|
| pred | predictions for class labels on the new dataset |
| lik  | likelihood of each class on the new dataset     |

sGdaCV2                   *Cross-validation function*

### Description

Cross-validation function

### Usage

```
sGdaCV2(data = NULL, cv = 5, lam = 0)
```

### Arguments

data	data matrix with column names being the class labels and row names being the genes.
cv	cross-validation folds.
lam	a sequence of lambda's.

### Value

returns a list object with following item.

cv.error	cross-validation errors for each lambda
----------	---

simpleAGG3                   *Blockwise classifiers*

### Description

Blockwise classifiers

### Usage

```
simpleAGG3(data = NULL, data.new = NULL, len = 100, times = 100,
           lam = seq(0, 0.1, length = 10))
```

### Arguments

data	data matrix with column names being the class labels and row names being the genes.
data.new	the new data needs to be predicted.
len	block size
times	number of blocks
lam	a sequence of lambda's from cross-validation.

**Value**

returns a list object with following items.

cv.error	cross-validation errors for each block
pred	predictions for class labels on the new dataset
lik	likelihood of each class on the new dataset

---

sortgene

*Gene sorter*

---

**Description**

Gene sorter

**Usage**

```
sortgene(data = NULL)
```

**Arguments**

data	data matrix with column names being the class labels and row names being the genes.
------	---

**Value**

topTable data structure from limma.

---

sQDA

*Spase Quadratic Discriminant Analysis*

---

**Description**

Spase Quadratic Discriminant Analysis

**Usage**

```
sQDA(train.data = NULL, test.data = NULL, len = 100, lams = seq(0.02, 1,  
length = 10), presel = T, prelam = 0.2, margin = 0.05)
```

**Arguments**

<code>train.data</code>	data matrix with column names being the class labels and row names being the genes.
<code>test.data</code>	the new data needs to be predicted.
<code>len</code>	block size
<code>lams</code>	a sequence of lambda's from cross-validation.
<code>presel</code>	pre-selection indicator.
<code>prelam</code>	pre-selection sparsity parameter, only used when presel=T.
<code>margin</code>	error margin for pre-selection, only used when presel=T.

**Value**

returns a list object with following items.

<code>pred</code>	predictions for class labels on the test.data
<code>p</code>	the number of blocks selected

**References**

The application of sparse estimation of covariance matrix to quadratic discriminant analysis. Jiehuan Sun and Hongyu Zhao.

**Examples**

```
data(exampleddata)
res<-sQDA(train.data[1:100,],test.data[1:100,],lams=0.2,presel=FALSE)
sum(res$pred!=colnames(test.data))/ncol(test.data) ##prediction error
res$p ## number of blocks selected
res$pred ## predicted class labels on test.data
```

<code>test.data</code>	<i>testing data</i>
------------------------	---------------------

**Description**

simulated testing data

<code>train.data</code>	<i>training data</i>
-------------------------	----------------------

**Description**

simulated training data

# Index

\*Topic **data**

exampledada, [3](#)

test.data, [6](#)

train.data, [6](#)

\*Topic **package**

SQDA-package, [2](#)

cross, [2](#)

exampledada, [3](#)

sGda, [3](#)

sGdaCV2, [4](#)

simpleAGG3, [4](#)

sortgene, [5](#)

SQDA (SQDA-package), [2](#)

sQDA, [5](#)

SQDA-package, [2](#)

test.data, [6](#)

train.data, [6](#)