

# Package ‘sparsediscrim’

July 1, 2021

**Title** Sparse and Regularized Discriminant Analysis

**Version** 0.3.0

**Description** A collection of sparse and regularized discriminant analysis methods intended for small-sample, high-dimensional data sets. The package features the High-Dimensional Regularized Discriminant Analysis classifier from Ramey et al. (2017) <[arXiv:1602.01182](https://arxiv.org/abs/1602.01182)>. Other classifiers include those from Dudoit et al. (2002) <[doi:10.1198/016214502753479248](https://doi.org/10.1198/016214502753479248)>, Pang et al. (2009) <[doi:10.1111/j.1541-0420.2009.01200.x](https://doi.org/10.1111/j.1541-0420.2009.01200.x)>, and Tong et al. (2012) <[doi:10.1093/bioinformatics/btr690](https://doi.org/10.1093/bioinformatics/btr690)>.

**Imports** bdsmatrix, corpcor, dplyr, ggplot2, mvtnorm, rlang

**Suggests** testthat, MASS, covr, modeldata, spelling

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**URL** <https://github.com/topepo/sparsediscrim>,  
<https://topepo.github.io/sparsediscrim/>

**RoxygenNote** 7.1.1.9001

**Depends** R (>= 2.10)

**Encoding** UTF-8

**Language** en-US

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-07-01 07:50:02 UTC

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center_data	<i>Centers the observations in a matrix by their respective class sample means</i>
-------------	--

---

**Description**

Centers the observations in a matrix by their respective class sample means

**Usage**

```
center_data(x, y)
```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
y	vector of class labels for each training observation

**Value**

matrix with observations centered by its corresponding class sample mean

---

cov_autocorrelation	<i>Generates a <math>p \times p</math> autocorrelated covariance matrix</i>
---------------------	---

---

**Description**

This function generates a  $p \times p$  autocorrelated covariance matrix with autocorrelation parameter rho. The variance sigma2 is constant for each feature and defaulted to 1.

**Usage**

```
cov_autocorrelation(p, rho, sigma2 = 1)
```

**Arguments**

p	the size of the covariance matrix
rho	the autocorrelation parameter. Must be less than 1 in absolute value.
sigma2	the variance of each feature

**Details**

The autocorrelated covariance matrix is defined as: The  $(i, j)$ th entry of the autocorrelated covariance matrix is defined as:  $\rho^{|i-j|}$ .

The value of rho must be such that  $|\rho| < 1$  to ensure that the covariance matrix is positive definite.

**Value**

autocorrelated covariance matrix

---

cov\_block\_autocorrelation

*Generates a  $p \times p$  block-diagonal covariance matrix with autocorrelated blocks.*

---

**Description**

This function generates a  $p \times p$  covariance matrix with autocorrelated blocks. The autocorrelation parameter is rho. There are num\_blocks blocks each with size, block\_size. The variance, sigma2, is constant for each feature and defaulted to 1.

**Usage**

```
cov_block_autocorrelation(num_blocks, block_size, rho, sigma2 = 1)
```

**Arguments**

num_blocks	the number of blocks in the covariance matrix
block_size	the size of each square block within the covariance matrix
rho	the autocorrelation parameter. Must be less than 1 in absolute value.
sigma2	the variance of each feature

**Details**

The autocorrelated covariance matrix is defined as:

$$\Sigma = \Sigma^{(\rho)} \oplus \Sigma^{(-\rho)} \oplus \dots \oplus \Sigma^{(\rho)},$$

where  $\oplus$  denotes the direct sum and the  $(i, j)$ th entry of  $\Sigma^{(\rho)}$  is

$$\Sigma_{ij}^{(\rho)} = \{\rho^{|i-j|}\}.$$

The matrix  $\Sigma^{(\rho)}$  is the autocorrelated block discussed above.

The value of rho must be such that  $|\rho| < 1$  to ensure that the covariance matrix is positive definite.

The size of the resulting matrix is  $p \times p$ , where  $p = \text{num\_blocks} * \text{block\_size}$ .

**Value**

autocorrelated covariance matrix

---

cov_eigen	<i>Computes the eigenvalue decomposition of the maximum likelihood estimators (MLE) of the covariance matrices for the given data matrix</i>
-----------	--

---

### Description

For the classes given in the vector `y`, we compute the eigenvalue (spectral) decomposition of the class sample covariance matrices (MLEs) using the data matrix `x`.

### Usage

```
cov_eigen(x, y, pool = FALSE, fast = FALSE, tol = 1e-06)
```

### Arguments

<code>x</code>	data matrix with <code>n</code> observations and <code>p</code> feature vectors
<code>y</code>	class labels for observations (rows) in <code>x</code>
<code>pool</code>	logical. Should the sample covariance matrices be pooled?
<code>fast</code>	logical. Should the Fast SVD be used? See details.
<code>tol</code>	tolerance value below which the singular values of <code>x</code> are considered zero.

### Details

If the `fast` argument is selected, we utilize the so-called Fast Singular Value Decomposition (SVD) to quickly compute the eigenvalue decomposition. To compute the Fast SVD, we use the `corpcor::fast.svd()` function, which employs a well-known trick for tall data (large `n`, small `p`) and wide data (large `p`, small `n`) to compute the SVD corresponding to the nonzero singular values. For more information about the Fast SVD, see `corpcor::fast.svd()`.

### Value

a list containing the eigendecomposition for each class. If `pool = TRUE`, then a single list is returned.

### Examples

```
cov_eigen(x = iris[, -5], y = iris[, 5])
cov_eigen(x = iris[, -5], y = iris[, 5], pool = TRUE)
cov_eigen(x = iris[, -5], y = iris[, 5], pool = TRUE, fast = TRUE)

# Generates a data set having fewer observations than features.
# We apply the Fast SVD to compute the eigendecomposition corresponding to the
# nonzero eigenvalues of the covariance matrices.
set.seed(42)
n <- 5
p <- 20
num_classes <- 3
x <- lapply(seq_len(num_classes), function(k) {
```

```

  replicate(p, rnorm(n, mean = k))
})
x <- do.call(rbind, x)
colnames(x) <- paste0("x", 1:ncol(x))
y <- gl(num_classes, n)
cov_eigen(x = x, y = y, fast = TRUE)
cov_eigen(x = x, y = y, pool = TRUE, fast = TRUE)

```

---

cov_intraclass	<i>Generates a <math>p \times p</math> intraclass covariance matrix</i>
----------------	---

---

### Description

This function generates a  $p \times p$  intraclass covariance matrix with correlation  $\rho$ . The variance  $\sigma^2$  is constant for each feature and defaulted to 1.

### Usage

```
cov_intraclass(p, rho, sigma2 = 1)
```

### Arguments

<code>p</code>	the size of the covariance matrix
<code>rho</code>	the value of the off-diagonal elements
<code>sigma2</code>	the variance of each feature

### Details

The intraclass covariance matrix is defined as:

$$\sigma^2 * (\rho * J_p + (1 - \rho) * I_p),$$

where  $J_p$  is the  $p \times p$  matrix of ones and  $I_p$  is the  $p \times p$  identity matrix.

By default, with `sigma2 = 1`, the diagonal elements of the intraclass covariance matrix are all 1, while the off-diagonal elements of the matrix are all  $\rho$ .

The value of  $\rho$  must be between  $1/(1-p)$  and 1, exclusively, to ensure that the covariance matrix is positive definite.

### Value

intraclass covariance matrix

---

cov_list	<i>Computes the covariance-matrix maximum likelihood estimators for each class and returns a list.</i>
----------	--

---

**Description**

For a sample matrix,  $x$ , we compute the MLE for the covariance matrix for each class given in the vector,  $y$ .

**Usage**

```
cov_list(x, y)
```

**Arguments**

$x$	data matrix with $n$ observations and $p$ feature vectors
$y$	class labels for observations (rows) in $x$

**Value**

list of the sample covariance matrices of size  $p \times p$  for each class given in  $y$ .

---

cov_mle	<i>Computes the maximum likelihood estimator for the sample covariance matrix under the assumption of multivariate normality.</i>
---------	---

---

**Description**

For a sample matrix,  $x$ , we compute the sample covariance matrix of the data as the maximum likelihood estimator (MLE) of the population covariance matrix.

**Usage**

```
cov_mle(x, diag = FALSE)
```

**Arguments**

$x$	data matrix with $n$ observations and $p$ feature vectors
diag	logical value. If TRUE, assumes the population covariance matrix is diagonal. By default, we assume that diag is FALSE.

**Details**

If the `diag` option is set to TRUE, then we assume the population covariance matrix is diagonal, and the MLE is computed under this assumption. In this case, we return a vector of length  $p$  instead.

**Value**

sample covariance matrix of size  $p \times p$ . If `diag` is TRUE, then a vector of length  $p$  is returned instead.

---

cov_pool	<i>Computes the pooled maximum likelihood estimator (MLE) for the common covariance matrix</i>
----------	--

---

**Description**

For the matrix `x`, we compute the MLE for the population covariance matrix under the assumption that the data are sampled from  $K$  multivariate normal populations having equal covariance matrices.

**Usage**

```
cov_pool(x, y)
```

**Arguments**

<code>x</code>	data matrix with $n$ observations and $p$ feature vectors
<code>y</code>	class labels for observations (rows) in <code>x</code>

**Value**

pooled sample covariance matrix of size  $p \times p$

**Examples**

```
cov_pool(iris[, -5], iris$Species)
```

---

cov_shrink_diag	<i>Computes a shrunken version of the maximum likelihood estimator for the sample covariance matrix under the assumption of multivariate normality.</i>
-----------------	---

---

**Description**

For a sample matrix, `x`, we compute the sample covariance matrix as the maximum likelihood estimator (MLE) of the population covariance matrix and shrink it towards its diagonal.

**Usage**

```
cov_shrink_diag(x, gamma = 1)
```



**Arguments**

x	data matrix with n observations and p feature vectors
gamma	the shrinkage parameter. Must be between 0 and 1, inclusively. By default, the shrinkage parameter is 1, which simply yields the MLE.

**Details**

Let  $\hat{\Sigma}$  be the MLE of the covariance matrix  $\Sigma$ . Then, we shrink the MLE towards its diagonal by computing

$$\hat{\Sigma}(\gamma) = \gamma \hat{\Sigma} + (1 - \gamma) \hat{\Sigma} \circ I_p,$$

where  $\circ$  denotes the Hadamard product and  $\gamma \in [0, 1]$ .

For  $\gamma < 1$ , the resulting shrunken covariance matrix estimator is positive definite, and for  $\gamma = 1$ , we simply have the MLE, which can potentially be positive semidefinite (singular).

The estimator given here is based on Section 18.3.1 of the Hastie et al. (2008) text.

**Value**

shrunken sample covariance matrix of size  $p \times p$

**References**

Hastie, T., Tibshirani, R., and Friedman, J. (2008), "The Elements of Statistical Learning: Data Mining, Inference, and Prediction," 2nd edition. <http://web.stanford.edu/~hastie/ElemStatLearn/>

cv\_partition                      *Randomly partitions data for cross-validation.*

**Description**

For a vector of training labels, we return a list of cross-validation folds, where each fold has the indices of the observations to leave out in the fold. In terms of classification error rate estimation, one can think of a fold as the observations to hold out as a test sample set. Either the hold\_out size or the number of folds, num\_folds, can be specified. The number of folds defaults to 10, but if the hold\_out size is specified, then num\_folds is ignored.

**Usage**

```
cv_partition(y, num_folds = 10, hold_out = NULL, seed = NULL)
```

**Arguments**

y	a vector of class labels
num_folds	the number of cross-validation folds. Ignored if hold_out is not NULL. See Details.
hold_out	the hold-out size for cross-validation. See Details.
seed	optional random number seed for splitting the data for cross-validation

**Details**

We partition the vector  $y$  based on its length, which we treat as the sample size, 'n'. If an object other than a vector is used in  $y$ , its length can yield unexpected results. For example, the output of `length(diag(3))` is 9.

**Value**

list the indices of the training and test observations for each fold.

**Examples**

```
# The following three calls to `cv_partition` yield the same partitions.
set.seed(42)
cv_partition(iris$Species)
cv_partition(iris$Species, num_folds = 10, seed = 42)
cv_partition(iris$Species, hold_out = 15, seed = 42)
```

---

diag\_estimates

*Computes estimates and ancillary information for diagonal classifiers*


---

**Description**

Computes the maximum likelihood estimators (MLEs) for each class under the assumption of multivariate normality for each class. Also, computes ancillary information necessary for classifier summary, such as sample size, the number of features, etc.

**Usage**

```
diag_estimates(x, y, prior = NULL, pool = FALSE, est_mean = c("mle", "tong"))
```

**Arguments**

<code>x</code>	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
<code>y</code>	Vector of class labels for each training observation. Only complete data are retained.
<code>prior</code>	Vector with prior probabilities for each class. If <code>NULL</code> (default), then equal probabilities are used. See details.
<code>pool</code>	logical value. If <code>TRUE</code> , calculates the pooled sample variances for each class.
<code>est_mean</code>	the estimator for the class means. By default, we use the maximum likelihood estimator (MLE). To improve the estimation, we provide the option to use a shrunken mean estimator proposed by Tong et al. (2012).

**Details**

This function computes the common estimates and ancillary information used in all of the diagonal classifiers in the `sparsediscrim` package.

The matrix of training observations are given in `x`. The rows of `x` contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in `y` are coerced to a factor. The length of `y` should match the number of rows in `x`.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations. If other data have zero variances, these will be removed with a warning.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in `y`. The prior probabilities should be nonnegative and sum to one.

**Value**

named list with estimators for each class and necessary ancillary information

**References**

Tong, T., Chen, L., and Zhao, H. (2012), "Improved Mean Estimation and Its Application to Diagonal Discriminant Analysis," *Bioinformatics*, 28, 4, 531-537. <https://academic.oup.com/bioinformatics/article/28/4/531/211887>

---

dmvnorm_diag	<i>Computes multivariate normal density with a diagonal covariance matrix</i>
--------------	---

---

**Description**

Alternative to `mvtnorm::dmvnorm`

**Usage**

```
dmvnorm_diag(x, mean, sigma)
```

**Arguments**

<code>x</code>	matrix
<code>mean</code>	vector of means
<code>sigma</code>	vector containing diagonal covariance matrix

**Value**

multivariate normal density

---

generate_blockdiag	<i>Generates data from K multivariate normal data populations, where each population (class) has a covariance matrix consisting of block-diagonal autocorrelation matrices.</i>
--------------------	---

---

### Description

This function generates K multivariate normal data sets, where each class is generated with a constant mean vector and a covariance matrix consisting of block-diagonal autocorrelation matrices. The data are returned as a single matrix  $x$  along with a vector of class labels  $y$  that indicates class membership.

### Usage

```
generate_blockdiag(n, mu, num_blocks, block_size, rho, sigma2 = rep(1, K))
```

### Arguments

n	vector of the sample sizes of each class. The length of n determines the number of classes K.
mu	matrix containing the mean vectors for each class. Expected to have p rows and K columns.
num_blocks	the number of block matrices. See details.
block_size	the dimensions of the square block matrix. See details.
rho	vector of the values of the autocorrelation parameter for each class covariance matrix. Must equal the length of n (i.e., equal to K).
sigma2	vector of the variance coefficients for each class covariance matrix. Must equal the length of n (i.e., equal to K).

### Details

For simplicity, we assume that a class mean vector is constant for each feature. That is, we assume that the mean vector of the  $k$ th class is  $c_k * j_p$ , where  $j_p$  is a  $p \times 1$  vector of ones and  $c_k$  is a real scalar.

The  $k$ th class covariance matrix is defined as

$$\Sigma_k = \Sigma^{(\rho)} \oplus \Sigma^{(-\rho)} \oplus \dots \oplus \Sigma^{(\rho)},$$

where  $\oplus$  denotes the direct sum and the  $(i, j)$ th entry of  $\Sigma^{(\rho)}$  is

$$\Sigma_{ij}^{(\rho)} = \{\rho^{|i-j|}\}.$$

The matrix  $\Sigma^{(\rho)}$  is referred to as a block. Its dimensions are provided in the block\_size argument, and the number of blocks are specified in the num\_blocks argument.

Each matrix  $\Sigma_k$  is generated by the `cov_block_autocorrelation()` function.

The number of classes K is determined with lazy evaluation as the length of n.

The number of features p is computed as block\_size \* num\_blocks.

**Value**

named list with elements:

- x: matrix of observations with n rows and p columns
- y: vector of class labels that indicates class membership for each observation (row) in x.

**Examples**

```
# Generates data from K = 3 classes.
means <- matrix(rep(1:3, each=9), ncol=3)
data <- generate_blockdiag(n = c(15, 15, 15), block_size = 3, num_blocks = 3,
rho = seq(.1, .9, length = 3), mu = means)
data$x
data$y

# Generates data from K = 4 classes. Notice that we use specify a variance.
means <- matrix(rep(1:4, each=9), ncol=4)
data <- generate_blockdiag(n = c(15, 15, 15, 20), block_size = 3, num_blocks = 3,
rho = seq(.1, .9, length = 4), mu = means)
data$x
data$y
```

---

generate\_intraclass     *Generates data from K multivariate normal data populations, where each population (class) has an intraclass covariance matrix.*

---

**Description**

This function generates K multivariate normal data sets, where each class is generated with a constant mean vector and an intraclass covariance matrix. The data are returned as a single matrix x along with a vector of class labels y that indicates class membership.

**Usage**

```
generate_intraclass(n, p, rho, mu, sigma2 = rep(1, K))
```

**Arguments**

n	vector of the sample sizes of each class. The length of n determines the number of classes K.
p	the number of features (variables) in the data
rho	vector of the values of the off-diagonal elements for each intraclass covariance matrix. Must equal the length of n.
mu	vector containing the mean for each class. Must equal the length of n (i.e., equal to K).
sigma2	vector of variances for each class. Must equal the length of n. Default is 1 for each class.

## Details

For simplicity, we assume that a class mean vector is constant for each feature. That is, we assume that the mean vector of the  $k$ th class is  $c_k * j_p$ , where  $j_p$  is a  $p \times 1$  vector of ones and  $c_k$  is a real scalar.

The intraclass covariance matrix for the  $k$ th class is defined as:

$$\sigma_k^2 * (\rho_k * J_p + (1 - \rho_k) * I_p),$$

where  $J_p$  is the  $p \times p$  matrix of ones and  $I_p$  is the  $p \times p$  identity matrix.

By default, with  $\sigma_k^2 = 1$ , the diagonal elements of the intraclass covariance matrix are all 1, while the off-diagonal elements of the matrix are all rho.

The values of rho must be between  $1/(1 - p)$  and 1, exclusively, to ensure that the covariance matrix is positive definite.

The number of classes K is determined with lazy evaluation as the length of n.

## Value

named list with elements:

- x: matrix of observations with n rows and p columns
- y: vector of class labels that indicates class membership for each observation (row) in x.

## Examples

```
# Generates data from K = 3 classes.
data <- generate_intraclass(n = 3:5, p = 5, rho = seq(.1, .9, length = 3),
                          mu = c(0, 3, -2))

data$x
data$y

# Generates data from K = 4 classes. Notice that we use specify a variance.
data <- generate_intraclass(n = 3:6, p = 4, rho = seq(0, .9, length = 4),
                          mu = c(0, 3, -2, 6), sigma2 = 1:4)

data$x
data$y
```

---

h

*Bias correction function from Pang et al. (2009).*

---

## Description

This function computes the function  $h_{\nu,p}(t)$  on page 1023 of Pang et al. (2009).

## Usage

```
h(nu, p, t = -1)
```

**Arguments**

nu	a specified constant (nu = N - K)
p	the feature space dimension.
t	a constant specified by the user that indicates the exponent to use with the variance estimator. By default, t = -1 as in Pang et al. See the paper for more details.

**Value**

the bias correction value

**References**

Pang, H., Tong, T., & Zhao, H. (2009). "Shrinkage-based Diagonal Discriminant Analysis and Its Applications in High-Dimensional Data," *Biometrics*, 65, 4, 1021-1029. <https://onlinelibrary.wiley.com/doi/abs/10.1111/j.1541-0420.2009.01200.x>

---

 lda\_diag

---

*Diagonal Linear Discriminant Analysis (DLDA)*


---

**Description**

Given a set of training data, this function builds the Diagonal Linear Discriminant Analysis (DLDA) classifier, which is often attributed to Dudoit et al. (2002). The DLDA classifier belongs to the family of Naive Bayes classifiers, where the distributions of each class are assumed to be multivariate normal and to share a common covariance matrix.

The DLDA classifier is a modification to LDA, where the off-diagonal elements of the pooled sample covariance matrix are set to zero.

**Usage**

```
lda_diag(x, ...)

## Default S3 method:
lda_diag(x, y, prior = NULL, ...)

## S3 method for class 'formula'
lda_diag(formula, data, prior = NULL, ...)

## S3 method for class 'lda_diag'
predict(object, newdata, type = c("class", "prob", "score"), ...)
```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
formula	A formula of the form $\text{groups} \sim x_1 + x_2 + \dots$ . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in <code>formula</code> are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

**Details**

The DLDA classifier is a modification to the well-known LDA classifier, where the off-diagonal elements of the pooled sample covariance matrix are assumed to be zero – the features are assumed to be uncorrelated. Under multivariate normality, the assumption uncorrelated features is equivalent to the assumption of independent features. The feature-independence assumption is a notable attribute of the Naive Bayes classifier family. The benefit of these classifiers is that they are fast and have much fewer parameters to estimate, especially when the number of features is quite large.

The matrix of training observations are given in `x`. The rows of `x` contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in `y` are coerced to a factor. The length of `y` should match the number of rows in `x`.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in `y`. The `prior` probabilities should be nonnegative and sum to one.

**Value**

The model fitting function returns the fitted classifier. The `predict()` method returns either a vector (type = "class") or a data frame (all other type values).

**References**

Dudoit, S., Fridlyand, J., & Speed, T. P. (2002). "Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data," *Journal of the American Statistical Association*, 97, 457, 77-87.



**Examples**

```

library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
dlda_out <- lda_diag(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(dlda_out, penguins[pred_rows, -1], type = "class")

dlda_out2 <- lda_diag(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(dlda_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)

```

---

lda_eigen	<i>The Minimum Distance Rule using Moore-Penrose Inverse (MDMP) classifier</i>
-----------	--

---

**Description**

Given a set of training data, this function builds the MDMP classifier from Srivastava and Kubokawa (2007). The MDMP classifier is an adaptation of the linear discriminant analysis (LDA) classifier that is designed for small-sample, high-dimensional data. Srivastava and Kubokawa (2007) have proposed a modification of the standard maximum likelihood estimator of the pooled covariance matrix, where only the largest 95% of the eigenvalues and their corresponding eigenvectors are kept. The value of 95% is the default and can be changed via the `eigen_pct` argument.

The MDMP classifier from Srivastava and Kubokawa (2007) is an adaptation of the linear discriminant analysis (LDA) classifier that is designed for small-sample, high-dimensional data. Srivastava and Kubokawa (2007) have proposed a modification of the standard maximum likelihood estimator of the pooled covariance matrix, where only the largest 95% of the eigenvalues and their corresponding eigenvectors are kept.

**Usage**

```

lda_eigen(x, ...)

## Default S3 method:
lda_eigen(x, y, prior = NULL, eigen_pct = 0.95, ...)

## S3 method for class 'formula'
lda_eigen(formula, data, prior = NULL, ...)

## S3 method for class 'lda_eigen'
predict(object, newdata, type = c("class", "prob", "score"), ...)

```

**Arguments**

`x` Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.

...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
eigen_pct	the percentage of eigenvalues kept
formula	A formula of the form $\text{groups} \sim x_1 + x_2 + \dots$ . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in formula are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

### Details

The matrix of training observations are given in  $x$ . The rows of  $x$  contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in  $y$  are coerced to a factor. The length of  $y$  should match the number of rows in  $x$ .

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in  $y$ . The prior probabilities should be nonnegative and sum to one.

### Value

lda\_eigen object that contains the trained MDMP classifier

### References

Srivastava, M. and Kubokawa, T. (2007). "Comparison of Discrimination Methods for High Dimensional Data," Journal of the Japanese Statistical Association, 37, 1, 123-134.

### Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
mdmp_out <- lda_eigen(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(mdmp_out, penguins[pred_rows, -1], type = "class")

mdmp_out2 <- lda_eigen(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
```

```
predicted2 <- predict(mdmp_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

lda_emp_bayes	<i>The Minimum Distance Empirical Bayesian Estimator (MDEB) classifier</i>
---------------	--

---

## Description

Given a set of training data, this function builds the MDEB classifier from Srivastava and Kubokawa (2007). The MDEB classifier is an adaptation of the linear discriminant analysis (LDA) classifier that is designed for small-sample, high-dimensional data. Rather than using the standard maximum likelihood estimator of the pooled covariance matrix, Srivastava and Kubokawa (2007) have proposed an Empirical Bayes estimator where the eigenvalues of the pooled sample covariance matrix are shrunken towards the identity matrix: the shrinkage constant has a closed form and is quick to calculate.

The MDEB classifier from Srivastava and Kubokawa (2007) is an adaptation of the linear discriminant analysis (LDA) classifier that is designed for small-sample, high-dimensional data. Rather than using the standard maximum likelihood estimator of the pooled covariance matrix, Srivastava and Kubokawa (2007) have proposed an Empirical Bayes estimator where the eigenvalues of the pooled sample covariance matrix are shrunken towards the identity matrix: the shrinkage constant has a closed form and is quick to calculate

## Usage

```
lda_emp_bayes(x, ...)

## Default S3 method:
lda_emp_bayes(x, y, prior = NULL, ...)

## S3 method for class 'formula'
lda_emp_bayes(formula, data, prior = NULL, ...)

## S3 method for class 'lda_emp_bayes'
predict(object, newdata, type = c("class", "prob", "score"), ...)
```

## Arguments

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.

formula	A formula of the form $\text{groups} \sim x_1 + x_2 + \dots$ . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in formula are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

### Details

The matrix of training observations are given in  $x$ . The rows of  $x$  contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in  $y$  are coerced to a factor. The length of  $y$  should match the number of rows in  $x$ .

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in  $y$ . The prior probabilities should be nonnegative and sum to one.

### Value

lda\_emp\_bayes object that contains the trained MDEB classifier

### References

Srivastava, M. and Kubokawa, T. (2007). "Comparison of Discrimination Methods for High Dimensional Data," *Journal of the Japanese Statistical Association*, 37, 1, 123-134.

### Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
mdeb_out <- lda_emp_bayes(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(mdeb_out, penguins[pred_rows, -1], type = "class")

mdeb_out2 <- lda_emp_bayes(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(mdeb_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

lda_emp_bayes_eigen	<i>The Minimum Distance Rule using Modified Empirical Bayes (MD-MEB) classifier</i>
---------------------	---

---

## Description

Given a set of training data, this function builds the MDMEB classifier from Srivastava and Kubokawa (2007). The MDMEB classifier is an adaptation of the linear discriminant analysis (LDA) classifier that is designed for small-sample, high-dimensional data. Srivastava and Kubokawa (2007) have proposed a modification of the standard maximum likelihood estimator of the pooled covariance matrix, where only the largest 95% of the eigenvalues and their corresponding eigenvectors are kept. The resulting covariance matrix is then shrunken towards a scaled identity matrix. The value of 95% is the default and can be changed via the `eigen_pct` argument.

The MDMEB classifier is an adaptation of the linear discriminant analysis (LDA) classifier that is designed for small-sample, high-dimensional data. Srivastava and Kubokawa (2007) have proposed a modification of the standard maximum likelihood estimator of the pooled covariance matrix, where only the largest 95% of the eigenvalues and their corresponding eigenvectors are kept. The resulting covariance matrix is then shrunken towards a scaled identity matrix.

## Usage

```
lda_emp_bayes_eigen(x, ...)

## Default S3 method:
lda_emp_bayes_eigen(x, y, prior = NULL, eigen_pct = 0.95, ...)

## S3 method for class 'formula'
lda_emp_bayes_eigen(formula, data, prior = NULL, ...)

## S3 method for class 'lda_emp_bayes_eigen'
predict(object, newdata, type = c("class", "prob", "score"), ...)
```

## Arguments

<code>x</code>	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
<code>...</code>	additional arguments (not currently used).
<code>y</code>	Vector of class labels for each training observation. Only complete data are retained.
<code>prior</code>	Vector with prior probabilities for each class. If <code>NULL</code> (default), then equal probabilities are used. See details.
<code>eigen_pct</code>	the percentage of eigenvalues kept
<code>formula</code>	A formula of the form <code>groups ~ x1 + x2 + ...</code> . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.

data	data frame from which variables specified in formula are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

### Details

The matrix of training observations are given in `x`. The rows of `x` contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in `y` are coerced to a factor. The length of `y` should match the number of rows in `x`.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in `y`. The `prior` probabilities should be nonnegative and sum to one.

### Value

lda\_emp\_bayes\_eigen object that contains the trained MDMEB classifier

### References

Srivastava, M. and Kubokawa, T. (2007). "Comparison of Discrimination Methods for High Dimensional Data," *Journal of the Japanese Statistical Association*, 37, 1, 123-134.

### Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
mdmeh_out <- lda_emp_bayes_eigen(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(mdmeh_out, penguins[pred_rows, -1], type = "class")

mdmeh_out2 <- lda_emp_bayes_eigen(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(mdmeh_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

lda\_pseudo

*Linear Discriminant Analysis (LDA) with the Moore-Penrose Pseudo-Inverse***Description**

Given a set of training data, this function builds the Linear Discriminant Analysis (LDA) classifier, where the distributions of each class are assumed to be multivariate normal and share a common covariance matrix. When the pooled sample covariance matrix is singular, the linear discriminant function is incalculable. A common method to overcome this issue is to replace the inverse of the pooled sample covariance matrix with the Moore-Penrose pseudo-inverse, which is unique and always exists. Note that when the pooled sample covariance matrix is nonsingular, it is equal to the pseudo-inverse.

The Linear Discriminant Analysis (LDA) classifier involves the assumption that the distributions of each class are assumed to be multivariate normal and share a common covariance matrix. When the pooled sample covariance matrix is singular, the linear discriminant function is incalculable. A common method to overcome this issue is to replace the inverse of the pooled sample covariance matrix with the Moore-Penrose pseudo-inverse, which is unique and always exists. Note that when the pooled sample covariance matrix is nonsingular, it is equal to the pseudo-inverse.

**Usage**

```
lda_pseudo(x, ...)

## Default S3 method:
lda_pseudo(x, y, prior = NULL, tol = 1e-08, ...)

## S3 method for class 'formula'
lda_pseudo(formula, data, prior = NULL, tol = 1e-08, ...)

## S3 method for class 'lda_pseudo'
predict(object, newdata, type = c("class", "prob", "score"), ...)
```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
tol	tolerance value below which eigenvalues are considered numerically equal to 0
formula	A formula of the form groups ~ x1 + x2 + ... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.

data	data frame from which variables specified in formula are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

### Details

The matrix of training observations are given in  $x$ . The rows of  $x$  contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in  $y$  are coerced to a factor. The length of  $y$  should match the number of rows in  $x$ .

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in  $y$ . The prior probabilities should be nonnegative and sum to one.

### Value

lda\_pseudo object that contains the trained lda\_pseudo classifier

### Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
lda_pseudo_out <- lda_pseudo(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(lda_pseudo_out, penguins[pred_rows, -1], type = "class")

lda_pseudo_out2 <- lda_pseudo(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(lda_pseudo_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```



## Description

Given a set of training data, this function builds the Linear Discriminant Analysis (LDA) classifier, where the distributions of each class are assumed to be multivariate normal and share a common covariance matrix. When the pooled sample covariance matrix is singular, the linear discriminant function is in calculable. This function replaces the inverse of pooled sample covariance matrix with an estimator proposed by Schafer and Strimmer (2005). The estimator is calculated via `corpcor::invcov.shrink()`.

The Linear Discriminant Analysis (LDA) classifier involves the assumption that the distributions of each class are assumed to be multivariate normal and share a common covariance matrix. When the pooled sample covariance matrix is singular, the linear discriminant function is in calculable. Here, the inverse of the pooled sample covariance matrix is replaced with an estimator from Schafer and Strimmer (2005).

## Usage

```
lda_schafer(x, ...)

## Default S3 method:
lda_schafer(x, y, prior = NULL, ...)

## S3 method for class 'formula'
lda_schafer(formula, data, prior = NULL, ...)

## S3 method for class 'lda_schafer'
predict(object, newdata, type = c("class", "prob", "score"), ...)
```

## Arguments

<code>x</code>	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
<code>...</code>	Options passed to <code>corpcor::invcov.shrink()</code>
<code>y</code>	Vector of class labels for each training observation. Only complete data are retained.
<code>prior</code>	Vector with prior probabilities for each class. If <code>NULL</code> (default), then equal probabilities are used. See details.
<code>formula</code>	A formula of the form <code>groups ~ x1 + x2 + ...</code> . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
<code>data</code>	data frame from which variables specified in <code>formula</code> are preferentially to be taken.
<code>object</code>	Fitted model object
<code>newdata</code>	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
<code>type</code>	Prediction type: either <code>"class"</code> , <code>"prob"</code> , or <code>"score"</code> .

## Details

The matrix of training observations are given in  $x$ . The rows of  $x$  contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in  $y$  are coerced to a factor. The length of  $y$  should match the number of rows in  $x$ .

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in  $y$ . The prior probabilities should be nonnegative and sum to one.

## Value

`lda_schafer` object that contains the trained classifier

## References

Schafer, J., and Strimmer, K. (2005). "A shrinkage approach to large-scale covariance estimation and implications for functional genomics," *Statist. Appl. Genet. Mol. Biol.* 4, 32.

## Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
lda_schafer_out <- lda_schafer(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(lda_schafer_out, penguins[pred_rows, -1], type = "class")

lda_schafer_out2 <- lda_schafer(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(lda_schafer_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

lda\_shrink\_cov

*Shrinkage-based Diagonal Linear Discriminant Analysis (SDLDA)*

---

## Description

Given a set of training data, this function builds the Shrinkage-based Diagonal Linear Discriminant Analysis (SDLDA) classifier, which is based on the DLDA classifier, often attributed to Dudoit et al. (2002). The DLDA classifier belongs to the family of Naive Bayes classifiers, where the distributions of each class are assumed to be multivariate normal and to share a common covariance matrix. To improve the estimation of the pooled variances, Pang et al. (2009) proposed the SDLDA classifier which uses a shrinkage-based estimators of the pooled covariance matrix.

The SDLDA classifier is a modification to LDA, where the off-diagonal elements of the pooled sample covariance matrix are set to zero. To improve the estimation of the pooled variances, we use a shrinkage method from Pang et al. (2009).

**Usage**

```
lda_shrink_cov(x, ...)

## Default S3 method:
lda_shrink_cov(x, y, prior = NULL, num_alphas = 101, ...)

## S3 method for class 'formula'
lda_shrink_cov(formula, data, prior = NULL, num_alphas = 101, ...)

## S3 method for class 'lda_shrink_cov'
predict(object, newdata, type = c("class", "prob", "score"), ...)
```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
num_alphas	the number of values used to find the optimal amount of shrinkage
formula	A formula of the form groups ~ x1 + x2 + ... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in formula are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

**Details**

The DLDA classifier is a modification to the well-known LDA classifier, where the off-diagonal elements of the pooled covariance matrix are assumed to be zero – the features are assumed to be uncorrelated. Under multivariate normality, the assumption uncorrelated features is equivalent to the assumption of independent features. The feature-independence assumption is a notable attribute of the Naive Bayes classifier family. The benefit of these classifiers is that they are fast and have much fewer parameters to estimate, especially when the number of features is quite large.

The matrix of training observations are given in x. The rows of x contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in y are coerced to a factor. The length of y should match the number of rows in x.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is `NULL` (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in `y`. The prior probabilities should be nonnegative and sum to one.

## Value

`lda_shrink_cov` object that contains the trained SDLDA classifier

## References

Dudoit, S., Fridlyand, J., & Speed, T. P. (2002). "Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data," *Journal of the American Statistical Association*, 97, 457, 77-87.

Pang, H., Tong, T., & Zhao, H. (2009). "Shrinkage-based Diagonal Discriminant Analysis and Its Applications in High-Dimensional Data," *Biometrics*, 65, 4, 1021-1029.

## Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
sdlda_out <- lda_shrink_cov(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(sdlda_out, penguins[pred_rows, -1], type = "class")

sdlda_out2 <- lda_shrink_cov(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(sdlda_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

<code>lda_shrink_mean</code>	<i>Shrinkage-mean-based Diagonal Linear Discriminant Analysis (SmDLDA) from Tong, Chen, and Zhao (2012)</i>
------------------------------	---

---

## Description

Given a set of training data, this function builds the Shrinkage-mean-based Diagonal Linear Discriminant Analysis (SmDLDA) classifier from Tong, Chen, and Zhao (2012). The SmDLDA classifier incorporates a Lindley-type shrunken mean estimator into the DLDA classifier from Dudoit et al. (2002). For more about the DLDA classifier, see `lda_diag()`.

The SmDLDA classifier is a modification to LDA, where the off-diagonal elements of the pooled sample covariance matrix are set to zero.

**Usage**

```
lda_shrink_mean(x, ...)

## Default S3 method:
lda_shrink_mean(x, y, prior = NULL, ...)

## S3 method for class 'formula'
lda_shrink_mean(formula, data, prior = NULL, ...)

## S3 method for class 'lda_shrink_mean'
predict(object, newdata, type = c("class", "prob", "score"), ...)
```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
formula	A formula of the form $\text{groups} \sim x_1 + x_2 + \dots$ . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in formula are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

**Details**

The DLDA classifier belongs to the family of Naive Bayes classifiers, where the distributions of each class are assumed to be multivariate normal and to share a common covariance matrix.

The DLDA classifier is a modification to the well-known LDA classifier, where the off-diagonal elements of the pooled sample covariance matrix are assumed to be zero – the features are assumed to be uncorrelated. Under multivariate normality, the assumption uncorrelated features is equivalent to the assumption of independent features. The feature-independence assumption is a notable attribute of the Naive Bayes classifier family. The benefit of these classifiers is that they are fast and have much fewer parameters to estimate, especially when the number of features is quite large.

The matrix of training observations are given in *x*. The rows of *x* contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in *y* are coerced to a factor. The length of *y* should match the number of rows in *x*.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is `NULL` (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in `y`. The prior probabilities should be nonnegative and sum to one.

### Value

`lda_shrink_mean` object that contains the trained `SmDLDA` classifier

### References

Tong, T., Chen, L., and Zhao, H. (2012), "Improved Mean Estimation and Its Application to Diagonal Discriminant Analysis," *Bioinformatics*, 28, 4, 531-537. <https://academic.oup.com/bioinformatics/article/28/4/531/211887>

Dudoit, S., Fridlyand, J., & Speed, T. P. (2002). "Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data," *Journal of the American Statistical Association*, 97, 457, 77-87.

### Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
smdllda_out <- lda_shrink_mean(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(smdllda_out, penguins[pred_rows, -1], type = "class")

smdllda_out2 <- lda_shrink_mean(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(smdllda_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

lda\_thomaz

*Linear Discriminant Analysis using the Thomaz-Kitani-Gillies Covariance Matrix Estimator*

---

### Description

Given a set of training data, this function builds the Linear Discriminant Analysis (LDA) classifier, where the distributions of each class are assumed to be multivariate normal and share a common covariance matrix. When the pooled sample covariance matrix is singular, the linear discriminant function is incalculable. This function replaces the pooled sample covariance matrix with a regularized estimator from Thomaz et al. (2006), where the smallest eigenvalues are replaced with the average eigenvalue. Specifically, small eigenvalues here means that the eigenvalues are less than the average eigenvalue.

Given a set of training data, this function builds the Linear Discriminant Analysis (LDA) classifier, where the distributions of each class are assumed to be multivariate normal and share a common

covariance matrix. When the pooled sample covariance matrix is singular, the linear discriminant function is in calculable. This function replaces the pooled sample covariance matrix with a regularized estimator from Thomaz et al. (2006), where the smallest eigenvalues are replaced with the average eigenvalue. Specifically, small eigenvalues here means that the eigenvalues are less than the average eigenvalue.

### Usage

```
lda_thomaz(x, ...)

## Default S3 method:
lda_thomaz(x, y, prior = NULL, ...)

## S3 method for class 'formula'
lda_thomaz(formula, data, prior = NULL, ...)

## S3 method for class 'lda_thomaz'
predict(object, newdata, type = c("class", "prob", "score"), ...)
```

### Arguments

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
formula	A formula of the form $\text{groups} \sim x_1 + x_2 + \dots$ . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in <code>formula</code> are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

### Details

The matrix of training observations are given in `x`. The rows of `x` contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in `y` are coerced to a factor. The length of `y` should match the number of rows in `x`.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is `NULL` (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in `y`. The prior probabilities should be nonnegative and sum to one.

### Value

`lda_thomaz` object that contains the trained classifier

### References

Thomaz, C. E., Kitani, E. C., and Gillies, D. F. (2006). "A maximum uncertainty LDA-based approach for limited sample size problems with application to face recognition," *J. Braz. Comp. Soc.*, 12, 2, 7-18.

### Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
lda_thomaz_out <- lda_thomaz(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(lda_thomaz_out, penguins[pred_rows, -1], type = "class")

lda_thomaz_out2 <- lda_thomaz(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(lda_thomaz_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

log\_determinant

*Computes the log determinant of a matrix.*

---

### Description

Computes the log determinant of a matrix.

### Usage

```
log_determinant(x)
```

### Arguments

`x`                    matrix

### Value

log determinant of `x`



---

no_intercept	<i>Removes the intercept term from a formula if it is included</i>
--------------	--

---

### Description

Often, we prefer not to have an intercept term in a model, but user-specified formulas might have included the intercept term. In this case, we wish to update the formula but without the intercept term. This is especially true in numerous classification models, where errors and doom can occur if an intercept is included in the model.

### Usage

```
no_intercept(formula, data)
```

### Arguments

formula	a model formula to remove its intercept term
data	data frame

### Value

formula with no intercept term

### Examples

```
iris_formula <- formula(Species ~ .)
no_intercept(iris_formula, data = iris)
```

---

plot.rda_high_dim_cv	<i>Plots a heatmap of cross-validation error grid for a HDRDA classifier object.</i>
----------------------	--

---

### Description

Uses `ggplot2::ggplot2()` to plot a heatmap of the training error grid.

### Usage

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

### Arguments

x	object to plot
...	unused

**Value**

A ggplot object.

---

posterior_probs	<i>Computes posterior probabilities via Bayes Theorem under normality</i>
-----------------	---

---

**Description**

Computes posterior probabilities via Bayes Theorem under normality

**Usage**

```
posterior_probs(x, means, covs, priors)
```

**Arguments**

x	matrix of observations
means	list of means for each class
covs	list of covariance matrices for each class
priors	list of prior probabilities for each class

**Value**

matrix of posterior probabilities for each observation

---

qda_diag	<i>Diagonal Quadratic Discriminant Analysis (DQDA)</i>
----------	--

---

**Description**

Given a set of training data, this function builds the Diagonal Quadratic Discriminant Analysis (DQDA) classifier, which is often attributed to Dudoit et al. (2002). The DQDA classifier belongs to the family of Naive Bayes classifiers, where the distributions of each class are assumed to be multivariate normal. Note that the DLDA classifier is a special case of the DQDA classifier.

The DQDA classifier is a modification to QDA, where the off-diagonal elements of the pooled sample covariance matrix are set to zero.

**Usage**

```

qda_diag(x, ...)

## Default S3 method:
qda_diag(x, y, prior = NULL, ...)

## S3 method for class 'formula'
qda_diag(formula, data, prior = NULL, ...)

## S3 method for class 'qda_diag'
predict(object, newdata, type = c("class", "prob", "score"), ...)

```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
formula	A formula of the form $\text{groups} \sim x_1 + x_2 + \dots$ . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in <code>formula</code> are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

**Details**

The DQDA classifier is a modification to the well-known QDA classifier, where the off-diagonal elements of each class covariance matrix are assumed to be zero – the features are assumed to be uncorrelated. Under multivariate normality, the assumption uncorrelated features is equivalent to the assumption of independent features. The feature-independence assumption is a notable attribute of the Naive Bayes classifier family. The benefit of these classifiers is that they are fast and have much fewer parameters to estimate, especially when the number of features is quite large.

The matrix of training observations are given in `x`. The rows of `x` contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in `y` are coerced to a factor. The length of `y` should match the number of rows in `x`.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, *prior*, contains the *a priori* class membership for each class. If *prior* is `NULL` (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, *prior* should be a vector with the same length as the number of classes in *y*. The prior probabilities should be nonnegative and sum to one.

## Value

`qda_diag` object that contains the trained DQDA classifier

## References

Dudoit, S., Fridlyand, J., & Speed, T. P. (2002). "Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data," *Journal of the American Statistical Association*, 97, 457, 77-87.

## Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
dqda_out <- qda_diag(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(dqda_out, penguins[pred_rows, -1], type = "class")

dqda_out2 <- qda_diag(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(dqda_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

<code>qda_shrink_cov</code>	<i>Shrinkage-based Diagonal Quadratic Discriminant Analysis (SDQDA)</i>
-----------------------------	---

---

## Description

Given a set of training data, this function builds the Shrinkage-based Diagonal Quadratic Discriminant Analysis (SDQDA) classifier, which is based on the DQDA classifier, often attributed to Dudoit et al. (2002). The DQDA classifier belongs to the family of Naive Bayes classifiers, where the distributions of each class are assumed to be multivariate normal. To improve the estimation of the class variances, Pang et al. (2009) proposed the SDQDA classifier which uses a shrinkage-based estimators of each class covariance matrix.

The SDQDA classifier is a modification to QDA, where the off-diagonal elements of the pooled sample covariance matrix are set to zero. To improve the estimation of the pooled variances, we use a shrinkage method from Pang et al. (2009).

**Usage**

```

qda_shrink_cov(x, ...)

## Default S3 method:
qda_shrink_cov(x, y, prior = NULL, num_alphas = 101, ...)

## S3 method for class 'formula'
qda_shrink_cov(formula, data, prior = NULL, num_alphas = 101, ...)

## S3 method for class 'qda_shrink_cov'
predict(object, newdata, type = c("class", "prob", "score"), ...)

```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	Vector of class labels for each training observation. Only complete data are retained.
prior	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
num_alphas	the number of values used to find the optimal amount of shrinkage
formula	A formula of the form $\text{groups} \sim x_1 + x_2 + \dots$ . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in formula are preferentially to be taken.
object	Fitted model object
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
type	Prediction type: either "class", "prob", or "score".

**Details**

The DQDA classifier is a modification to the well-known QDA classifier, where the off-diagonal elements of the pooled covariance matrix are assumed to be zero – the features are assumed to be uncorrelated. Under multivariate normality, the assumption uncorrelated features is equivalent to the assumption of independent features. The feature-independence assumption is a notable attribute of the Naive Bayes classifier family. The benefit of these classifiers is that they are fast and have much fewer parameters to estimate, especially when the number of features is quite large.

The matrix of training observations are given in *x*. The rows of *x* contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in *y* are coerced to a factor. The length of *y* should match the number of rows in *x*.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is `NULL` (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in `y`. The prior probabilities should be nonnegative and sum to one.

## Value

`qda_shrink_cov` object that contains the trained SDQDA classifier

## References

Dudoit, S., Fridlyand, J., & Speed, T. P. (2002). "Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data," *Journal of the American Statistical Association*, 97, 457, 77-87.

Pang, H., Tong, T., & Zhao, H. (2009). "Shrinkage-based Diagonal Discriminant Analysis and Its Applications in High-Dimensional Data," *Biometrics*, 65, 4, 1021-1029.

## Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]# set.seed(42)
sdqda_out <- qda_shrink_cov(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(sdqda_out, penguins[pred_rows, -1], type = "class")

sdqda_out2 <- qda_shrink_cov(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(sdqda_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

<code>qda_shrink_mean</code>	<i>Shrinkage-mean-based Diagonal Quadratic Discriminant Analysis (SmDQDA) from Tong, Chen, and Zhao (2012)</i>
------------------------------	--

---

## Description

Given a set of training data, this function builds the Shrinkage-mean-based Diagonal Quadratic Discriminant Analysis (SmDQDA) classifier from Tong, Chen, and Zhao (2012). The SmDQDA classifier incorporates a Lindley-type shrunken mean estimator into the DQDA classifier from Dudoit et al. (2002). For more about the DQDA classifier, see [qda\\_diag\(\)](#).

The SmDQDA classifier is a modification to QDA, where the off-diagonal elements of the pooled sample covariance matrix are set to zero.

**Usage**

```

qda_shrink_mean(x, ...)

## Default S3 method:
qda_shrink_mean(x, y, prior = NULL, ...)

## S3 method for class 'formula'
qda_shrink_mean(formula, data, prior = NULL, ...)

## S3 method for class 'qda_shrink_mean'
predict(object, newdata, type = c("class", "prob", "score"), ...)

```

**Arguments**

<code>x</code>	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
<code>...</code>	additional arguments (not currently used).
<code>y</code>	Vector of class labels for each training observation. Only complete data are retained.
<code>prior</code>	Vector with prior probabilities for each class. If NULL (default), then equal probabilities are used. See details.
<code>formula</code>	A formula of the form <code>groups ~ x1 + x2 + ...</code> . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
<code>data</code>	data frame from which variables specified in <code>formula</code> are preferentially to be taken.
<code>object</code>	Fitted model object
<code>newdata</code>	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
<code>type</code>	Prediction type: either "class", "prob", or "score".

**Details**

The DQDA classifier is a modification to the well-known QDA classifier, where the off-diagonal elements of each class covariance matrix are assumed to be zero – the features are assumed to be uncorrelated. Under multivariate normality, the assumption uncorrelated features is equivalent to the assumption of independent features. The feature-independence assumption is a notable attribute of the Naive Bayes classifier family. The benefit of these classifiers is that they are fast and have much fewer parameters to estimate, especially when the number of features is quite large.

The matrix of training observations are given in `x`. The rows of `x` contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in `y` are coerced to a factor. The length of `y` should match the number of rows in `x`.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, *prior*, contains the *a priori* class membership for each class. If *prior* is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, *prior* should be a vector with the same length as the number of classes in *y*. The prior probabilities should be nonnegative and sum to one.

### Value

`qda_shrink_mean` object that contains the trained SmdQDA classifier

### References

Tong, T., Chen, L., and Zhao, H. (2012), "Improved Mean Estimation and Its Application to Diagonal Discriminant Analysis," *Bioinformatics*, 28, 4, 531-537. <https://academic.oup.com/bioinformatics/article/28/4/531/211887>

Dudoit, S., Fridlyand, J., & Speed, T. P. (2002). "Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data," *Journal of the American Statistical Association*, 97, 457, 77-87.

### Examples

```
library(modeldata)
data(penguins)
pred_rows <- seq(1, 344, by = 20)
penguins <- penguins[, c("species", "body_mass_g", "flipper_length_mm")]
smdqda_out <- qda_shrink_mean(species ~ ., data = penguins[-pred_rows, ])
predicted <- predict(smdqda_out, penguins[pred_rows, -1], type = "class")

smdqda_out2 <- qda_shrink_mean(x = penguins[-pred_rows, -1], y = penguins$species[-pred_rows])
predicted2 <- predict(smdqda_out2, penguins[pred_rows, -1], type = "class")
all.equal(predicted, predicted2)
```

---

quadform

*Quadratic form of a matrix and a vector*

---

### Description

We compute the quadratic form of a vector and a matrix in an efficient manner. Let  $x$  be a real vector of length  $p$ , and let  $A$  be a  $p \times p$  real matrix. Then, we compute the quadratic form  $q = x'Ax$ .

### Usage

```
quadform(A, x)
```

### Arguments

$A$	matrix of dimension $p \times p$
$x$	vector of length $p$



**Details**

A naive way to compute the quadratic form is to explicitly write  $t(x) \%*\% A \%*\% x$ , but for large  $p$ , this operation is inefficient. We provide a more efficient method below.

Note that we have adapted the code from: <https://stat.ethz.ch/pipermail/r-help/2005-November/081940.html>

**Value**

scalar value

---

quadform\_inv

*Quadratic Form of the inverse of a matrix and a vector*

---

**Description**

We compute the quadratic form of a vector and the inverse of a matrix in an efficient manner. Let  $x$  be a real vector of length  $p$ , and let  $A$  be a  $p \times p$  nonsingular matrix. Then, we compute the quadratic form  $q = x' A^{-1} x$ .

**Usage**

```
quadform_inv(A, x)
```

**Arguments**

A	matrix that is $p \times p$ and nonsingular
x	vector of length $p$

**Details**

A naive way to compute the quadratic form is to explicitly write  $t(x) \%*\% solve(A) \%*\% x$ , but for large  $p$ , this operation is inefficient. We provide a more efficient method below.

Note that we have adapted the code from: <https://stat.ethz.ch/pipermail/r-help/2005-November/081940.html>

**Value**

scalar value

---

rda_cov	<i>Calculates the RDA covariance-matrix estimators for each class</i>
---------	---

---

### Description

For the classes given in the vector `y`, this function calculates the class covariance-matrix estimators employed in the HDRDA classifier, implemented in `rda_high_dim()`.

### Usage

```
rda_cov(x, y, lambda = 1)
```

### Arguments

<code>x</code>	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
<code>y</code>	vector of class labels for each training observation
<code>lambda</code>	the RDA pooling parameter. Must be between 0 and 1, inclusively.

### Value

list containing the RDA covariance-matrix estimators for each class given in `y`

### References

Ramey, J. A., Stein, C. K., and Young, D. M. (2013), "High-Dimensional Regularized Discriminant Analysis."

---

rda_high_dim	<i>High-Dimensional Regularized Discriminant Analysis (HDRDA)</i>
--------------	---

---

### Description

Given a set of training data, this function builds the HDRDA classifier from Ramey, Stein, and Young (2017). Specially designed for small-sample, high-dimensional data, the HDRDA classifier incorporates dimension reduction and covariance-matrix shrinkage to enable a computationally efficient classifier.

For a given `rda_high_dim` object, we predict the class of each observation (row) of the the matrix given in `newdata`.

**Usage**

```

rda_high_dim(x, ...)

## Default S3 method:
rda_high_dim(
  x,
  y,
  lambda = 1,
  gamma = 0,
  shrinkage_type = c("ridge", "convex"),
  prior = NULL,
  tol = 1e-06,
  ...
)

## S3 method for class 'formula'
rda_high_dim(formula, data, ...)

## S3 method for class 'rda_high_dim'
predict(
  object,
  newdata,
  projected = FALSE,
  type = c("class", "prob", "score"),
  ...
)

```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
...	additional arguments (not currently used).
y	vector of class labels for each training observation
lambda	the HDRDA pooling parameter. Must be between 0 and 1, inclusively.
gamma	a numeric values used for the shrinkage parameter.
shrinkage_type	the type of covariance-matrix shrinkage to apply. By default, a ridge-like shrinkage is applied. If convex is given, then shrinkage similar to Friedman (1989) is applied. See Ramey et al. (2017) for details.
prior	vector with prior probabilities for each class. If NULL (default), then the sample proportion of observations belonging to each class equal probabilities are used. See details.
tol	a threshold for determining nonzero eigenvalues.
formula	A formula of the form groups ~ x1 + x2 + ... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	data frame from which variables specified in formula are preferentially to be taken.

object	Object of type <code>rda_high_dim</code> that contains the trained HDRDA classifier
newdata	Matrix or data frame of observations to predict. Each row corresponds to a new observation.
projected	logical indicating whether <code>newdata</code> have already been projected to a $q$ -dimensional subspace. This argument can yield large gains in speed when the linear transformation has already been performed.
type	Prediction type: either <code>"class"</code> , <code>"prob"</code> , or <code>"score"</code> .

## Details

The HDRDA classifier utilizes a covariance-matrix estimator that is a convex combination of the covariance-matrix estimators used in the Linear Discriminant Analysis (LDA) and Quadratic Discriminant Analysis (QDA) classifiers. For each of the  $K$  classes given in  $y$ , ( $k = 1, \dots, K$ ), we first define this convex combination as

$$\hat{\Sigma}_k(\lambda) = (1 - \lambda)\hat{\Sigma}_k + \lambda\hat{\Sigma},$$

where  $\lambda \in [0, 1]$  is the *pooling* parameter. We then calculate the covariance-matrix estimator

$$\tilde{\Sigma}_k = \alpha_k \hat{\Sigma}_k(\lambda) + \gamma I_p,$$

where  $I_p$  is the  $p \times p$  identity matrix. The matrix  $\tilde{\Sigma}_k$  is substituted into the HDRDA classifier. See Ramey et al. (2017) for more details.

The matrix of training observations are given in  $x$ . The rows of  $x$  contain the sample observations, and the columns contain the features for each training observation. The vector of class labels given in  $y$  are coerced to a factor. The length of  $y$  should match the number of rows in  $x$ .

The vector `prior` contains the *a priori* class membership for each class. If `prior` is `NULL` (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in  $y$ . The prior probabilities should be nonnegative and sum to one. The order of the prior probabilities is assumed to match the levels of `factor(y)`.

## Value

`rda_high_dim` object that contains the trained HDRDA classifier  
 list with predicted class and discriminant scores for each of the  $K$  classes

## References

- Ramey, J. A., Stein, C. K., and Young, D. M. (2017), "High-Dimensional Regularized Discriminant Analysis." <https://arxiv.org/abs/1602.01182>.
- Friedman, J. H. (1989), "Regularized Discriminant Analysis," *Journal of American Statistical Association*, 84, 405, 165-175. <http://www.jstor.org/stable/2289860> (Requires full-text access).

---

rda\_high\_dim\_cv      *Helper function to optimize the HDRDA classifier via cross-validation*

---

### Description

For a given data set, we apply cross-validation (cv) to select the optimal HDRDA tuning parameters.

### Usage

```
rda_high_dim_cv(  
  x,  
  y,  
  num_folds = 10,  
  num_lambda = 21,  
  num_gamma = 8,  
  shrinkage_type = c("ridge", "convex"),  
  verbose = FALSE,  
  ...  
)
```

### Arguments

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
y	vector of class labels for each training observation
num_folds	the number of cross-validation folds.
num_lambda	The number of values of lambda to consider
num_gamma	The number of values of gamma to consider
shrinkage_type	the type of covariance-matrix shrinkage to apply. By default, a ridge-like shrinkage is applied. If convex is given, then shrinkage similar to Friedman (1989) is applied. See Ramey et al. (2017) for details.
verbose	If set to TRUE, summary information will be outputted as the optimal model is being determined.
...	Options passed to <code>rda_high_dim()</code> .

### Details

The number of cross-validation folds is given in `num_folds`.

### Value

list containing the HDRDA model that minimizes cross-validation as well as a data.frame that summarizes the cross-validation results.

---

rda_weights	<i>Computes the observation weights for each class for the HDRDA classifier</i>
-------------	---

---

### Description

This function calculates the weight for each observation in the data matrix  $x$  in order to calculate the covariance matrices employed in the HDRDA classifier, implemented in `rda_high_dim()`.

### Usage

```
rda_weights(x, y, lambda = 1)
```

### Arguments

$x$	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
$y$	vector of class labels for each training observation
$\lambda$	the RDA pooling parameter. Must be between 0 and 1, inclusively.

### Value

list containing the observations for each class given in  $y$

### References

Ramey, J. A., Stein, C. K., and Young, D. M. (2013), "High-Dimensional Regularized Discriminant Analysis."

---

regdiscrim_estimates	<i>Computes estimates and ancillary information for regularized discriminant classifiers</i>
----------------------	--

---

### Description

Computes the maximum likelihood estimators (MLEs) for each class under the assumption of multivariate normality for each class. Also, computes ancillary information necessary for classifier summary, such as sample size, the number of features, etc.

### Usage

```
regdiscrim_estimates(x, y, cov = TRUE, prior = NULL)
```

**Arguments**

x	Matrix or data frame containing the training data. The rows are the sample observations, and the columns are the features. Only complete data are retained.
y	vector of class labels for each training observation
cov	logical. Should the sample covariance matrices be computed? (Default: yes)
prior	vector with prior probabilities for each class. If NULL (default), then the sample proportions are used. See details.

**Details**

This function computes the common estimates and ancillary information used in all of the regularized discriminant classifiers in the `sparsediscrim` package.

The matrix of training observations are given in `x`. The rows of `x` contain the sample observations, and the columns contain the features for each training observation.

The vector of class labels given in `y` are coerced to a factor. The length of `y` should match the number of rows in `x`.

An error is thrown if a given class has less than 2 observations because the variance for each feature within a class cannot be estimated with less than 2 observations.

The vector, `prior`, contains the *a priori* class membership for each class. If `prior` is NULL (default), the class membership probabilities are estimated as the sample proportion of observations belonging to each class. Otherwise, `prior` should be a vector with the same length as the number of classes in `y`. The `prior` probabilities should be nonnegative and sum to one.

**Value**

named list with estimators for each class and necessary ancillary information

---

risk\_stein

*Stein Risk function from Pang et al. (2009).*

---

**Description**

This function finds the value for  $\alpha \in [0, 1]$  that empirically minimizes the average risk under a Stein loss function, which is given on page 1023 of Pang et al. (2009).

**Usage**

```
risk_stein(N, K, var_feature, num_alphas = 101, t = -1)
```

**Arguments**

N	the sample size.
K	the number of classes.
var_feature	a vector of the sample variances for each dimension.
num_alphas	The number of values used to find the optimal amount of shrinkage.
t	a constant specified by the user that indicates the exponent to use with the variance estimator. By default, t = -1 as in Pang et al. See the paper for more details.

**Value**

list with

- alpha: the alpha that minimizes the average risk under a Stein loss function. If the minimum is not unique, we randomly select an alpha from the minimizers.
- risk: the minimum average risk attained.

**References**

Pang, H., Tong, T., & Zhao, H. (2009). "Shrinkage-based Diagonal Discriminant Analysis and Its Applications in High-Dimensional Data," *Biometrics*, 65, 4, 1021-1029. <https://onlinelibrary.wiley.com/doi/abs/10.1111/j.1541-0420.2009.01200.x>

---

solve_chol	<i>Computes the inverse of a symmetric, positive-definite matrix using the Cholesky decomposition</i>
------------	---

---

**Description**

This is often faster than `solve()` for larger matrices. See, for example: <http://blog.phytools.org/2012/12/faster-inversion-of-square-symmetric.html> and <https://stats.stackexchange.com/questions/14951/efficient-calculation-of-matrix-inverse-in-r>.

**Usage**

```
solve_chol(x)
```

**Arguments**

x	symmetric, positive-definite matrix
---	-------------------------------------

**Value**

the inverse of x



---

tong\_mean\_shrinkage    *Tong et al. (2012)'s Lindley-type Shrunken Mean Estimator*

---

### Description

An implementation of the Lindley-type shrunken mean estimator utilized in shrinkage-mean-based diagonal linear discriminant analysis (SmDLDA).

### Usage

```
tong_mean_shrinkage(x, r_opt = NULL)
```

### Arguments

`x`                    a matrix with  $n$  rows and  $p$  columns.  
`r_opt`                the shrinkage coefficient. If `NULL` (default), we calculate the shrinkage coefficient with the formula given just above Equation 5 on page 533 and denoted by  $\hat{r}_{opt}$ . We allow the user to specify an alternative value to investigate better approximations.

### Value

vector of length  $p$  with the shrunken mean estimator

### References

Tong, T., Chen, L., and Zhao, H. (2012), "Improved Mean Estimation and Its Application to Diagonal Discriminant Analysis," *Bioinformatics*, 28, 4, 531-537. <https://academic.oup.com/bioinformatics/article/28/4/531/211887>

---

two\_class\_sim\_data    *Example bivariate classification data from caret*

---

### Description

Example bivariate classification data from caret

### Details

These data were generated using by invoking the `twoClassSim()` function in the `caret` package.

### Value

```
two_class_sim_data
  a tibble
```

**Examples**

```
data(two_class_sim_data)
```

---

```
update_rda_high_dim     Helper function to update tuning parameters for the HDRDA classifier
```

---

**Description**

This function updates some of the quantities in the HDRDA classifier based on updated values of lambda and gamma. The update can greatly expedite cross-validation to examine a large grid of values for lambda and gamma.

**Usage**

```
update_rda_high_dim(obj, lambda = 1, gamma = 0)
```

**Arguments**

obj	a rda_high_dim object
lambda	a numeric value between 0 and 1, inclusively
gamma	a numeric value (nonnegative)

**Value**

a rda\_high\_dim object with updated estimates

---

```
var_shrinkage             Shrinkage-based estimator of variances for each feature from Pang et al. (2009).
```

---

**Description**

This function computes the shrinkage-based estimator of variance of each feature (variable) from Pang et al. (2009) for the SDLDA classifier.

**Usage**

```
var_shrinkage(N, K, var_feature, num_alphas = 101, t = -1)
```

**Arguments**

N	the sample size.
K	the number of classes.
var_feature	a vector of the sample variances for each feature.
num_alphas	The number of values used to find the optimal amount of shrinkage.
t	a constant specified by the user that indicates the exponent to use with the variance estimator. By default, t = -1 as in Pang et al. See the paper for more details.

**Value**

a vector of the shrunken variances for each feature.

**References**

Pang, H., Tong, T., & Zhao, H. (2009). "Shrinkage-based Diagonal Discriminant Analysis and Its Applications in High-Dimensional Data," *Biometrics*, 65, 4, 1021-1029. <https://onlinelibrary.wiley.com/doi/abs/10.1111/j.1541-0420.2009.01200.x>

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