

Package ‘binda’

November 20, 2021

Version 1.0.4

Date 2021-11-20

Title Multi-Class Discriminant Analysis using Binary Predictors

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Depends R (>= 3.0.2), entropy (>= 1.3.1)

Imports graphics, stats, utils

Suggests crossval

Description Implements functions for multi-class discriminant analysis using binary predictors, for corresponding variable selection, and for dichotomizing continuous data.

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URL <https://strimmerlab.github.io/software/binda/>

NeedsCompilation no

Repository CRAN

Date/Publication 2021-11-20 18:00:02 UTC

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binda-package	<i>The binda Package</i>
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Description

The "binda" package implements functions for multi-class discriminant analysis using binary predictors, for corresponding variable selection, and for dichotomizing continuous data.

Author(s)

Sebastian Gibb and Korbinian Strimmer (<https://strimmerlab.github.io/>)

References

Gibb, S., and K. Strimmer. 2015. Differential protein expression and peak selection in mass spectrometry data by binary discriminant analysis. *Bioinformatics* 31:3156-3162. <DOI:10.1093/bioinformatics/btv334>
 Website: <https://strimmerlab.github.io/software/binda/>

See Also

[binda](#), [binda.ranking](#), [dichotomize](#), [chances](#).

binda	<i>Binary Discriminant Analysis: Model Fit and Class Prediction</i>
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Description

binda trains a diagonal multivariate Bernoulli model. predict.binda performs corresponding class prediction.

Usage

```
binda(Xtrain, L, lambda.freqs, verbose=TRUE)
## S3 method for class 'binda'
predict(object, Xtest, verbose=TRUE, ...)
```

Arguments

Xtrain	A matrix containing the training data set. Note that the rows correspond to observations and the columns to variables.
L	A factor with the class labels of the training samples.
lambda.freqs	Shrinkage intensity for the frequencies. If not specified it is estimated from the data. lambda.freqs=0 implies no shrinkage (i.e. empirical frequencies) and lambda.freqs=1 complete shrinkage (i.e. uniform frequencies).
verbose	Report shrinkage intensities (binda) and number of used features (predict.binda).


```
colnames(Xtest) = paste0("V", 1:ncol(Xtest))
predict(binda.fit, Xtest)
```

binda.ranking

Binary Discriminant Analysis: Variable Ranking

Description

binda.ranking determines a ranking of predictors by computing corresponding t-scores between the group means and the pooled mean.

plot.binda.ranking provides a graphical visualization of the top ranking variables

Usage

```
binda.ranking(Xtrain, L, lambda.freqs, verbose=TRUE)
## S3 method for class 'binda.ranking'
plot(x, top=40, arrow.col="blue", zeroaxis.col="red", ylab="Variables", main, ...)
```

Arguments

Xtrain	A matrix containing the training data set. Note that the rows correspond to observations and the columns to variables.
L	A factor with the class labels of the training samples.
lambda.freqs	Shrinkage intensity for the class frequencies. If not specified it is estimated from the data. lambda.freqs=0 implies no shrinkage (i.e. empirical frequencies) and lambda.freqs=1 complete shrinkage (i.e. uniform frequencies).
verbose	Print out some info while computing.
x	A "binda.ranking" object – this is produced by the binda.ranking() function.
top	The number of top-ranking variables shown in the plot (default: 40).
arrow.col	Color of the arrows in the plot (default is "blue").
zeroaxis.col	Color for the center zero axis (default is "red").
ylab	Label written next to feature list (default is "Variables").
main	Main title (if missing, "The", top, "Top Ranking Variables" is used).
...	Other options passed on to generic plot().

Details

The overall ranking of a feature is determined by computing a weighted sum of the squared t-scores. This is approximately equivalent to the mutual information between the response and each variable. The same criterion is used in [dichotomize](#). For precise details see Gibb and Strimmer (2015).

Value

binda.ranking returns a matrix with the following columns:

idx	original feature number
score	the score determining the overall ranking of a variable
t	for each group and feature the t-score of the class mean versus the pooled mean

Author(s)

Sebastian Gibb and Korbinian Strimmer (<https://strimmerlab.github.io>).

References

Gibb, S., and K. Strimmer. 2015. Differential protein expression and peak selection in mass spectrometry data by binary discriminant analysis. *Bioinformatics* 31:3156-3162. <DOI:10.1093/bioinformatics/btv334>

See Also

[binda](#), [predict.binda](#), [dichotomize](#).

Examples

```
# load "binda" library
library("binda")

# training data set with labels
Xtrain = matrix(c(1, 1, 0, 1, 0, 0,
                 1, 1, 1, 1, 0, 0,
                 1, 0, 0, 0, 1, 1,
                 1, 0, 0, 0, 1, 1), nrow=4, byrow=TRUE)
colnames(Xtrain) = paste0("V", 1:ncol(Xtrain))
is.binaryMatrix(Xtrain) # TRUE
L = factor(c("Treatment", "Treatment", "Control", "Control") )

# ranking variables
br = binda.ranking(Xtrain, L)
br
#   idx   score t.Control t.Treatment
#V2  2 4.000000 -2.000000  2.000000
#V4  4 4.000000 -2.000000  2.000000
#V5  5 4.000000  2.000000 -2.000000
#V6  6 4.000000  2.000000 -2.000000
#V3  3 1.333333 -1.154701  1.154701
#V1  1 0.000000  0.000000  0.000000
#attr(,"class")
#[1] "binda.ranking"
#attr(,"cl.count")
#[1] 2

# show plot
plot(br)
```

```
# result: variable V1 is irrelevant for distinguishing the two groups
```

chances

Estimate Bernoulli Parameters from Binary Matrix with Class Labels

Description

chances estimates Bernoulli parameters (=chances) from a binary matrix and associated class labels.

Usage

```
chances(X, L, lambda.freqs, verbose=TRUE)
```

Arguments

X	data matrix (columns correspond to variables, rows to samples).
L	factor containing the class labels, one for each sample (row).
lambda.freqs	shrinkage parameter for class frequencies (if not specified it is estimated).
verbose	report shrinkage intensity and other information.

Details

The class-specific chances are estimated using the empirical means over the 0s and 1s in each class. For estimating the pooled mean the class-specific means are weighted using the estimated class frequencies. Class frequencies are estimated using [freqs.shrink](#).

Value

chances returns a list with the following components:

samples: the samples in each class,

regularization: the shrinkage intensity used to estimate the class frequencies,

freqs: the estimated class frequencies,

means: the estimated chances (parameters of Bernoulli distribution, expectations of 1s) for each variable conditional on class, as well as the marginal changes (pooled means).

Author(s)

Sebastian Gibb and Korbinian Strimmer (<https://strimmerlab.github.io>).

See Also

[is.binaryMatrix](#).

Examples

```
# load binda library
library("binda")

# example binary matrix with 6 variables (in columns) and 4 samples (in rows)
Xb = matrix(c(1, 1, 0, 1, 0, 0,
             1, 1, 1, 1, 0, 0,
             1, 0, 0, 0, 1, 1,
             1, 0, 0, 0, 1, 1), nrow=4, byrow=TRUE)
colnames(Xb) = paste0("V", 1:ncol(Xb))

# Test for binary matrix
is.binaryMatrix(Xb) # TRUE

L = factor(c("Treatment", "Treatment", "Control", "Control") )

chances(Xb, L)
```

dichotomize

*Dichotomize Continuous Data Set With Labels***Description**

dichotomize converts a matrix containing continuous measurements into a binary matrix.

optimizeThreshold determines optimal thresholds for dichotomization.

Usage

```
dichotomize(X, thresh)
optimizeThreshold(X, L, lambda.freqs, verbose=FALSE)
```

Arguments

X	data matrix (columns correspond to variables, rows to samples).
thresh	vector of thresholds, one for each variable (column).
L	factor containing the class labels, one for each sample (row).
lambda.freqs	shrinkage parameter for class frequencies (if not specified it is estimated).
verbose	report shrinkage intensity and other information.

Details

dichotomize assigns 0 if a matrix entry is lower than given column-specific threshold, otherwise it assigns 1.

optimizeThreshold uses (approximate) mutual information to determine the optimal thresholds. Specifically, the thresholds are chosen to maximize the mutual information between response and each variable. The same criterion is also used in [binda.ranking](#). For detailed description of the dichotomization procedure see Gibb and Strimmer (2015).

Class frequencies are estimated using [freqs.shrink](#).

Value

dichotomize returns a binary matrix.

optimizeThreshold returns a vector containing the variable thresholds.

Author(s)

Sebastian Gibb and Korbinian Strimmer (<https://strimmerlab.github.io>).

References

Gibb, S., and K. Strimmer. 2015. Differential protein expression and peak selection in mass spectrometry data by binary discriminant analysis. *Bioinformatics* 31:3156-3162. <DOI:10.1093/bioinformatics/btv334>

See Also

[binda.ranking](#), [freqs.shrink](#), [mi.plugin](#), [is.binaryMatrix](#).

Examples

```
# load binda library
library("binda")

# example data with 6 variables (in columns) and 4 samples (in rows)
X = matrix(c(1, 1, 1, 1.75, 0.4, 0,
            1, 1, 2, 2, 0.4, 0.09,
            1, 0, 1, 1, 0.5, 0.1,
            1, 0, 1, 0.5, 0.6, 0.1), nrow=4, byrow=TRUE)
colnames(X) = paste0("V", 1:ncol(X))

# class labels
L = factor(c("Treatment", "Treatment", "Control", "Control") )
rownames(X) = paste0(L, rep(1:2, times=2))

X
#           V1 V2 V3  V4  V5  V6
#Treatment1  1  1  1 1.75 0.4 0.00
#Treatment2  1  1  2 2.00 0.4 0.09
#Control1    1  0  1 1.00 0.5 0.10
#Control2    1  0  1 0.50 0.6 0.10

# find optimal thresholds (one for each variable)
thr = optimizeThreshold(X, L)
thr
# V1  V2  V3  V4  V5  V6
#1.00 1.00 2.00 1.75 0.50 0.10

# convert into binary matrix
# if value is lower than threshold -> 0 otherwise -> 1
Xb = dichotomize(X, thr)
is.binaryMatrix(Xb) # TRUE
Xb
```



```
#           V1 V2 V3 V4 V5 V6
#Treatment1 1 1 0 1 0 0
#Treatment2 1 1 1 1 0 0
#Control1   1 0 0 0 1 1
#Control2   1 0 0 0 1 1
#attr("thresh")
# V1  V2  V3  V4  V5  V6
#1.00 1.00 2.00 1.75 0.50 0.10
```

is.binaryMatrix *Check For Binary Matrix*

Description

is.binaryMatrix tests whether `m` is a matrix and whether it contains only 0s and 1s. Note that functions like `binda.ranking` and `binda` require a binary matrix as input.

Usage

```
is.binaryMatrix(m)
```

Arguments

`m` a matrix.

Value

is.binaryMatrix returns either TRUE or FALSE.

Author(s)

Sebastian Gibb and Korbinian Strimmer (<https://strimmerlab.github.io>).

Examples

```
# load binda library
library("binda")

# test matrix
m = matrix(c(1, 1, 0, 1, 0, 0,
            1, 1, 1, 1, 0, 0,
            1, 0, 0, 0, 1, 1,
            1, 0, 0, 0, 1, 1), nrow=4, byrow=TRUE)

# Test for binary matrix
is.binaryMatrix(m) # TRUE
```

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