

Package ‘lpda’

March 12, 2026

Type Package

Title Linear Programming Discriminant Analysis

Version 1.2.3

Description Classification method obtained through linear programming.

It is advantageous with respect to the classical developments when the distribution of the variables involved is unknown or when the number of variables is much greater than the number of individuals.

Mathematical details behind the method are published in Nueda, et al. (2022) “LPDA: A new classification method based on linear programming”.

[doi:10.1371/journal.pone.0270403](https://doi.org/10.1371/journal.pone.0270403).

Depends R (>= 3.5.0)

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports Rglpk, multiway

Suggests rmarkdown, knitr, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

Author María José Nueda [aut, cre]

Maintainer María José Nueda <mj.nueda@ua.es>

Repository CRAN

Date/Publication 2026-03-12 16:40:03 UTC

Contents

lpda	2
lpda.3D	4
lpda.fit	6

lpda.pca	7
lpdaCV	8
lpdaCV.3D	9
palmdates	10
PCA	11
plot.lpda	12
plot.lpda.3D	13
predict.lpda	14
predict.lpda.3D	15
RNAseq	16
stand	16
stand2	17
summary.lpda	17
summary.lpda.3D	18

Index	20
--------------	-----------

lpda	<i>Computing discriminating hyperplane for two groups</i>
------	---

Description

This function computes a discriminating hyperplane for two groups with original data (calling lpda.fit) or with principal components (calling lpda.pca)

Usage

```
lpda(data, group, scale = FALSE, pca = FALSE, PC = 2, Variability = NULL,
      f1 = NULL, f2 = NULL)
## S3 method for class 'lpda'
print(x, ...)
```

Arguments

data	Matrix containing data. Individuals in rows and variables in columns
group	Vector with the variable group
scale	Logical indicating if it is required standardize data. When pca=TRUE data is always scaled.
pca	Logical indicating if Principal Components Analysis is required
PC	Number of Principal Components (PC) for PCA. By default it is 2. When the number of PC is not decided, it can be determined choosing the desired proportion of explained variability (Variability parameter).
Variability	Parameter for Principal Components (PC) selection. This is the minimum desired proportion of variability explained for the PC of the variables. The analysis is always done with a minimum of 2 PCs. If it is NULL the PCA will be computed with PC parameter.

f1	Vector with weights for individuals of the first group. If NULL they are equally weighted.
f2	Vector with weights for individuals of the second group. If NULL they are equally weighted.
x	An object of class "lpda", a result of a call to lpda.
...	Other arguments passed.

Value

lpda returns an object of class "lpda".

coef	Hyperplane coefficients
data	Input data matrix
group	Input group vector
scale	Input scale argument
pca	Input pca argument
loadings	Principal Components loadings. Shown when pca = TRUE
scores	Principal Components scores. Shown when pca = TRUE
var.exp	A matrix containing the explained variance for each component and the cumulative variance. Shown when pca = TRUE
PCs	Number of Principal Components in the analysis. Shown when pca = TRUE

The functions `predict` and `plot` can be used to obtain the predicted classes and a plot in two dimensions with the distances to the computed hyperplane for the two classes.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

References

Nueda MJ, Gandía C, Molina MD (2022) LPDA: A new classification method based on linear programming. PLoS ONE 17(7): e0270403. <<https://doi.org/10.1371/journal.pone.0270403>>

See Also

[lpda.pca](#), [lpda.fit](#)

Examples

```
##### palmdates example in lpda package:
data(palmdates)
group = as.factor( c(rep("Spanish",11),rep("Foreign",10)) )

# with concentration data:
model = lpda(data = palmdates$conc, group = group )
summary(model)
```

```

predict(model)
plot(model, main = "Palmdates example")

model.pca = lpda(data = palmdates$conc, group = group, pca=TRUE, PC = 2)
plot(model.pca, PCscores = TRUE, main = "Palmdates example")

# with spectra data
model.pca = lpda(data = palmdates$spectra, group = group, pca=TRUE, Variability = 0.9)
model.pca$PCs # 4 PCs to explain 90% of the variability
plot(model.pca, PCscores = TRUE, main = "Spectra palmdates")

```

lpda.3D

Classification with lpda for 3way array data

Description

This function applies lpda methodology to classify individuals in two or more groups with original data (by applying lpda through the third dimension) or by applying lpda to the parafac scores.

Usage

```

lpda.3D(data, group, scale = FALSE, pfac = FALSE, nfac = 2,
        nstart = 10, seed=2, f1 = NULL, f2 = NULL)
## S3 method for class 'lpda.3D'
print(x, ...)

```

Arguments

data	Array containing data. Individuals in the first mode, variables in the second mode and third mode with time or similar.
group	Vector with the variable group.
scale	Logical indicating if it is required standardize data.
pfac	Logical indicating if Parafac Analysis is required
nfac	Number of factors for Parafac Analysis.
nstart	Number of random starts for multiway analysis.
seed	A single value to reproduce same results in multiway methods.
f1	Vector with weights for individuals of the first group. If NULL they are equally weighted.
f2	Vector with weights for individuals of the second group. If NULL they are equally weighted.
x	An object of class "lpda.3D", a result of a call to lpda.3D.
...	Other arguments passed.

Value

lpda.3D returns an object of class "lpda.3D".

MOD	When pfac=FALSE, MOD is a list of lpda objects obtained from the application of lpda to each slide matrix of the third node. When pfac=TRUE, MOD is a list of two elements: (1) mod.pfac the parafac model obtained with Multiway package and (2) the lpda object, obtained from the application of lpda to the parafac scores.
data	Input array data
group	Input group vector
pfac	Input pfac argument

The functions `predict` and `plot` can be used to obtain the predicted classes and a plot in two dimensions with the distances to the computed hyperplane for the two classes.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

References

Nueda MJ, Gandía C, Molina MD (2022) LPDA: A new classification method based on linear programming. PLoS ONE 17(7): e0270403. <<https://doi.org/10.1371/journal.pone.0270403>>

See Also

[lpda](#), [parafac](#)

Examples

```
### RNAseq is a 3-dimensional array
data(RNAseq)
group = as.factor(rep(c("G1", "G2"), each = 10))

## Strategy 1
model3D = lpda.3D(RNAseq, group)
summary(model3D)
predict(model3D)
plot(model3D, mfrow=c(2,2))

## Strategy 2: with parafac
model3Ds2 = lpda.3D(RNAseq, group, pfac=TRUE, nfac=2)
model3Ds2$MOD$mod.pfac$Rsqr
predict(model3Ds2)
summary(model3Ds2)
plot(model3Ds2, pfacscores=FALSE, main="Parafac Model", mfrow=c(1,1))
plot(model3Ds2, pfacscores=TRUE, cex=1.5, main="Parafac components")
legend("bottomright", levels(group), col=c(2,3), pch=20)
```

`lpda.fit`*lpda.fit computes the discriminating hyperplane for two groups*

Description

`lpda.fit` computes the discriminating hyperplane for two groups, giving as a result the coefficients of the hyperplane.

Usage

```
lpda.fit(data, group, f1 = NULL, f2 = NULL)
```

Arguments

<code>data</code>	Matrix containing data. Individuals in rows and variables in columns
<code>group</code>	Vector with the variable group
<code>f1</code>	Vector with weights for individuals of the first group
<code>f2</code>	Vector with weights for individuals of the second group

Value

<code>coef</code>	Hyperplane coefficients
-------------------	-------------------------

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

References

Nueda MJ, Gandía C, Molina MD (2022) LPDA: A new classification method based on linear programming. PLoS ONE 17(7): e0270403. <<https://doi.org/10.1371/journal.pone.0270403>>

See Also

[lpda](#)

lpda.pca	<i>lpda.pca computes a PCA to the original data and selects the desired PCs when Variability is supplied</i>
----------	--

Description

lpda.pca computes the discriminating hyperplane for two groups with Principal Components (PC)

Usage

```
lpda.pca(data, group, PC = 2, Variability = NULL)
```

Arguments

data	Matrix containing data. Individuals in rows and variables in columns
group	Vector with the variable group
PC	Number of Principal Components (PC) for PCA. By default it is 2. When the number of PC is not decided, it can be determined choosing the desired proportion of explained variability (Variability parameter).
Variability	Parameter for Principal Components (PC) selection. This is the minimum desired proportion of variability explained for the PC of the variables. The analysis is always done with a minimum of 2 PCs. If it is NULL the PCA will be computed with PC parameter.

Value

loadings	Principal Components loadings.
scores	Principal Components scores.
var.exp	A matrix containing the explained variance for each component and the cumulative variance.
PCs	Number of Principal Components in the analysis.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

References

Nueda MJ, Gandía C, Molina MD (2022) LPDA: A new classification method based on linear programming. PLoS ONE 17(7): e0270403. <<https://doi.org/10.1371/journal.pone.0270403>>

See Also

[lpda](#)

lpdaCV

*Crossvalidation procedure for lpda evaluation***Description**

lpdaCV evaluates the error rate classification with a crossvalidation procedure

Usage

```
lpdaCV(data, group, scale = FALSE, pca = FALSE, PC = 2, Variability = NULL,
        CV = "ktest", ntest = 10, R = 10, f1 = NULL, f2 = NULL)
```

```
## S3 method for class 'lpdaCV'
print(x, ...)
```

Arguments

data	Matrix containing data. Individuals in rows and variables in columns
group	Vector with the variable group
scale	Logical indicating if it is required standardize data.
pca	Logical indicating if a reduction of dimension is required
PC	Number of Principal Components (PC) for PCA. By default it is 2. When the number of PC is not decided, it can be determined choosing the desired proportion of explained variability (Variability parameter) or choosing the maximum number of errors allowed in the training set (Error.max).
Variability	Parameter for Principal Components (PC) selection. This is the desired proportion of variability explained for the PC of the variables.
CV	Crossvalidation mode: loo "leave one out" or ktest: that leaves k in the test set.
ntest	Number of samples to evaluate in the test-set.
R	Number of times that the error is evaluated.
f1	Vector with weights for individuals of the first group. If NULL they are equally weighted.
f2	Vector with weights for individuals of the second group. If NULL they are equally weighted.
x	An object of class "lpdaCV", a result of a call to lpdaCV or lpdaCV.3D.
...	Other arguments passed.

Value

lpdaCV returns the prediction error rate classification.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

See Also[lpda](#)**Examples**

```
### RNAseq is a 3-dimensional array
data(RNAseq)
data = RNAseq[, ,3]
group = as.factor(rep(c("G1","G2"), each = 10))
lpdaCV(data, group, pca = TRUE, CV = "ktest", ntest = 2)
```

lpdaCV.3D

*Crossvalidation procedure for lpda3D evaluation***Description**

lpdaCV.3D evaluates the error rate classification with a crossvalidation procedure

Usage

```
lpdaCV.3D(data, group, scale = FALSE, pfac = FALSE, nfac = 2, nstart = 10, seed=2,
          CV = "ktest", ntest = 10, R = 10, f1 = NULL, f2 = NULL)
```

Arguments

data	Array containing data. Individuals in the first mode, variables in the second mode and third mode with time or similar.
group	Vector with the variable group.
scale	Logical indicating if it is required standardize data.
pfac	Logical indicating if Parafac Analysis is required
nfac	Number of factors for Parafac Analysis. By default it is 2.
nstart	Number of random starts for multiway analysis.
seed	A single value to reproduce same results in multiway methods. If NULL the start will be random.
CV	Crossvalidation mode: loo "leave one out" or ktest: that leaves k in the test set.
ntest	Number of samples to evaluate in the test-set.
R	Number of times that the error is evaluated.
f1	Vector with weights for individuals of the first group. If NULL they are equally weighted.
f2	Vector with weights for individuals of the second group. If NULL they are equally weighted.

Value

lpda.3D returns the prediction error rate classification.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

See Also

[lpda.3D](#), [lpdaCV](#)

Examples

```
### RNAseq is a 3-dimensional array

data(RNAseq)
group = as.factor(rep(c("G1", "G2"), each = 10))
lpdaCV.3D(RNAseq, group, CV = "ktest", R=5, ntest=5, pfac=TRUE, nfac=c(2,10))
```

palmdates

Spectrometry and composition chemical of Spanish and Arabian palm dates

Description

A data set with scores of 21 dates on spectrometry and concentration measurements of the substances that better define the quality of the dates: fibre, sorbitol, fructose, glucose and myo-inositol. The first 11 dates are Spanish (from Elche, Alicante) and the last 10 are from other countries, mainly Arabian.

Usage

```
palmdates
```

Format

A data frame with 2 elements:

conc a data frame with 5 columns: fibre, sorbitol, fructose, glucose and myo-inositol.

spectra a data frame with 2050 columns.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

References

Abdrabo, S.S., Gras, L., Grindlay, G. and Mora, J. (2021) Evaluation of Fourier Transform-Raman Spectroscopy for palm dates characterization. Journal of food composition and analysis. Submitted.

PCA

Principal Component Analysis

Description

Computes a Principal Component Analysis when $p > n$ and when $p \leq n$.

Usage

PCA(X)

Arguments

X Matrix or data.frame with variables in columns and observations in rows.

Value

eigen A eigen class object with eigenvalues and eigenvectors of the analysis.
var.exp A matrix containing the explained variance for each component and the cumulative variance.
scores Scores of the PCA analysis.
loadings Loadings of the PCA analysis.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

Examples

```
## Simulate data matrix with 500 variables and 10 observations
datasim = matrix(sample(0:100, 5000, replace = TRUE), nrow = 10)
## PCA
myPCA = PCA(datasim)
## Extracting the variance explained by each principal component
myPCA$var.exp
```

`plot.lpda`*Plot method for lpda classification*

Description

`plot.lpda` is applied to an `lpda` class object. It shows a plot in two dimensions with the distances to the computed hyperplane of each individual coloring each case with the real class.

Usage

```
## S3 method for class 'lpda'
plot(x, PCscores = FALSE, main = NULL, xlab = NULL, ylab = NULL,
      col= NULL, pch = NULL, lty = NULL,
      legend.pos = "topright",...)
```

Arguments

<code>x</code>	Object of class inheriting from "lpda"
<code>PCscores</code>	Logical to show the first 2 PCscores. Only possible when PCA is applied.
<code>main</code>	An optional title for the plot.
<code>xlab</code>	An optional title for x-axis.
<code>ylab</code>	An optional title for y-axis.
<code>col</code>	An optional vector with colours for the groups.
<code>pch</code>	An integer specifying the symbol to be used in plotting points. When NULL, <code>pch=20</code> .
<code>lty</code>	The line type. If it is not specified, <code>lty = 2</code> for the distances to the hiperplane and <code>lty = 1</code> for PCs plot
<code>legend.pos</code>	The position for the legend. By default it is <code>topright</code> . NULL when no legend is required.
<code>...</code>	Other arguments passed.

Value

Two dimensional plot representing the distances to the computed hyperplane of each individual colored with the real class.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

See Also

[lpda](#)

plot.lpda.3D	<i>Plot method for lpda classification</i>
--------------	--

Description

plot.lpda.3D is applied to an lpda.3D class object. It shows a plot in two dimensions with the distances to the computed hyperplane of each individual coloring each case with the real class.

Usage

```
## S3 method for class 'lpda.3D'  
plot(x, pfacscores = FALSE, main = NULL,  
     legend.pos = "topright", ...)
```

Arguments

x	Object of class inheriting from "lpda"
pfacscores	Logical to show the first 2 parafac scores. Only possible when parafac is applied.
main	An optional title for the plot.
legend.pos	The position for the legend. By default it is topright. NULL when no legend is required.
...	Other arguments passed.

Value

Two dimensional plot representing the distances to the computed hyperplane of each individual colored with the real class.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

See Also

[lpda.3D](#), [plot.lpda](#)

predict.lpda	<i>Predict method for lpda classification</i>
--------------	---

Description

Predict method for lpda classification

Usage

```
## S3 method for class 'lpda'  
predict(object, datatest = object$data,...)  
  
## S3 method for class 'predict.lpda'  
print(x, ...)
```

Arguments

object	Object of class inheriting from "lpda"
datatest	An optional data to predict their class. If omitted, the original data is used.
x	An object of class "predict.lpda", a result of a call to predict.lpda.
...	Other arguments passed.

Value

fitted	Predicted class
eval	Evaluation of each individual in the fitted model

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

See Also

[lpda](#)

predict.lpda.3D	<i>Predict method for lpda.3D classification</i>
-----------------	--

Description

Predict method for lpda.3D classification

Usage

```
## S3 method for class 'lpda.3D'  
predict(object, datatest = NULL,...)  
  
## S3 method for class 'predict.lpda.3D'  
print(x, ...)
```

Arguments

object	Object of class inheriting from "lpda.3D"
datatest	An optional data to predict their class. If omitted, the original data is used.
x	An object of class "predict.lpda.3D", a result of a call to predict.lpda.3D.
...	Other arguments passed.

Value

fitted	Predicted class
eval	Evaluation of each individual in all the fitted models

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

See Also

[lpda](#)

RNAseq

Simulated RNA-Seq Time Series 3-dimensional dataset example

Description

A simulated RNA-Seq dataset example.

Usage

RNAseq

Format

An array data frame with 20 samples (1st dimension), 600 genes (2nd dimension) and 4 time-points (3rd dimension).

Details

This dataset is a RNA-Seq simulated example. It has been simulated as Negative Binomial distributed and transformed to rpk (Reads per kilo base per million mapped reads). It contains gene expression from 600 genes measured to 60 samples through 4 time-points. First 10 samples are from first group and the remaining samples from the second one.

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

stand

stand center and scale a data matrix

Description

stand center and scale a data matrix

Usage

stand(X)

Arguments

X a data matrix with individuals in rows and variables in columns

Value

Scaled data matrix

stand2	<i>stand2 center and scale a data matrix with the parameters of another one</i>
--------	---

Description

stand2 center and scale a data matrix with the parameters of another one

Usage

```
stand2(X, X2)
```

Arguments

X	the data matrix from which mean and standard deviation is computed
X2	the data matrix to center and scale

Value

Scaled X2 data matrix

summary.lpda	<i>Summarizing lpda classification</i>
--------------	--

Description

summary method for class "lpda"

Usage

```
## S3 method for class 'lpda'
summary(object, datatest = object$data, grouptest=object$group,...)

## S3 method for class 'summary.lpda'
print(x, ...)
```

Arguments

object	Object of class inheriting from "lpda"
datatest	An optional data to predict their class and compare with real in the confusion matrix. If omitted, the original data is used.
grouptest	When datatest is specified, grouptest must also be specified and viceversa.
x	An object of class "summary.lpda", a result of a call to summary.lpda.
...	Other arguments passed.

Value

Confusion.Matrix

Table of confusion. Predicted classes in rows and real classes in columns, giving the hit (in the diagonal) and misclassification counts (out of the diagonal)

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

See Also

[lpda](#)

summary.lpda.3D

Summarizing lpda.3D classification

Description

summary method for class "lpda.3D"

Usage

```
## S3 method for class 'lpda.3D'
summary(object, datatest = NULL, grouptest=NULL,...)

## S3 method for class 'summary.lpda.3D'
print(x, ...)
```

Arguments

object	Object of class inheriting from "lpda.3D"
datatest	An optional data to predict their class and compare with real in the confusion matrix. If omitted, the original data is used.
grouptest	When datatest is specified, grouptest must also be specified and viceversa.
x	An object of class "summary.lpda.3D", a result of a call to summary.lpda.3D.
...	Other arguments passed.

Value

Confusion.Matrix

Table of confusion. Predicted classes in rows and real classes in columns, giving the hit (in the diagonal) and misclassification counts (out of the diagonal)

Author(s)

Maria Jose Nueda, <mj.nueda@ua.es>

See Also

[lpda.3D](#)

Index

* classification

- lpda, [2](#)
- lpda.3D, [4](#)
- lpda.fit, [6](#)
- lpda.pca, [7](#)
- lpdaCV, [8](#)
- lpdaCV.3D, [9](#)
- plot.lpda, [12](#)
- plot.lpda.3D, [13](#)
- predict.lpda, [14](#)
- predict.lpda.3D, [15](#)
- summary.lpda, [17](#)
- summary.lpda.3D, [18](#)

* datasets

- palmdates, [10](#)
- RNAseq, [16](#)

lpda, [2](#), [5–7](#), [9](#), [12](#), [14](#), [15](#), [18](#)

lpda.3D, [4](#), [10](#), [13](#), [19](#)

lpda.fit, [3](#), [6](#)

lpda.pca, [3](#), [7](#)

lpdaCV, [8](#), [10](#)

lpdaCV.3D, [9](#)

palmdates, [10](#)

parafac, [5](#)

PCA, [11](#)

plot.lpda, [12](#), [13](#)

plot.lpda.3D, [13](#)

predict.lpda, [14](#)

predict.lpda.3D, [15](#)

print.lpda (lpda), [2](#)

print.lpda.3D (lpda.3D), [4](#)

print.lpdaCV (lpdaCV), [8](#)

print.predict.lpda (predict.lpda), [14](#)

print.predict.lpda.3D

(predict.lpda.3D), [15](#)

print.summary.lpda (summary.lpda), [17](#)

print.summary.lpda.3D

(summary.lpda.3D), [18](#)

RNAseq, [16](#)

stand, [16](#)

stand2, [17](#)

summary.lpda, [17](#)

summary.lpda.3D, [18](#)