

WEEK-7

Linear Discriminant Analysis

Linear Discriminant Analysis (LDA) is a supervised learning algorithm used for classification tasks in machine learning. It is a technique used to find a linear combination of features that best separates the classes in a dataset. LDA works by projecting the data onto a lower-dimensional space that maximizes the separation between the classes. It does this by finding a set of linear discriminants that maximize the ratio of between-class variance to within-class variance. In other words, it finds the directions in the feature space that best separate the different classes of data.

```
import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
import seaborn as sn
from sklearn.datasets import load_wine

wine_info=load_wine()
X=pd.DataFrame(wine_info.data,columns=wine_info.feature_names)

X.head()

  alcohol  malic_acid  ash  alkalinity_of_ash  magnesium  total_phenols \
0   14.23     1.71  2.43         15.6      127.0         2.80
1   13.20     1.78  2.14         11.2     100.0         2.65
2   13.16     2.36  2.67         18.6     101.0         2.80
3   14.37     1.95  2.50         16.8     113.0         3.85
4   13.24     2.59  2.87         21.0     118.0         2.80

  flavanoids  nonflavanoid_phenols  proanthocyanins  color_intensity  hue \
0      3.06           0.28           2.29           5.64  1.04
1      2.76           0.26           1.28           4.38  1.05
2      3.24           0.30           2.81           5.68  1.03
3      3.49           0.24           2.18           7.80  0.86
4      2.69           0.39           1.82           4.32  1.04

  od280/od315_of_diluted_wines  proline
0              3.92  1065.0
1              3.40  1050.0
2              3.17  1185.0
3              3.45  1480.0
4              2.93   735.0

X.shape

(178, 13)

X.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 178 entries, 0 to 177
```

Data columns (total 13 columns):

#	Column	Non-Null Count	Dtype
0	alcohol	178 non-null	float64
1	malic_acid	178 non-null	float64
2	ash	178 non-null	float64
3	alcalinity_of_ash	178 non-null	float64
4	magnesium	178 non-null	float64
5	total_phenols	178 non-null	float64
6	flavanoids	178 non-null	float64
7	nonflavanoid_phenols	178 non-null	float64
8	proanthocyanins	178 non-null	float64
9	color_intensity	178 non-null	float64
10	hue	178 non-null	float64
11	od280/od315_of_diluted_wines	178 non-null	float64
12	proline	178 non-null	float64

dtypes: float64(13)

memory usage: 18.2 KB

X.describe()

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium \
count	178.000000	178.000000	178.000000	178.000000	178.000000
mean	13.000618	2.336348	2.366517	19.494944	99.741573
std	0.811827	1.117146	0.274344	3.339564	14.282484
min	11.030000	0.740000	1.360000	10.600000	70.000000
25%	12.362500	1.602500	2.210000	17.200000	88.000000
50%	13.050000	1.865000	2.360000	19.500000	98.000000
75%	13.677500	3.082500	2.557500	21.500000	107.000000
max	14.830000	5.800000	3.230000	30.000000	162.000000

	total_phenols	flavanoids	nonflavanoid_phenols	proanthocyanins \
count	178.000000	178.000000	178.000000	178.000000
mean	2.295112	2.029270	0.361854	1.590899
std	0.625851	0.998859	0.124453	0.572359
min	0.980000	0.340000	0.130000	0.410000
25%	1.742500	1.205000	0.270000	1.250000
50%	2.355000	2.135000	0.340000	1.555000
75%	2.800000	2.875000	0.437500	1.950000
max	3.880000	5.080000	0.660000	3.580000

	color_intensity	hue	od280/od315_of_diluted_wines	proline
count	178.000000	178.000000	178.000000	178.000000
mean	5.058090	0.957449	2.611685	746.893258
std	2.318286	0.228572	0.709990	314.907474
min	1.280000	0.480000	1.270000	278.000000
25%	3.220000	0.782500	1.937500	500.500000
50%	4.690000	0.965000	2.780000	673.500000
75%	6.200000	1.120000	3.170000	985.000000
max	13.000000	1.710000	4.000000	1680.000000

```
Y=pd.Categorical.from_codes(wine_info.target,wine_info.target_names)
```

```
Y.unique()
```

```
['class_0', 'class_1', 'class_2']
```

```
Categories (3, object): ['class_0', 'class_1', 'class_2']
```

```
df=X.join(pd.Series(Y,name="class"))
```

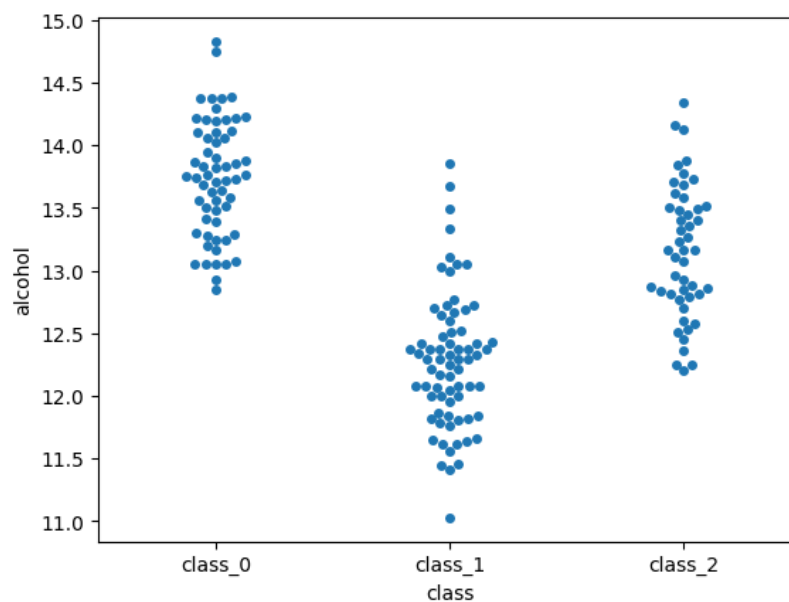
```
df.head()
```

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols \
0	14.23	1.71	2.43	15.6	127.0	2.80
1	13.20	1.78	2.14	11.2	100.0	2.65
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	flavanoids	nonflavanoid_phenols	proanthocyanins	color_intensity	hue \
0	3.06	0.28	2.29	5.64	1.04
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3	3.49	0.24	2.18	7.80	0.86
4	2.69	0.39	1.82	4.32	1.04

	od280/od315_of_diluted_wines	proline	class
0	3.92	1065.0	class_0
1	3.40	1050.0	class_0
2	3.17	1185.0	class_0
3	3.45	1480.0	class_0
4	2.93	735.0	class_0

```
sn.swarmplot(x=df["class"],y=df["alcohol"])
```



```
from sklearn.preprocessing import LabelEncoder
le=LabelEncoder()
y_labelled=le.fit_transform(Y)
y_labelled[0:5]

array([0, 0, 0, 0, 0])

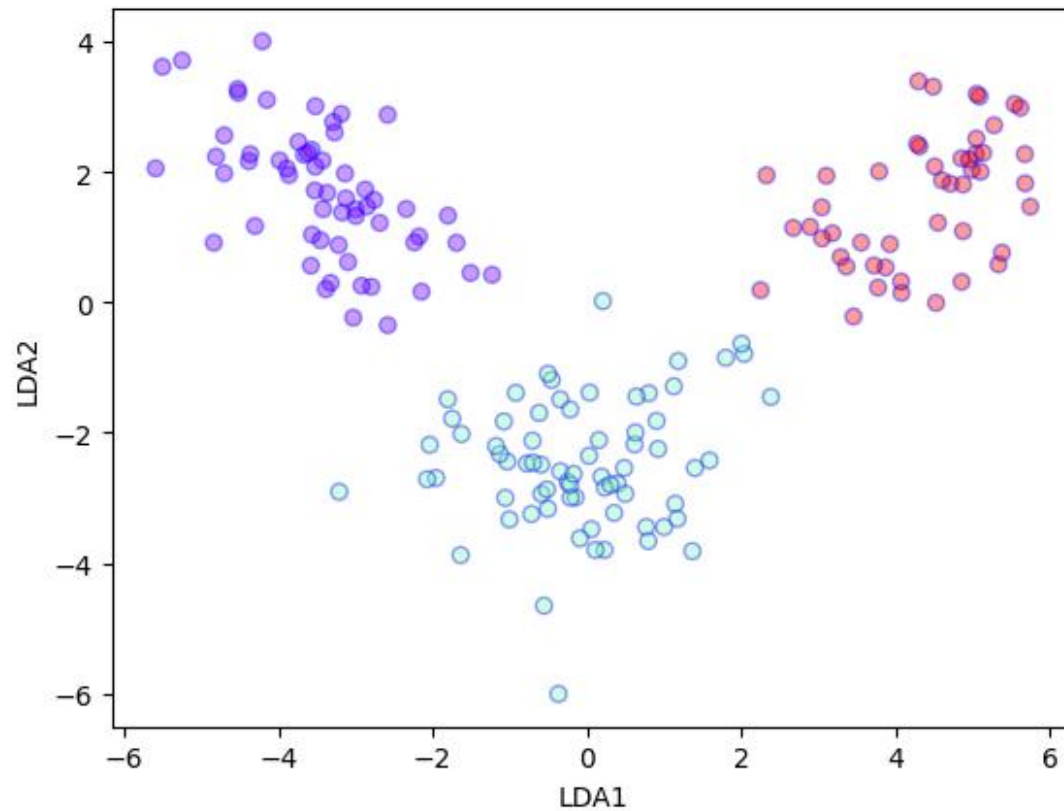
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.model_selection import train_test_split

lda=LinearDiscriminantAnalysis()
X_lda=lda.fit_transform(X,y_labelled)
lda.explained_variance_ratio_

array([0.68747889, 0.31252111])

plt.xlabel("LDA1")
plt.ylabel("LDA2")
plt.scatter(
    X_lda[:,0],
    X_lda[:,1],
    c=y_labelled,
    cmap="rainbow",
    alpha=0.4,
    edgecolors='b'
)

<matplotlib.collections.PathCollection at 0x1b1c890a500>
```



```
X_train,X_test,Y_train,Y_test=train_test_split(X_lda,y_labelled,random_state=20,test_size=0.4)
```

```
from sklearn.tree import DecisionTreeClassifier
```

```
model=DecisionTreeClassifier()
```

```
model.fit(X_train,Y_train)
```

```
model.score(X_test,Y_test)
```

```
0.9861111111111112
```