LDA_with_LDA_PCA_Comparision

September 30, 2020

[91]:
```
import time
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from matplotlib.pyplot import figure
import seaborn as sns
from sklearn import preprocessing
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report,confusion_matrix
```

[92]:
```
df=pd.read_csv('D:\msc3\machine learning\mushroom.csv')
print(df)
```

```
     class cap-shape cap-surface cap-color bruises odor gill-attachment  \
0        p         x           s         n       t    p               f
1        e         x           s         y       t    a               f
2        e         b           s         w       t    l               f
3        p         x           y         w       t    p               f
4        e         x           s         g       f    n               f
…      …       …         …       …     …  …               …
8119     e         k           s         n       f    n               a
8120     e         x           s         n       f    n               a
8121     e         f           s         n       f    n               a
8122     p         k           y         n       f    y               f
8123     e         x           s         n       f    n               a

     gill-spacing gill-size gill-color  … stalk-surface-below-ring  \
0               c         n          k  …                        s
1               c         b          k  …                        s
2               c         b          n  …                        s
3               c         n          n  …                        s
4               w         b          k  …                        s
…             …       …        …   …                      …
8119            c         b          y  …                        s
8120            c         b          y  …                        s
8121            c         b          n  …                        s
```

```
8122            c         n          b  …                       k
8123            c         b          y  …                       s

     stalk-color-above-ring stalk-color-below-ring veil-type veil-color  \
0                         w                      w         p          w
1                         w                      w         p          w
2                         w                      w         p          w
3                         w                      w         p          w
4                         w                      w         p          w
…                       …                      …       …        …
8119                      o                      o         p          o
8120                      o                      o         p          n
8121                      o                      o         p          o
8122                      w                      w         p          w
8123                      o                      o         p          o

     ring-number ring-type spore-print-color population habitat
0              o         p                 k          s       u
1              o         p                 n          n       g
2              o         p                 n          n       m
3              o         p                 k          s       u
4              o         e                 n          a       g
…            …       …               …        …     …
8119           o         p                 b          c       l
8120           o         p                 b          v       l
8121           o         p                 b          c       l
8122           o         e                 w          v       l
8123           o         p                 o          c       l

[8124 rows x 23 columns]
```

[93]:
```
df.describe().T
```

[93]:

	count	unique	top	freq
class	8124	2	e	4208
cap-shape	8124	6	x	3656
cap-surface	8124	4	y	3244
cap-color	8124	10	n	2284
bruises	8124	2	f	4748
odor	8124	9	n	3528
gill-attachment	8124	2	f	7914
gill-spacing	8124	2	c	6812
gill-size	8124	2	b	5612
gill-color	8124	12	b	1728
stalk-shape	8124	2	t	4608
stalk-root	8124	5	b	3776
stalk-surface-above-ring	8124	4	s	5176

```
stalk-surface-below-ring  8124      4   s  4936
stalk-color-above-ring    8124      9   w  4464
stalk-color-below-ring    8124      9   w  4384
veil-type                 8124      1   p  8124
veil-color                8124      4   w  7924
ring-number               8124      3   o  7488
ring-type                 8124      5   p  3968
spore-print-color         8124      9   w  2388
population                8124      6   v  4040
habitat                   8124      7   d  3148
```

[94]:
```
X = df.drop(['class'], axis = 1)
Y = df['class']
X = pd.get_dummies(X, prefix_sep='_')
Y = LabelEncoder().fit_transform(Y)
X = StandardScaler().fit_transform(X)
```

[95]:
```
print(X)
```

```
[[-0.24272523 -0.02219484 -0.79620985 … -0.40484176  4.59086996
  -0.15558197]
 [-0.24272523 -0.02219484 -0.79620985 … -0.40484176 -0.21782364
  -0.15558197]
 [ 4.11988487 -0.02219484 -0.79620985 … -0.40484176 -0.21782364
  -0.15558197]
 …
 [-0.24272523 -0.02219484  1.2559503  … -0.40484176 -0.21782364
  -0.15558197]
 [-0.24272523 -0.02219484 -0.79620985 … -0.40484176 -0.21782364
  -0.15558197]
 [-0.24272523 -0.02219484 -0.79620985 … -0.40484176 -0.21782364
  -0.15558197]]
```

[96]:
```
print(Y)
```

```
[1 0 0 … 0 1 0]
```

[97]:
```
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis

lda = LinearDiscriminantAnalysis(n_components=1)

# run an LDA and use it to transform the features
X_lda = lda.fit(X, Y).transform(X)
print('Original number of features:', X.shape[1])
print('Reduced number of features:', X_lda.shape[1])
print(X.shape)
print(X_lda.shape)
```

```
Original number of features: 117
Reduced number of features: 1
(8124, 117)
(8124, 1)
```

[98]:
```
X_Reduced, X_Test_Reduced, Y_Reduced, Y_Test_Reduced = train_test_split(X_lda,␣
↪Y,
                                                                        ␣
↪test_size = 0.30,
                                                                        ␣
↪random_state = 101)

start = time.process_time()
lda = LinearDiscriminantAnalysis().fit(X_Reduced,Y_Reduced)
print('time taken:')
print(time.process_time() - start)
```

```
time taken:
0.0
```

[101]:
```
predictionlda = lda.predict(X_Test_Reduced)
print('confusion matrix:')
print(confusion_matrix(Y_Test_Reduced,predictionlda))
```

```
confusion matrix:
[[1274    0]
 [   2 1162]]
[1 0 1 … 0 0 1]
```

[2]:
```
print('classification report:')
print(classification_report(Y_Test_Reduced,predictionlda))
disp = plot_confusion_matrix(classifier, X_test, y_test,
                                 display_labels=class_names,
                                 cmap=plt.cm.Blues,
                                 normalize=normalize)
```

```
classification report:


      ␣
↪---------------------------------------------------------------------------

       NameError                                 Traceback (most recent call␣
↪last)

       <ipython-input-2-85ba16b8a7f1> in <module>
         1 print('classification report:')
   ----> 2 print(classification_report(Y_Test_Reduced,predictionlda))
```

```
3 disp = plot_confusion_matrix(classifier, X_test, y_test,
4                                display_labels=class_names,
5                                cmap=plt.cm.Blues,


NameError: name 'classification_report' is not defined
```

[104]:
```
from sklearn.decomposition import PCA

pca = PCA(n_components=2)
X_pca = pca.fit_transform(X)
PCA_df = pd.DataFrame(data = X_pca, columns = ['PC1', 'PC2'])
PCA_df = pd.concat([PCA_df, df['class']], axis = 1)
PCA_df['class'] = LabelEncoder().fit_transform(PCA_df['class'])
PCA_df.head()
```

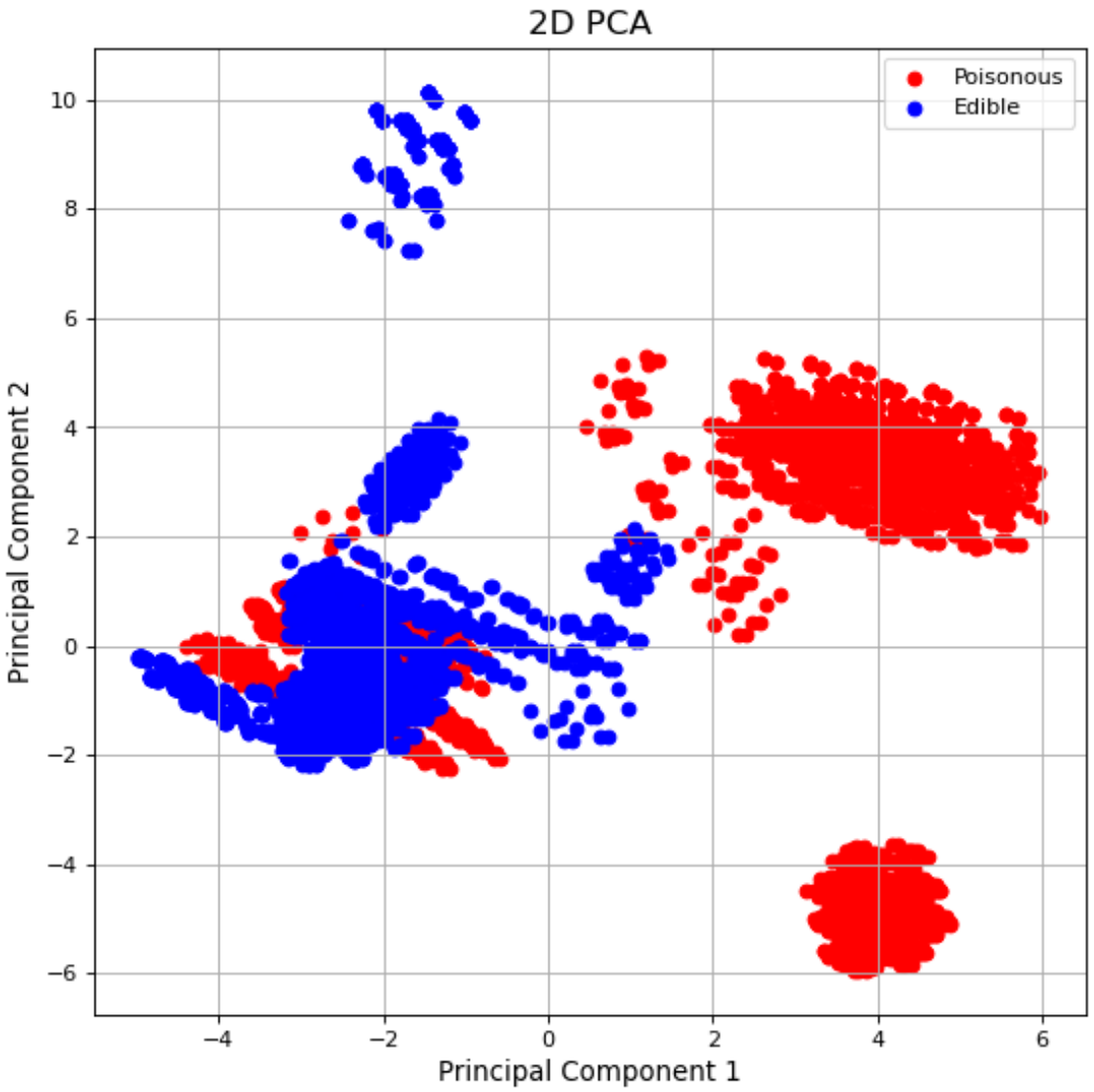
[104]:

	PC1	PC2	class
0	-3.284740	1.020129	1
1	-3.969485	-0.856876	0
2	-4.958587	-0.211117	0
3	-3.469969	0.337959	1
4	-2.726583	0.889655	0

[105]:
```
figure(num=None, figsize=(8, 8), dpi=80, facecolor='w', edgecolor='k')

classes = [1, 0]
colors = ['r', 'b']
for clas, color in zip(classes, colors):
    plt.scatter(PCA_df.loc[PCA_df['class'] == clas, 'PC1'],
                PCA_df.loc[PCA_df['class'] == clas, 'PC2'],
                c = color)

plt.xlabel('Principal Component 1', fontsize = 12)
plt.ylabel('Principal Component 2', fontsize = 12)
plt.title('2D PCA', fontsize = 15)
plt.legend(['Poisonous', 'Edible'])
plt.grid()
```



[106]:
```
pca = PCA(n_components=3,svd_solver='full')
X_pca = pca.fit_transform(X)
print(pca.explained_variance_)
```

```
[10.31484926  9.42671062  8.35720548]
```

[107]:
```
from sklearn.ensemble import RandomForestClassifier
def forest_test(X, Y):
    X_Train, X_Test, Y_Train, Y_Test = train_test_split(X, Y,
                                                        test_size = 0.30,
                                                        random_state = 101)
    start = time.process_time()
```

```
    trainedforest = RandomForestClassifier(n_estimators=700).
↪fit(X_Train,Y_Train)
    print(time.process_time() - start)
    predictionforest = trainedforest.predict(X_Test)
    print(confusion_matrix(Y_Test,predictionforest))
    print(classification_report(Y_Test,predictionforest))
```

[108]:
```
forest_test(X_pca, Y)
```

```
3.828125
[[1262   12]
 [  40 1124]]
              precision    recall  f1-score   support

           0       0.97      0.99      0.98      1274
           1       0.99      0.97      0.98      1164

    accuracy                           0.98      2438
   macro avg       0.98      0.98      0.98      2438
weighted avg       0.98      0.98      0.98      2438
```

[ ]:
```

```