ECE657A_assignment2_report

March 12, 2023

[155]:
```
from IPython.display import HTML

HTML('''<script>
code_show=true;
function code_toggle() {
 if (code_show){
 $('div.input').hide();
 } else {
 $('div.input').show();
 }
 code_show = !code_show
}
$( document ).ready(code_toggle);
</script>
<form action="javascript:code_toggle()"><input type="submit" value="Click here␣
↪to toggle on/off the raw code."></form>''')
```

[155]:
```
<IPython.core.display.HTML object>
```

[4]:
```
#Preprocessing of Abalone dataset
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
import scipy.stats as st
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
import warnings
df = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                     'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
↪'Rings'], sep = ',')
warnings.filterwarnings('ignore')
```

[5]:
```
df.head()
```

[5]:
```
  Sex  Length  Diameter  Height  Whole_weight  Sucked_weight  Viscera_weight  \
0   M   0.455     0.365   0.095        0.5140         0.2245          0.1010
1   M   0.350     0.265   0.090        0.2255         0.0995          0.0485
2   F   0.530     0.420   0.135        0.6770         0.2565          0.1415
3   M   0.440     0.365   0.125        0.5160         0.2155          0.1140
4   I   0.330     0.255   0.080        0.2050         0.0895          0.0395

   Shell_weight  Rings
0         0.150     15
1         0.070      7
2         0.210      9
3         0.155     10
4         0.055      7
```

[6]:
```python
#Data Summarization
abalone_describe = df.describe()
print(abalone_describe)

summarize = pd.DataFrame(columns=['mean',
 ↪'median','variance','skew','kurtosis'])
summarize['mean'] = df.mean()
summarize['median'] = df.median()
summarize['variance'] = df.var()
summarize['skew'] = df.skew()
summarize['kurtosis'] = df.kurtosis()
display(summarize)
```

```
            Length     Diameter       Height  Whole_weight  Sucked_weight  \
count  4177.000000  4177.000000  4177.000000   4177.000000    4177.000000
mean      0.523992     0.407881     0.139516      0.828742       0.359367
std       0.120093     0.099240     0.041827      0.490389       0.221963
min       0.075000     0.055000     0.000000      0.002000       0.001000
25%       0.450000     0.350000     0.115000      0.441500       0.186000
50%       0.545000     0.425000     0.140000      0.799500       0.336000
75%       0.615000     0.480000     0.165000      1.153000       0.502000
max       0.815000     0.650000     1.130000      2.825500       1.488000

       Viscera_weight  Shell_weight        Rings
count     4177.000000   4177.000000  4177.000000
mean         0.180594      0.238831     9.933684
std          0.109614      0.139203     3.224169
min          0.000500      0.001500     1.000000
25%          0.093500      0.130000     8.000000
50%          0.171000      0.234000     9.000000
75%          0.253000      0.329000    11.000000
max          0.760000      1.005000    29.000000
```

```
                    mean  median   variance      skew  kurtosis
```

```
Length          0.523992  0.5450   0.014422 -0.639873   0.064621
Diameter        0.407881  0.4250   0.009849 -0.609198  -0.045476
Height          0.139516  0.1400   0.001750  3.128817  76.025509
Whole_weight    0.828742  0.7995   0.240481  0.530959  -0.023644
Sucked_weight   0.359367  0.3360   0.049268  0.719098   0.595124
Viscera_weight  0.180594  0.1710   0.012015  0.591852   0.084012
Shell_weight    0.238831  0.2340   0.019377  0.620927   0.531926
Rings           9.933684  9.0000  10.395266  1.114102   2.330687
```

[7]:
```python
missing_values = df.isna().sum()
print(missing_values)
```

```
Sex               0
Length            0
Diameter          0
Height            0
Whole_weight      0
Sucked_weight     0
Viscera_weight    0
Shell_weight      0
Rings             0
dtype: int64
```

Is there any missing data? Answer to this question can given by observing the output of isna(), we can see that for for all the columns we have got value 0, which means that there are no missing values for any of the columns in the abalone dataset.

[8]:
```python
if (missing_values>0).any():
    print("There are {} missing values\n".format(np.sum(missing_values)))
else:
    print("there are no missing data")
```

```
there are no missing data
```

[9]:
```python
sex_describe = df['Sex'].describe()
sex_unique = df['Sex'].unique()
print(sex_describe)
print("Total Unique Sex: ", sex_unique)
df['Sex'].value_counts()
```

```
count     4177
unique       3
top          M
freq      1528
Name: Sex, dtype: object
Total Unique Sex:  ['M' 'F' 'I']
```

[9]:
```
M    1528
I    1342
F    1307
```

```
Name: Sex, dtype: int64
```

Finding correlations between 2 variables/columns in abalone dataset

[10]:
```python
features = df.select_dtypes(include=[np.number])
features_correlation = features.corr()
print(features_correlation)
```

```
                  Length  Diameter    Height  Whole_weight  Sucked_weight  \
Length          1.000000  0.986812  0.827554      0.925261       0.897914
Diameter        0.986812  1.000000  0.833684      0.925452       0.893162
Height          0.827554  0.833684  1.000000      0.819221       0.774972
Whole_weight    0.925261  0.925452  0.819221      1.000000       0.969405
Sucked_weight   0.897914  0.893162  0.774972      0.969405       1.000000
Viscera_weight  0.903018  0.899724  0.798319      0.966375       0.931961
Shell_weight    0.897706  0.905330  0.817338      0.955355       0.882617
Rings           0.556720  0.574660  0.557467      0.540390       0.420884

                Viscera_weight  Shell_weight     Rings
Length                0.903018      0.897706  0.556720
Diameter              0.899724      0.905330  0.574660
Height                0.798319      0.817338  0.557467
Whole_weight          0.966375      0.955355  0.540390
Sucked_weight         0.931961      0.882617  0.420884
Viscera_weight        1.000000      0.907656  0.503819
Shell_weight          0.907656      1.000000  0.627574
Rings                 0.503819      0.627574  1.000000
```

finding the correlation w.r.t to rings

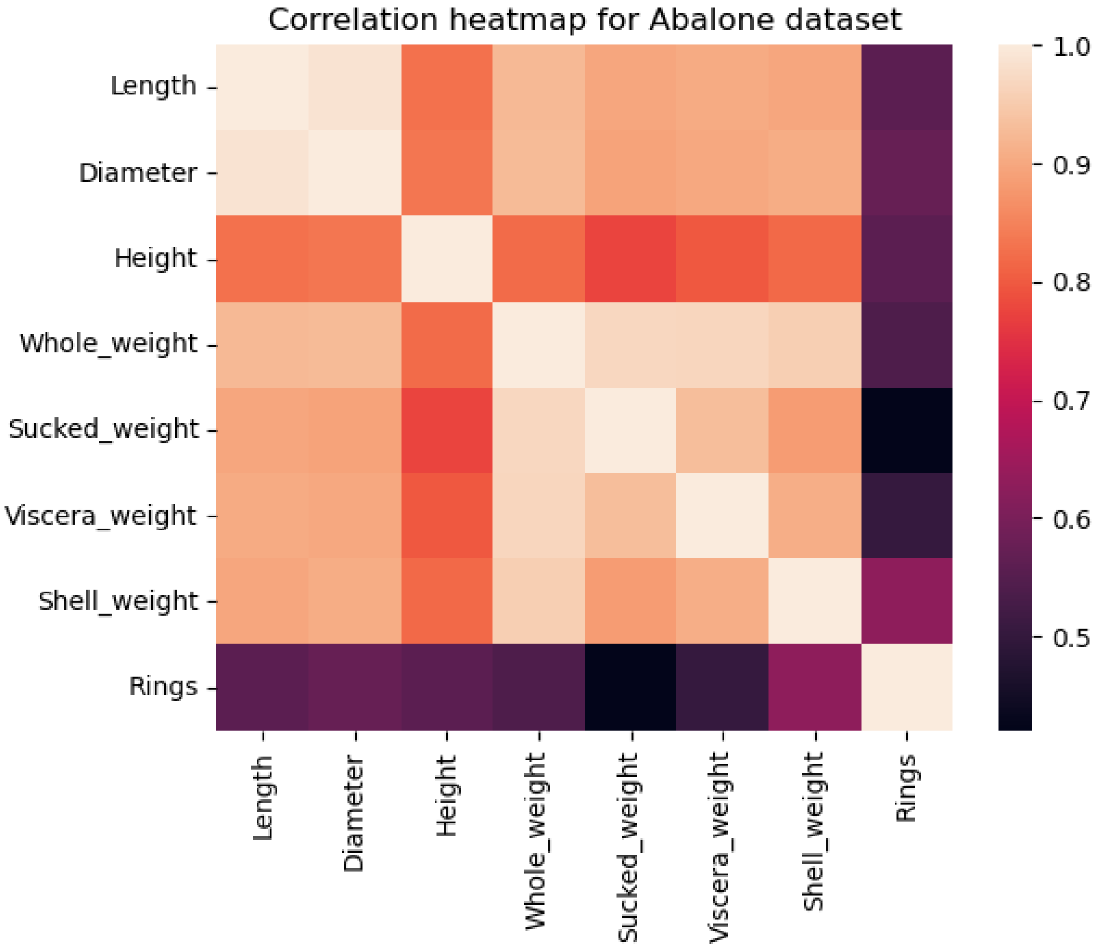
[11]:
```python
print(features_correlation['Rings'])
```

```
Length            0.556720
Diameter          0.574660
Height            0.557467
Whole_weight      0.540390
Sucked_weight     0.420884
Viscera_weight    0.503819
Shell_weight      0.627574
Rings             1.000000
Name: Rings, dtype: float64
```

from the above block, we can see that only shell weight is somewhat correlated with rings columns. apart from this all other columns/parameters are not that much correlated with the rings. this would cause problem in the ring classification. 1 represents that the variables are highly correlated and 0 represents that variableas are not correlated.

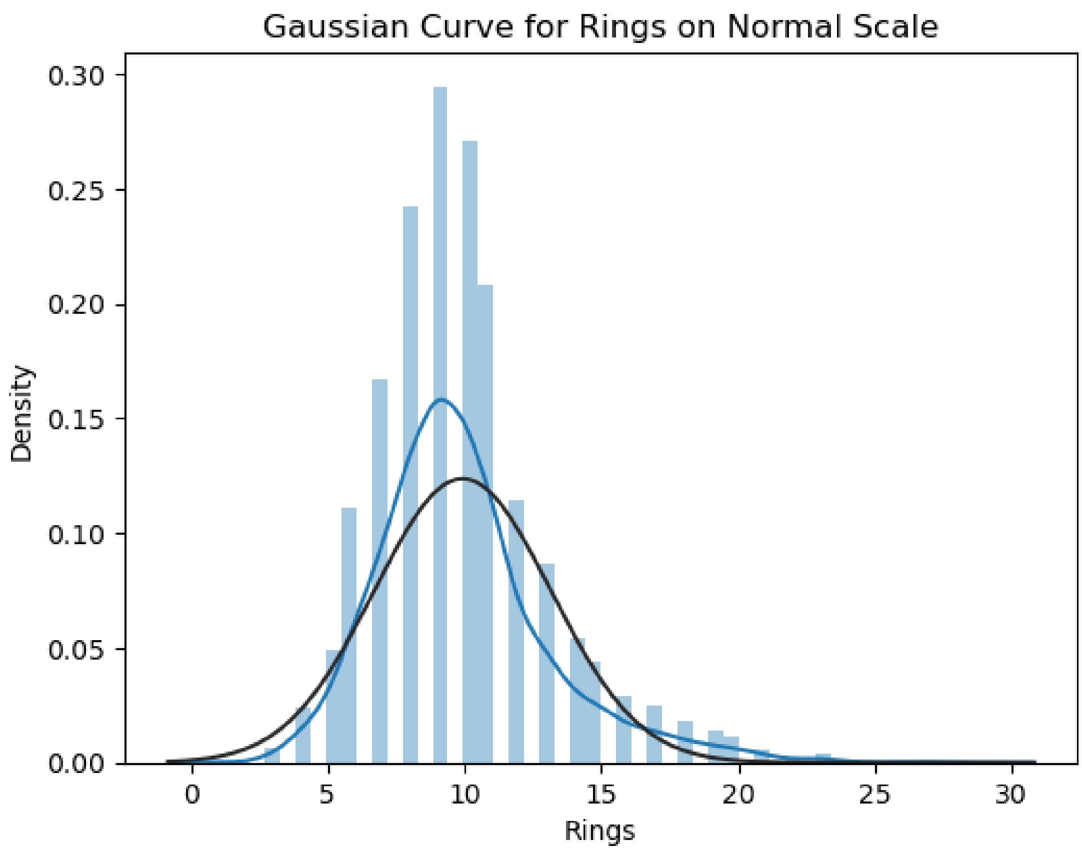
[12]:
```python
plt.title("Correlation heatmap for Abalone dataset")
sns.heatmap(features_correlation)
```

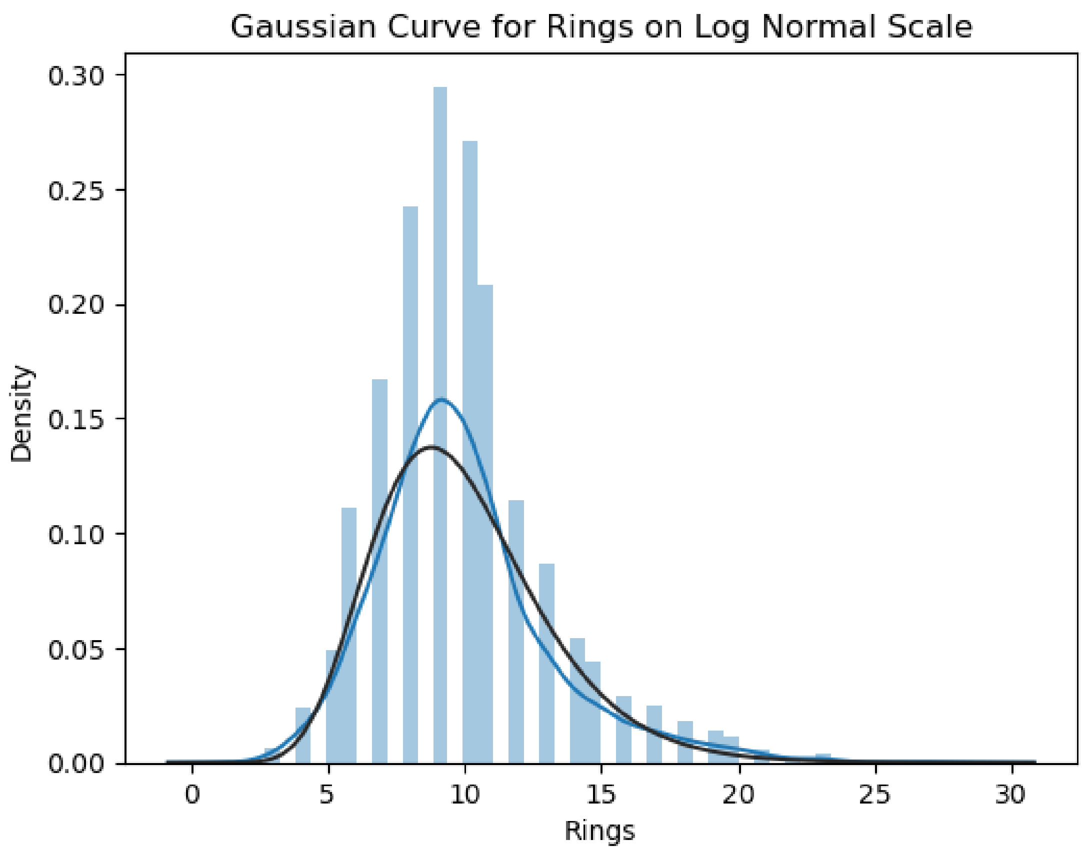
[12]: <AxesSubplot:title={'center':'Correlation heatmap for Abalone dataset'}>



[13]:
```
#Checking the histogram for Rings
rings = df['Rings']
plt.figure(1)
plt.title("Gaussian Curve for Rings on Normal Scale")
sns.distplot(rings,kde=True,fit=st.norm)

plt.figure(2)
plt.title("Gaussian Curve for Rings on Log Normal Scale")
sns.distplot(rings,kde=True,fit=st.lognorm)
```

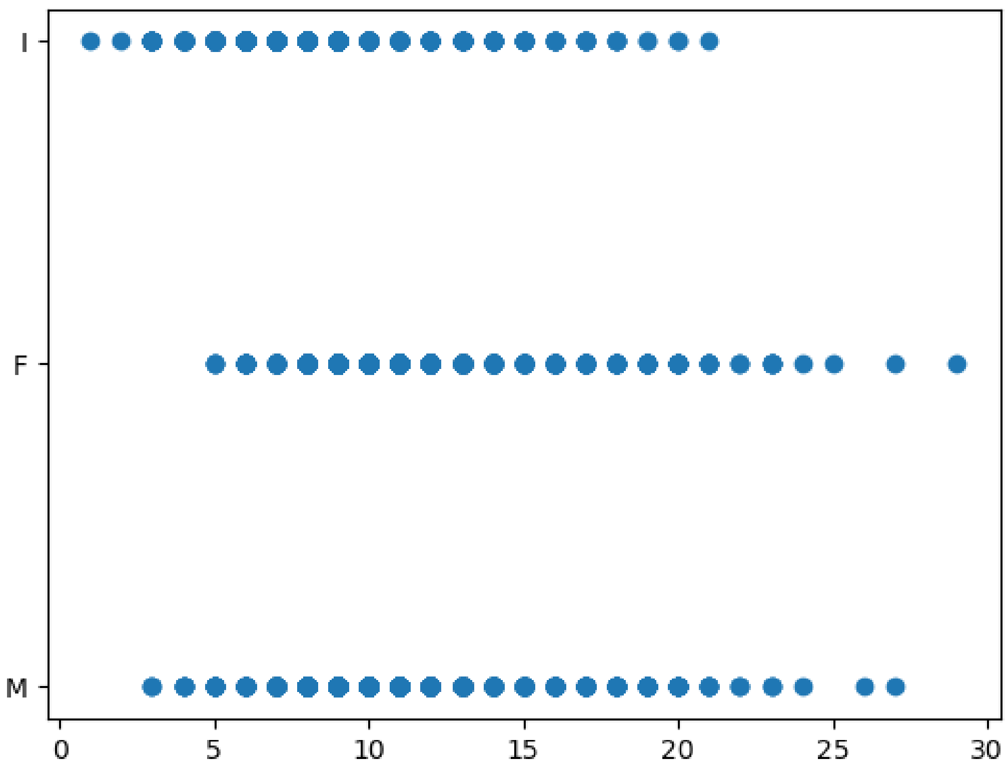
[13]: <AxesSubplot:title={'center':'Gaussian Curve for Rings on Log Normal Scale'}, xlabel='Rings', ylabel='Density'>


Gaussian Curve for Rings on Normal Scale
Density
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0
5
10
15
20
25
30
Rings

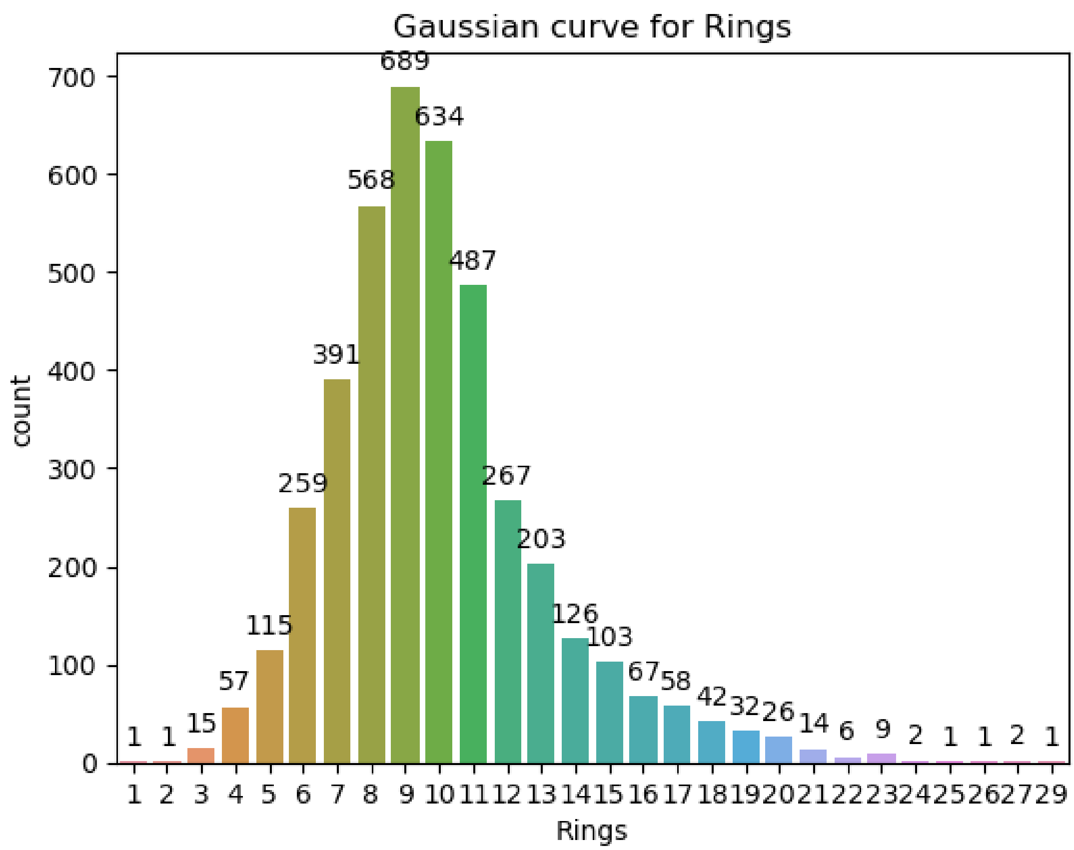


[14]:
```
# Check any relationship between Sex and Rings
plt.scatter(y=df['Sex'], x=df['Rings'])
```

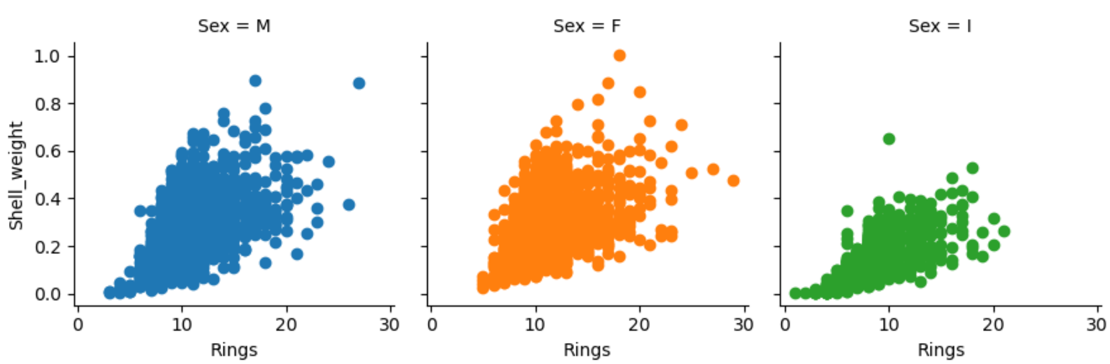
[14]: <matplotlib.collections.PathCollection at 0x1bbd045bbe0>



[15]:
```
ax = sns.countplot(df['Rings'])
plt.title('Gaussian curve for Rings')
for p in ax.patches:
    ax.annotate(format(p.get_height(), '.0f'),
                (p.get_x() + p.get_width() / 2., p.get_height()),
                ha = 'center', va = 'center',
                xytext = (0, 9),
                textcoords = 'offset points')
```

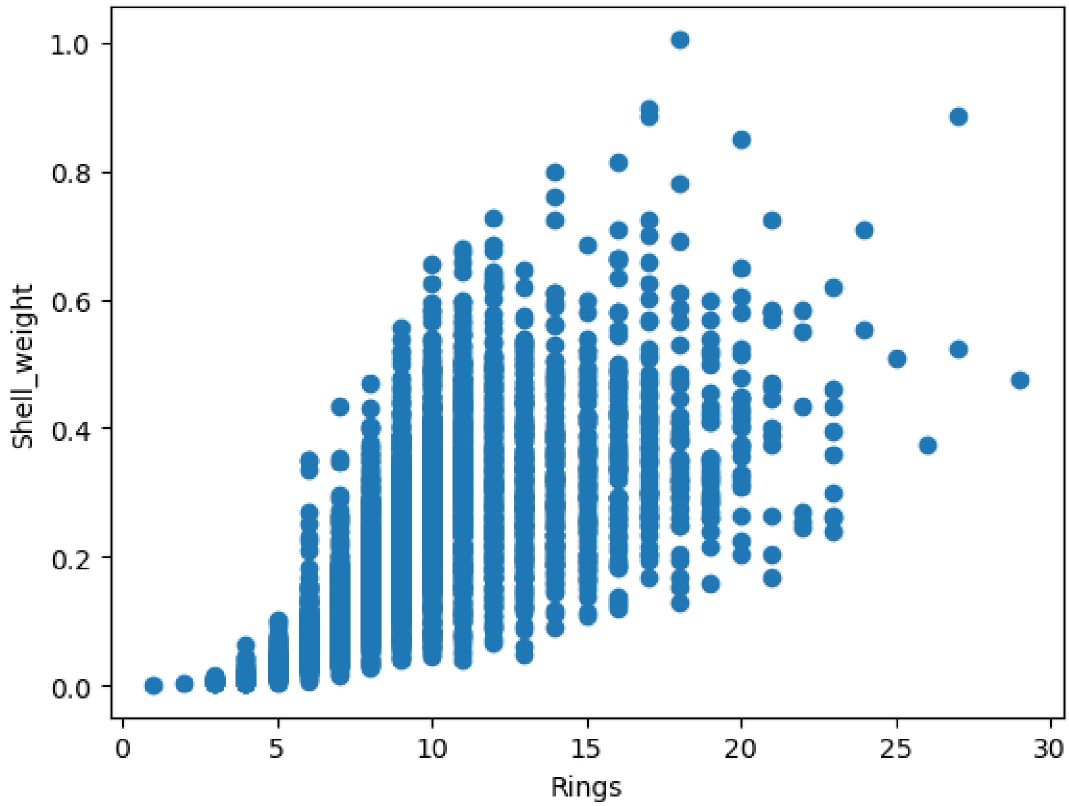


[16]:
```
Rings_facet = sns.FacetGrid(df, col="Sex", hue="Sex")
Rings_facet=Rings_facet.map(plt.scatter,"Rings", "Shell_weight")
```



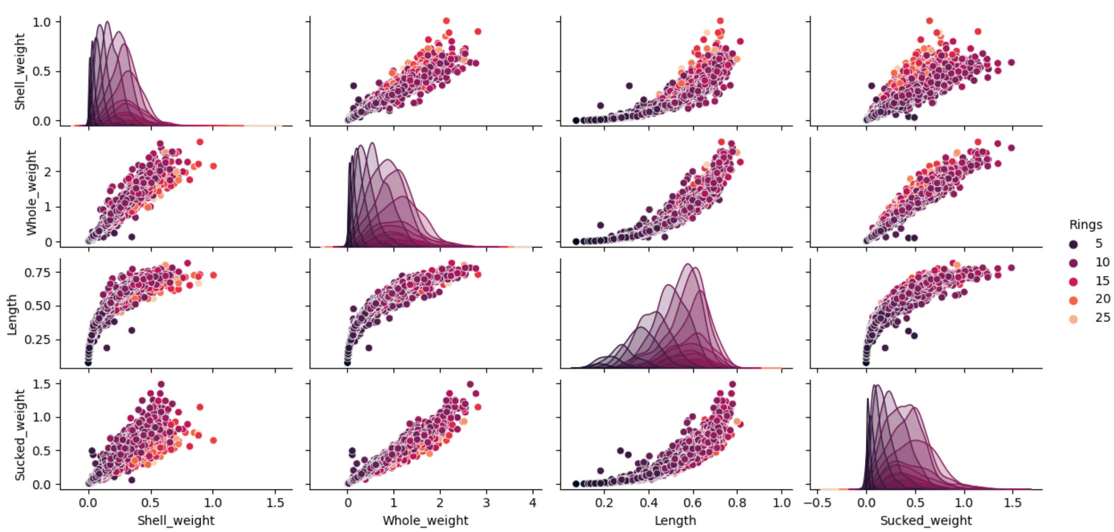
[17]:
```
plt.scatter(x=df['Rings'], y=df['Shell_weight'])
plt.xlabel('Rings')
plt.ylabel('Shell_weight')
```

[17]: Text(0, 0.5, 'Shell_weight')



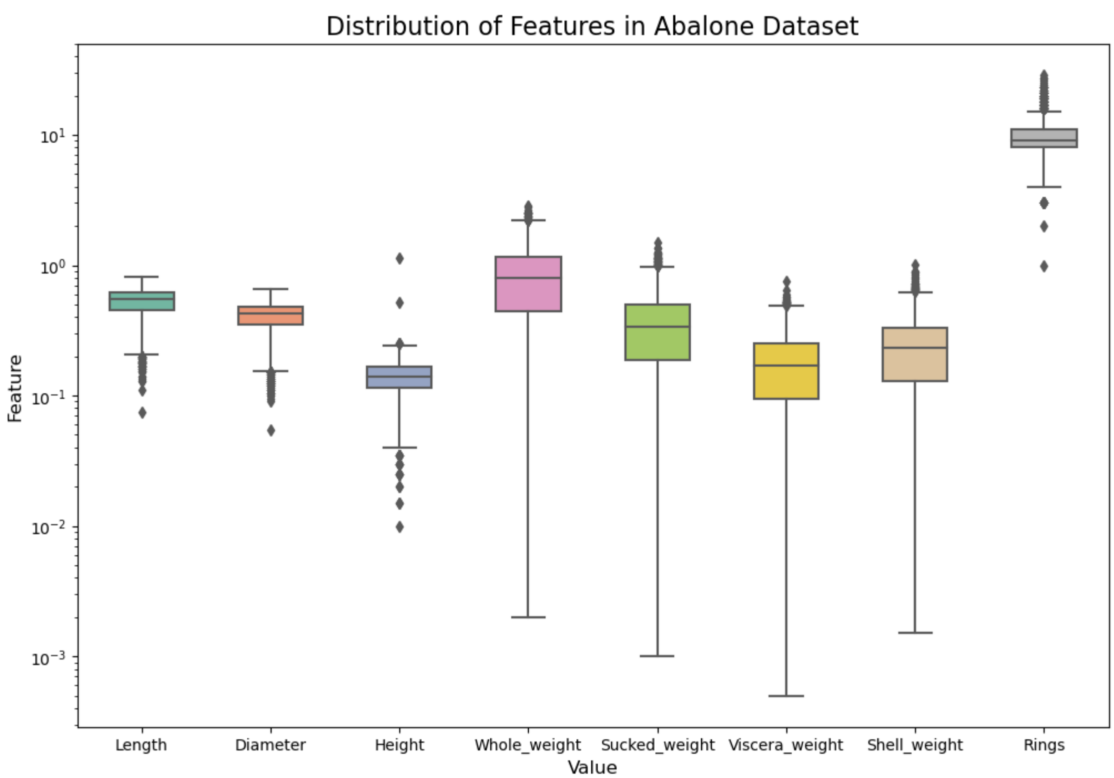
[18]:
```
sns.pairplot(df, vars=["Shell_weight", "Whole_weight", "Length",␣
↪"Sucked_weight"], hue='Rings', palette="rocket", height=1.5, aspect=2)
```

[18]: <seaborn.axisgrid.PairGrid at 0x1bbd1809df0>



[19]:
```
plt.figure(figsize=(12,8))
sns.boxplot(data=df, orient="v", palette="Set2", whis=1.5, width=0.5)
plt.yscale('log')
plt.title("Distribution of Features in Abalone Dataset", fontsize=16)
plt.xlabel("Value", fontsize=12)
plt.ylabel("Feature", fontsize=12)
```

[19]: Text(0, 0.5, 'Feature')



Starting Normalization from here

[20]:
```
numeric_cols = df.select_dtypes(include='number').columns.tolist()
scaler = StandardScaler()
scaler.fit(df[numeric_cols])
abalone_norm = df.copy()
abalone_norm[numeric_cols] = scaler.transform(df[numeric_cols])
print(df.head())
```

```
  Sex  Length  Diameter  Height  Whole_weight  Sucked_weight  Viscera_weight  \
0   M   0.455     0.365   0.095        0.5140         0.2245          0.1010
1   M   0.350     0.265   0.090        0.2255         0.0995          0.0485
```

```
2    F   0.530    0.420   0.135        0.6770       0.2565         0.1415
3    M   0.440    0.365   0.125        0.5160       0.2155         0.1140
4    I   0.330    0.255   0.080        0.2050       0.0895         0.0395

   Shell_weight  Rings
0         0.150     15
1         0.070      7
2         0.210      9
3         0.155     10
4         0.055      7
```

[21]:
```
X = df.drop(['Rings','Sex'], axis=1)
y = df['Rings']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state = 40)

X_Norm = abalone_norm.drop(['Rings','Sex'], axis=1)
#y_Norm = abalone_norm['Rings']
y_Norm = y
X_train_Norm, X_test_Norm, y_train_Norm, y_test_Norm = train_test_split(X_Norm,␣
↪y_Norm, test_size=0.2, random_state = 40)
```

[22]:
```
display("Training Data Original")
display(X_train.head())
display(X_train.describe())

display("Testing Data Original")
display(X_test.head())
display(X_test.describe())

display("Training Data Z Normalized")
display(X_train_Norm.head())
display(X_train_Norm.describe())

display("Testing Data Z Normalized")
display(X_test_Norm.head())
display(X_test_Norm.describe())
```

```
'Training Data Original'

      Length  Diameter  Height  Whole_weight  Sucked_weight  Viscera_weight  \
1794   0.575     0.450   0.130        0.8145         0.4030          0.1715
1466   0.515     0.425   0.145        0.9365         0.4970          0.1810
2275   0.655     0.525   0.185        1.2590         0.4870          0.2215
3929   0.650     0.515   0.215        1.4980         0.5640          0.3230
1955   0.645     0.510   0.180        1.6195         0.7815          0.3220

      Shell_weight
1794        0.2130
```

1466	0.2185
2275	0.4450
3929	0.4250
1955	0.4675

	Length	Diameter	Height	Whole_weight	Sucked_weight	\
count	3341.000000	3341.000000	3341.000000	3341.000000	3341.000000	
mean	0.523590	0.407685	0.139397	0.829025	0.360037	
std	0.120856	0.099806	0.042632	0.493738	0.223379	
min	0.075000	0.055000	0.000000	0.002000	0.001000	
25%	0.450000	0.350000	0.115000	0.438500	0.184500	
50%	0.545000	0.425000	0.140000	0.797000	0.336000	
75%	0.615000	0.480000	0.165000	1.153000	0.505500	
max	0.815000	0.650000	1.130000	2.825500	1.488000	

	Viscera_weight	Shell_weight
count	3341.000000	3341.000000
mean	0.180496	0.238490
std	0.110090	0.139733
min	0.000500	0.001500
25%	0.092500	0.130000
50%	0.170500	0.233000
75%	0.253000	0.326000
max	0.760000	1.005000

'Testing Data Original'

	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	\
341	0.62	0.510	0.205	1.3475	0.4775	0.2565	
3413	0.49	0.395	0.120	0.6740	0.3325	0.1235	
1088	0.45	0.340	0.120	0.4925	0.2410	0.1075	
98	0.47	0.370	0.130	0.5225	0.2010	0.1330	
3661	0.55	0.415	0.150	0.7915	0.3535	0.1760	

	Shell_weight
341	0.480
3413	0.185
1088	0.120
98	0.165
3661	0.236

	Length	Diameter	Height	Whole_weight	Sucked_weight	\
count	836.000000	836.000000	836.000000	836.000000	836.000000	
mean	0.525598	0.408666	0.139994	0.827610	0.356690	
std	0.117049	0.096998	0.038462	0.477058	0.216322	
min	0.160000	0.110000	0.015000	0.014500	0.005500	
25%	0.453750	0.350000	0.115000	0.451500	0.190500	
50%	0.545000	0.425000	0.140000	0.806000	0.336750	
75%	0.615000	0.481250	0.165000	1.157125	0.492625	
max	0.800000	0.630000	0.240000	2.526000	1.351000	

	Viscera_weight	Shell_weight
count	836.000000	836.000000
mean	0.180982	0.240193
std	0.107758	0.137137
min	0.002500	0.005000
25%	0.095375	0.130875
50%	0.171000	0.235000
75%	0.252875	0.332625
max	0.590000	0.885000

'Training Data Z Normalized'

	Length	Diameter	Height	Whole_weight	Sucked_weight	\
1794	0.424788	0.424464	-0.227545	-0.029046	0.196599	
1466	-0.074885	0.172519	0.131117	0.219766	0.620144	
2275	1.091018	1.180300	1.087551	0.877486	0.575086	
3929	1.049379	1.079522	1.804876	1.364912	0.922032	
1955	1.007740	1.029133	0.967997	1.612704	1.902043	

	Viscera_weight	Shell_weight
1794	-0.082970	-0.185585
1466	0.003708	-0.146070
2275	0.373230	1.481249
3929	1.299315	1.337556
1955	1.290191	1.642903

	Length	Diameter	Height	Whole_weight	Sucked_weight	\
count	3341.000000	3341.000000	3341.000000	3341.000000	3341.000000	
mean	-0.003347	-0.001980	-0.002858	0.000578	0.003019	
std	1.006478	1.005828	1.019371	1.006950	1.006500	
min	-3.739154	-3.556267	-3.335953	-1.686092	-1.614731	
25%	-0.616198	-0.583316	-0.586208	-0.795876	-0.787917	
50%	0.174951	0.172519	0.011563	-0.064736	-0.105289	
75%	0.757903	0.726798	0.609334	0.661305	0.658443	
max	2.423480	2.440025	23.683287	4.072271	5.085388	

	Viscera_weight	Shell_weight
count	3341.000000	3341.000000
mean	-0.000887	-0.002449
std	1.004457	1.003930
min	-1.643173	-1.705134
25%	-0.803766	-0.781909
50%	-0.092094	-0.041893
75%	0.660635	0.626278
max	5.286500	5.504642

'Testing Data Z Normalized'

	Length	Diameter	Height	Whole_weight	Sucked_weight	\

```
341   0.799543  1.029133  1.565767      1.057976       0.532281
3413 -0.283082 -0.129815 -0.466653     -0.315588      -0.121059
1088 -0.616198 -0.684094 -0.466653     -0.685746      -0.533340
98   -0.449640 -0.381760 -0.227545     -0.624563      -0.713572
3661  0.216591  0.071741  0.250672     -0.075953      -0.026438

      Viscera_weight  Shell_weight
341         0.692569      1.732711
3413       -0.520922     -0.386755
1088       -0.666906     -0.853756
98         -0.434244     -0.530447
3661       -0.041912     -0.020339
           Length    Diameter      Height  Whole_weight  Sucked_weight  \
count  836.000000  836.000000  836.000000    836.000000     836.000000
mean     0.013374    0.007911    0.011420     -0.002309      -0.012063
std      0.974773    0.977526    0.919654      0.972932       0.974702
min     -3.031284   -3.001988   -2.977291     -1.660599      -1.594455
25%     -0.584968   -0.583316   -0.586208     -0.769363      -0.760882
50%      0.174951    0.172519    0.011563     -0.046381      -0.101910
75%      0.757903    0.739396    0.609334      0.669718       0.600431
max      2.298562    2.238469    2.402646      3.461458       4.468094

       Viscera_weight  Shell_weight
count      836.000000    836.000000
mean         0.003544      0.009788
std          0.983182      0.985280
min         -1.624925     -1.679988
25%         -0.777534     -0.775623
50%         -0.087532     -0.027523
75%          0.659495      0.673876
max          3.735421      4.642486
```

[23]:

```
# Apply KNN classification for original Data
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score
knn = KNeighborsClassifier(n_neighbors=3)
knn.fit(X_train, y_train)
knn_pred = knn.predict(X_test)
knn_initial_score = accuracy_score(y_test, knn_pred)
knn_initial_score
```

[23]: 0.20334928229665072

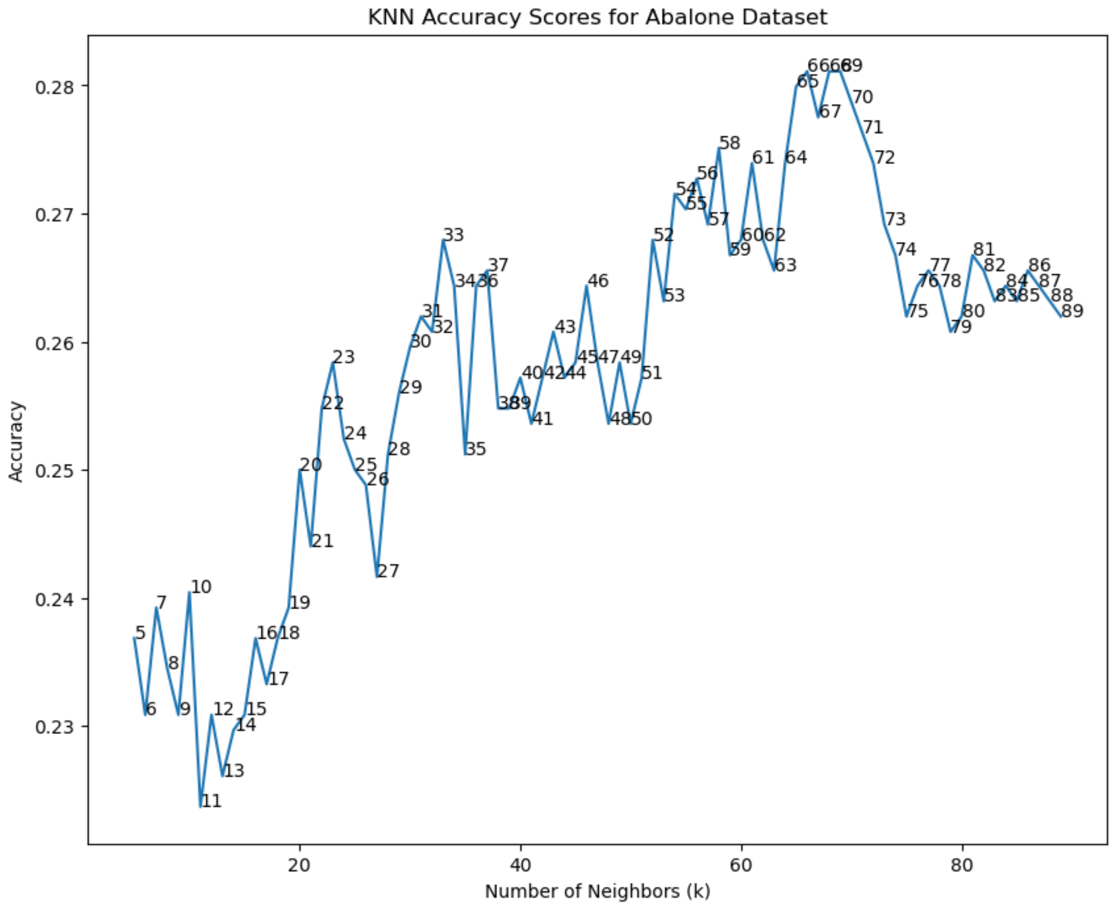
[24]:

```
# Apply KNN classification for Normalized Data
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score
knn = KNeighborsClassifier(n_neighbors=3)
```

```
knn.fit(X_train_Norm, y_train)
knn_pred = knn.predict(X_test_Norm)
knn_initial_score = accuracy_score(y_test, knn_pred)
knn_initial_score
```

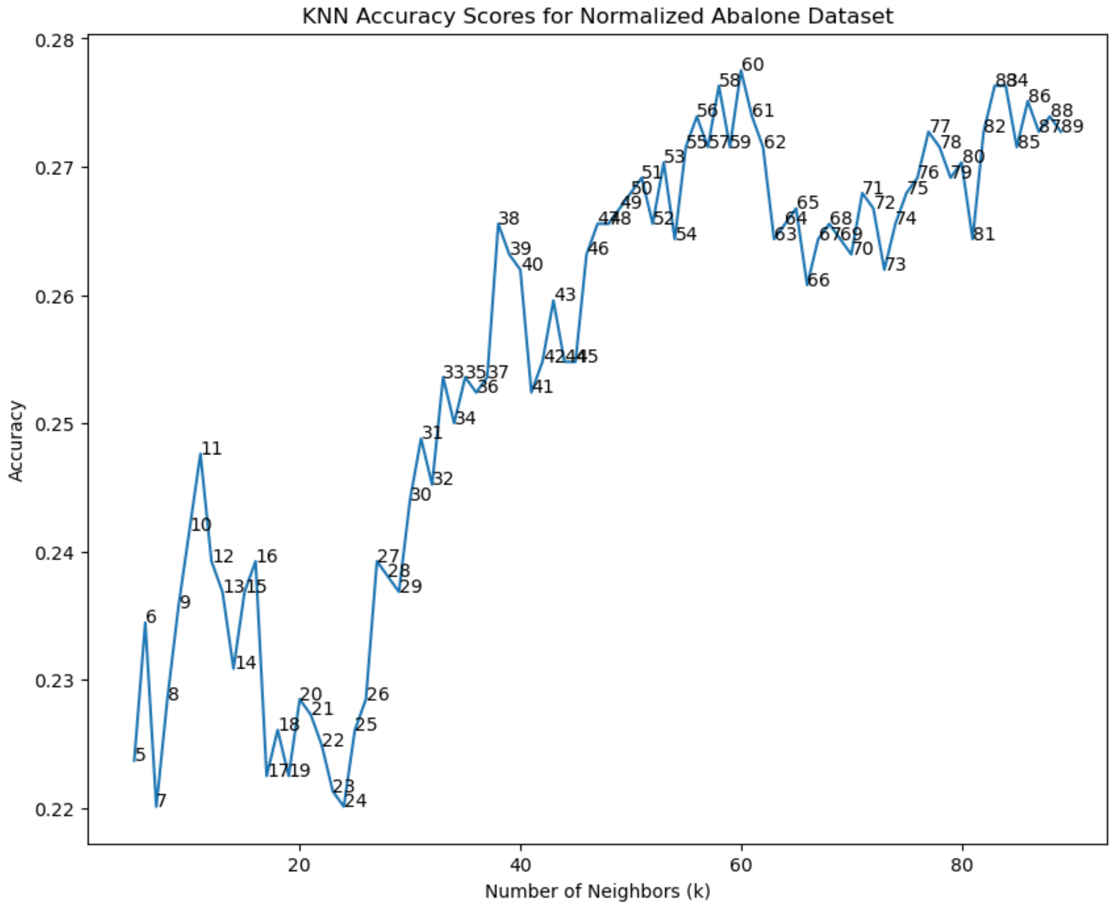
[24]: 0.215311004784689

[25]:
```
from sklearn.metrics import accuracy_score, recall_score, precision_score
from sklearn.metrics import confusion_matrix
accuracy_score = []
for k in range(5,90):
    knn = KNeighborsClassifier(n_neighbors=k)
    knn.fit(X_train, y_train)
    knn_pred = knn.predict(X_test)
    knn_accuracy_score = recall_score(y_test, knn_pred, average='micro')
    accuracy_score.append(knn_accuracy_score)
    #knn_accuracy_score = accuracy_score(y_test, knn_pred)
    #knn_accuracy_score
    #print("The Accuracy for k={} is {}".format(k, knn_accuracy_score))

plt.figure(figsize=(10,8))
for i, k in enumerate(range(5, 90)):
    plt.text(k, accuracy_score[i], str(k), fontsize=10)


plt.plot(range(5,90), accuracy_score)
plt.xlabel('Number of Neighbors (k)')
plt.ylabel('Accuracy')
plt.title('KNN Accuracy Scores for Abalone Dataset')
plt.show()
```



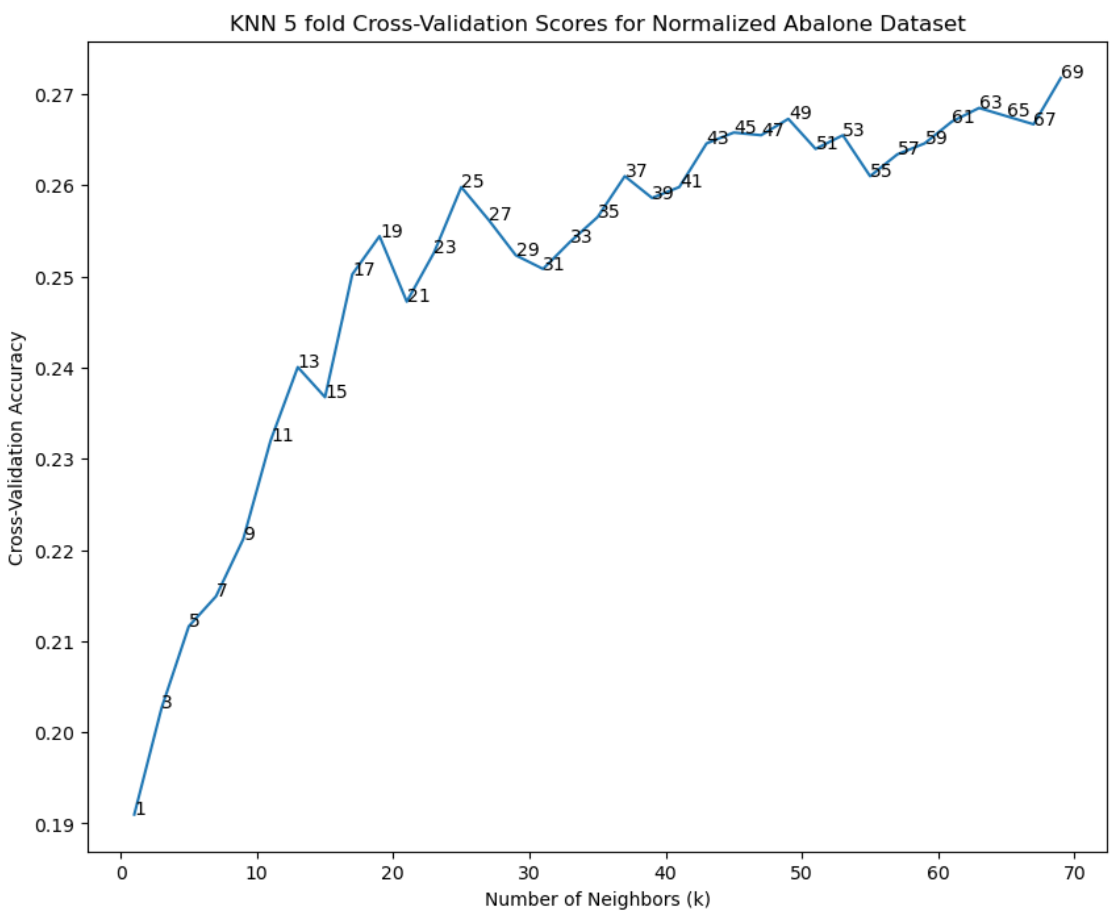

```
[26]: from sklearn.metrics import accuracy_score, recall_score, precision_score
from sklearn.metrics import confusion_matrix
accuracy_score = []
for k in range(5,90):
    knn = KNeighborsClassifier(n_neighbors=k)
    knn.fit(X_train_Norm, y_train)
    knn_pred = knn.predict(X_test_Norm)
    knn_accuracy_score = recall_score(y_test, knn_pred, average='micro')
    accuracy_score.append(knn_accuracy_score)
    #knn_accuracy_score = accuracy_score(y_test, knn_pred)
    #knn_accuracy_score
    #print("The Accuracy for k={} is {}".format(k, knn_accuracy_score))

plt.figure(figsize=(10,8))
plt.plot(range(5,90), accuracy_score)
plt.xlabel('Number of Neighbors (k)')
plt.ylabel('Accuracy')
plt.title('KNN Accuracy Scores for Normalized Abalone Dataset')
```

```
for i, k in enumerate(range(5, 90)):
    plt.text(k, accuracy_score[i], str(k), fontsize=10)

plt.show()
```



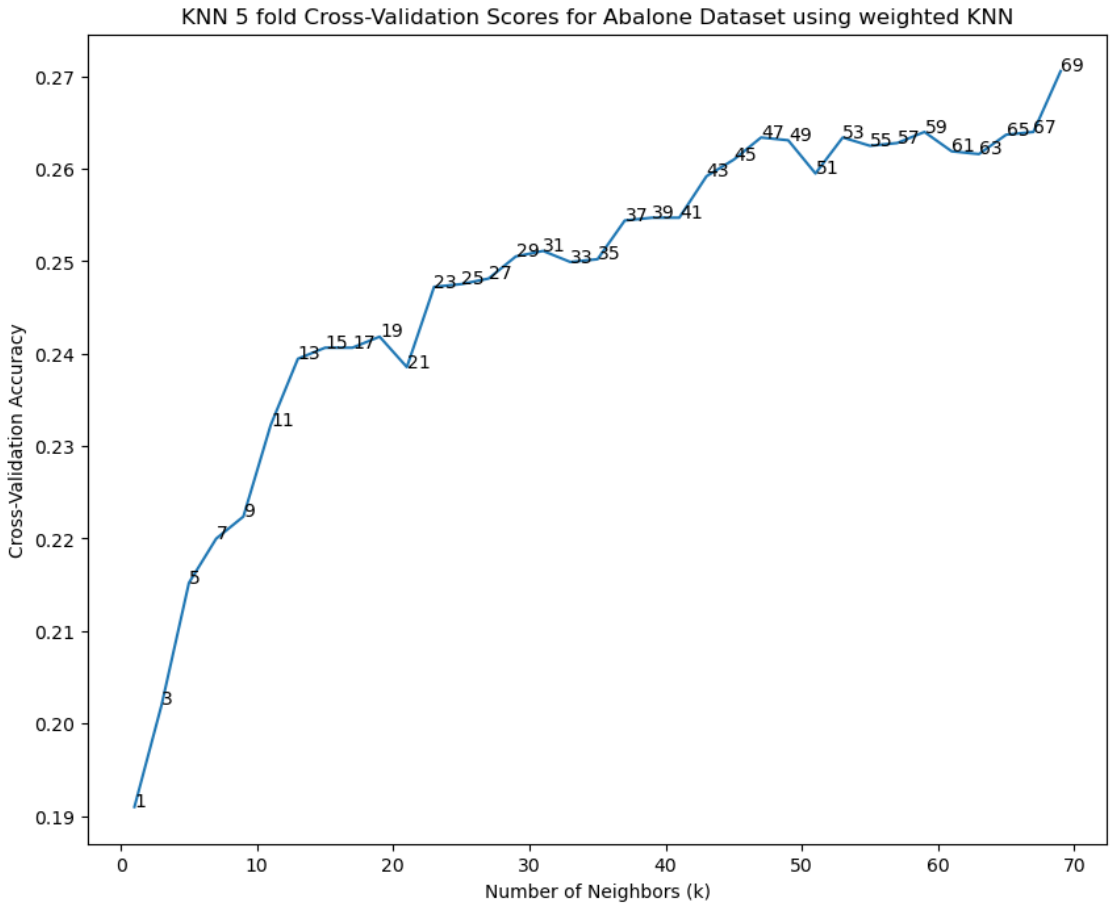
[27]:
```
from sklearn.metrics import accuracy_score
from sklearn.model_selection import StratifiedKFold
from sklearn.model_selection import cross_val_score

k_list = np.arange(1, 70, 2)
# Create an empty list to store cross-validation scores
cross_validate_scores = []

# Use 5-fold cross-validation to evaluate model performance for each value of k
cross_validation = 5
for k in k_list:
    knn = KNeighborsClassifier(n_neighbors=k)
```

```
    scores = cross_val_score(knn, X_train_Norm, y_train, cv=cross_validation,␣
↪scoring='accuracy')
    cross_validate_scores.append(scores.mean())

# Plot the cross-validation scores for each value of k
import matplotlib.pyplot as plt
plt.figure(figsize=(10,8))
plt.plot(k_list, cross_validate_scores)
plt.xlabel('Number of Neighbors (k)')
plt.ylabel('Cross-Validation Accuracy')
plt.title('KNN {} fold Cross-Validation Scores for Normalized Abalone Dataset'.
↪format(cross_validation))

for i, k in enumerate(range(1, 70, 2)):
    plt.text(k, cross_validate_scores[i], str(k), fontsize=10)

plt.show()
```



[28]:
```
from sklearn.metrics import accuracy_score
from sklearn.model_selection import StratifiedKFold
from sklearn.model_selection import cross_val_score

k_list = np.arange(1, 70, 2)
# Create an empty list to store cross-validation scores
cross_validate_scores = []

# Use 5-fold cross-validation to evaluate model performance for each value of k
cross_validation = 5
for k in k_list:
    knn = KNeighborsClassifier(n_neighbors=k, weights='distance')
    scores = cross_val_score(knn, X_train_Norm, y_train, cv=cross_validation,␣
↪scoring='accuracy')
    cross_validate_scores.append(scores.mean())

# Plot the cross-validation scores for each value of k
import matplotlib.pyplot as plt
plt.figure(figsize=(10,8))
plt.plot(k_list, cross_validate_scores)
plt.xlabel('Number of Neighbors (k)')
plt.ylabel('Cross-Validation Accuracy')
plt.title('KNN {} fold Cross-Validation Scores for Abalone Dataset using␣
↪weighted KNN'.format(cross_validation))

print(cross_validate_scores)

for i, k in enumerate(range(1, 70, 2)):
    plt.text(k, cross_validate_scores[i], str(k), fontsize=10)

plt.show()
```

```
[0.19096604996285454, 0.20203807631374024, 0.2152068061187043,
0.21999185485531178, 0.22238706443615014, 0.2322668564216858,
0.23945248516420076, 0.24064964241919745, 0.2406478522775078,
0.2418432193908148, 0.2385533865005415, 0.24723467862481313,
0.24753139460988338, 0.24813064454051537, 0.25052316890881915,
0.25112197130402875, 0.249924814049032, 0.25022421524663674, 0.2544131468005693,
0.2547147856752862, 0.2547147856752862, 0.25920267089140103, 0.2609946027228055,
0.2633902598390663, 0.2630922012477287, 0.25950117701816094, 0.2633916024453335,
0.2624969791358986, 0.2627945901918137, 0.2639917474468104, 0.2618968341344218,
0.2615983280076618, 0.26369324132005045, 0.26399264251765525,
0.2705758885815812]
```



0.1 Assignment 2 Question 1 implementation starts here

0.1.1 Question 1

1 Representation Learning You will apply PCA and LDA onto the dataset, analyse the resulting new representations in terms of interpretability and classifier impact, then create new reduced dimension datasets for use in later questions. 1. Run PCA on each dataset, look at the total variance explained by the principle components. At least, show a plot of the first two principle components using easily distinguishable colours and markers to indicate the labels of each datapoint. 2. Plot and show a scree-plot to look at the cumulative variance represented by the PCA eigenvectors. 3. You now want to experimentally find the best reduced dimensionality for the dataset with respect to how it impacts the accuracy of a classifier. • Produce a plot that shows accuracy of the kNN classifier on the PCA features using different numbers of dimensions. The accuracy should be listed in increasing order from 2 up to D, the original dimensionality of the dataset. • For the kNN classifier, you should choose the best one you found from asg1, one of the weighted versions using a normalized dataset. • Comment briefly on the difference in accuracy from asg1. • How do the best number of features suggested by the scree plot and this analysis compare? 4. Try using the t-SNE method to visualize the datasets by producing a 2D plot, comment on any useful patterns that this shows. Once you've completed the above analysis, you can create two new versions of your datasets using

the best reduced dimensionality representation, as measured against kNN performance or the scree plot analysis, whichever you choose. For the rest of the assignment you will have the following datasets Original Dataset Feature Extraction Datasets wine-raw wine-pca / wine-lda abalone-raw abalone-pca / abalone-lda Include summary accuracy scores for kNN on all six datasets in the table in the last question.

1 Using Abalone Dataset

[29]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
import sys

df = pd.read_csv(r"C:
 ↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
 ↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                        'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
 ↪'Rings'], sep = ',')
X = df.iloc[:, 1:8].values  # extract features
y = df.iloc[:, -1].values   # extract labels
print(y)

scaler = StandardScaler()
X_std = scaler.fit_transform(X)

cov_mat = np.cov(X_std.T)
print("Covariance Matrix Calculated using numpy:\n")
np.savetxt(sys.stdout, cov_mat, fmt='%.4f', delimiter='\t')
```

```
[15  7  9 …  9 10 12]
Covariance Matrix Calculated using numpy:

1.0002  0.9870  0.8278  0.9255  0.8981  0.9032  0.8979
0.9870  1.0002  0.8339  0.9257  0.8934  0.8999  0.9055
0.8278  0.8339  1.0002  0.8194  0.7752  0.7985  0.8175
0.9255  0.9257  0.8194  1.0002  0.9696  0.9666  0.9556
0.8981  0.8934  0.7752  0.9696  1.0002  0.9322  0.8828
0.9032  0.8999  0.7985  0.9666  0.9322  1.0002  0.9079
0.8979  0.9055  0.8175  0.9556  0.8828  0.9079  1.0002
```

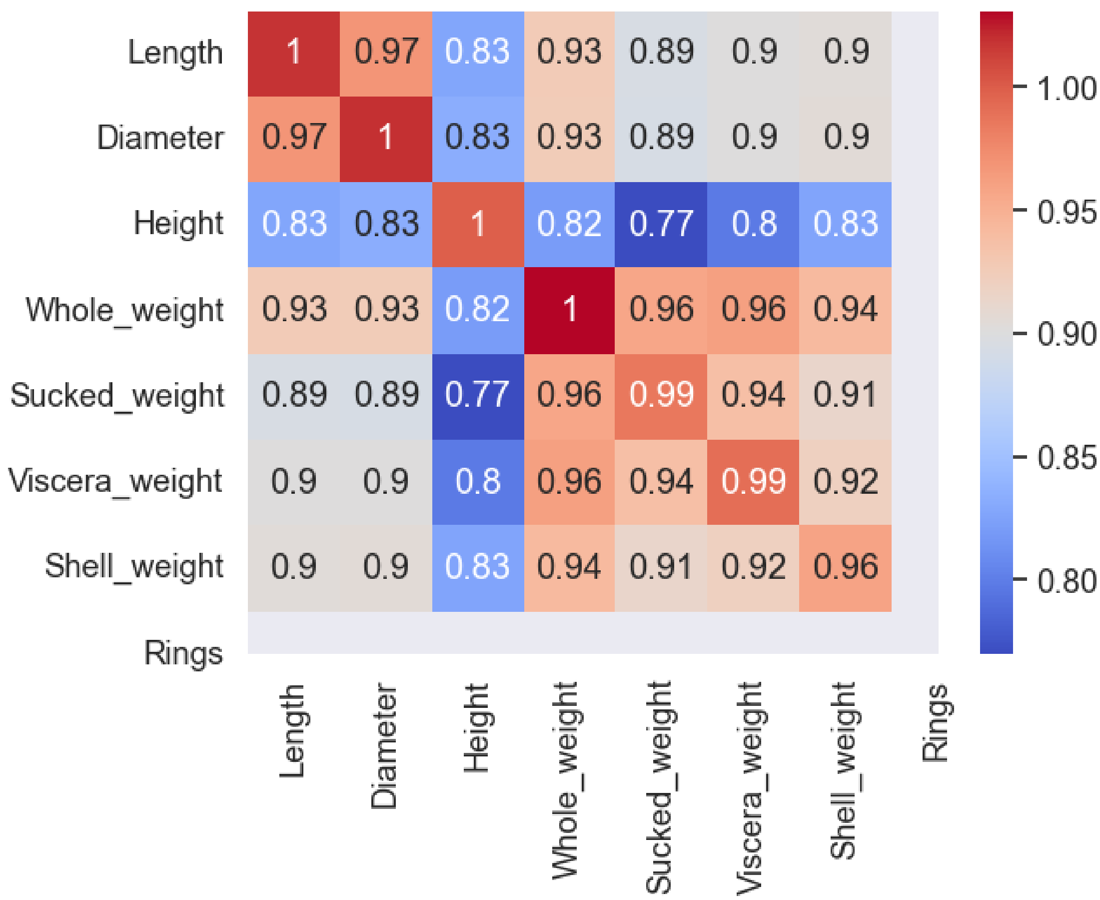
In the above we block, we calculated the covariance matrix in order to find the similarity between two feature variables.instead of using Direct PCA, we calculated it using numpy array to study the data. We can see that the feature points are quite correlated with each other. 1. The diagonal elements are the variances of each variable, which represent the spread or variability of each variable around its mean. 2. The off-diagonal elements are the covariances between each pair of variables, which represent the degree to which the variables vary together. 3. The covariance matrix shows that the length and diameter of abalone have a high positive covariance, indicating that they tend to vary together. Similarly, the weight measurements have a positive covariance with each other. 4. The covariance matrix also shows that the height of abalone has a low covariance with the other variables, indicating that it is less related to the other variables.

1.1 Using LDA as a preprocessing step for abalone dataset

[30]:
```
eig_vals, eig_vecs = np.linalg.eig(cov_mat)

tot = sum(eig_vals)
var_exp = [(i / tot) for i in sorted(eig_vals, reverse=True)]
cum_var_exp = np.cumsum(var_exp)
print("Variance explained by each principal component:\n", var_exp)
print("Cumulative variance explained by each principal component:\n",␣
↪cum_var_exp)

# Calculate the number of principal components needed to explain 95% of the␣
↪variance
n_components = np.argmax(cum_var_exp >= 0.95) + 1
print("Number of principal components needed to explain 95% of the variance:",␣
↪n_components)

pca = PCA(n_components=n_components)
#pca = PCA(n_components=np.argmax(cum_var_exp)+1)
X_pca = pca.fit_transform(X_std)

covariance = pca.get_covariance()
eigen_values = pca.explained_variance_
eigen_vectors = pca.components_

plt.figure()
sns.set(font_scale=1.2)
sns.heatmap(covariance, xticklabels=features.columns, yticklabels=features.
↪columns, cmap="coolwarm", annot=True)
plt.show()

print("Covariance matrix of the principal components:")
np.savetxt(sys.stdout, covariance, fmt='%.4f', delimiter='\t')
print("\n")
print("Eigenvalues of the principal components:")
np.savetxt(sys.stdout, eigen_values, fmt='%.4f', delimiter='\t')
print("\n")
print("Eigenvectors of the principal components:")
np.savetxt(sys.stdout, eigen_vectors, fmt='%.4f', delimiter='\t')
print("\n")

colors = ['r', 'g', 'b']
```

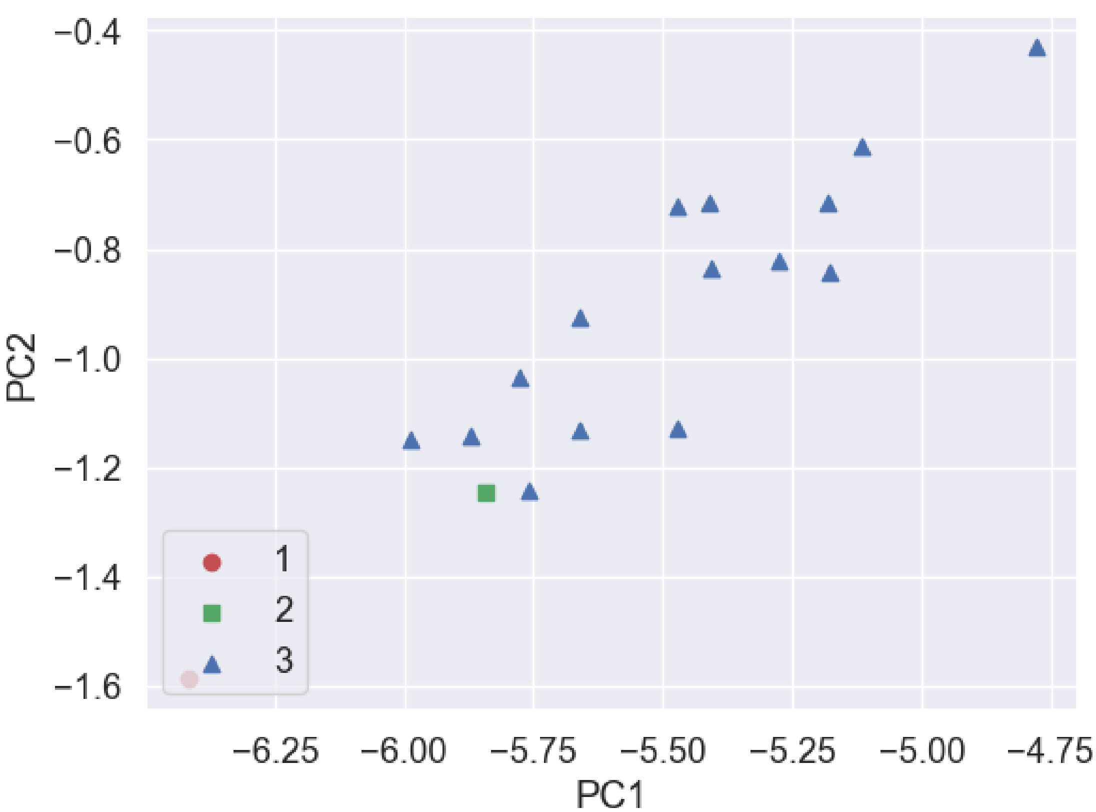
```
markers = ['o', 's', '^']
for label, color, marker in zip(np.unique(y), colors, markers):
    plt.scatter(X_pca[y == label, 0], X_pca[y == label, 1], color=color,␣
 ↪marker=marker, label=label)
plt.xlabel('PC1')
plt.ylabel('PC2')
plt.legend(loc='lower left')
plt.show()
```

```
Variance explained by each principal component:
 [0.9078731478516083, 0.03991890899342265, 0.023906381975154992,
0.016295977883821613, 0.009236274060776192, 0.0018182993981407179,
0.0009510098370754434]
Cumulative variance explained by each principal component:
 [0.90787315 0.94779206 0.97169844 0.98799442 0.99723069 0.99904899
 1.        ]
Number of principal components needed to explain 95% of the variance: 3
```



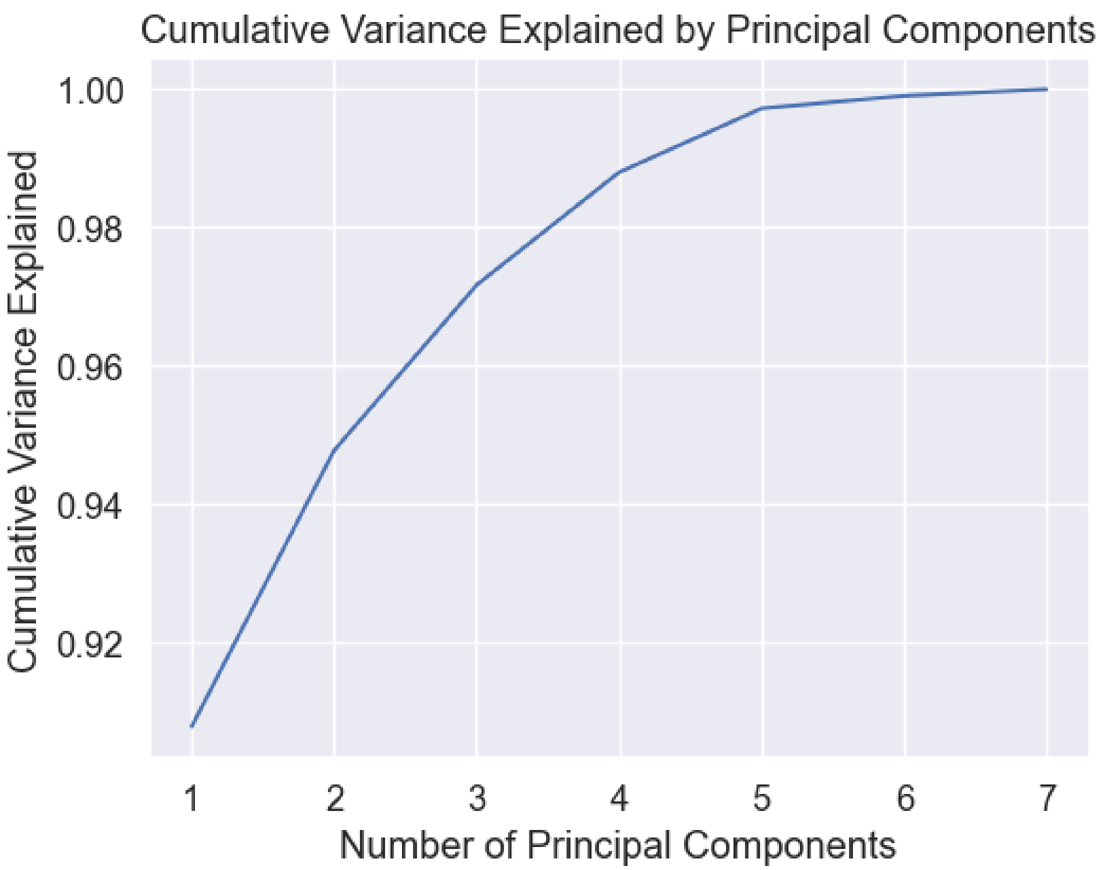

```
Covariance matrix of the principal components:
```

```
1.0177  0.9687  0.8271  0.9262  0.8949  0.9011  0.9041
0.9687  1.0189  0.8335  0.9257  0.8937  0.9005  0.9046
0.8271  0.8335  0.9985  0.8199  0.7696  0.7973  0.8264
0.9262  0.9257  0.8199  1.0310  0.9568  0.9610  0.9412
0.8949  0.8937  0.7696  0.9568  0.9858  0.9376  0.9129
0.9011  0.9005  0.7973  0.9610  0.9376  0.9909  0.9203
0.9041  0.9046  0.8264  0.9412  0.9129  0.9203  0.9590


Eigenvalues of the principal components:
6.3566
0.2795
0.1674


Eigenvectors of the principal components:
0.3833  0.3836  0.3481  0.3907  0.3782  0.3815  0.3789
0.0379  0.0653  0.8668  -0.2333 -0.3480 -0.2529 -0.0584
-0.5933 -0.5854 0.3149  0.2308  0.2316  0.2703  0.1621
```

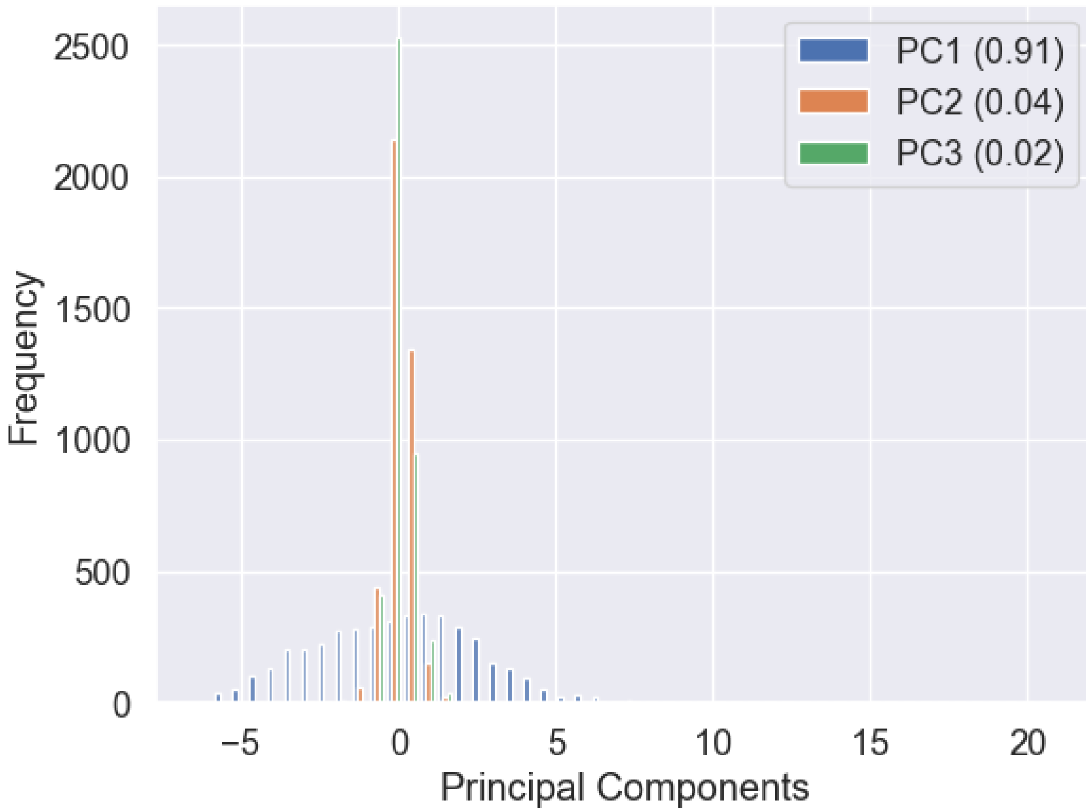


from the eigen values, we can see that the first principal components captures most variance.

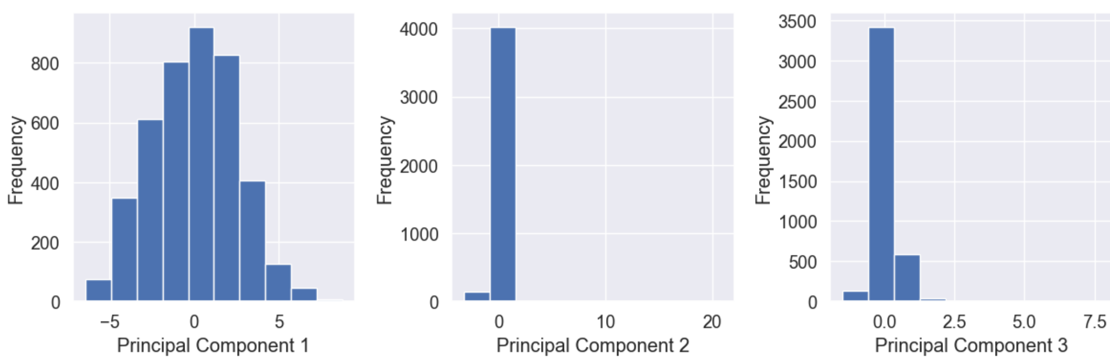
[31]:
```
# Plot the cumulative variance explained
plt.plot(range(1, len(cum_var_exp) + 1), cum_var_exp)
plt.xlabel('Number of Principal Components')
plt.ylabel('Cumulative Variance Explained')
plt.title('Cumulative Variance Explained by Principal Components')
plt.show()
```



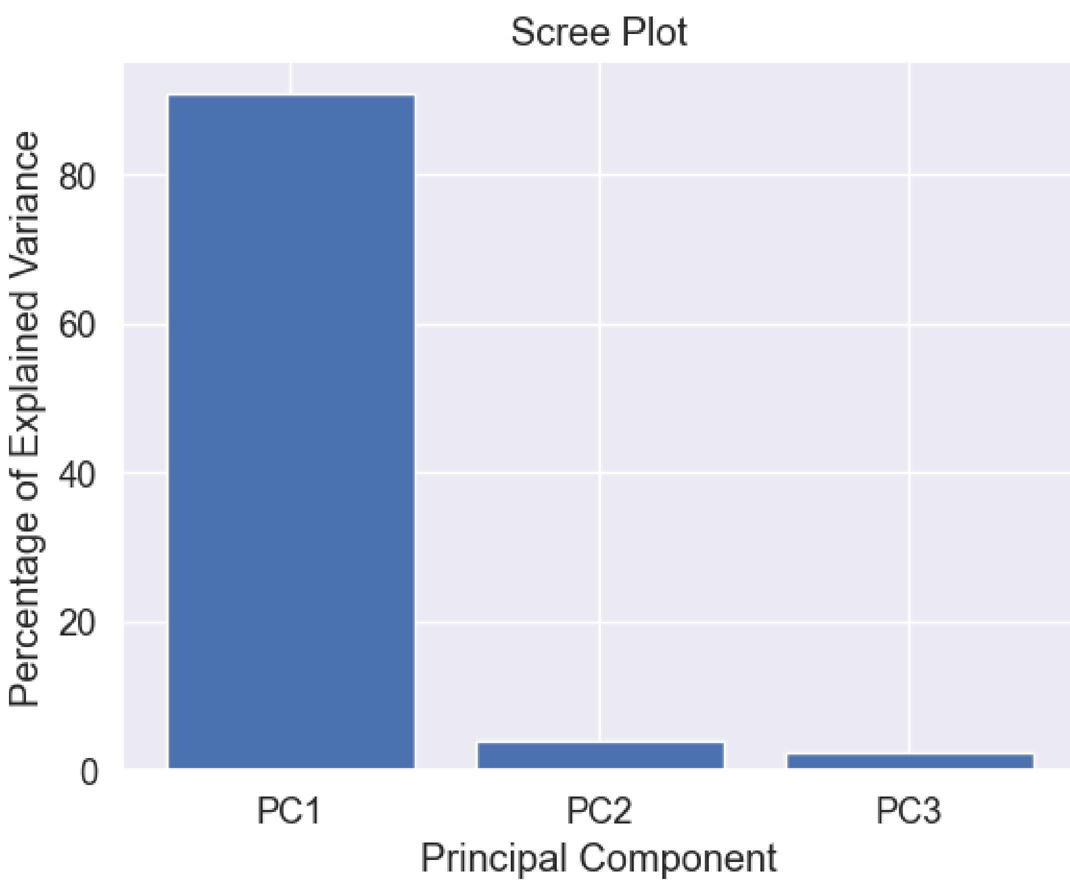
[32]:
```
n_components = pca.n_components_
plt.hist(X_pca, bins=50, label=[f'PC{i+1} ({var:.2f})' for i,var in␣
 ↪enumerate(pca.explained_variance_ratio_)])
plt.xlabel('Principal Components')
plt.ylabel('Frequency')
plt.legend()
plt.show()
```



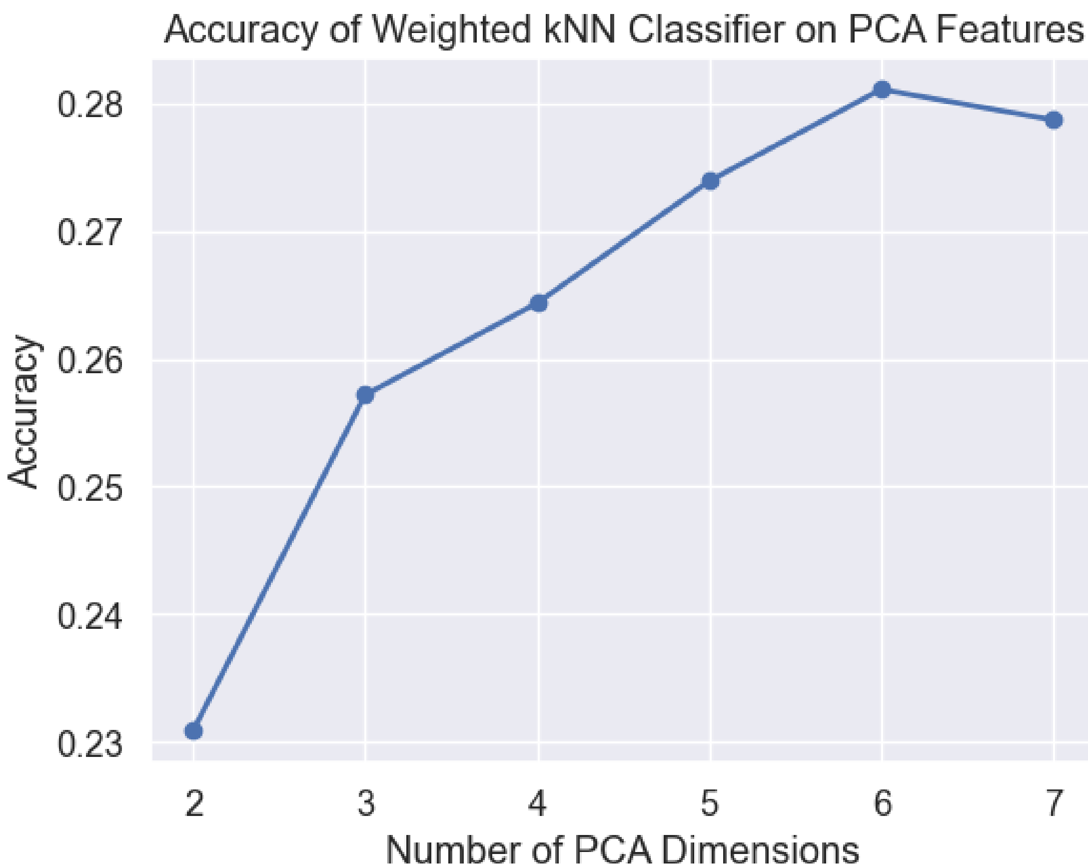
[33]:
```
fig, axs = plt.subplots(1, 3, figsize=(12, 4))
for i in range(3):
    axs[i].hist(X_pca[:, i], bins=10)
    axs[i].set_xlabel(f"Principal Component {i+1}")
    axs[i].set_ylabel("Frequency")
fig.tight_layout()
plt.show()
```



[34]:
```
# plt.plot(np.arange(1, len(pca.explained_variance_ratio_) + 1), pca.
↪explained_variance_ratio_, 'bo-', linewidth=2)
# plt.xlabel('Principal Component')
# plt.ylabel('Proportion of Variance Explained')
# plt.title('Scree Plot')
# for i, explained_var in enumerate(pca.explained_variance_ratio_):
#     plt.text(i + 1, explained_var + 0.01, f'PC{i+1}', ha='center')
# plt.show()

per_var = np.round(pca.explained_variance_ratio_ * 100, decimals=1)
labels = ['PC' + str(x) for x in range(1, len(per_var)+1)]

plt.bar(x=range(1,len(per_var)+1), height=per_var, tick_label=labels)
plt.ylabel('Percentage of Explained Variance')
plt.xlabel('Principal Component')
plt.title('Scree Plot')
plt.show()
```



[35]:
```python
# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_std, y, test_size=0.2,␣
↪random_state=42)

dims = np.arange(2, X.shape[1]+1)
accs = []
for d in dims:
    pca = PCA(n_components=d)
    X_train_pca = pca.fit_transform(X_train)
    X_test_pca = pca.transform(X_test)

    knn = KNeighborsClassifier(n_neighbors=68, weights='distance')
    knn.fit(X_train_pca, y_train)
    acc = knn.score(X_test_pca, y_test)
    accs.append(acc)

import matplotlib.pyplot as plt
plt.plot(dims, accs, 'bo-', linewidth=2)
plt.xlabel('Number of PCA Dimensions')
plt.ylabel('Accuracy')
plt.title('Accuracy of Weighted kNN Classifier on PCA Features')
plt.grid(True)
plt.show()
```



[36]:
```
#Printing Accuracy for abalone using 3 PC and K=68
# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_std, y, test_size=0.2,␣
↪random_state=42)

# Apply PCA and select the first 3 principal components
pca = PCA(n_components=3)
X_train_pca = pca.fit_transform(X_train)
X_test_pca = pca.transform(X_test)

# Apply weighted KNN with k=68 and weights=distance
knn = KNeighborsClassifier(n_neighbors=68, weights='distance')
knn.fit(X_train_pca, y_train)

# Evaluate the model
accuracy = knn.score(X_test_pca, y_test)
print("Accuracy:", accuracy)
```

```
Accuracy: 0.25717703349282295
```

1.2 Using LDA as a preprocessing step for abalone dataset

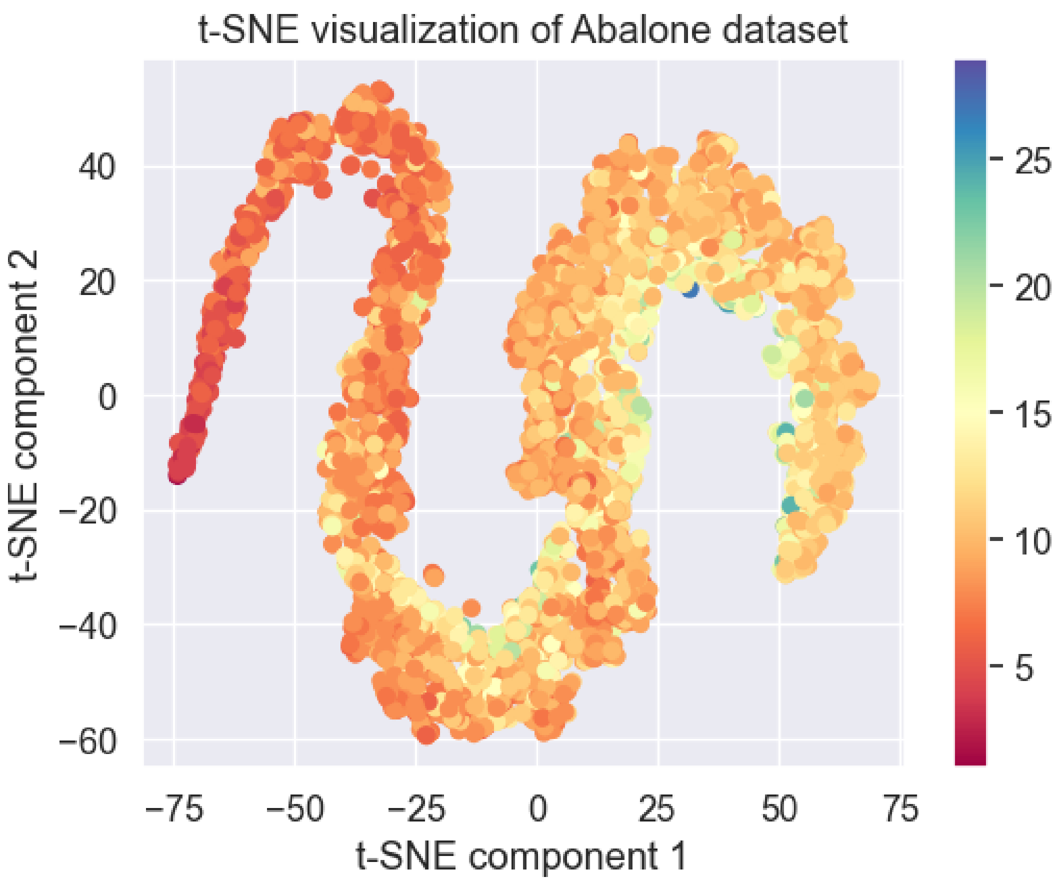
[37]:
```
#Implementing LDA and calculating accuracy using KNN k=68
import pandas as pd
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.neighbors import KNeighborsClassifier

# Load the dataset
dataset = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                      'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
↪'Rings'], sep = ',')



# Prepare the dataset
X = dataset.iloc[:, 1:8].values
y = dataset.iloc[:, -1].values
y = pd.cut(y, bins=[0, 8, 11, 30], labels=['young', 'middle-aged', 'old'])

print(y)

scaler = StandardScaler()
X_std = scaler.fit_transform(X)

# Split the dataset
X_train, X_test, y_train, y_test = train_test_split(X_std, y, test_size=0.2,␣
↪random_state=0)

# Perform LDA with cross-validation
lda = LinearDiscriminantAnalysis()
scores = cross_val_score(lda, X_train, y_train, cv=5)
print("Mean cv accuracy:", scores.mean())

# Project the training and test sets onto the LDA projection
lda.fit(X_train, y_train)
X_train_lda = lda.transform(X_train)
X_test_lda = lda.transform(X_test)

# Apply KNN with k=68
knn = KNeighborsClassifier(n_neighbors=68, weights='distance')
knn.fit(X_train_lda, y_train)

# Evaluate the model
accuracy = knn.score(X_test_lda, y_test)
```

```
print("Test Accuracy:", accuracy)

accuracy_scores = cross_val_score(lda, X_train_lda, y_train, cv=5)

print("CV Accuracy scores:", accuracy_scores)
print("CV Average accuracy:", accuracy_scores.mean())
```

```
['old', 'young', 'middle-aged', 'middle-aged', 'young', …, 'middle-aged',
'middle-aged', 'middle-aged', 'middle-aged', 'old']
Length: 4177
Categories (3, object): ['young' < 'middle-aged' < 'old']
Mean cv accuracy: 0.6692637147230204
Test Accuracy: 0.6961722488038278
CV Accuracy scores: [0.66367713 0.68263473 0.69011976 0.67215569 0.65568862]
CV Average accuracy: 0.6728551864880105
```

[38]:

```
from sklearn.preprocessing import LabelEncoder
from sklearn.manifold import TSNE
le = LabelEncoder()
df['Sex'] = le.fit_transform(df['Sex'])

X = df.iloc[:, 1:8].values
y = df.iloc[:, -1].values

tsne = TSNE(n_components=2, perplexity=30.0, random_state=0)
X_tsne = tsne.fit_transform(X)

plt.scatter(X_tsne[:,0], X_tsne[:,1], c=y, cmap=plt.cm.Spectral)
plt.colorbar()
plt.xlabel('t-SNE component 1')
plt.ylabel('t-SNE component 2')
plt.title('t-SNE visualization of Abalone dataset')
plt.show()
```



1. The t-SNE plot shows the abalone samples projected onto a two-dimensional space based on their similarity in the original high-dimensional space.
2. Each point in the plot represents an abalone sample, and the color of the point corresponds to the number of rings in the abalone (an indicator of age).
3. The t-SNE plot reveals that the abalone samples with similar numbers of rings tend to cluster together, indicating that age is an important factor in the variability of the data.
4. The plot also shows that the length and diameter measurements of the abalone are strongly correlated, as points that are close together in the plot tend to have similar values for these variables.
5. There is some overlap between the clusters corresponding to different numbers of rings, indicating that other variables in the dataset also contribute to the variability of the data.
6. Overall, the t-SNE visualization provides an intuitive way to explore the structure of the abalone dataset and can reveal interesting patterns and relationships between the variables.

1.3 Using Wine Dataset

[39]:
```
wine_r = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
```

```python
wine_r["colour"]=1
wine_w = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_w["colour"]=0
D = pd.concat([wine_w,wine_r], ignore_index=True)

import warnings
warnings.filterwarnings('ignore')
D
```

[39]:

```
      fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0               7.0             0.270         0.36            20.7      0.045
1               6.3             0.300         0.34             1.6      0.049
2               8.1             0.280         0.40             6.9      0.050
3               7.2             0.230         0.32             8.5      0.058
4               7.2             0.230         0.32             8.5      0.058
…             …               …          …              …        …
6492            6.2             0.600         0.08             2.0      0.090
6493            5.9             0.550         0.10             2.2      0.062
6494            6.3             0.510         0.13             2.3      0.076
6495            5.9             0.645         0.12             2.0      0.075
6496            6.0             0.310         0.47             3.6      0.067

      free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                    45.0                 170.0  1.00100  3.00       0.45
1                    14.0                 132.0  0.99400  3.30       0.49
2                    30.0                  97.0  0.99510  3.26       0.44
3                    47.0                 186.0  0.99560  3.19       0.40
4                    47.0                 186.0  0.99560  3.19       0.40
…                   …                   …      …    …        …
6492                 32.0                  44.0  0.99490  3.45       0.58
6493                 39.0                  51.0  0.99512  3.52       0.76
6494                 29.0                  40.0  0.99574  3.42       0.75
6495                 32.0                  44.0  0.99547  3.57       0.71
6496                 18.0                  42.0  0.99549  3.39       0.66

      alcohol  quality  colour
0         8.8        6       0
1         9.5        6       0
2        10.1        6       0
3         9.9        6       0
4         9.9        6       0
…       …      …      …
6492     10.5        5       1
6493     11.2        6       1
6494     11.0        6       1
```

```
6495     10.2        5       1
6496     11.0        6       1

[6497 rows x 13 columns]
```

[40]:

```
D.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 6497 entries, 0 to 6496
Data columns (total 13 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   fixed acidity         6497 non-null   float64
 1   volatile acidity      6497 non-null   float64
 2   citric acid           6497 non-null   float64
 3   residual sugar        6497 non-null   float64
 4   chlorides             6497 non-null   float64
 5   free sulfur dioxide   6497 non-null   float64
 6   total sulfur dioxide  6497 non-null   float64
 7   density               6497 non-null   float64
 8   pH                    6497 non-null   float64
 9   sulphates             6497 non-null   float64
 10  alcohol               6497 non-null   float64
 11  quality               6497 non-null   int64
 12  colour                6497 non-null   int64
dtypes: float64(11), int64(2)
memory usage: 660.0 KB
```

[41]:

```
D.describe()
```

[41]:

```
       fixed acidity  volatile acidity  citric acid  residual sugar  \
count    6497.000000       6497.000000  6497.000000     6497.000000
mean        7.215307          0.339666     0.318633        5.443235
std         1.296434          0.164636     0.145318        4.757804
min         3.800000          0.080000     0.000000        0.600000
25%         6.400000          0.230000     0.250000        1.800000
50%         7.000000          0.290000     0.310000        3.000000
75%         7.700000          0.400000     0.390000        8.100000
max        15.900000          1.580000     1.660000       65.800000

         chlorides  free sulfur dioxide  total sulfur dioxide      density  \
count  6497.000000          6497.000000           6497.000000  6497.000000
mean      0.056034            30.525319            115.744574     0.994697
std       0.035034            17.749400             56.521855     0.002999
min       0.009000             1.000000              6.000000     0.987110
25%       0.038000            17.000000             77.000000     0.992340
50%       0.047000            29.000000            118.000000     0.994890
75%       0.065000            41.000000            156.000000     0.996990
```

```
max       0.611000            289.000000            440.000000      1.038980

                  pH    sulphates      alcohol      quality       colour
count  6497.000000  6497.000000  6497.000000  6497.000000  6497.000000
mean      3.218501     0.531268    10.491801     5.818378     0.246114
std       0.160787     0.148806     1.192712     0.873255     0.430779
min       2.720000     0.220000     8.000000     3.000000     0.000000
25%       3.110000     0.430000     9.500000     5.000000     0.000000
50%       3.210000     0.510000    10.300000     6.000000     0.000000
75%       3.320000     0.600000    11.300000     6.000000     0.000000
max       4.010000     2.000000    14.900000     9.000000     1.000000
```

There are no missing values, so now we can start with EDA. More samples of quality 5 or 6 have been observed in the dataset, which shows that it is not a balanced dataset. The standard deviation for most features vary over a range and hence, we require normalization of the features before applying PCA.

[42]:
```python
D.shape
```

[42]:
```
(6497, 13)
```

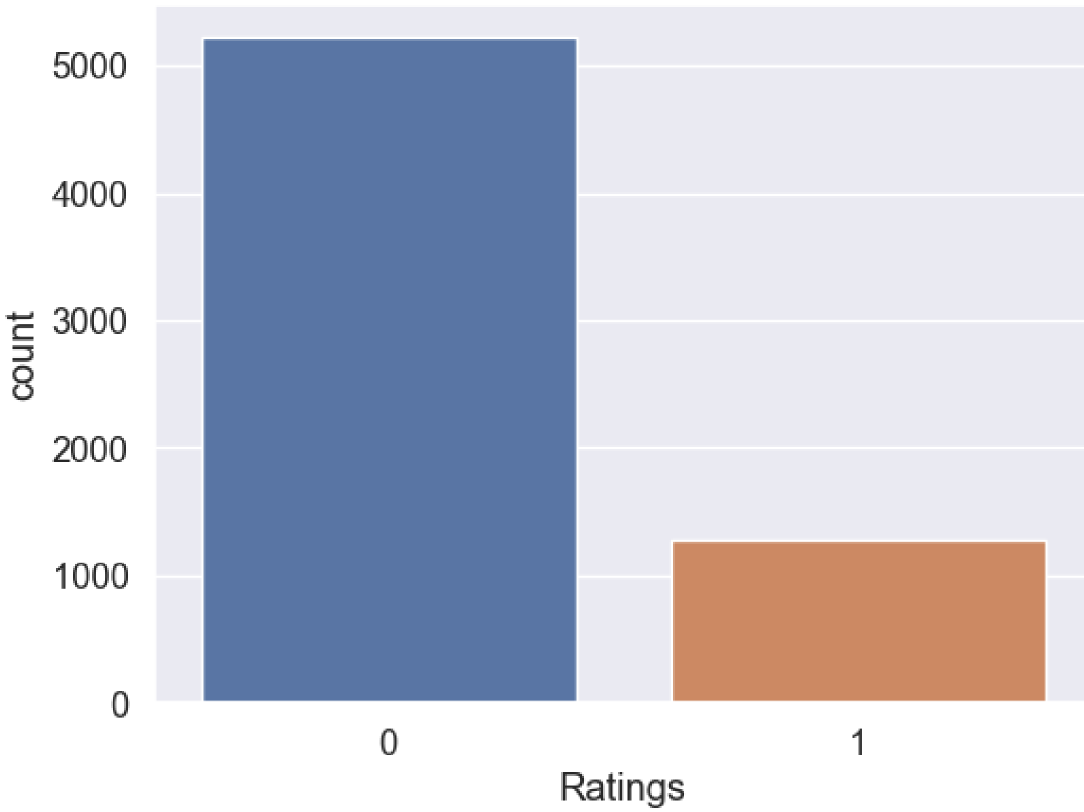
Most of the wines in this dataset has a quality score of 5 or 6. We will now add a feature called 'rating' depending on the quality score of each wine data point. If quality is <5, we assign them as 'Bad' (value of 0) and if quality is >=5, we assign it as 'Good' (value of 1).

[43]:
```python
rating=[]
for i in D["quality"]:
    if i <= 6:
        rating.append(0)
    else:
        rating.append(1)

D["Ratings"] =  rating
D
```

[43]:
```
      fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0               7.0             0.270         0.36            20.7      0.045
1               6.3             0.300         0.34             1.6      0.049
2               8.1             0.280         0.40             6.9      0.050
3               7.2             0.230         0.32             8.5      0.058
4               7.2             0.230         0.32             8.5      0.058
…               …               …           …               …         …
6492            6.2             0.600         0.08             2.0      0.090
6493            5.9             0.550         0.10             2.2      0.062
6494            6.3             0.510         0.13             2.3      0.076
6495            5.9             0.645         0.12             2.0      0.075
6496            6.0             0.310         0.47             3.6      0.067
```

```
      free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                    45.0                 170.0  1.00100  3.00       0.45
1                    14.0                 132.0  0.99400  3.30       0.49
2                    30.0                  97.0  0.99510  3.26       0.44
3                    47.0                 186.0  0.99560  3.19       0.40
4                    47.0                 186.0  0.99560  3.19       0.40
…                   …                   …      …    …        …
6492                 32.0                  44.0  0.99490  3.45       0.58
6493                 39.0                  51.0  0.99512  3.52       0.76
6494                 29.0                  40.0  0.99574  3.42       0.75
6495                 32.0                  44.0  0.99547  3.57       0.71
6496                 18.0                  42.0  0.99549  3.39       0.66

      alcohol  quality  colour  Ratings
0         8.8        6       0        0
1         9.5        6       0        0
2        10.1        6       0        0
3         9.9        6       0        0
4         9.9        6       0        0
…       …      …      …      …
6492     10.5        5       1        0
6493     11.2        6       1        0
6494     11.0        6       1        0
6495     10.2        5       1        0
6496     11.0        6       1        0

[6497 rows x 14 columns]
```

[44]:
```
sns.countplot(D['Ratings'])
plt.show()
```



Almost 5200 of the total number of wines seem to be “Bad” and the remaining 1297 wines “Good”.

[45]:
```
#Data Summarization
wine_describe = D.describe()
print(wine_describe)

summarize = pd.DataFrame(columns=['mean',␣
 ↪'median','variance','skew','kurtosis'])
summarize['mean'] = D.mean()
summarize['median'] = D.median()
summarize['variance'] = D.var()
summarize['skew'] = D.skew()
summarize['kurtosis'] = D.kurtosis()
display(summarize)
```

```
       fixed acidity  volatile acidity  citric acid  residual sugar  \
count    6497.000000       6497.000000  6497.000000     6497.000000
mean        7.215307          0.339666     0.318633        5.443235
std         1.296434          0.164636     0.145318        4.757804
min         3.800000          0.080000     0.000000        0.600000
25%         6.400000          0.230000     0.250000        1.800000
50%         7.000000          0.290000     0.310000        3.000000
```

75%	7.700000	0.400000	0.390000	8.100000
max	15.900000	1.580000	1.660000	65.800000

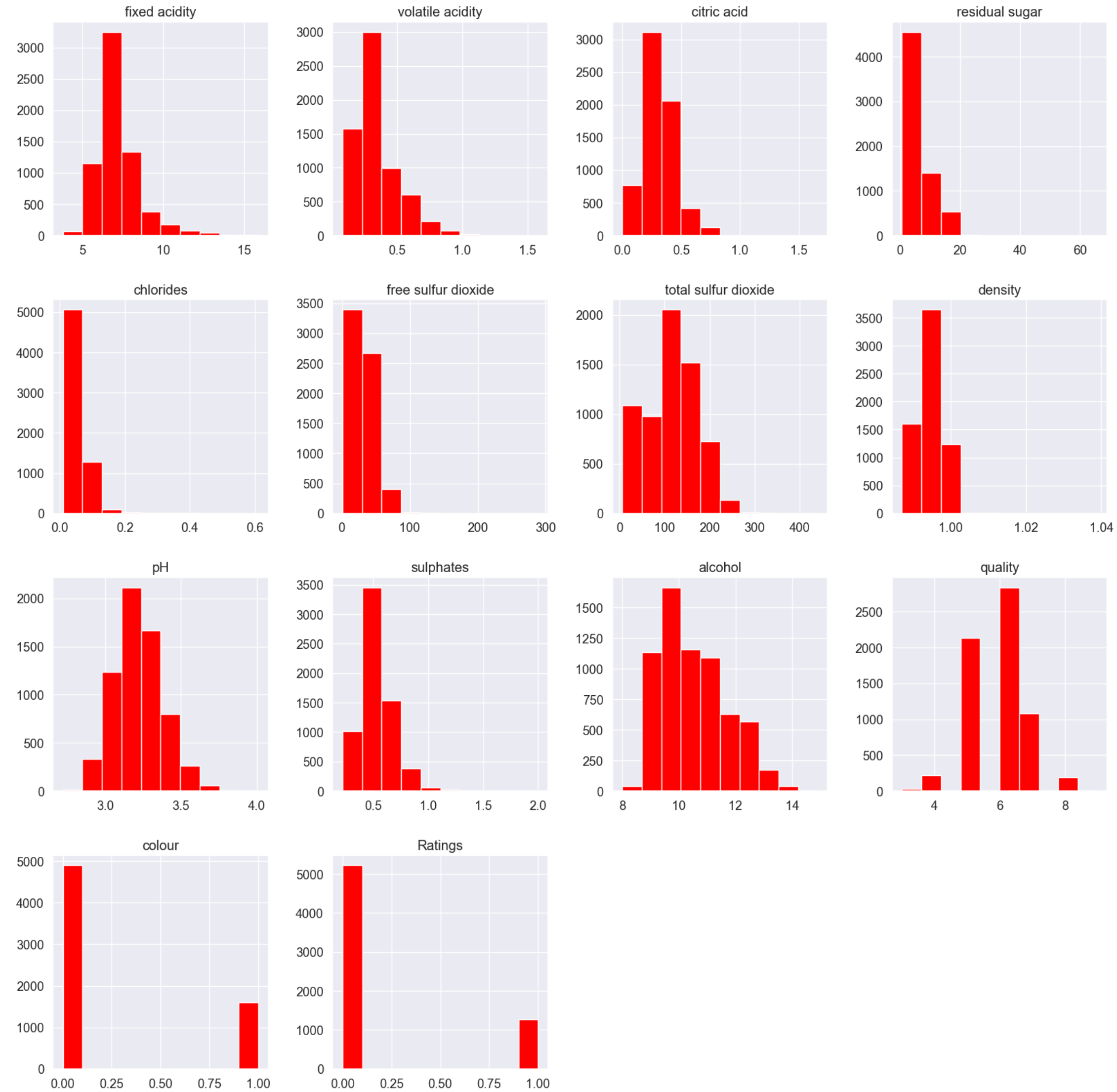
	chlorides	free sulfur dioxide	total sulfur dioxide	density	\
count	6497.000000	6497.000000	6497.000000	6497.000000	
mean	0.056034	30.525319	115.744574	0.994697	
std	0.035034	17.749400	56.521855	0.002999	
min	0.009000	1.000000	6.000000	0.987110	
25%	0.038000	17.000000	77.000000	0.992340	
50%	0.047000	29.000000	118.000000	0.994890	
75%	0.065000	41.000000	156.000000	0.996990	
max	0.611000	289.000000	440.000000	1.038980	

	pH	sulphates	alcohol	quality	colour	\
count	6497.000000	6497.000000	6497.000000	6497.000000	6497.000000	
mean	3.218501	0.531268	10.491801	5.818378	0.246114	
std	0.160787	0.148806	1.192712	0.873255	0.430779	
min	2.720000	0.220000	8.000000	3.000000	0.000000	
25%	3.110000	0.430000	9.500000	5.000000	0.000000	
50%	3.210000	0.510000	10.300000	6.000000	0.000000	
75%	3.320000	0.600000	11.300000	6.000000	0.000000	
max	4.010000	2.000000	14.900000	9.000000	1.000000	

	Ratings
count	6497.000000
mean	0.196552
std	0.397421
min	0.000000
25%	0.000000
50%	0.000000
75%	0.000000
max	1.000000

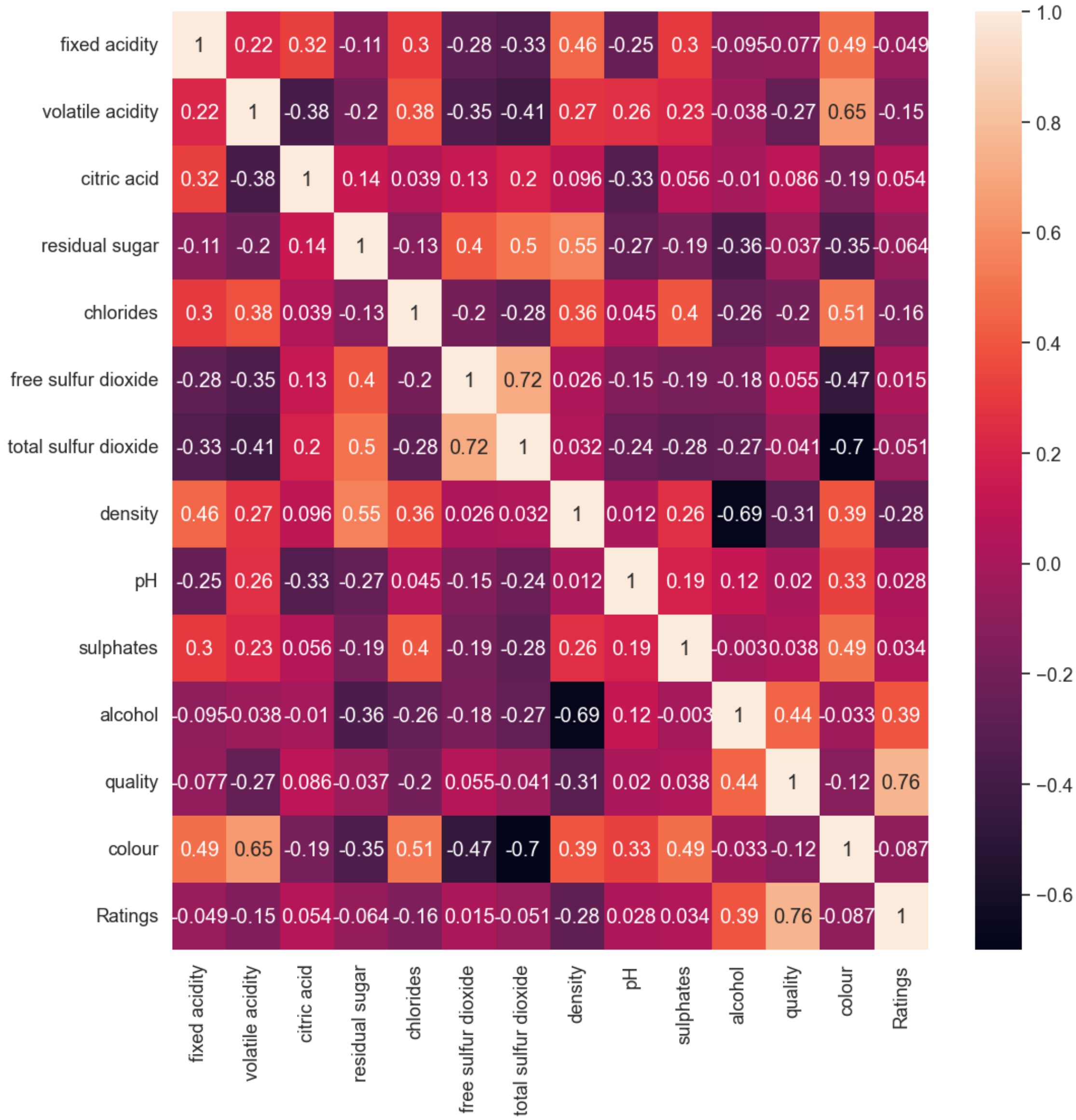
	mean	median	variance	skew	kurtosis
fixed acidity	7.215307	7.00000	1.680740	1.723290	5.061161
volatile acidity	0.339666	0.29000	0.027105	1.495097	2.825372
citric acid	0.318633	0.31000	0.021117	0.471731	2.397239
residual sugar	5.443235	3.00000	22.636696	1.435404	4.359272
chlorides	0.056034	0.04700	0.001227	5.399828	50.898051
free sulfur dioxide	30.525319	29.00000	315.041192	1.220066	7.906238
total sulfur dioxide	115.744574	118.00000	3194.720039	-0.001177	-0.371664
density	0.994697	0.99489	0.000009	0.503602	6.606067
pH	3.218501	3.21000	0.025853	0.386839	0.367657
sulphates	0.531268	0.51000	0.022143	1.797270	8.653699
alcohol	10.491801	10.30000	1.422561	0.565718	-0.531687
quality	5.818378	6.00000	0.762575	0.189623	0.232322
colour	0.246114	0.00000	0.185570	1.179095	-0.609922
Ratings	0.196552	0.00000	0.157944	1.527553	0.333522

[46]:
```python
D.hist(figsize=(20,20), color='red')
plt.show()
```



[47]:
```python
mycor= D.corr()
plt.subplots(figsize=(12,12))
sns.heatmap(mycor,annot=True)
```

[47]:
```
<AxesSubplot:>
```



Alcohol has the maximum correlation with quality followed by sulphates and citric acid and then fixed acidity. We can also observe that residual sugar has a significant positive correlation with density and total sulfur dioxide is strongly correlated with the type of wine.

Apply Z-score Normalization on wine dataset:

[48]:
```
#Split dataset into X and Y
X = D.iloc[:, :-1]
y = D.iloc[:, -3]
print(y)
sc_wine = StandardScaler()
X = sc_wine.fit_transform(X)
```

```
print("The normalized dataset is: \n", X)
```

```
0       6
1       6
2       6
3       6
4       6
       ..
6492    5
6493    6
6494    6
6495    5
6496    6
Name: quality, Length: 6497, dtype: int64
The normalized dataset is:
 [[-0.16608919 -0.42318303  0.28468605 … -1.41855821  0.20799905
  -0.57136659]
 [-0.70607349 -0.24094936  0.14704613 … -0.83161516  0.20799905
  -0.57136659]
 [ 0.68245757 -0.36243847  0.55996589 … -0.32852111  0.20799905
  -0.57136659]
 …
 [-0.70607349  1.03468634 -1.29817304 …  0.42611996  0.20799905
   1.75018984]
 [-1.01463595  1.85473786 -1.366993   … -0.2446721  -0.93722961
   1.75018984]
 [-0.93749534 -0.1802048   1.04170561 …  0.42611996  0.20799905
   1.75018984]]
```

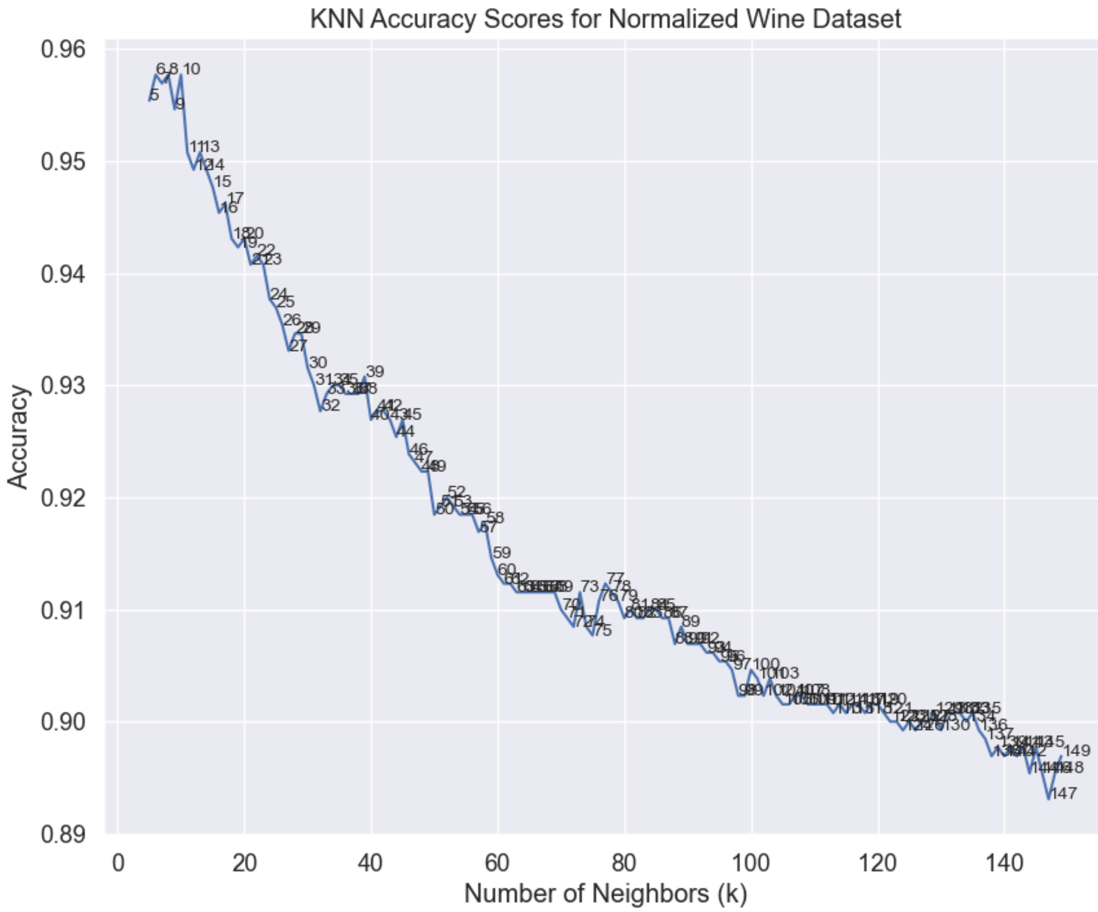
[49]:
```
cov_mat = np.cov(X.T)
print("Covariance Matrix Calculated using numpy:\n")
np.savetxt(sys.stdout, cov_mat, fmt='%.4f', delimiter='\t')
```

```
Covariance Matrix Calculated using numpy:

1.0002  0.2190  0.3245  -0.1120 0.2982  -0.2828 -0.3291 0.4590  -0.2527 0.2996
-0.0955 -0.0768 0.4868
0.2190  1.0002  -0.3780 -0.1960 0.3772  -0.3526 -0.4145 0.2713  0.2615  0.2260
-0.0376 -0.2657 0.6531
0.3245  -0.3780 1.0002  0.1425  0.0390  0.1331  0.1953  0.0962  -0.3299 0.0562
-0.0105 0.0855  -0.1874
-0.1120 -0.1960 0.1425  1.0002  -0.1290 0.4029  0.4956  0.5526  -0.2674 -0.1860
-0.3595 -0.0370 -0.3489
0.2982  0.3772  0.0390  -0.1290 1.0002  -0.1951 -0.2797 0.3627  0.0447  0.3957
-0.2570 -0.2007 0.5128
-0.2828 -0.3526 0.1331  0.4029  -0.1951 1.0002  0.7210  0.0257  -0.1459 -0.1885
-0.1799 0.0555  -0.4717
-0.3291 -0.4145 0.1953  0.4956  -0.2797 0.7210  1.0002  0.0324  -0.2384 -0.2758
```

```
-0.2658 -0.0414 -0.7005
0.4590  0.2713  0.0962  0.5526  0.3627  0.0257  0.0324  1.0002  0.0117  0.2595
-0.6869 -0.3059 0.3907
-0.2527 0.2615  -0.3299 -0.2674 0.0447  -0.1459 -0.2384 0.0117  1.0002  0.1922
0.1213  0.0195  0.3292
0.2996  0.2260  0.0562  -0.1860 0.3957  -0.1885 -0.2758 0.2595  0.1922  1.0002
-0.0030 0.0385  0.4873
-0.0955 -0.0376 -0.0105 -0.3595 -0.2570 -0.1799 -0.2658 -0.6869 0.1213  -0.0030
1.0002  0.4444  -0.0330
-0.0768 -0.2657 0.0855  -0.0370 -0.2007 0.0555  -0.0414 -0.3059 0.0195  0.0385
0.4444  1.0002  -0.1193
0.4868  0.6531  -0.1874 -0.3489 0.5128  -0.4717 -0.7005 0.3907  0.3292  0.4873
-0.0330 -0.1193 1.0002
```

[50]:

```python
# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
 ↪random_state=42)

from sklearn.metrics import accuracy_score, recall_score, precision_score
from sklearn.metrics import confusion_matrix
accuracy_score = []
for k in range(5,150):
    knn = KNeighborsClassifier(n_neighbors=k, weights='distance')
    knn.fit(X_train, y_train)
    knn_pred = knn.predict(X_test)
    knn_accuracy_score = recall_score(y_test, knn_pred, average='micro')
    accuracy_score.append(knn_accuracy_score)
    #knn_accuracy_score = accuracy_score(y_test, knn_pred)
    #knn_accuracy_score
    #print("The Accuracy for k={} is {}".format(k, knn_accuracy_score))

plt.figure(figsize=(10,8))
plt.plot(range(5,150), accuracy_score)
plt.xlabel('Number of Neighbors (k)')
plt.ylabel('Accuracy')
plt.title('KNN Accuracy Scores for Normalized Wine Dataset')

for i, k in enumerate(range(5, 150)):
    plt.text(k, accuracy_score[i], str(k), fontsize=10)

plt.show()
```



from the above graph, we have selected value of K = 40 as the accuracy is decreasing when K is inreasing. so we chosed the middle value i.e. K=40

[51]:
```
scaler = StandardScaler()
X_std = scaler.fit_transform(X)

# Split the dataset
X_train, X_test, y_train, y_test = train_test_split(X_std, y, test_size=0.2,␣
 ↪random_state=0)

# Apply KNN with K=40 and weights=distance
knn = KNeighborsClassifier(n_neighbors=40, weights='distance')
knn.fit(X_train, y_train)

#Evaluate the model
accuracy = knn.score(X_test, y_test)
print("Test Accuracy:", accuracy)
```

```
cv_accuracy_scores = cross_val_score(knn, X, y, cv=5)
# Print the accuracy scores
print("CV Accuracy scores:", accuracy_scores)
print("CV Average accuracy:", accuracy_scores.mean())
```

```
Test Accuracy: 0.9176923076923077
CV Accuracy scores: [0.66367713 0.68263473 0.69011976 0.67215569 0.65568862]
CV Average accuracy: 0.6728551864880105
```

The above accuracy is for raw wine dataset with only normalization done as a pre-processing step

1.4 PCA preprocessing on Wine dataset

[52]:
```
''' Using Principal Component Analysis or PCA in short to reduce the␣
↪dimensionality of the data in order to optimize the result
of the clustering. '''
pca = PCA()
principalComponents = pca.fit_transform(X)
principalComponents
```

[52]:
```
array([[-2.06707183,  3.48606943, -0.12160483, …,  0.355487  ,
         0.09523024,  0.03915981],
       [-0.27234588, -0.50787251, -0.41460196, …, -0.14436514,
         0.04905848,  0.16266364],
       [-0.38931517,  0.29383078,  0.53340294, …, -0.20948338,
        -0.65935401, -0.18165748],
       …,
       [ 2.720703  , -0.90429614, -1.28925071, …,  0.71079279,
         0.17217269,  0.25399957],
       [ 3.05387095, -0.52363091, -2.62264968, …,  0.87445042,
        -0.15998844, -0.06881234],
       [ 1.79287529, -0.72259628,  0.31706237, …,  1.30046828,
         0.76258543,  0.16620553]])
```

[53]:
```
PCA_dataset = pd.DataFrame(data = principalComponents, columns = ['component1',␣
↪'component2', 'component3', 'component4',
                                                                   'component5',␣
↪'component6','component7', 'component8', 'component9',
                                                                  'component10',␣
↪'component11', 'component12', 'component13'] )
PCA_dataset.head()
```

[53]:

	component1	component2	component3	component4	component5	component6	\
0	-2.067072	3.486069	-0.121605	0.225732	1.926477	0.354486	
1	-0.272346	-0.507873	-0.414602	-0.251146	-0.448951	-0.855633	
2	-0.389315	0.293831	0.533403	-0.253599	0.420879	-0.646033	
3	-1.708927	0.968794	-0.219406	0.149823	0.055460	0.226626	
4	-1.708927	0.968794	-0.219406	0.149823	0.055460	0.226626	

```
   component7  component8  component9  component10  component11  component12  \
0   -0.672678    0.121818    0.495242     0.164076     0.355487     0.095230
1   -0.837531   -0.026002   -0.358875    -1.135174    -0.144365     0.049058
2   -0.108228   -0.519626   -0.328810     0.029797    -0.209483    -0.659354
3   -0.012470   -0.479977   -0.543434     0.084188    -0.458196     0.232972
4   -0.012470   -0.479977   -0.543434     0.084188    -0.458196     0.232972

   component13
0     0.039160
1     0.162664
2    -0.181657
3    -0.046354
4    -0.046354
```

[54]:
```
# The amount of variance that each PCA explains is
var = pca.explained_variance_ratio_
var
```

[54]:
```
array([0.29492412, 0.20484445, 0.12627433, 0.08311596, 0.06536559,
       0.05083677, 0.04407412, 0.04007519, 0.03618948, 0.02352702,
       0.01975193, 0.00917425, 0.00184679])
```

[55]:
```
# Cumulative variance
var1 = np.cumsum(np.round(var,decimals = 4)*100)
var1
```

[55]:
```
array([ 29.49,  49.97,  62.6 ,  70.91,  77.45,  82.53,  86.94,  90.95,
        94.57,  96.92,  98.9 ,  99.82, 100.  ])
```

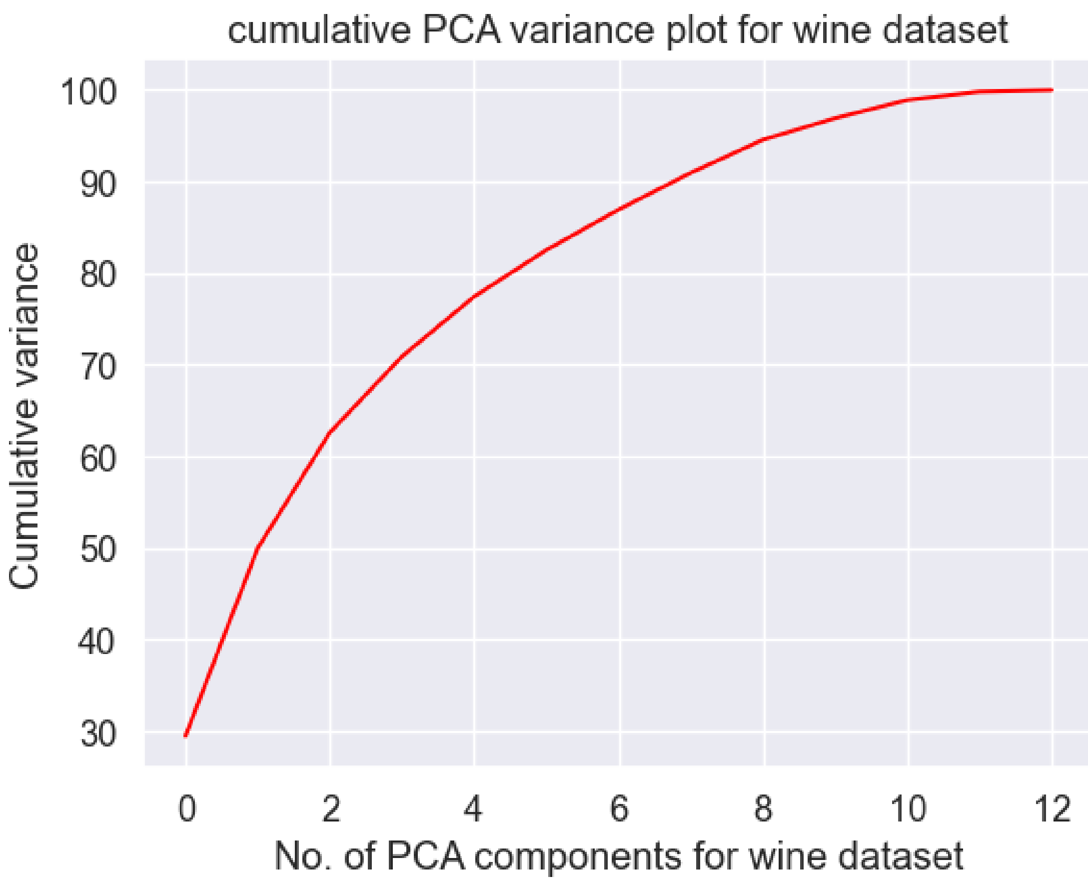
[56]:
```
pca.components_
```

[56]:
```
array([[ 0.26022761,  0.36378537, -0.11319392, -0.23277398,  0.30248902,
        -0.33871316, -0.40228457,  0.16134445,  0.17486612,  0.27953014,
        -0.00438771, -0.09658937,  0.46988304],
       [ 0.21697768,  0.04063327,  0.1652622 ,  0.38999091,  0.21461462,
         0.18038247,  0.21801564,  0.53387129, -0.18258784,  0.06996466,
        -0.49463822, -0.27584039,  0.04159581],
       [ 0.46915601, -0.27753553,  0.58755451, -0.07691544,  0.04901716,
        -0.10171768, -0.10349402, -0.05064624, -0.40644534,  0.17017062,
         0.21223488,  0.29407328, -0.00515413],
       [-0.15221794, -0.0988973 ,  0.05585934,  0.1409448 ,  0.11802731,
         0.33598581,  0.15119611,  0.14728961,  0.45593175,  0.54443786,
         0.0924771 ,  0.49999028,  0.09931403],
       [ 0.16420616,  0.13567635, -0.22703334,  0.50195548, -0.4279513 ,
        -0.21043504, -0.20327797,  0.30757457, -0.03611788, -0.25574119,
         0.12151437,  0.44307302,  0.09994023],
```

```
[-0.02600784,  0.38249628, -0.35416504,  0.05274959,  0.41655005,
  0.30502379,  0.11684492, -0.16177157, -0.56167229,  0.00674719,
  0.1729653 ,  0.26868635,  0.02824745],
[ 0.3868432 ,  0.40294671,  0.10595656, -0.13885955, -0.45217669,
  0.44036475,  0.24390134, -0.00370185,  0.11276566,  0.03066965,
  0.31551766, -0.25917623,  0.13860244],
[ 0.03181395, -0.18196056, -0.4133581 , -0.03047916, -0.41017361,
 -0.13581435,  0.0184071 , -0.0299972 , -0.33985109,  0.66555974,
 -0.11850286, -0.15297009, -0.10122474],
[-0.32809868,  0.27168218,  0.2906849 ,  0.47464037,  0.08487095,
 -0.29460432,  0.02474758, -0.03542723, -0.03627823,  0.24884103,
  0.46895273, -0.32552487, -0.15419297],
[ 0.10889424, -0.51968453, -0.2497291 ,  0.23754043,  0.16676955,
  0.36129991, -0.37140759,  0.0430805 ,  0.01712679, -0.07384153,
  0.38220047, -0.3352888 ,  0.1920652 ],
[-0.4722093 ,  0.12979518,  0.32485317, -0.00408122, -0.28055358,
  0.32649347, -0.46716453, -0.06333852, -0.25560562,  0.04477967,
 -0.24688386,  0.01512309,  0.34430043],
[-0.21912105, -0.24108752, -0.00161111, -0.05294132, -0.05238527,
 -0.23414618,  0.53145939,  0.05878588, -0.15947249, -0.10382993,
  0.14265139, -0.01467474,  0.70057617],
[-0.27041153, -0.01273268, -0.00846961, -0.45657506, -0.0166051 ,
  0.03258504, -0.05491676,  0.72967519, -0.1601302 , -0.04557912,
  0.31007441,  0.01434882, -0.23944217]])
```

[157]:
```python
# Variance plot for PCA components obtained
import matplotlib.pyplot as plt
plt.plot(var1,color="red")
plt.xlabel("No. of PCA components for wine dataset")
plt.ylabel("Cumulative variance")
plt.title("cumulative PCA variance plot for wine dataset")
```

[157]:
```
Text(0.5, 1.0, 'cumulative PCA variance plot for wine dataset')
```



Our problem suggests to use the first 3 principal components.

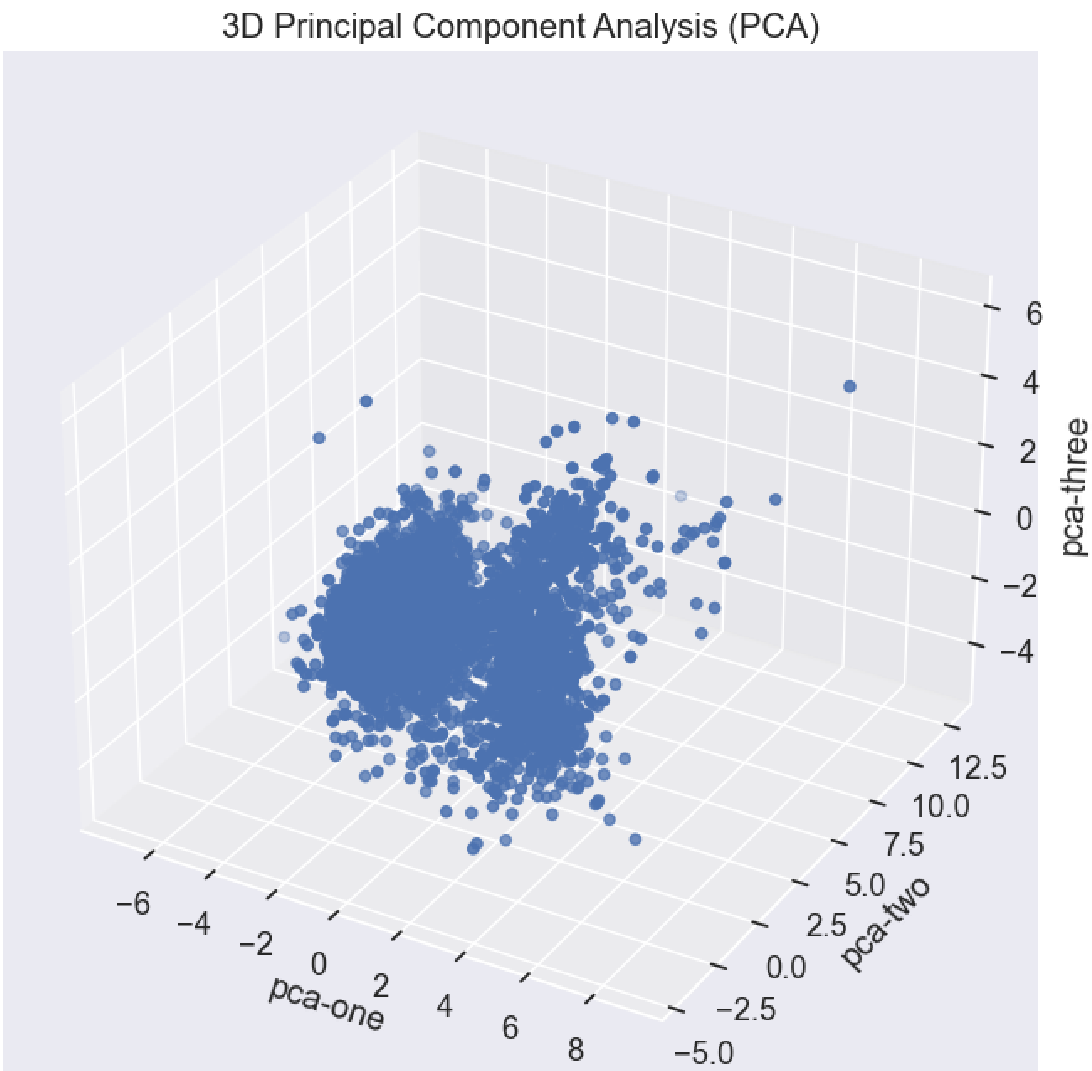
[58]:
```
principal_component1 = PCA_dataset['component1']
principal_component2 = PCA_dataset['component2']
principal_component3 = PCA_dataset['component3']
```

[59]:
```
# Creating dataframe for further clusering algorithms
pca_df = pd.concat([principal_component1, principal_component2,␣
 ↪principal_component3], axis = 1)
pca_df.head()
```

[59]:

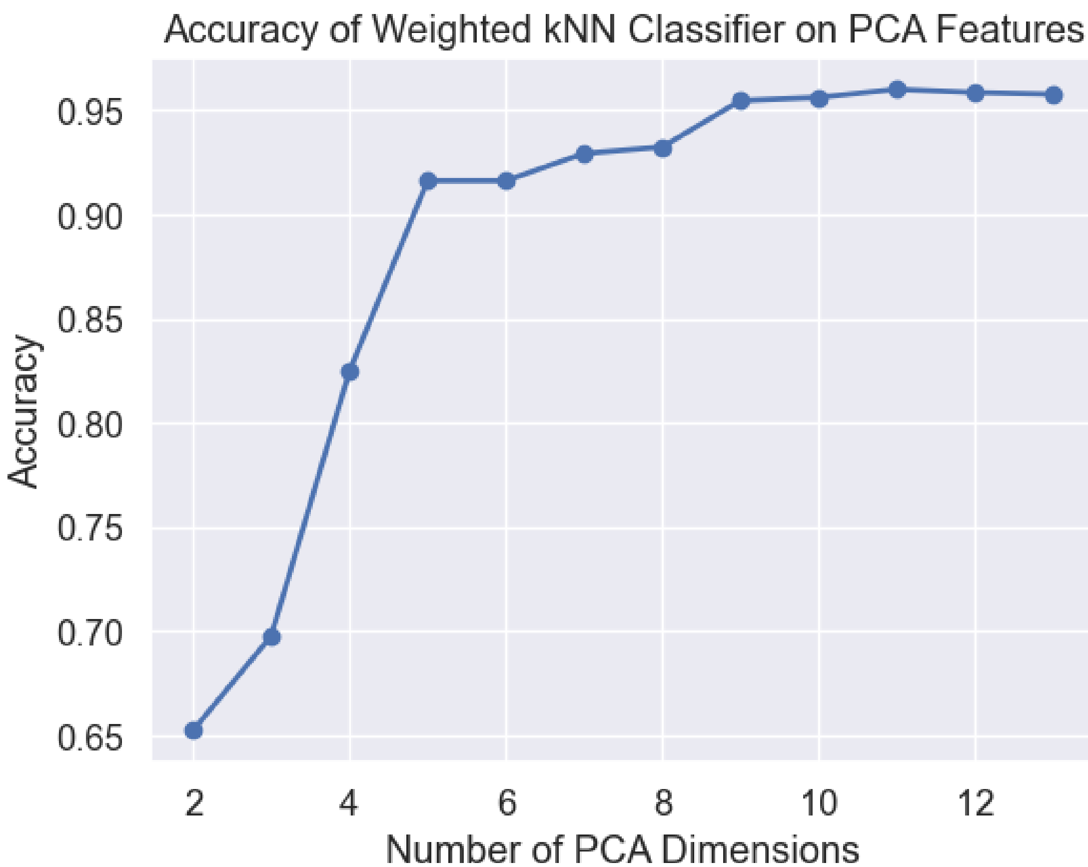
	component1	component2	component3
0	-2.067072	3.486069	-0.121605
1	-0.272346	-0.507873	-0.414602
2	-0.389315	0.293831	0.533403
3	-1.708927	0.968794	-0.219406
4	-1.708927	0.968794	-0.219406

[60]:
```
# Visualizing the results of the 3D PCA.
ax = plt.figure(figsize=(8,8)).gca(projection='3d')
plt.title('3D Principal Component Analysis (PCA)')
ax.scatter(
    xs=principal_component1,
    ys=principal_component2,
    zs=principal_component3,
)
ax.set_xlabel('pca-one')
ax.set_ylabel('pca-two')
ax.set_zlabel('pca-three')
plt.show()
```



[61]:

```
# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)

dims = np.arange(2, X.shape[1]+1)
accs = []
for d in dims:
    pca = PCA(n_components=d)
    X_train_pca = pca.fit_transform(X_train)
    X_test_pca = pca.transform(X_test)

    knn = KNeighborsClassifier(n_neighbors=10, weights='distance')
    knn.fit(X_train_pca, y_train)
    acc = knn.score(X_test_pca, y_test)
    accs.append(acc)

import matplotlib.pyplot as plt
plt.plot(dims, accs, 'bo-', linewidth=2)
plt.xlabel('Number of PCA Dimensions')
plt.ylabel('Accuracy')
plt.title('Accuracy of Weighted kNN Classifier on PCA Features')
plt.grid(True)
plt.show()
```



[62]:
```
# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_std, y, test_size=0.2,␣
 ↪random_state=42)

# Apply PCA and select the first 3 principal components
pca = PCA(n_components=3)
X_train_pca = pca.fit_transform(X_train)
X_test_pca = pca.transform(X_test)

# Apply weighted KNN with k=68 and weights=distance
knn = KNeighborsClassifier(n_neighbors=40, weights='distance')
knn.fit(X_train_pca, y_train)

# Evaluate the model
accuracy = knn.score(X_test_pca, y_test)
print("Test Accuracy:", accuracy)

accuracy_scores = cross_val_score(knn, X_train_pca, y_train, cv=5)
```

```python
print("CV Accuracy scores:", accuracy_scores)
print("CV Average accuracy:", accuracy_scores.mean())
```

```
Test Accuracy: 0.7115384615384616
CV Accuracy scores: [0.67980769 0.70865385 0.67853705 0.68046198 0.70452358]
CV Average accuracy: 0.6903968312726734
```

[63]:

```python
import pandas as pd
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.neighbors import KNeighborsClassifier

scaler = StandardScaler()
X_std = scaler.fit_transform(X)

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_std, y, test_size=0.2,␣
 ↪random_state=0)

# Perform LDA with 3 components and cr oss-validation
lda = LinearDiscriminantAnalysis(n_components=3)
scores = cross_val_score(lda, X_train, y_train, cv=5)
print("Mean CV accuracy:", scores.mean())

# Project the training and testing sets onto the LDA projection
lda.fit(X_train, y_train)
X_train_lda = lda.transform(X_train)
X_test_lda = lda.transform(X_test)

# Apply KNN with k=40
knn = KNeighborsClassifier(n_neighbors=40, weights='distance')
knn.fit(X_train_lda, y_train)

# Evaluate the model
accuracy = knn.score(X_test_lda, y_test)
print("Test Accuracy:", accuracy)

# Compute cross-validation accuracy scores
accuracy_scores = cross_val_score(knn, X_train_lda, y_train, cv=5)
print("CV Accuracy scores:", accuracy_scores)
print("CV Average accuracy:", accuracy_scores.mean())
```

```
Mean CV accuracy: 1.0
Test Accuracy: 1.0
CV Accuracy scores: [1. 1. 1. 1. 1.]
CV Average accuracy: 1.0
```

1.5 Assignment 2 Question 2 implementation starts here

1.5.1 Question

2 Naive Bayes Classifier Now you will classify the two datasets using the Naive Bayes Classifier. There are a number of these available, for our datasets, the Multinomial Naive Bayes and Complement Naive Bayes forms seem most appropriate, so we will experiment with those. 1. Use 5-fold cross validation to compare both versions of Naive Bayes against your previous best results from kNN. Do this on all 6 of your datasets. 2. You can have some analysis here or plot to highlight any interesting issues. There are also variants of Naive Bayes you may want to explore. 3. Produce a table comparing the accuracies on the different datasets. Include summary accuracy scores on all six datasets in the table in the last question.

[64]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.decomposition import PCA
import warnings
warnings.filterwarnings('ignore')
```

[65]:
```
# Load raw abalone dataset
abalone_df = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                        'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
↪'Rings'], sep = ',')

# Separate indep and dep features
X_abalone = abalone_df.iloc[:, 1:-1] # Removed the sex feature
y_abalone = abalone_df.iloc[:, -1]

# Normalize dataset
sc1 = MinMaxScaler()
X_abalone = sc1.fit_transform(X_abalone)
X_abalone
```

[65]:
```
array([[0.51351351, 0.5210084 , 0.0840708 , …, 0.15030262, 0.1323239 ,
        0.14798206],
       [0.37162162, 0.35294118, 0.07964602, …, 0.06624075, 0.06319947,
        0.06826109],
       [0.61486486, 0.61344538, 0.11946903, …, 0.17182246, 0.18564845,
        0.2077728 ],
       …,
       [0.70945946, 0.70588235, 0.18141593, …, 0.3527236 , 0.37788018,
        0.30543099],
       [0.74324324, 0.72268908, 0.13274336, …, 0.35642233, 0.34298881,
```

```
 0.29347285],
[0.85810811, 0.84033613, 0.17256637, …, 0.63517149, 0.49506254,
 0.49177877]])
```

[66]:
```python
# Apply PCA on abalone dataset
pca = PCA(n_components=3)
abalone_pca = pca.fit_transform(X_abalone)
abalone_pca_df = pd.DataFrame(data=abalone_pca, columns=['PC1', 'PC2', 'PC3'])
abalone_pca_df
```

[66]:
```
           PC1       PC2       PC3
0    -0.230816 -0.026563 -0.006786
1    -0.497671  0.043791  0.003049
2    -0.068857 -0.081454  0.011720
3    -0.230997 -0.012962  0.004214
4    -0.532797  0.057362 -0.000513
…          …         …         …
4172  0.100632 -0.034549 -0.011468
4173  0.128141 -0.023082 -0.028686
4174  0.273938  0.019037 -0.025086
4175  0.262282 -0.027659 -0.045737
4176  0.739028  0.130322 -0.046922

[4177 rows x 3 columns]
```

[67]:
```python
# Apply LDA on raw abalone dataset
X_abalone_lda = X_abalone
y_abalone_lda = y_abalone
lda = LinearDiscriminantAnalysis(n_components=3)
X_abalone_lda = lda.fit(X_abalone_lda, y_abalone_lda).transform(X_abalone_lda)
abalone_lda_df = pd.DataFrame(X_abalone_lda, y_abalone_lda)
abalone_lda_df
```

[67]:
```
              0         1         2
Rings
15    -0.791003 -0.235208  0.359351
7     -2.355522  0.336978  0.214024
9      0.766719 -0.246564  1.129422
10    -0.611434  0.098075  0.230542
7     -2.674301  0.527509  0.102575
…           …         …         …
11     0.921330 -0.612381 -0.272399
10     0.425796 -0.894428 -0.034727
9      1.064523 -0.385654 -0.787231
10     0.840757 -1.513723 -0.864217
12     0.843580  0.352389 -2.262564
```

```
[4177 rows x 3 columns]
```

2 Wine Datasets

[68]:
```
wine_r = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_r["colour"]=1
wine_w = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_w["colour"]=0
wine_raw = pd.concat([wine_w,wine_r], ignore_index=True)
wine_raw.head(100)
```

[68]:
```
    fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0             7.0             0.270         0.36            20.7      0.045
1             6.3             0.300         0.34             1.6      0.049
2             8.1             0.280         0.40             6.9      0.050
3             7.2             0.230         0.32             8.5      0.058
4             7.2             0.230         0.32             8.5      0.058
..            …                 …          …              …        …
95            7.1             0.260         0.29            12.4      0.044
96            6.0             0.340         0.66            15.9      0.046
97            8.6             0.265         0.36             1.2      0.034
98            9.8             0.360         0.46            10.5      0.038
99            6.0             0.340         0.66            15.9      0.046

    free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                  45.0                 170.0   1.0010  3.00       0.45
1                  14.0                 132.0   0.9940  3.30       0.49
2                  30.0                  97.0   0.9951  3.26       0.44
3                  47.0                 186.0   0.9956  3.19       0.40
4                  47.0                 186.0   0.9956  3.19       0.40
..                  …                   …       …     …         …
95                 62.0                 240.0   0.9969  3.04       0.42
96                 26.0                 164.0   0.9979  3.14       0.50
97                 15.0                  80.0   0.9913  2.95       0.36
98                  4.0                  83.0   0.9956  2.89       0.30
99                 26.0                 164.0   0.9979  3.14       0.50

    alcohol  quality  colour
0       8.8        6       0
1       9.5        6       0
2      10.1        6       0
3       9.9        6       0
```

```
4       9.9        6       0
..       …       …       …
95      9.2        6       0
96      8.8        6       0
97     11.4        7       0
98     10.1        4       0
99      8.8        6       0

[100 rows x 13 columns]
```

[69]:
```
# Separate indep and dep features
X_wine1 = wine_raw.iloc[:, :-2]
y_wine = wine_raw.iloc[:, -2]
X_wine = pd.concat([X_wine1, wine_raw.iloc[:, -1]], axis=1)

# Normalize dataset
sc2 = MinMaxScaler()
X_wine = sc2.fit_transform(X_wine)
X_wine.shape, y_wine.shape
```

[69]:
```
((6497, 12), (6497,))
```

[70]:
```
# Apply PCA on wine dataset for dimensionality reduction
pca = PCA(n_components=2)
wine_pca = pca.fit_transform(X_wine)
wine_pca_df = pd.DataFrame(data=wine_pca, columns=['PC1', 'PC2'])
wine_pca_df
```

[70]:
```
           PC1       PC2
0    -0.298897 -0.337622
1    -0.241913 -0.084556
2    -0.225052 -0.036821
3    -0.290807 -0.123910
4    -0.290807 -0.123910
…          …         …
6492  0.793106  0.054298
6493  0.789921  0.151012
6494  0.790787  0.111938
6495  0.808678  0.031407
6496  0.751111  0.102306

[6497 rows x 2 columns]
```

[71]:
```
# Apply LDA on raw wine dataset
X_wine_lda = X_wine
y_wine_lda = y_wine
lda = LinearDiscriminantAnalysis(n_components=2)
```

```
X_wine_lda = lda.fit(X_wine_lda, y_wine_lda).transform(X_wine_lda)
wine_lda_df = pd.DataFrame(X_wine_lda, y_wine_lda)
print(wine_lda_df.shape)
wine_lda_df
```

```
(6497, 2)
```

[71]:

```
                0         1
quality
6        0.752078 -1.466209
6        1.445150  0.392049
6       -0.123015  0.911451
6        0.288961 -0.721769
6        0.288961 -0.721769
…             …         …
5        0.512278 -0.224430
6       -0.514707 -0.597340
6       -0.231160 -0.831907
5        0.630811  0.158871
6       -0.668993 -2.296580

[6497 rows x 2 columns]
```

3 Abalone - raw dataset - Multimonial naive bayes:

If we apply Standardisation to the Abalone dataset, values become negative and that is not acceptable as a values to Naive Bayes classifiers. Hence, we need to use MinMaxScaler (Normalization) to scale down values only within 0 and 1. However, this will decrease the accuracy of the model.

[72]:

```
from sklearn.metrics import accuracy_score
from sklearn.model_selection import StratifiedKFold
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import MultinomialNB, ComplementNB

kf = StratifiedKFold(n_splits=5)
acc_list = []
acc_all = []
for train_index, test_index in kf.split(X_abalone, y_abalone):
    X_train, X_test = X_abalone[train_index], X_abalone[test_index]
    y_train, y_test = y_abalone[train_index], y_abalone[test_index]
    # Create model for every fold
    # Multinimial NB
    multi = MultinomialNB()
    multi.fit(X_train, y_train)
    y_pred = multi.predict(X_test)
    acc_list.append(accuracy_score(y_test, y_pred))
```

```
avg_acc = sum(acc_list)/5
acc_all.append(avg_acc)
```

The accuracy of a model on the Raw abalone dataset has significantly reduced from 26% to 16.5% with Naive Bayes compared to KNN using 10 neighbors measured in the previous assignment. While it's likely that neither algorithm is adequate for predicting the abalone age, the KNN model is more accurate so far

4 Wine - Raw dataset - Multinomial Naive Bayes:

[73]:
```
# Running KNN on the Wine Raw dataset

# Separate indep and dep features
X_wine1 = wine_raw.iloc[:, :-2]
y_wine = wine_raw.iloc[:, -2]
X_wine = pd.concat([X_wine1, wine_raw.iloc[:, -1]], axis=1)

# Normalize dataset
sc2 = MinMaxScaler(feature_range=(0, 1))
X_wine = sc2.fit_transform(X_wine)
X_wine.shape, y_wine.shape

kf = StratifiedKFold(n_splits=5)
acc_list = []

for train_index, test_index in kf.split(X_wine, y_wine):
    X_train, X_test = X_wine[train_index], X_wine[test_index]
    y_train, y_test = y_wine[train_index], y_wine[test_index]
    # Create model for every fold
    # Multinimial NB
    multi = KNeighborsClassifier(n_neighbors=10)
    multi.fit(X_train, y_train)
    y_pred = multi.predict(X_test)
    acc_list.append(accuracy_score(y_test, y_pred))

avg_acc = sum(acc_list)/5
avg_acc
```

[73]: 0.46159223071001365

[74]:
```
kf = StratifiedKFold(n_splits=5)
acc_list = []

for train_index, test_index in kf.split(X_wine, y_wine):
    X_train, X_test = X_wine[train_index], X_wine[test_index]
    y_train, y_test = y_wine[train_index], y_wine[test_index]
    # Create model for every fold
```

```
    # Multinimial NB
    multi = MultinomialNB()
    multi.fit(X_train, y_train)
    y_pred = multi.predict(X_test)
    acc_list.append(accuracy_score(y_test, y_pred))

avg_acc = sum(acc_list)/5
acc_all.append(avg_acc)
```

[75]:
```
acc_all
```

[75]: [0.16495086382259405, 0.414954106709303]

KNN Algorithm has worked slightly better on the Wine (Raw) dataset compared to Multinomial Naive Bayes as the accuracy has gone down from 46.15% to an average of 41.5% accross 5-folds. A combination of Standardisation and then KNN has no significant effect on the accuracy improvement.

5 Abalone - Raw - Complement NB

[76]:
```
kf = StratifiedKFold(n_splits=5)
acc_list = []
for train_index, test_index in kf.split(X_abalone, y_abalone):
    X_train, X_test = X_abalone[train_index], X_abalone[test_index]
    y_train, y_test = y_abalone[train_index], y_abalone[test_index]
    # Create model for every fold
    comp = ComplementNB()
    comp.fit(X_train, y_train)
    y_pred = comp.predict(X_test)
    acc_list.append(accuracy_score(y_test, y_pred))

avg_acc = sum(acc_list)/5
avg_acc
```

[76]: 0.17500329484571525

6 Wine dataset - raw - complement NB

[77]:
```
X_wine1 = wine_raw.iloc[:, :-2]
y_wine = wine_raw.iloc[:, -2]
X_wine = pd.concat([X_wine1, wine_raw.iloc[:, -1]], axis=1)

# Normalize dataset
sc2 = MinMaxScaler()
X_wine = sc2.fit_transform(X_wine)
X_wine.shape, y_wine.shape
```

```
kf = StratifiedKFold(n_splits=5)
acc_list = []

for train_index, test_index in kf.split(X_wine, y_wine):
    X_train, X_test = X_wine[train_index], X_wine[test_index]
    y_train, y_test = y_wine[train_index], y_wine[test_index]
    # Create model for every fold
    multi = ComplementNB()
    multi.fit(X_train, y_train)
    y_pred = multi.predict(X_test)
    acc_list.append(accuracy_score(y_test, y_pred))

avg_acc = sum(acc_list)/5
avg_acc
```

[77]: 0.38971090187718366

[78]:

```
#X_abalone = abalone_df.iloc[:, 1:-1] # Removed the sex feature
#y_abalone = abalone_df.iloc[:, -1]
#abalone_pca = pca.fit_transform(X_abalone)
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
abalone_df = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                      'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
↪'Rings'], sep = ',')

# Separate indep and dep features
X_abalone = abalone_df.iloc[:, 1:-1] # Removed the sex feature
y_abalone = abalone_df.iloc[:, -1]
# print(y_abalone)

# Normalize dataset
sc1 = MinMaxScaler(feature_range=(0, 1))
X_abalone = sc1.fit_transform(X_abalone)
X_abalone

# Split data into features and target variable
X = X_abalone
y = y_abalone

# Apply PCA with 3 components
pca = PCA(n_components=3)
X_pca_fit = pca.fit_transform(X)

# Normalize the values between 0 and 1 using MinMaxScaler
```

```
scaler = MinMaxScaler(feature_range=(0, 1))
X_pca = scaler.fit_transform(X_pca_fit)

# Apply LDA with 3 components
lda = LinearDiscriminantAnalysis(n_components=3)
X_lda_fit = lda.fit_transform(X, y)

scaler = MinMaxScaler(feature_range=(0, 1))
X_lda = scaler.fit_transform(X_lda_fit)

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)

mnb_clf = MultinomialNB()

cnb_clf = ComplementNB()

mnb_cv_scores = cross_val_score(mnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of Raw abalone using Multinomial Naive Bayes␣
↪classifier: {:.2f}%".format(mnb_cv_scores.mean() * 100))

cnb_cv_scores = cross_val_score(cnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of Raw abalone using Complement Naive Bayes␣
↪classifier: {:.2f}%".format(cnb_cv_scores.mean() * 100))

mnb_clf.fit(X_train, y_train)
mnb_test_acc = mnb_clf.score(X_test, y_test)
print("Test accuracy of Raw abalone using Multinomial Naive Bayes classifier: {:
↪.2f}%".format(mnb_test_acc * 100))

cnb_clf.fit(X_train, y_train)
cnb_test_acc = cnb_clf.score(X_test, y_test)
print("Test accuracy of Raw abalone using Complement Naive Bayes classifier: {:.
↪2f}%".format(cnb_test_acc * 100))
```

```
Cross-validation accuracy of Raw abalone using Multinomial Naive Bayes
classifier: 16.37%
Cross-validation accuracy of Raw abalone using Complement Naive Bayes
classifier: 18.14%
Test accuracy of Raw abalone using Multinomial Naive Bayes classifier: 16.99%
Test accuracy of Raw abalone using Complement Naive Bayes classifier: 19.14%
```

[79]:
```
X_train, X_test, y_train, y_test = train_test_split(X_pca, y, test_size=0.2,␣
↪random_state=42)

mnb_clf = MultinomialNB()
```

```
cnb_clf = ComplementNB()

pca_mnb_cv_scores = cross_val_score(mnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of processed abalone using Multinomial Naive␣
↪Bayes classifier with PCA: {:.2f}%".format(pca_mnb_cv_scores.mean() * 100))

pca_cnb_cv_scores = cross_val_score(cnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of processed abalone using Complement Naive␣
↪Bayes classifier with PCA: {:.2f}%".format(pca_cnb_cv_scores.mean() * 100))

mnb_clf.fit(X_train, y_train)
pca_mnb_test_acc = mnb_clf.score(X_test, y_test)
print("Test accuracy of processed abalone using Multinomial Naive Bayes␣
↪classifier with PCA: {:.2f}%".format(pca_mnb_test_acc * 100))

cnb_clf.fit(X_train, y_train)
pca_cnb_test_acc = cnb_clf.score(X_test, y_test)
print("Test accuracy of processed abalone using Complement Naive Bayes␣
↪classifier with PCA: {:.2f}%".format(pca_cnb_test_acc * 100))
```

```
Cross-validation accuracy of processed abalone using Multinomial Naive Bayes
classifier with PCA: 16.37%
Cross-validation accuracy of processed abalone using Complement Naive Bayes
classifier with PCA: 18.26%
Test accuracy of processed abalone using Multinomial Naive Bayes classifier with
PCA: 16.99%
Test accuracy of processed abalone using Complement Naive Bayes classifier with
PCA: 17.22%
```

[80]:
```
X_train, X_test, y_train, y_test = train_test_split(X_lda, y, test_size=0.2,␣
↪random_state=42)

lda_mnb_cv_scores = cross_val_score(mnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of processed abalone using Multinomial Naive␣
↪Bayes classifier with LDA: {:.2f}%".format(lda_mnb_cv_scores.mean() * 100))

lda_cnb_cv_scores = cross_val_score(cnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of processed abalone using Complement Naive␣
↪Bayes classifier with LDA: {:.2f}%".format(lda_cnb_cv_scores.mean() * 100))

mnb_clf.fit(X_train, y_train)
lda_mnb_test_acc = mnb_clf.score(X_test, y_test)
print("Test accuracy of processed abalone using Multinomial Naive Bayes␣
↪classifier LDA: {:.2f}%".format(lda_mnb_test_acc * 100))

cnb_clf.fit(X_train, y_train)
lda_cnb_test_acc = cnb_clf.score(X_test, y_test)
```

```
print("Test accuracy of processed abalone using Complement Naive Bayes␣
↪classifier LDA: {:.2f}%".format(lda_cnb_test_acc * 100))
```

```
Cross-validation accuracy of processed abalone using Multinomial Naive Bayes
classifier with LDA: 16.37%
Cross-validation accuracy of processed abalone using Complement Naive Bayes
classifier with LDA: 23.97%
Test accuracy of processed abalone using Multinomial Naive Bayes classifier LDA:
16.99%
Test accuracy of processed abalone using Complement Naive Bayes classifier LDA:
21.53%
```

7 Using Wine Dataset

[81]:
```
wine_r = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_r["colour"]=1
wine_w = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_w["colour"]=0
wine_raw = pd.concat([wine_w,wine_r], ignore_index=True)
wine_raw.head(100)
```

[81]:
```
    fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0             7.0             0.270         0.36            20.7      0.045
1             6.3             0.300         0.34             1.6      0.049
2             8.1             0.280         0.40             6.9      0.050
3             7.2             0.230         0.32             8.5      0.058
4             7.2             0.230         0.32             8.5      0.058
..            …                …           …              …         …
95            7.1             0.260         0.29            12.4      0.044
96            6.0             0.340         0.66            15.9      0.046
97            8.6             0.265         0.36             1.2      0.034
98            9.8             0.360         0.46            10.5      0.038
99            6.0             0.340         0.66            15.9      0.046

    free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                  45.0                 170.0   1.0010  3.00       0.45
1                  14.0                 132.0   0.9940  3.30       0.49
2                  30.0                  97.0   0.9951  3.26       0.44
3                  47.0                 186.0   0.9956  3.19       0.40
4                  47.0                 186.0   0.9956  3.19       0.40
..                  …                   …       …    …        …
95                 62.0                 240.0   0.9969  3.04       0.42
96                 26.0                 164.0   0.9979  3.14       0.50
```

```
97                 15.0                    80.0   0.9913  2.95       0.36
98                  4.0                    83.0   0.9956  2.89       0.30
99                 26.0                   164.0   0.9979  3.14       0.50

    alcohol  quality  colour
0       8.8        6       0
1       9.5        6       0
2      10.1        6       0
3       9.9        6       0
4       9.9        6       0
..      …      …     …
95      9.2        6       0
96      8.8        6       0
97     11.4        7       0
98     10.1        4       0
99      8.8        6       0

[100 rows x 13 columns]
```

[82]:

```
#Split dataset into X and Y
X_wine = wine_raw.iloc[:, :-1]
y_wine = wine_raw.iloc[:, -2]
print(y)
sc_wine = MinMaxScaler(feature_range=(0, 1))
X_wine = sc_wine.fit_transform(X_wine)
print("The normalized dataset is: \n", X)
```

```
0       15
1        7
2        9
3       10
4        7
        ..
4172    11
4173    10
4174     9
4175    10
4176    12
Name: Rings, Length: 4177, dtype: int64
The normalized dataset is:
 [[0.51351351 0.5210084  0.0840708  … 0.15030262 0.1323239  0.14798206]
 [0.37162162 0.35294118 0.07964602 … 0.06624075 0.06319947 0.06826109]
 [0.61486486 0.61344538 0.11946903 … 0.17182246 0.18564845 0.2077728 ]
 …
 [0.70945946 0.70588235 0.18141593 … 0.3527236  0.37788018 0.30543099]
 [0.74324324 0.72268908 0.13274336 … 0.35642233 0.34298881 0.29347285]
 [0.85810811 0.84033613 0.17256637 … 0.63517149 0.49506254 0.49177877]]
```

[83]:
```
# Apply PCA with 3 components
pca = PCA(n_components=3)
X_wine_pca_fit = pca.fit_transform(X_wine)

# Normalize the values between 0 and 1 using MinMaxScaler
scaler = MinMaxScaler(feature_range=(0, 1))
X_wine_pca = scaler.fit_transform(X_wine_pca_fit)

# Apply LDA with 3 components
lda = LinearDiscriminantAnalysis(n_components=3)
X_wine_lda_fit = lda.fit_transform(X_wine, y_wine)

# Normalize the values between 0 and 1 using MinMaxScaler
scaler = MinMaxScaler(feature_range=(0, 1))
X_wine_lda = scaler.fit_transform(X_wine_lda_fit)
```

[84]:
```
X_train, X_test, y_train, y_test = train_test_split(X_wine, y_wine, test_size=0.
 ↪2, random_state=42)

mnb_clf = MultinomialNB()

cnb_clf = ComplementNB()

mnb_cv_scores = cross_val_score(mnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of raw wine using Multinomial Naive Bayes␣
 ↪classifier: {:.2f}%".format(mnb_cv_scores.mean() * 100))

cnb_cv_scores = cross_val_score(cnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of raw wine using Complement Naive Bayes␣
 ↪classifier: {:.2f}%".format(cnb_cv_scores.mean() * 100))

mnb_clf.fit(X_train, y_train)
mnb_test_acc = mnb_clf.score(X_test, y_test)
print("Test accuracy of raw wine using Multinomial Naive Bayes classifier: {:.
 ↪2f}%".format(mnb_test_acc * 100))

cnb_clf.fit(X_train, y_train)
cnb_test_acc = cnb_clf.score(X_test, y_test)
print("Test accuracy of raw wine using Complement Naive Bayes classifier: {:.
 ↪2f}%".format(cnb_test_acc * 100))
```

```
Cross-validation accuracy of raw wine using Multinomial Naive Bayes classifier:
43.54%
Cross-validation accuracy of raw wine using Complement Naive Bayes classifier:
47.51%
Test accuracy of raw wine using Multinomial Naive Bayes classifier: 44.62%
Test accuracy of raw wine using Complement Naive Bayes classifier: 48.54%
```

[85]:
```
X_train, X_test, y_train, y_test = train_test_split(X_wine_pca, y_wine,␣
↪test_size=0.2, random_state=42)

mnb_clf = MultinomialNB()

cnb_clf = ComplementNB()

pca_mnb_cv_scores = cross_val_score(mnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of processed wine using Multinomial Naive␣
↪Bayes classifier with PCA: {:.2f}%".format(pca_mnb_cv_scores.mean() * 100))

pca_cnb_cv_scores = cross_val_score(cnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of processed wine using Complement Naive Bayes␣
↪classifier with PCA: {:.2f}%".format(pca_cnb_cv_scores.mean() * 100))

mnb_clf.fit(X_train, y_train)
pca_mnb_test_acc = mnb_clf.score(X_test, y_test)
print("Test accuracy of processed wine using Multinomial Naive Bayes classifier␣
↪with PCA: {:.2f}%".format(pca_mnb_test_acc * 100))

cnb_clf.fit(X_train, y_train)
pca_cnb_test_acc = cnb_clf.score(X_test, y_test)
print("Test accuracy of processed wine using Complement Naive Bayes classifier␣
↪with PCA: {:.2f}%".format(pca_cnb_test_acc * 100))
```

```
Cross-validation accuracy of processed wine using Multinomial Naive Bayes
classifier with PCA: 43.43%
Cross-validation accuracy of processed wine using Complement Naive Bayes
classifier with PCA: 45.41%
Test accuracy of processed wine using Multinomial Naive Bayes classifier with
PCA: 44.54%
Test accuracy of processed wine using Complement Naive Bayes classifier with
PCA: 46.92%
```

[86]:
```
X_train, X_test, y_train, y_test = train_test_split(X_wine_lda, y_wine,␣
↪test_size=0.2, random_state=42)

lda_mnb_cv_scores = cross_val_score(mnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of processed wine using Multinomial Naive␣
↪Bayes classifier with LDA: {:.2f}%".format(lda_mnb_cv_scores.mean() * 100))

lda_cnb_cv_scores = cross_val_score(cnb_clf, X_train, y_train, cv=5)
print("Cross-validation accuracy of processed wine using Complement Naive Bayes␣
↪classifier with LDA: {:.2f}%".format(lda_cnb_cv_scores.mean() * 100))

mnb_clf.fit(X_train, y_train)
lda_mnb_test_acc = mnb_clf.score(X_test, y_test)
```

```
print("Test accuracy of processed wine using Multinomial Naive Bayes classifier␣
↪with LDA: {:.2f}%".format(lda_mnb_test_acc * 100))

cnb_clf.fit(X_train, y_train)
lda_cnb_test_acc = cnb_clf.score(X_test, y_test)
print("Test accuracy of processed wine using Complement Naive Bayes classifier␣
↪with LDA: {:.2f}%".format(lda_cnb_test_acc * 100))
```

```
Cross-validation accuracy of processed wine using Multinomial Naive Bayes
classifier with LDA: 43.43%
Cross-validation accuracy of processed wine using Complement Naive Bayes
classifier with LDA: 0.54%
Test accuracy of processed wine using Multinomial Naive Bayes classifier with
LDA: 44.54%
Test accuracy of processed wine using Complement Naive Bayes classifier with
LDA: 0.15%
```

8 Assignment 2 Question 3 implementation starts here

8.0.1 Question 3:

3 Decision Trees Classifier You will now do classification on your datasets using Decision Trees. Decision Trees have a number of parameters that can effect peformance. You can use the GridSearchCV function for this question. 1. Use 5-fold cross validation and a range of parameter values to evaluate the best settings for classification on each dataset. • the maximum depth of trees 2. Produce a plot showing the mean accuracy vs. relative to tree depth. 3. Interpretability: Use the decision tree library functions, to examine the final resulting splitting rules used for the trees. Do they indicate any interesting patterns that explain the data? Can you find support for this from any analysis you've done or see on this dataset previously? For this part, use the original raw feature space only, not the PCA/LDA space. (Why not?) • Relevant decision tree visualizers, whichever one you use, make sure it is readable in useful way, don't show information that isn't helpful: • tree.plot tree(): the built-in tree plot function for • sklearn.tree.DecisionTree tree.export graphviz : another simple visualizer • sklearn.tree.export text : text view of the tree data Include summary accuracy scores on all six datasets in the table in the last question.

8.1 Using Abalone Dataset

[87]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.decomposition import PCA
import warnings
warnings.filterwarnings('ignore')
```

```
[88]: # Load raw abalone dataset
abalone_df = pd.read_csv(r"C:
 ↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
 ↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                      'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
 ↪'Rings'], sep = ',')

# Separate indep and dep features
X_abalone = abalone_df.iloc[:, 1:-1] # Removed the sex feature
y_abalone = abalone_df.iloc[:, -1]

# Normalize dataset
sc1 = MinMaxScaler()
X_abalone = sc1.fit_transform(X_abalone)
X_abalone
```

```
[88]: array([[0.51351351, 0.5210084 , 0.0840708 , …, 0.15030262, 0.1323239 ,
         0.14798206],
        [0.37162162, 0.35294118, 0.07964602, …, 0.06624075, 0.06319947,
         0.06826109],
        [0.61486486, 0.61344538, 0.11946903, …, 0.17182246, 0.18564845,
         0.2077728 ],
        …,
        [0.70945946, 0.70588235, 0.18141593, …, 0.3527236 , 0.37788018,
         0.30543099],
        [0.74324324, 0.72268908, 0.13274336, …, 0.35642233, 0.34298881,
         0.29347285],
        [0.85810811, 0.84033613, 0.17256637, …, 0.63517149, 0.49506254,
         0.49177877]])
```

```
[89]: # Apply PCA on abalone dataset
pca = PCA(n_components=3)
abalone_pca = pca.fit_transform(X_abalone)
abalone_pca_df = pd.DataFrame(data=abalone_pca, columns=['PC1', 'PC2', 'PC3'])
abalone_pca_df
```

[89]:

	PC1	PC2	PC3
0	-0.230816	-0.026563	-0.006786
1	-0.497671	0.043791	0.003049
2	-0.068857	-0.081454	0.011720
3	-0.230997	-0.012962	0.004214
4	-0.532797	0.057362	-0.000513
…	…	…	…
4172	0.100632	-0.034549	-0.011468
4173	0.128141	-0.023082	-0.028686
4174	0.273938	0.019037	-0.025086
4175	0.262282	-0.027659	-0.045737

```
4176  0.739028  0.130322 -0.046922

[4177 rows x 3 columns]
```

[90]:
```python
# Apply LDA on raw abalone dataset
X_abalone_lda = X_abalone
y_abalone_lda = y_abalone
lda = LinearDiscriminantAnalysis(n_components=3)
X_abalone_lda = lda.fit(X_abalone_lda, y_abalone_lda).transform(X_abalone_lda)
abalone_lda_df = pd.DataFrame(X_abalone_lda, y_abalone_lda)
abalone_lda_df
```

[90]:
```
              0         1         2
Rings
15    -0.791003 -0.235208  0.359351
7     -2.355522  0.336978  0.214024
9      0.766719 -0.246564  1.129422
10    -0.611434  0.098075  0.230542
7     -2.674301  0.527509  0.102575
…           …         …         …
11     0.921330 -0.612381 -0.272399
10     0.425796 -0.894428 -0.034727
9      1.064523 -0.385654 -0.787231
10     0.840757 -1.513723 -0.864217
12     0.843580  0.352389 -2.262564

[4177 rows x 3 columns]
```

8.1.1 Wine Dataset

[91]:
```python
wine_r = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_r["colour"]=1
wine_w = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_w["colour"]=0
wine_raw = pd.concat([wine_w,wine_r], ignore_index=True)
wine_raw.head(100)
```

[91]:
```
   fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0            7.0             0.270         0.36            20.7      0.045
1            6.3             0.300         0.34             1.6      0.049
2            8.1             0.280         0.40             6.9      0.050
3            7.2             0.230         0.32             8.5      0.058
4            7.2             0.230         0.32             8.5      0.058
```

```
..           …           …          …          …      …
95         7.1       0.260       0.29       12.4   0.044
96         6.0       0.340       0.66       15.9   0.046
97         8.6       0.265       0.36        1.2   0.034
98         9.8       0.360       0.46       10.5   0.038
99         6.0       0.340       0.66       15.9   0.046

    free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                  45.0                 170.0   1.0010  3.00       0.45
1                  14.0                 132.0   0.9940  3.30       0.49
2                  30.0                  97.0   0.9951  3.26       0.44
3                  47.0                 186.0   0.9956  3.19       0.40
4                  47.0                 186.0   0.9956  3.19       0.40
..                  …                    …        …     …         …
95                 62.0                 240.0   0.9969  3.04       0.42
96                 26.0                 164.0   0.9979  3.14       0.50
97                 15.0                  80.0   0.9913  2.95       0.36
98                  4.0                  83.0   0.9956  2.89       0.30
99                 26.0                 164.0   0.9979  3.14       0.50

    alcohol  quality  colour
0       8.8        6       0
1       9.5        6       0
2      10.1        6       0
3       9.9        6       0
4       9.9        6       0
..      …       …      …
95      9.2        6       0
96      8.8        6       0
97     11.4        7       0
98     10.1        4       0
99      8.8        6       0

[100 rows x 13 columns]
```

[92]:
```
# Separate indep and dep features
X_wine1 = wine_raw.iloc[:, :-2]
y_wine = wine_raw.iloc[:, -2]
X_wine = pd.concat([X_wine1, wine_raw.iloc[:, -1]], axis=1)

# Normalize dataset
sc2 = MinMaxScaler()
X_wine = sc2.fit_transform(X_wine)
X_wine.shape, y_wine.shape
```

[92]:
```
((6497, 12), (6497,))
```

[93]:
```
# Apply PCA on wine dataset for dimensionality reduction
pca = PCA(n_components=2)
wine_pca = pca.fit_transform(X_wine)
wine_pca_df = pd.DataFrame(data=wine_pca, columns=['PC1', 'PC2'])
wine_pca_df
```

[93]:
```
           PC1       PC2
0    -0.298897 -0.337622
1    -0.241913 -0.084556
2    -0.225052 -0.036821
3    -0.290807 -0.123910
4    -0.290807 -0.123910
…          …         …
6492  0.793106  0.054298
6493  0.789921  0.151012
6494  0.790787  0.111938
6495  0.808678  0.031407
6496  0.751111  0.102306

[6497 rows x 2 columns]
```

[94]:
```
# Apply LDA on raw wine dataset
X_wine_lda = X_wine
y_wine_lda = y_wine
lda = LinearDiscriminantAnalysis(n_components=2)
X_wine_lda = lda.fit(X_wine_lda, y_wine_lda).transform(X_wine_lda)
wine_lda_df = pd.DataFrame(X_wine_lda, y_wine_lda)
print(wine_lda_df.shape)
wine_lda_df
```

```
(6497, 2)
```

[94]:
```
                0         1
quality
6        0.752078 -1.466209
6        1.445150  0.392049
6       -0.123015  0.911451
6        0.288961 -0.721769
6        0.288961 -0.721769
…              …         …
5        0.512278 -0.224430
6       -0.514707 -0.597340
6       -0.231160 -0.831907
5        0.630811  0.158871
6       -0.668993 -2.296580

[6497 rows x 2 columns]
```

9 Decision Tree on Abalone dataset

The DecisionTreeRegressor is an algorithm used to estimate a continous variable instead of a discrete one.

[95]:
```
from sklearn.model_selection import StratifiedKFold
from sklearn.tree import DecisionTreeRegressor
score=[]
train_score=[]
kf = StratifiedKFold(n_splits=5)

for train_index, test_index in kf.split(X_abalone, y_abalone):
    X_train, X_test = X_abalone[train_index], X_abalone[test_index]
    y_train, y_test = y_abalone[train_index], y_abalone[test_index]

    model = DecisionTreeRegressor()
    model.fit(X_train, y_train)
    predicted_test_y = model.predict(X_test)
    predicted_train_y = model.predict(X_train)
    train_score.append(model.score(X_train, y_train))
    score.append(model.score(X_test, y_test))

print("Testing score: ", score)
print("Training score: ", train_score)
```

```
Testing score:  [-0.029170677339277695, 0.1593988145639289, 0.07566737009552604,
0.14899358230388193, 0.13245339011866875]
Training score:  [1.0, 1.0, 1.0, 1.0, 1.0]
```

This model overfits the dataset and that is why, validation error is very high.

[96]:
```
def scatter_y(true_y, predicted_y):

    fig, ax = plt.subplots(figsize=(4,4))
    ax.plot(true_y, predicted_y, '.k')

    ax.plot([0, 30], [0, 30], '--k')
    ax.plot([0, 30], [2, 32], ':k')
    ax.plot([2, 32], [0, 30], ':k')

    rms = (true_y - predicted_y).std()

    ax.text(28, 3,
            "Root Mean Square Error = %.2g" % rms,
            ha='right', va='bottom')

    ax.set_xlim(0, 30)
    ax.set_ylim(0, 30)
```

```
    ax.set_xlabel('True number of rings')
    ax.set_ylabel('Predicted number of rings')

    return rms
```

[97]:
```
scatter_y(y_train, predicted_train_y)
plt.title("Training data")
scatter_y(y_test, predicted_test_y)
plt.title("Test data");
```

The Decision Tree overfits the training set, i.e. its parameters are fine tuned to reproduce the results of the training set but generalized badly to data not seen previously.

[98]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X_abalone, y_abalone,␣
↪test_size=0.2, random_state=1)
acc=[]
for i in range(1,10):
    model = DecisionTreeRegressor(max_depth=i)
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    acc.append(model.score(X_test, y_test))
```

[99]:
```
acc
```

[99]:
```
[0.2743675926265253,
 0.32115270603998214,
 0.3433132428439525,
 0.40126800234349214,
 0.4278684960176351,
 0.4340850300095299,
 0.4390516759870713,
 0.35617530225868343,
```

```
0.3674679511109248]
```

9.0.1 Using GridSearchCV

[100]:
```
import pandas as pd
import numpy as np
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import accuracy_score
from sklearn.model_selection import KFold
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.tree import export_graphviz
from sklearn.tree import export_text
import graphviz
import matplotlib.pyplot as plt

# Load raw abalone dataset
abalone_df = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                    'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
↪'Rings'], sep = ',')

encoder = LabelEncoder()
abalone_df["Sex"] = encoder.fit_transform(abalone_df["Sex"])

# Split data into features and target
X = abalone_df.drop("Rings", axis=1)
y = abalone_df["Rings"]

param_grid = {
    "max_depth": [1, 2, 3, 4, 5]
}

# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
↪scoring="accuracy")

# Perform cross-validation
grid.fit(X, y)

print("Best parameters:", grid.best_params_)
```

```
print("Best accuracy score:", grid.best_score_)
```

```
Best parameters: {'max_depth': 4}
Best accuracy score: 0.26238260321462337
```

[101]:

```
# Print the final decision tree using export_graphviz
from sklearn.tree import export_graphviz
import graphviz

dot_data = export_graphviz(grid.best_estimator_, out_file=None,
                           feature_names=X.columns,
                           class_names=["0-8", "9-10", "11-12", "13-14",␣
↪"15-16", "17-18", "19-20", "21-22", "23-24", "25-26", "27-29", "30-31",␣
↪"32-34", "35-38", "39-42", "43-46", "47-50", "51-54", "55-58", "59-62",␣
↪"63-66", "67-70", "71-74", "75-78", "79-82", "83-86", "87-90", "91-96",␣
↪"97+"],
                           filled=True, rounded=True,
                           special_characters=True)
graph = graphviz.Source(dot_data)
graph.render("abalone_decision_tree")

# Print the final decision tree using text
from sklearn.tree import export_text
tree_rules = export_text(grid.best_estimator_, feature_names=X.columns.tolist())
print(tree_rules)
```

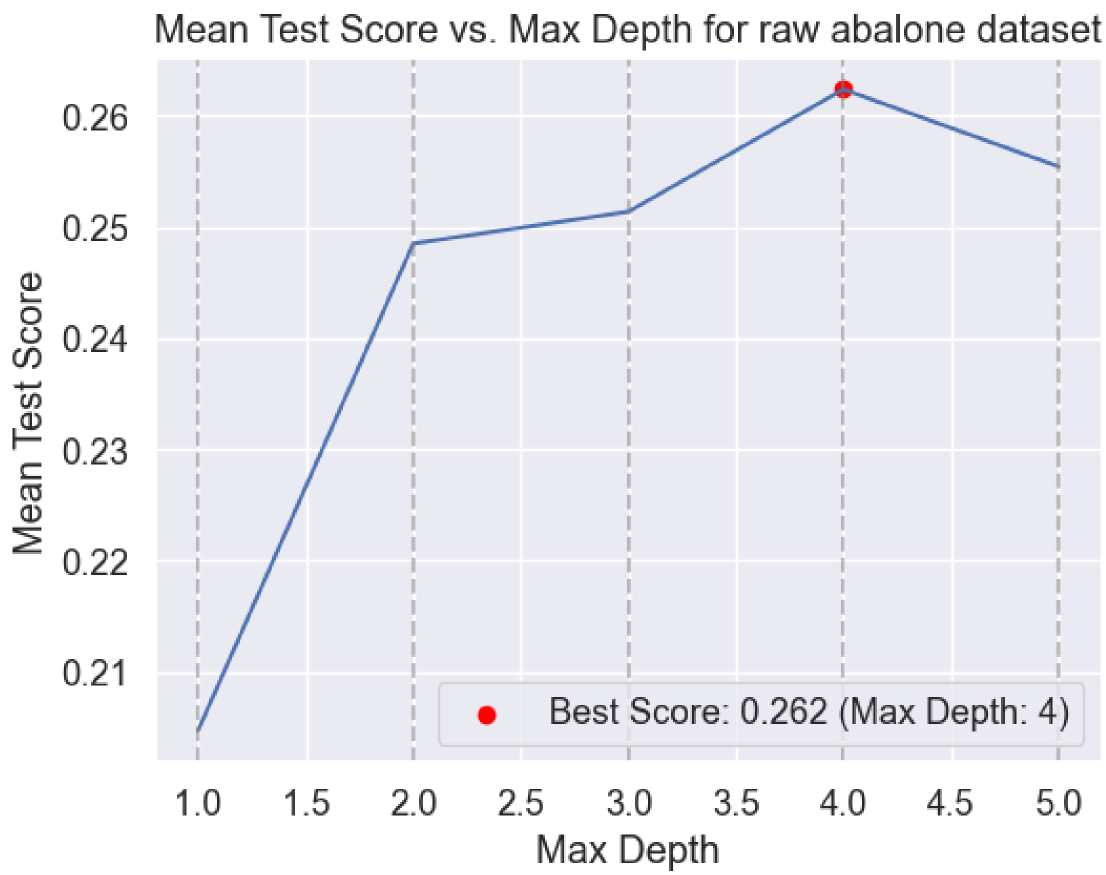
```
|--- Shell_weight <= 0.14
|   |--- Diameter <= 0.22
|   |   |--- Shell_weight <= 0.02
|   |   |   |--- Whole_weight <= 0.02
|   |   |   |   |--- class: 3
|   |   |   |--- Whole_weight >  0.02
|   |   |   |   |--- class: 4
|   |   |--- Shell_weight >  0.02
|   |   |   |--- Length <= 0.25
|   |   |   |   |--- class: 4
|   |   |   |--- Length >  0.25
|   |   |   |   |--- class: 5
|   |--- Diameter >  0.22
|   |   |--- Shell_weight <= 0.09
|   |   |   |--- Sex <= 1.50
|   |   |   |   |--- class: 7
|   |   |   |--- Sex >  1.50
|   |   |   |   |--- class: 9
|   |   |--- Shell_weight >  0.09
|   |   |   |--- Sex <= 0.50
|   |   |   |   |--- class: 8
|   |   |   |--- Sex >  0.50
```

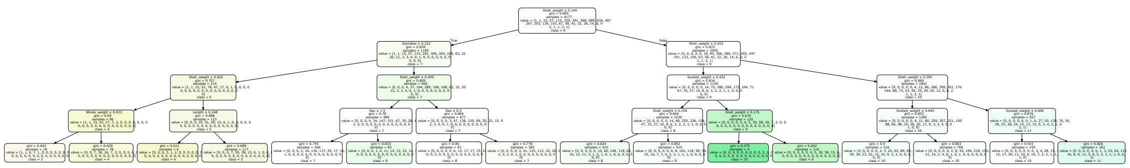
```
|   |   |   |   |--- class: 7
|--- Shell_weight >  0.14
|   |--- Shell_weight <= 0.25
|   |   |--- Sucked_weight <= 0.43
|   |   |   |--- Shell_weight <= 0.19
|   |   |   |   |--- class: 8
|   |   |   |--- Shell_weight >  0.19
|   |   |   |   |--- class: 9
|   |   |--- Sucked_weight >  0.43
|   |   |   |--- Shell_weight <= 0.18
|   |   |   |   |--- class: 10
|   |   |   |--- Shell_weight >  0.18
|   |   |   |   |--- class: 9
|   |--- Shell_weight >  0.25
|   |   |--- Shell_weight <= 0.39
|   |   |   |--- Sucked_weight <= 0.44
|   |   |   |   |--- class: 10
|   |   |   |--- Sucked_weight >  0.44
|   |   |   |   |--- class: 10
|   |   |--- Shell_weight >  0.39
|   |   |   |--- Sucked_weight <= 0.61
|   |   |   |   |--- class: 10
|   |   |   |--- Sucked_weight >  0.61
|   |   |   |   |--- class: 11
```

[102]:

```
# Extract the mean test scores for each value of max_depth
mean_test_scores = grid.cv_results_['mean_test_score']

# Plot the mean test scores vs. max_depth
plt.plot(param_grid['max_depth'], mean_test_scores)
plt.xlabel('Max Depth')
plt.ylabel('Mean Test Score')
plt.title('Mean Test Score vs. Max Depth for raw abalone dataset')

# Add vertical lines for each value of max_depth
for depth in param_grid['max_depth']:
    plt.axvline(depth, linestyle='--', color='gray', alpha=0.5)

# Annotate the plot with the best parameter value and score
best_score = grid.best_score_
best_depth = grid.best_params_['max_depth']
plt.scatter(best_depth, best_score, marker='o', color='red', label=f'Best Score:
 ↪ {best_score:.3f} (Max Depth: {best_depth})')
plt.legend()

plt.show()
```

```
# Print the final decision tree using export_graphviz
dot_data = export_graphviz(grid.best_estimator_,out_file=None,
feature_names=X.columns,
class_names=["1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11", "12",␣
↪"13", "14", "15", "16", "17", "18", "19", "20", "21", "22", "23", "24",␣
↪"25", "26", "27", "28", "29"],
filled=True,
rounded=True,
special_characters=True)

graph = graphviz.Source(dot_data)

graph.view()

from IPython.display import display

dot_data = export_graphviz(
    grid.best_estimator_,
    out_file=None,
    feature_names=X.columns,
    class_names=["1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11", "12",␣
↪"13", "14", "15", "16", "17", "18", "19", "20", "21", "22", "23", "24",␣
↪"25", "26", "27", "28", "29"],
    filled=True,
    rounded=True,
    special_characters=True
)

graph = graphviz.Source(dot_data)
display(graph)
```





from the above graph we can see that that maximum depth of 4 is yielding the high test accuracy score of 26.23%

[103]:
```
#Finding other best hyper parameters
param_grid = {
    "splitter": ["best", "random"],
    "max_depth": [1, 2, 3, 4, 5],
    "min_samples_leaf": [1, 2, 3, 4, 5],
    "min_weight_fraction_leaf": [0.0, 0.1, 0.2, 0.3, 0.4, 0.5],
    "max_features": ["sqrt", "log2"],
    "max_leaf_nodes": [None, 5, 10, 15, 20]
```

```
}

# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
 ↪scoring="accuracy")

# Perform cross-validation
grid.fit(X, y)

print("Best parameters:", grid.best_params_)
print("Best accuracy score:", grid.best_score_)
```

```
Best parameters: {'max_depth': 4, 'max_features': 'sqrt', 'max_leaf_nodes': 10,
'min_samples_leaf': 1, 'min_weight_fraction_leaf': 0.0, 'splitter': 'best'}
Best accuracy score: 0.2688488095579177
```

[104]:

```
#using GridSearchCV function as mentioned in the assignment
import pandas as pd
import numpy as np
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import accuracy_score
from sklearn.model_selection import KFold
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.decomposition import PCA

# Load raw abalone dataset
abalone_df = pd.read_csv(r"C:
 ↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
 ↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                      'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
 ↪'Rings'], sep = ',')

encoder = LabelEncoder()
abalone_df["Sex"] = encoder.fit_transform(abalone_df["Sex"])

X = abalone_df.drop("Rings", axis=1)
# Normalize dataset
sc1 = MinMaxScaler()
X = sc1.fit_transform(X)
```

```
# X = pd.DataFrame(data=X, columns=['Sex', 'Length', 'Diameter', 'Height',␣
↪'Whole_weight', 'Sucked_weight', 'Viscera_weight', 'Shell_weight'])

# print(X)

# Apply PCA to X
pca = PCA(n_components=3)
X = pca.fit_transform(X)

X = pd.DataFrame(data=X, columns=['PC1', 'PC2', 'PC3'])

y = abalone_df["Rings"]

param_grid = {
    "max_depth": [1, 2, 3, 4, 5]
}

# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid_pca = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
↪scoring="accuracy")

# Perform cross-validation
grid_pca.fit(X, y)

print("Best parameters:", grid_pca.best_params_)
print("Best accuracy score:", grid_pca.best_score_)
```

```
Best parameters: {'max_depth': 3}
Best accuracy score: 0.2542440477895883
```

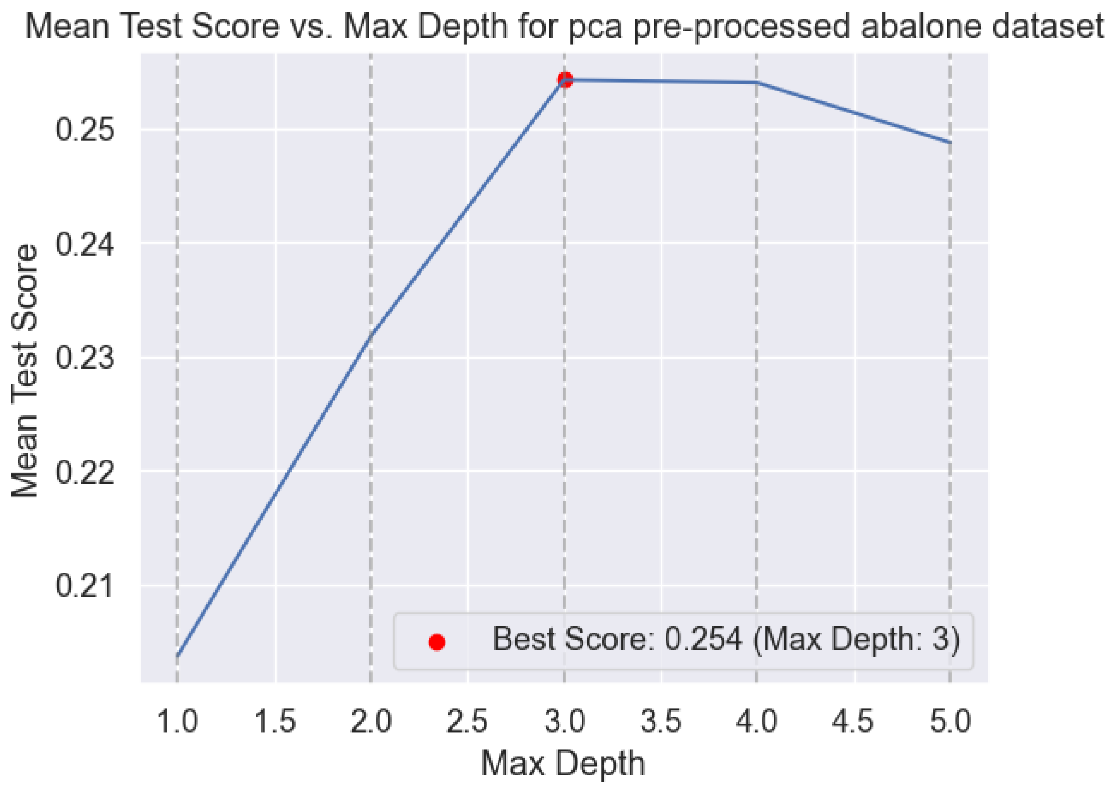
[105]:
```
# Print the final decision tree using export_graphviz
from sklearn.tree import export_graphviz
import graphviz

dot_data = export_graphviz(grid_pca.best_estimator_, out_file=None,
                           feature_names=X.columns,
                           class_names=["0-8", "9-10", "11-12", "13-14",␣
↪"15-16", "17-18", "19-20", "21-22", "23-24", "25-26", "27-29", "30-31",␣
↪"32-34", "35-38", "39-42", "43-46", "47-50", "51-54", "55-58", "59-62",␣
↪"63-66", "67-70", "71-74", "75-78", "79-82", "83-86", "87-90", "91-96",␣
↪"97+"],
                           filled=True, rounded=True,
                           special_characters=True)
```

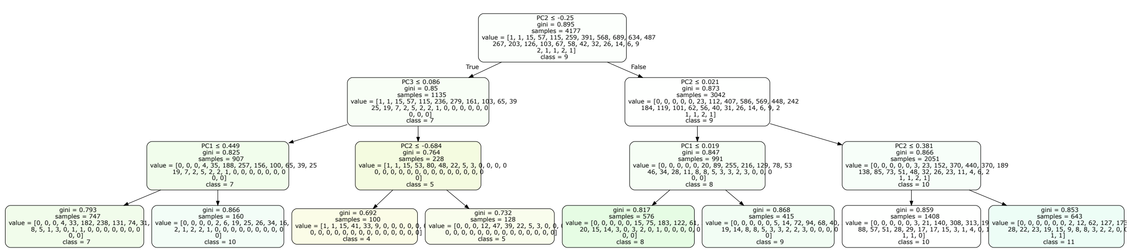
```
graph = graphviz.Source(dot_data)
graph.render("abalone_decision_tree")

# Print the final decision tree using text
from sklearn.tree import export_text
tree_rules = export_text(grid_pca.best_estimator_, feature_names=X.columns.
 ↪tolist())
print(tree_rules)
```

```
|--- PC2 <= -0.25
|   |--- PC3 <= 0.09
|   |   |--- PC1 <= 0.45
|   |   |   |--- class: 7
|   |   |--- PC1 >  0.45
|   |   |   |--- class: 10
|   |--- PC3 >  0.09
|   |   |--- PC2 <= -0.68
|   |   |   |--- class: 4
|   |   |--- PC2 >  -0.68
|   |   |   |--- class: 5
|--- PC2 >  -0.25
|   |--- PC2 <= 0.02
|   |   |--- PC1 <= 0.02
|   |   |   |--- class: 8
|   |   |--- PC1 >  0.02
|   |   |   |--- class: 9
|   |--- PC2 >  0.02
|   |   |--- PC2 <= 0.38
|   |   |   |--- class: 10
|   |   |--- PC2 >  0.38
|   |   |   |--- class: 11
```

[106]:
```
# Extract the mean test scores for each value of max_depth
mean_test_scores = grid_pca.cv_results_['mean_test_score']

# Plot the mean test scores vs. max_depth
plt.plot(param_grid['max_depth'], mean_test_scores)
plt.xlabel('Max Depth')
plt.ylabel('Mean Test Score')
plt.title('Mean Test Score vs. Max Depth for pca pre-processed abalone dataset')

# Add vertical lines for each value of max_depth
for depth in param_grid['max_depth']:
    plt.axvline(depth, linestyle='--', color='gray', alpha=0.5)

# Annotate the plot with the best parameter value and score
```

```
best_score = grid_pca.best_score_
best_depth = grid_pca.best_params_['max_depth']
plt.scatter(best_depth, best_score, marker='o', color='red', label=f'Best Score:
 ↪ {best_score:.3f} (Max Depth: {best_depth})')
plt.legend()

plt.show()

# Print the final decision tree using export_graphviz
dot_data = export_graphviz(grid_pca.best_estimator_,out_file=None,
feature_names=X.columns,
class_names=["1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11", "12",␣
 ↪"13", "14", "15", "16", "17", "18", "19", "20", "21", "22", "23", "24",␣
 ↪"25", "26", "27", "28", "29"],
filled=True,
rounded=True,
special_characters=True)

graph = graphviz.Source(dot_data)

graph.view()

# Print the final decision tree using export_graphviz
dot_data = export_graphviz(grid_pca.best_estimator_, out_file=None,
feature_names=X.columns,
class_names=["1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11", "12",␣
 ↪"13", "14", "15", "16", "17", "18", "19", "20", "21", "22", "23", "24",␣
 ↪"25", "26", "27", "28", "29"],
filled=True,
rounded=True,
special_characters=True)

graph = graphviz.Source(dot_data)

# graph.view()
display(graph)
```





from the above graph we can see that that maximum depth of 3 is yielding the high test accuracy score of 25.42%

[107]:
```python
#Finding the best hyperparameters
param_grid = {
    "splitter": ["best", "random"],
    "max_depth": [1, 2, 3, 4, 5],
    "min_samples_leaf": [1, 2, 3, 4, 5],
    "min_weight_fraction_leaf": [0.0, 0.1, 0.2, 0.3, 0.4, 0.5],
    "max_features": ["sqrt", "log2"],
    "max_leaf_nodes": [None, 5, 10, 15, 20]
}
```

```
# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid_pca = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
↪scoring="accuracy")

# Perform cross-validation
grid_pca.fit(X, y)

print("Best parameters:", grid_pca.best_params_)
print("Best accuracy score:", grid_pca.best_score_)
```

```
Best parameters: {'max_depth': 5, 'max_features': 'sqrt', 'max_leaf_nodes': 20,
'min_samples_leaf': 5, 'min_weight_fraction_leaf': 0.0, 'splitter': 'best'}
Best accuracy score: 0.25376471936509754
```

[108]:

```
##Using LDA

#using GridSearchCV function as mentioned in the assignment
import pandas as pd
import numpy as np
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import accuracy_score
from sklearn.model_selection import KFold
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.decomposition import PCA
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis

# Load raw abalone dataset
abalone_df = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                      'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
↪'Rings'], sep = ',')

encoder = LabelEncoder()
abalone_df["Sex"] = encoder.fit_transform(abalone_df["Sex"])

X = abalone_df.drop("Rings", axis=1)
y = abalone_df["Rings"]
# Normalize dataset
sc1 = MinMaxScaler()
X = sc1.fit_transform(X)
```

```
# X = pd.DataFrame(data=X, columns=['Sex', 'Length', 'Diameter', 'Height',␣
↪'Whole_weight', 'Sucked_weight', 'Viscera_weight', 'Shell_weight'])

# print(X)

# Apply LDA to X
lda = LinearDiscriminantAnalysis(n_components=3)
X = lda.fit_transform(X, y)

X = pd.DataFrame(data=X, columns=['LDA1', 'LDA2', 'LDA3'])

param_grid = {
    "max_depth": [1, 2, 3, 4, 5]
}

# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid_lda = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
↪scoring="accuracy")

# Perform cross-validation
grid_lda.fit(X, y)

print("Best parameters:", grid_lda.best_params_)
print("Best accuracy score:", grid_lda.best_score_)
```

```
Best parameters: {'max_depth': 5}
Best accuracy score: 0.2623840357562387
```

[109]:
```
# Print the final decision tree using export_graphviz
from sklearn.tree import export_graphviz
import graphviz

dot_data = export_graphviz(grid_lda.best_estimator_, out_file=None,
                           feature_names=X.columns,
                           class_names=["0-8", "9-10", "11-12", "13-14",␣
↪"15-16", "17-18", "19-20", "21-22", "23-24", "25-26", "27-29", "30-31",␣
↪"32-34", "35-38", "39-42", "43-46", "47-50", "51-54", "55-58", "59-62",␣
↪"63-66", "67-70", "71-74", "75-78", "79-82", "83-86", "87-90", "91-96",␣
↪"97+"],
                           filled=True, rounded=True,
                           special_characters=True)
graph = graphviz.Source(dot_data)
```

```python
graph.render("abalone_decision_tree")

# Print the final decision tree using text
from sklearn.tree import export_text
tree_rules = export_text(grid_lda.best_estimator_, feature_names=X.columns.
↪tolist())
print(tree_rules)
```

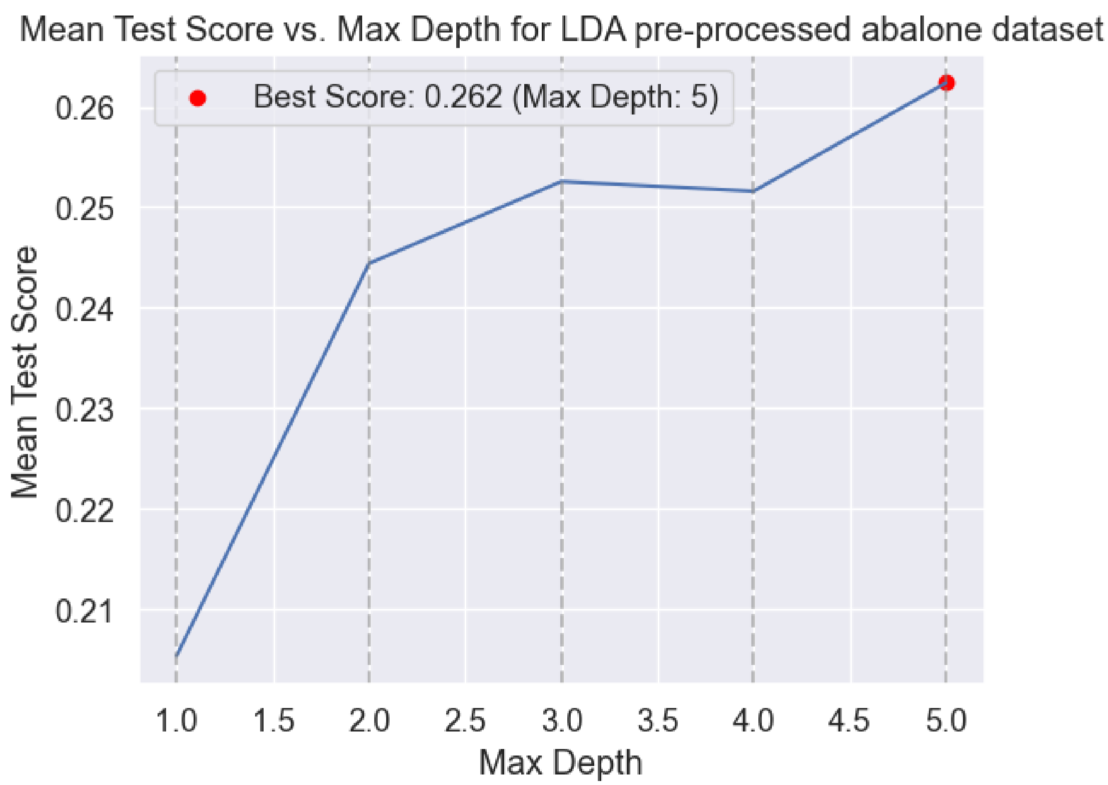
```
|--- LDA1 <= -0.60
|   |--- LDA1 <= -3.28
|   |   |--- LDA1 <= -4.13
|   |   |   |--- LDA2 <= -2.77
|   |   |   |   |--- LDA1 <= -6.99
|   |   |   |   |   |--- class: 1
|   |   |   |   |--- LDA1 >  -6.99
|   |   |   |   |   |--- class: 3
|   |   |   |--- LDA2 >  -2.77
|   |   |   |   |--- LDA3 <= -0.49
|   |   |   |   |   |--- class: 4
|   |   |   |   |--- LDA3 >  -0.49
|   |   |   |   |   |--- class: 4
|   |   |--- LDA1 >  -4.13
|   |   |   |--- LDA3 <= -0.17
|   |   |   |   |--- LDA1 <= -3.63
|   |   |   |   |   |--- class: 5
|   |   |   |   |--- LDA1 >  -3.63
|   |   |   |   |   |--- class: 6
|   |   |   |--- LDA3 >  -0.17
|   |   |   |   |--- LDA1 <= -3.64
|   |   |   |   |   |--- class: 7
|   |   |   |   |--- LDA1 >  -3.64
|   |   |   |   |   |--- class: 5
|   |--- LDA1 >  -3.28
|   |   |--- LDA1 <= -1.45
|   |   |   |--- LDA1 <= -2.01
|   |   |   |   |--- LDA1 <= -3.25
|   |   |   |   |   |--- class: 7
|   |   |   |   |--- LDA1 >  -3.25
|   |   |   |   |   |--- class: 6
|   |   |   |--- LDA1 >  -2.01
|   |   |   |   |--- LDA2 <= -0.08
|   |   |   |   |   |--- class: 7
|   |   |   |   |--- LDA2 >  -0.08
|   |   |   |   |   |--- class: 7
|   |   |--- LDA1 >  -1.45
|   |   |   |--- LDA2 <= 0.28
|   |   |   |   |--- LDA3 <= -1.12
|   |   |   |   |   |--- class: 9
```

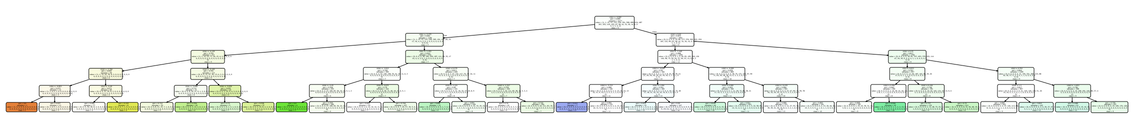
```
|   |   |   |   |--- LDA3 >  -1.12
|   |   |   |   |   |--- class: 8
|   |   |   |--- LDA2 >  0.28
|   |   |   |   |--- LDA3 <= -1.32
|   |   |   |   |   |--- class: 9
|   |   |   |   |--- LDA3 >  -1.32
|   |   |   |   |   |--- class: 7
|--- LDA1 >  -0.60
|   |--- LDA2 <= 0.09
|   |   |--- LDA2 <= -1.45
|   |   |   |--- LDA3 <= -0.02
|   |   |   |   |--- LDA2 <= -5.73
|   |   |   |   |   |--- class: 17
|   |   |   |   |--- LDA2 >  -5.73
|   |   |   |   |   |--- class: 11
|   |   |   |--- LDA3 >  -0.02
|   |   |   |   |--- LDA1 <= 1.20
|   |   |   |   |   |--- class: 13
|   |   |   |   |--- LDA1 >  1.20
|   |   |   |   |   |--- class: 16
|   |   |--- LDA2 >  -1.45
|   |   |   |--- LDA3 <= -0.31
|   |   |   |   |--- LDA1 <= 0.57
|   |   |   |   |   |--- class: 10
|   |   |   |   |--- LDA1 >  0.57
|   |   |   |   |   |--- class: 11
|   |   |   |--- LDA3 >  -0.31
|   |   |   |   |--- LDA2 <= -0.19
|   |   |   |   |   |--- class: 13
|   |   |   |   |--- LDA2 >  -0.19
|   |   |   |   |   |--- class: 10
|   |--- LDA2 >  0.09
|   |   |--- LDA1 <= 0.23
|   |   |   |--- LDA2 <= 0.63
|   |   |   |   |--- LDA2 <= 0.58
|   |   |   |   |   |--- class: 8
|   |   |   |   |--- LDA2 >  0.58
|   |   |   |   |   |--- class: 10
|   |   |   |--- LDA2 >  0.63
|   |   |   |   |--- LDA3 <= 0.23
|   |   |   |   |   |--- class: 9
|   |   |   |   |--- LDA3 >  0.23
|   |   |   |   |   |--- class: 8
|   |   |--- LDA1 >  0.23
|   |   |   |--- LDA2 <= 0.79
|   |   |   |   |--- LDA1 <= 1.30
|   |   |   |   |   |--- class: 9
|   |   |   |   |--- LDA1 >  1.30
```

```
|   |   |   |   |   |--- class: 11
|   |   |   |--- LDA2 >  0.79
|   |   |   |   |--- LDA3 <= -1.45
|   |   |   |   |   |--- class: 11
|   |   |   |   |--- LDA3 >  -1.45
|   |   |   |   |   |--- class: 9
```

[110]:
```
# Extract the mean test scores for each value of max_depth
mean_test_scores = grid_lda.cv_results_['mean_test_score']

# Plot the mean test scores vs. max_depth
plt.plot(param_grid['max_depth'], mean_test_scores)
plt.xlabel('Max Depth')
plt.ylabel('Mean Test Score')
plt.title('Mean Test Score vs. Max Depth for LDA pre-processed abalone dataset')

# Add vertical lines for each value of max_depth
for depth in param_grid['max_depth']:
    plt.axvline(depth, linestyle='--', color='gray', alpha=0.5)

# Annotate the plot with the best parameter value and score
best_score = grid_lda.best_score_
best_depth = grid_lda.best_params_['max_depth']
plt.scatter(best_depth, best_score, marker='o', color='red', label=f'Best Score:
 ↪ {best_score:.3f} (Max Depth: {best_depth})')
plt.legend()

plt.show()

# Print the final decision tree using export_graphviz
dot_data = export_graphviz(grid_lda.best_estimator_,out_file=None,
feature_names=X.columns,
class_names=["1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11", "12",␣
 ↪"13", "14", "15", "16", "17", "18", "19", "20", "21", "22", "23", "24",␣
 ↪"25", "26", "27", "28", "29"],
filled=True,
rounded=True,
special_characters=True)

graph = graphviz.Source(dot_data)

graph.view()

# Print the final decision tree using export_graphviz
dot_data = export_graphviz(grid_lda.best_estimator_, out_file=None,
feature_names=X.columns,
```

```python
class_names=["1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11", "12",␣
 ↪"13", "14", "15", "16", "17", "18", "19", "20", "21", "22", "23", "24",␣
 ↪"25", "26", "27", "28", "29"],
filled=True,
rounded=True,
special_characters=True)

graph = graphviz.Source(dot_data)

# graph.view()
display(graph)
```





from the above graph we can see that that maximum depth of 5 is yielding the high test accuracy score of 26.26%

[111]:

```
#Finding the best hyperparameters
param_grid = {
    "splitter": ["best", "random"],
    "max_depth": [1, 2, 3, 4, 5],
    "min_samples_leaf": [1, 2, 3, 4, 5],
    "min_weight_fraction_leaf": [0.0, 0.1, 0.2, 0.3, 0.4, 0.5],
    "max_features": ["sqrt", "log2"],
    "max_leaf_nodes": [None, 5, 10, 15, 20]
}

# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid_lda = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
 ↪scoring="accuracy")

# Perform cross-validation
grid_lda.fit(X, y)

print("Best parameters:", grid_lda.best_params_)
print("Best accuracy score:", grid_lda.best_score_)
```

```
Best parameters: {'max_depth': 5, 'max_features': 'sqrt', 'max_leaf_nodes': 20,
'min_samples_leaf': 5, 'min_weight_fraction_leaf': 0.0, 'splitter': 'best'}
Best accuracy score: 0.2583127524854597
```

[112]:

```
##Wine Dataset

wine_r = pd.read_csv(r"C:
 ↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
 ↪csv", sep=';')
wine_r["colour"]=1
wine_w = pd.read_csv(r"C:
 ↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
 ↪csv", sep=';')
wine_w["colour"]=0
wine_raw = pd.concat([wine_w,wine_r], ignore_index=True)
wine_raw.head(100)

# Separate indep and dep features
# X_wine1 = wine_raw.iloc[:, :-2]
y_wine = wine_raw.iloc[:, -2]
X_wine = pd.concat([X_wine1, wine_raw.iloc[:, -1]], axis=1)
# print(X_wine)
```

```
# print(X_wine.columns)

# Normalize dataset
sc2 = MinMaxScaler()
X_wine = sc2.fit_transform(X_wine)
# X_wine.shape, y_wine.shape

X_wine = pd.DataFrame(data=X_wine, columns=['fixed acidity', 'volatile␣
↪acidity', 'citric acid', 'residual sugar', 'chlorides', 'free sulfur␣
↪dioxide', 'total sulfur dioxide', 'density', 'pH', 'sulphates', 'alcohol',␣
↪'colour'])


# Apply PCA on wine dataset for dimensionality reduction
pca = PCA(n_components=3)
X_wine_pca = pca.fit_transform(X_wine)
# print(wine_pca_df)

# Apply LDA on raw wine dataset
X_wine_lda = X_wine
y_wine_lda = y_wine
lda = LinearDiscriminantAnalysis(n_components=3)
X_wine_lda = lda.fit(X_wine_lda, y_wine_lda).transform(X_wine_lda)
# wine_lda_df = pd.DataFrame(X_wine_lda, y_wine_lda)
# print(wine_lda_df.shape)
# print(X_wine_lda)
```

[113]:
```
#Decision tree using raw dataset
param_grid = {
    "splitter": ["best", "random"],
    "max_depth": [1, 2, 3, 4, 5],
    "min_samples_leaf": [1, 2, 3, 4, 5],
    "min_weight_fraction_leaf": [0.0, 0.1, 0.2, 0.3, 0.4, 0.5],
    "max_features": ["sqrt", "log2"],
    "max_leaf_nodes": [None, 5, 10, 15, 20]
}

# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid_wine = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
↪scoring="accuracy")

# Perform cross-validation
```

```
grid_wine.fit(X_wine, y_wine)

print("Best parameters:", grid_wine.best_params_)
print("Best accuracy score:", grid_wine.best_score_)
```

```
Best parameters: {'max_depth': 5, 'max_features': 'log2', 'max_leaf_nodes': 15,
'min_samples_leaf': 2, 'min_weight_fraction_leaf': 0.0, 'splitter': 'best'}
Best accuracy score: 0.5314768757032037
```

[114]:

```
#Decision tree using pca preprocessing on wine dataset
param_grid = {
    "splitter": ["best", "random"],
    "max_depth": [1, 2, 3, 4, 5],
    "min_samples_leaf": [1, 2, 3, 4, 5],
    "min_weight_fraction_leaf": [0.0, 0.1, 0.2, 0.3, 0.4, 0.5],
    "max_features": ["sqrt", "log2"],
    "max_leaf_nodes": [None, 5, 10, 15, 20]
}

# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid_wine = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
 ↪scoring="accuracy")

# Perform cross-validation
grid_wine.fit(X_wine_pca, y_wine)

print("Best parameters:", grid_wine.best_params_)
print("Best accuracy score:", grid_wine.best_score_)
```

```
Best parameters: {'max_depth': 5, 'max_features': 'log2', 'max_leaf_nodes':
None, 'min_samples_leaf': 3, 'min_weight_fraction_leaf': 0.0, 'splitter':
'best'}
Best accuracy score: 0.5023857405104518
```

[115]:

```
#Decision tree using lda preprocessing on wine dataset
param_grid = {
    "splitter": ["best", "random"],
    "max_depth": [1, 2, 3, 4, 5],
    "min_samples_leaf": [1, 2, 3, 4, 5],
    "min_weight_fraction_leaf": [0.0, 0.1, 0.2, 0.3, 0.4, 0.5],
    "max_features": ["sqrt", "log2"],
    "max_leaf_nodes": [None, 5, 10, 15, 20]
}
```

```
# Define the DecisionTreeClassifier
dt = DecisionTreeClassifier()

# Define the GridSearchCV object
cv = KFold(n_splits=5, shuffle=True, random_state=42)
grid_wine = GridSearchCV(estimator=dt, param_grid=param_grid, cv=cv,␣
↪scoring="accuracy")

# Perform cross-validation
grid_wine.fit(X_wine_lda, y_wine)

print("Best parameters:", grid_wine.best_params_)
print("Best accuracy score:", grid_wine.best_score_)
```

```
Best parameters: {'max_depth': 5, 'max_features': 'sqrt', 'max_leaf_nodes':
None, 'min_samples_leaf': 3, 'min_weight_fraction_leaf': 0.0, 'splitter':
'best'}
Best accuracy score: 0.5411726179901699
```

9.1 Assignment 2 Question 4

9.1.1 Question4

4 Random Forest Classifier You will now do classification on your datasets using Random Forests. Random Forests have a number of parameters that can effect performance. You can use the GridSearchCV function for this question. 1. Use 5-fold cross validation and a range of parameter values to evaluate the best settings for classification on each dataset. • the maximum depth of trees, you can try values as low as 2 or 3 and as high as needed, decision trees have an upper limit on how deep they can go determine by the size of the dataset. • the number of trees, try values at regular intervals, you can go as low as 3 and as high as a few hundred trees. 2. Produce a plot showing the mean accuracy vs. the above parameter settings. This can be individually or using a heat plot showing a grid of mean accuracies for different combinations of the two parameters. NOTE: do not produce a tree plot or export for each tree in the forest! Include summary accuracy scores on all six datasets in the table in the last question.

[116]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.decomposition import PCA
import warnings
warnings.filterwarnings('ignore')

# Load raw abalone dataset
```

```
abalone_df = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                    'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
↪'Rings'], sep = ',')

# Separate indep and dep features
X_abalone = abalone_df.iloc[:, 1:-1] # Removed the sex feature
y_abalone = abalone_df.iloc[:, -1]

# Normalize dataset
sc1 = StandardScaler()
X_abalone = sc1.fit_transform(X_abalone)
X_abalone
```

[116]:
```
array([[-0.57455813, -0.43214879, -1.06442415, …, -0.60768536,
        -0.72621157, -0.63821689],
       [-1.44898585, -1.439929  , -1.18397831, …, -1.17090984,
        -1.20522124, -1.21298732],
       [ 0.05003309,  0.12213032, -0.10799087, …, -0.4634999 ,
        -0.35668983, -0.20713907],
       …,
       [ 0.6329849 ,  0.67640943,  1.56576738, …,  0.74855917,
         0.97541324,  0.49695471],
       [ 0.84118198,  0.77718745,  0.25067161, …,  0.77334105,
         0.73362741,  0.41073914],
       [ 1.54905203,  1.48263359,  1.32665906, …,  2.64099341,
         1.78744868,  1.84048058]])
```

[117]:
```
# Apply PCA on abalone dataset
pca = PCA(n_components=3)
abalone_pca = pca.fit_transform(X_abalone)
abalone_pca_df = pd.DataFrame(data=abalone_pca, columns=['PC1', 'PC2', 'PC3'])
abalone_pca_df
```

[117]:

	PC1	PC2	PC3
0	-1.756019	-0.390532	-0.329928
1	-3.362734	-0.105153	0.252264
2	-0.482338	0.252055	-0.443918
3	-1.509041	0.207608	-0.000519
4	-3.654006	-0.272819	0.275035
…	…	…	…
4172	0.801361	0.385426	-0.064832
4173	0.719312	-0.329146	-0.293062
4174	2.167373	0.724010	0.402521
4175	1.647501	-0.305166	-0.306030
4176	4.894542	-0.705798	0.550942

```
[4177 rows x 3 columns]
```

[118]:
```
# Apply LDA on raw abalone dataset
X_abalone_lda = X_abalone
y_abalone_lda = y_abalone
lda = LinearDiscriminantAnalysis(n_components=3)
X_abalone_lda = lda.fit(X_abalone_lda, y_abalone_lda).transform(X_abalone_lda)
abalone_lda_df = pd.DataFrame(X_abalone_lda, y_abalone_lda)
abalone_lda_df
```

[118]:
```
              0         1         2
Rings
15    -0.791003 -0.235208  0.359351
7     -2.355522  0.336978  0.214024
9      0.766719 -0.246564  1.129422
10    -0.611434  0.098075  0.230542
7     -2.674301  0.527509  0.102575
…           …         …         …
11     0.921330 -0.612381 -0.272399
10     0.425796 -0.894428 -0.034727
9      1.064523 -0.385654 -0.787231
10     0.840757 -1.513723 -0.864217
12     0.843580  0.352389 -2.262564

[4177 rows x 3 columns]
```

[119]:
```
wine_r = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_r["colour"]=1
wine_w = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_w["colour"]=0
wine_raw = pd.concat([wine_w,wine_r], ignore_index=True)
wine_raw.head(100)
```

[119]:
```
    fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0             7.0             0.270         0.36            20.7      0.045
1             6.3             0.300         0.34             1.6      0.049
2             8.1             0.280         0.40             6.9      0.050
3             7.2             0.230         0.32             8.5      0.058
4             7.2             0.230         0.32             8.5      0.058
..            …                 …          …               …          …
95            7.1             0.260         0.29            12.4      0.044
96            6.0             0.340         0.66            15.9      0.046
```

```
97            8.6              0.265         0.36            1.2       0.034
98            9.8              0.360         0.46           10.5       0.038
99            6.0              0.340         0.66           15.9       0.046

    free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                  45.0                 170.0   1.0010  3.00       0.45
1                  14.0                 132.0   0.9940  3.30       0.49
2                  30.0                  97.0   0.9951  3.26       0.44
3                  47.0                 186.0   0.9956  3.19       0.40
4                  47.0                 186.0   0.9956  3.19       0.40
..                  …                     …       …    …          …
95                 62.0                 240.0   0.9969  3.04       0.42
96                 26.0                 164.0   0.9979  3.14       0.50
97                 15.0                  80.0   0.9913  2.95       0.36
98                  4.0                  83.0   0.9956  2.89       0.30
99                 26.0                 164.0   0.9979  3.14       0.50

    alcohol  quality  colour
0       8.8        6       0
1       9.5        6       0
2      10.1        6       0
3       9.9        6       0
4       9.9        6       0
..      …        …      …
95      9.2        6       0
96      8.8        6       0
97     11.4        7       0
98     10.1        4       0
99      8.8        6       0

[100 rows x 13 columns]
```

[120]:

```
# Separate indep and dep features
X_wine1 = wine_raw.iloc[:, :-2]
y_wine = wine_raw.iloc[:, -2]
X_wine = pd.concat([X_wine1, wine_raw.iloc[:, -1]], axis=1)

# Normalize dataset
sc2 = StandardScaler()
X_wine = sc2.fit_transform(X_wine)
X_wine.shape, y_wine.shape

# Apply PCA on wine dataset for dimensionality reduction
pca = PCA(n_components=2)
wine_pca = pca.fit_transform(X_wine)
wine_pca_df = pd.DataFrame(data=wine_pca, columns=['PC1', 'PC2'])
wine_pca_df
```

[120]:
```
           PC1       PC2
0    -2.185179  3.529983
1    -0.247707 -0.553177
2    -0.380592  0.365447
3    -1.735882  0.929351
4    -1.735882  0.929351
…          …         …
6492  2.699833 -0.854172
6493  2.524458 -1.161039
6494  2.775507 -0.761733
6495  2.984356 -0.767021
6496  1.852698 -0.516246

[6497 rows x 2 columns]
```

[121]:
```
# Apply LDA on raw wine dataset
X_wine_lda = X_wine
y_wine_lda = y_wine
lda = LinearDiscriminantAnalysis(n_components=2)
X_wine_lda = lda.fit(X_wine_lda, y_wine_lda).transform(X_wine_lda)
wine_lda_df = pd.DataFrame(X_wine_lda, y_wine_lda)
print(wine_lda_df.shape)
wine_lda_df
```

```
(6497, 2)
```

[121]:
```
                0         1
quality
6        0.752078 -1.466209
6        1.445150  0.392049
6       -0.123015  0.911451
6        0.288961 -0.721769
6        0.288961 -0.721769
…             …         …
5        0.512278 -0.224430
6       -0.514707 -0.597340
6       -0.231160 -0.831907
5        0.630811  0.158871
6       -0.668993 -2.296580

[6497 rows x 2 columns]
```

10 Random Forest on Abalone dataset

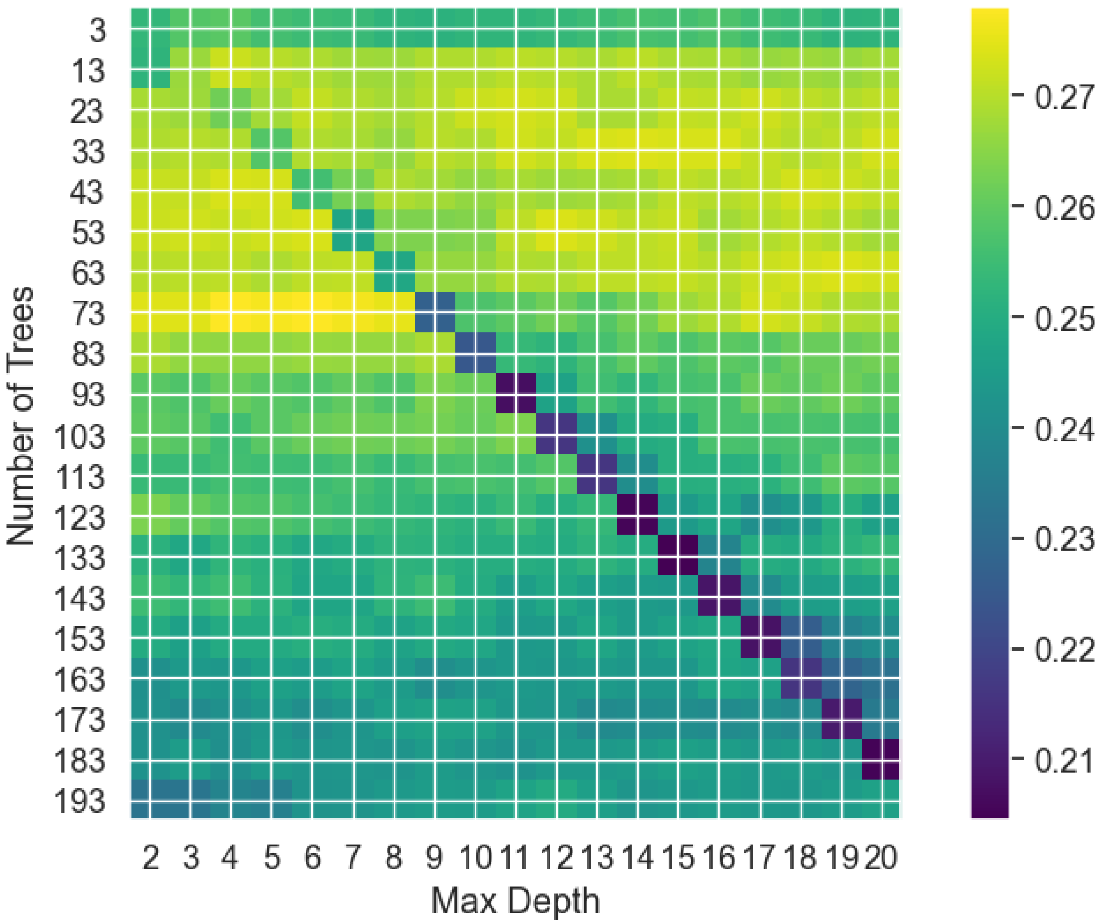
[122]:
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV, cross_val_score
```

[123]:
```
# define the range of parameter values
param_grid = {
    'max_depth': range(2, 21),
    'n_estimators': range(3, 201, 10)
}

# create the Random Forest classifier object
rf = RandomForestClassifier(random_state=42)

# perform the grid search with 5-fold cross validation
grid_search = GridSearchCV(rf, param_grid, cv=5, n_jobs=-1)

# fit the grid search to the data
grid_search.fit(X_abalone, y_abalone)

# print the best parameters and mean accuracy
print("Best Parameters:", grid_search.best_params_)
print("Mean Accuracy:", grid_search.best_score_)
```

```
Best Parameters: {'max_depth': 8, 'n_estimators': 153}
Mean Accuracy: 0.277958055181503
```

To produce a plot showing the mean accuracy vs. the above parameter settings, we can use the following code:

[124]:
```
mean_scores = np.array(grid_search.cv_results_['mean_test_score']).
 ↪reshape(len(param_grid['n_estimators']), len(param_grid['max_depth']))
plt.figure(figsize=(10, 6))
plt.imshow(mean_scores, cmap='viridis', interpolation='nearest')
plt.xticks(np.arange(len(param_grid['max_depth'])), param_grid['max_depth'])
plt.yticks(np.arange(len(param_grid['n_estimators'])),␣
 ↪param_grid['n_estimators'])
plt.xlabel('Max Depth')
plt.ylabel('Number of Trees')
plt.colorbar()
plt.show()
```



From the heat plot, we can see that the best mean accuracy is achieved with a maximum depth of 8 and 153 trees.

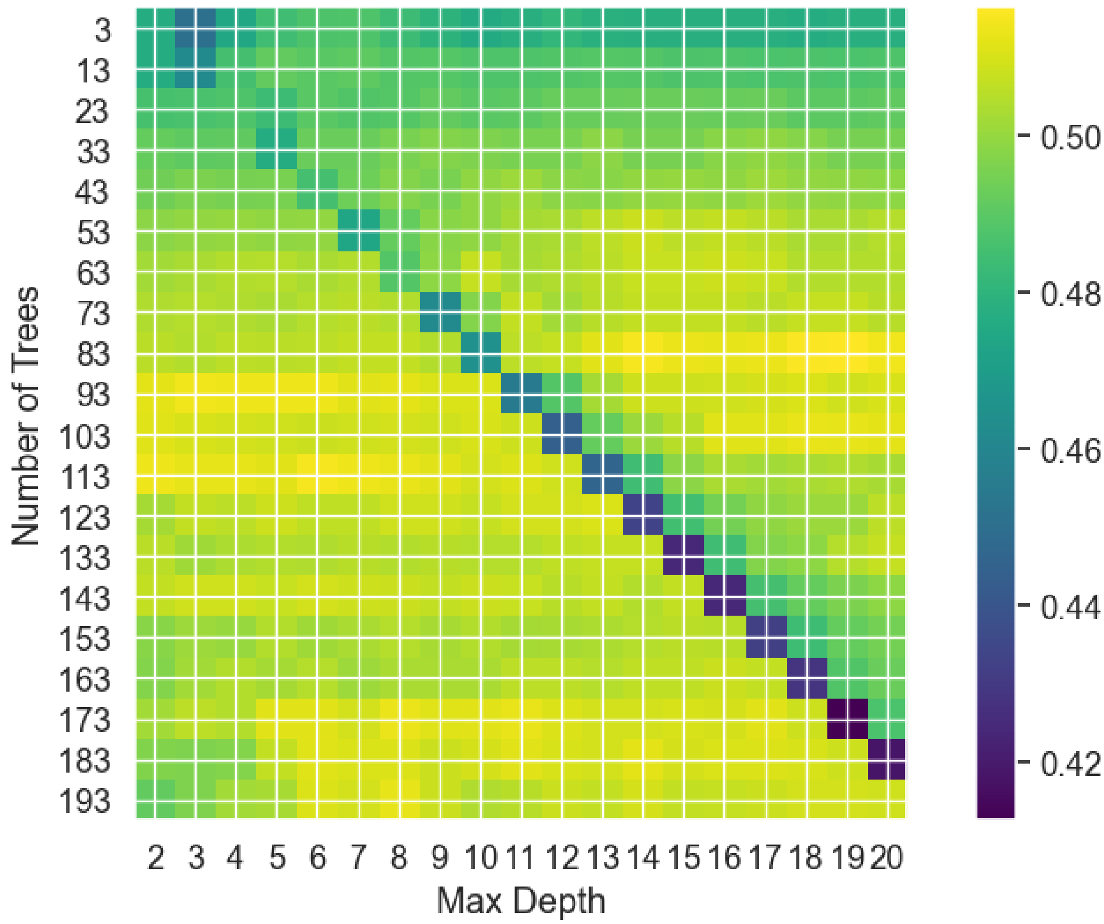
11 Random Forest on Wine - raw dataset:

[125]:
```
# define the range of parameter values
param_grid = {
    'max_depth': range(2, 21),
    'n_estimators': range(3, 201, 10)
}

# create the Random Forest classifier object
rf = RandomForestClassifier(random_state=42)

# perform the grid search with 5-fold cross validation
grid_search = GridSearchCV(rf, param_grid, cv=5, n_jobs=-1)
```

```
# fit the grid search to the data
grid_search.fit(X_wine, y_wine)

# print the best parameters and mean accuracy
print("Best Parameters:", grid_search.best_params_)
print("Mean Accuracy:", grid_search.best_score_)
```

```
Best Parameters: {'max_depth': 10, 'n_estimators': 93}
Mean Accuracy: 0.5163887013679161
```

[126]:
```
mean_scores = np.array(grid_search.cv_results_['mean_test_score']).
 ↪reshape(len(param_grid['n_estimators']), len(param_grid['max_depth']))
plt.figure(figsize=(10, 6))
plt.imshow(mean_scores, cmap='viridis', interpolation='nearest')
plt.xticks(np.arange(len(param_grid['max_depth'])), param_grid['max_depth'])
plt.yticks(np.arange(len(param_grid['n_estimators'])),␣
 ↪param_grid['n_estimators'])
plt.xlabel('Max Depth')
plt.ylabel('Number of Trees')
plt.colorbar()
plt.show()
```



From the heat plot, we can see that the best mean accuracy is achieved with a maximum depth of 10 and 93 trees.

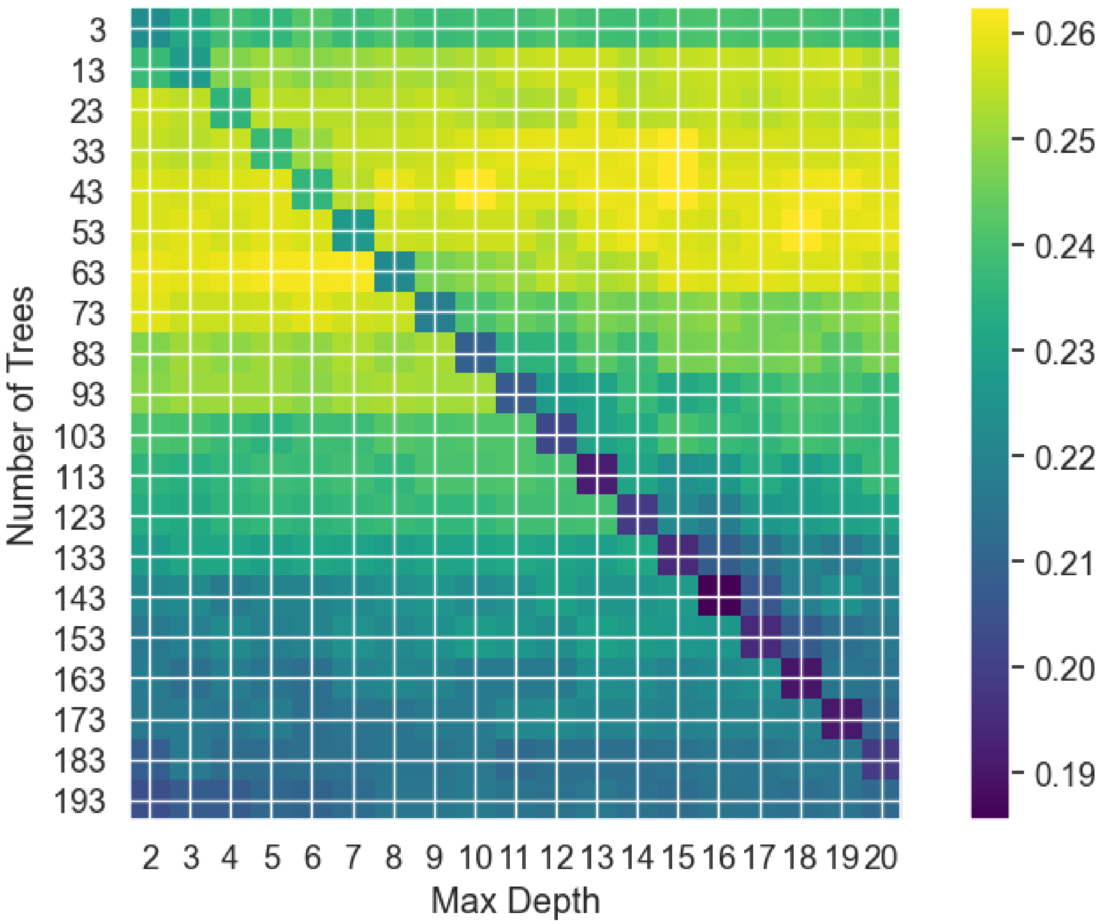
12 Random Forest - Abalone PCA dataset

[127]:
```python
# define the range of parameter values
param_grid = {
    'max_depth': range(2, 21),
    'n_estimators': range(3, 201, 10)
}

# create the Random Forest classifier object
rf = RandomForestClassifier(random_state=42)

# perform the grid search with 5-fold cross validation
grid_search = GridSearchCV(rf, param_grid, cv=5, n_jobs=-1)
```

```
# fit the grid search to the data
grid_search.fit(abalone_pca, y_abalone)

# print the best parameters and mean accuracy
print("Best Parameters:", grid_search.best_params_)
print("Mean Accuracy:", grid_search.best_score_)
```

```
Best Parameters: {'max_depth': 6, 'n_estimators': 43}
Mean Accuracy: 0.26239606910580754
```

[128]:
```
mean_scores = np.array(grid_search.cv_results_['mean_test_score']).
 ↪reshape(len(param_grid['n_estimators']), len(param_grid['max_depth']))
plt.figure(figsize=(10, 6))
plt.imshow(mean_scores, cmap='viridis', interpolation='nearest')
plt.xticks(np.arange(len(param_grid['max_depth'])), param_grid['max_depth'])
plt.yticks(np.arange(len(param_grid['n_estimators'])),␣
 ↪param_grid['n_estimators'])
plt.xlabel('Max Depth')
plt.ylabel('Number of Trees')
plt.colorbar()
plt.show()
```



13 Random Forest - Wine PCA dataset

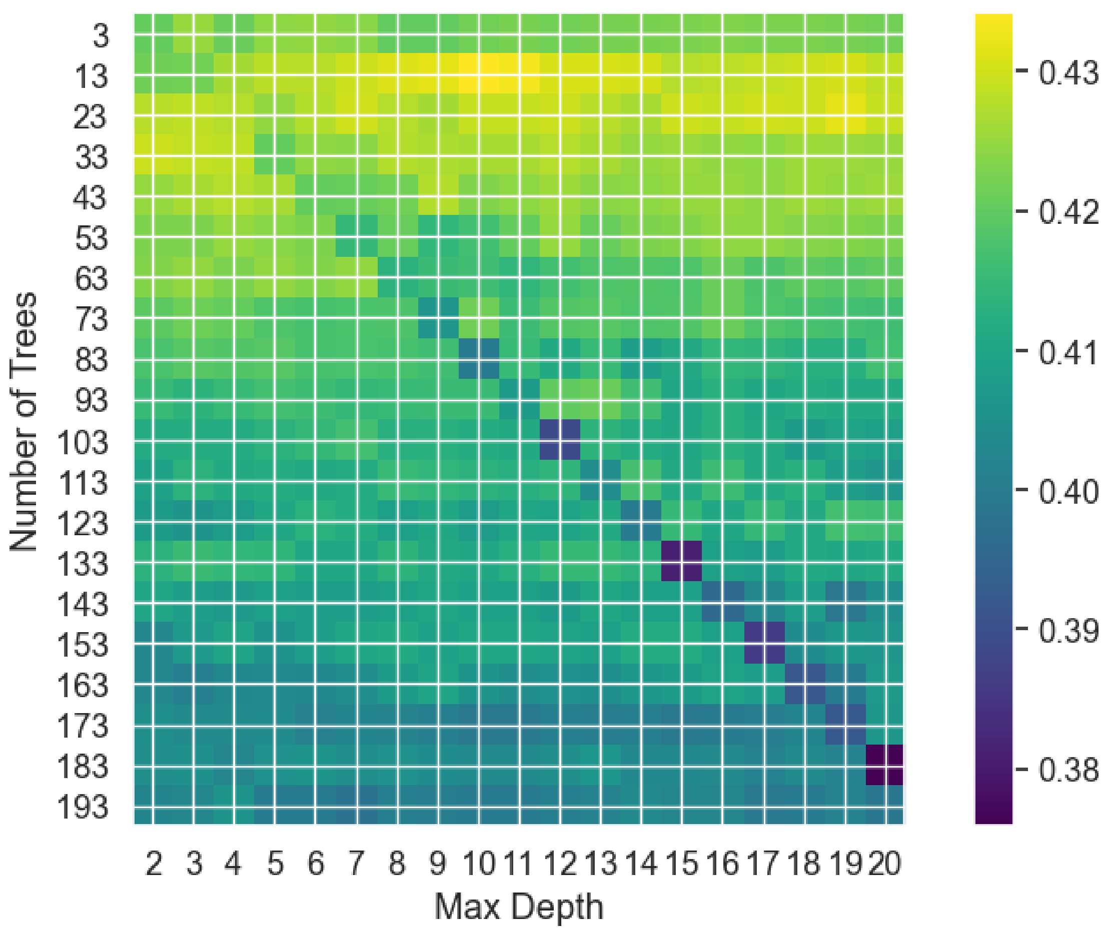
[129]:
```
# define the range of parameter values
param_grid = {
    'max_depth': range(2, 21),
    'n_estimators': range(3, 201, 10)
}

# create the Random Forest classifier object
rf = RandomForestClassifier(random_state=42)

# perform the grid search with 5-fold cross validation
grid_search = GridSearchCV(rf, param_grid, cv=5, n_jobs=-1)

# fit the grid search to the data
grid_search.fit(wine_pca, y_wine)
```

```python
# print the best parameters and mean accuracy
print("Best Parameters:", grid_search.best_params_)
print("Mean Accuracy:", grid_search.best_score_)
```

```
Best Parameters: {'max_depth': 3, 'n_estimators': 73}
Mean Accuracy: 0.4341899686149109
```

[130]:

```python
mean_scores = np.array(grid_search.cv_results_['mean_test_score']).
 ↪reshape(len(param_grid['n_estimators']), len(param_grid['max_depth']))
plt.figure(figsize=(10, 6))
plt.imshow(mean_scores, cmap='viridis', interpolation='nearest')
plt.xticks(np.arange(len(param_grid['max_depth'])), param_grid['max_depth'])
plt.yticks(np.arange(len(param_grid['n_estimators'])),␣
 ↪param_grid['n_estimators'])
plt.xlabel('Max Depth')
plt.ylabel('Number of Trees')
plt.colorbar()
plt.show()
```

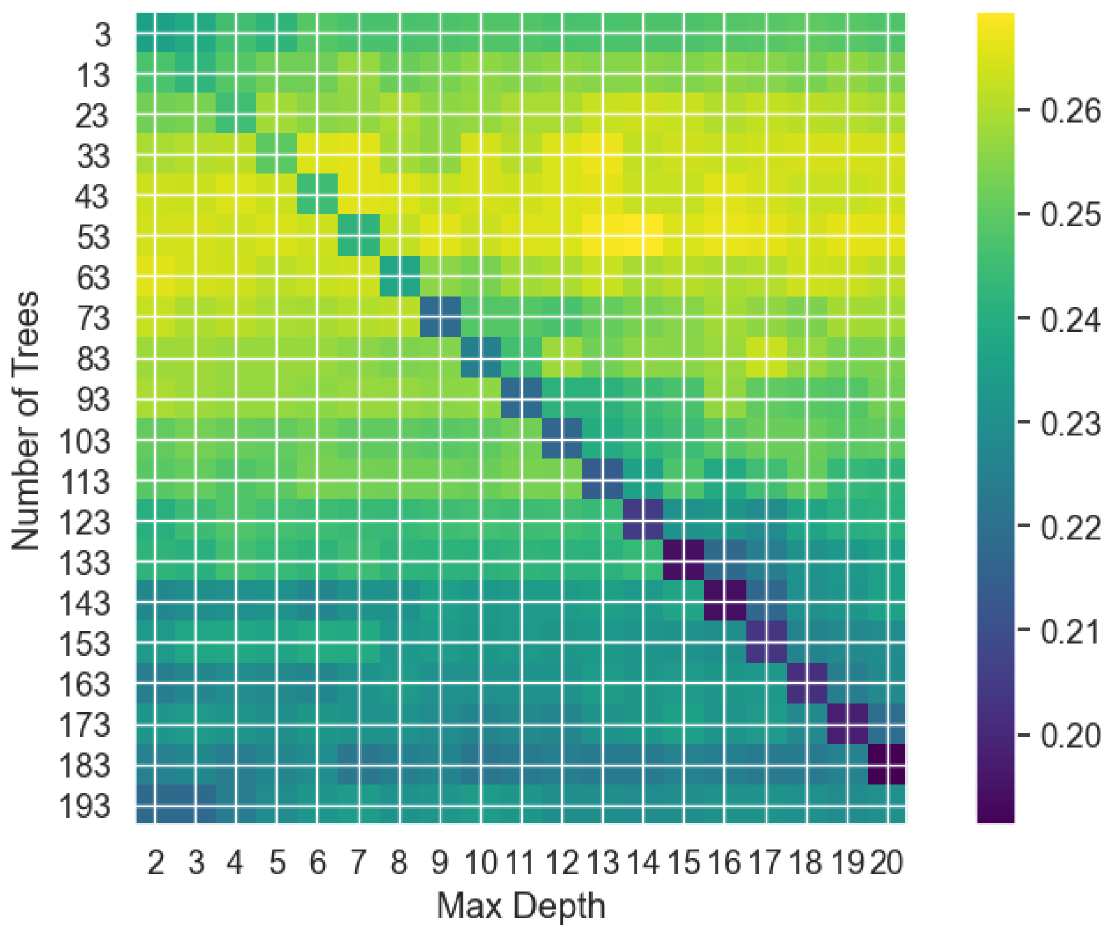


14 Random Forest - Abalone LDA dataset

[131]:
```
# define the range of parameter values
param_grid = {
    'max_depth': range(2, 21),
    'n_estimators': range(3, 201, 10)
}

# create the Random Forest classifier object
rf = RandomForestClassifier(random_state=42)

# perform the grid search with 5-fold cross validation
grid_search = GridSearchCV(rf, param_grid, cv=5, n_jobs=-1)

# fit the grid search to the data
grid_search.fit(X_abalone_lda, y_abalone)

# print the best parameters and mean accuracy
print("Best Parameters:", grid_search.best_params_)
print("Mean Accuracy:", grid_search.best_score_)
```

```
Best Parameters: {'max_depth': 7, 'n_estimators': 73}
Mean Accuracy: 0.26933701974042346
```

[132]:
```
mean_scores = np.array(grid_search.cv_results_['mean_test_score']).
 ↪reshape(len(param_grid['n_estimators']), len(param_grid['max_depth']))
plt.figure(figsize=(10, 6))
plt.imshow(mean_scores, cmap='viridis', interpolation='nearest')
plt.xticks(np.arange(len(param_grid['max_depth'])), param_grid['max_depth'])
plt.yticks(np.arange(len(param_grid['n_estimators'])),␣
 ↪param_grid['n_estimators'])
plt.xlabel('Max Depth')
plt.ylabel('Number of Trees')
plt.colorbar()
plt.show()
```



15 Random Forest - Wine LDA dataset

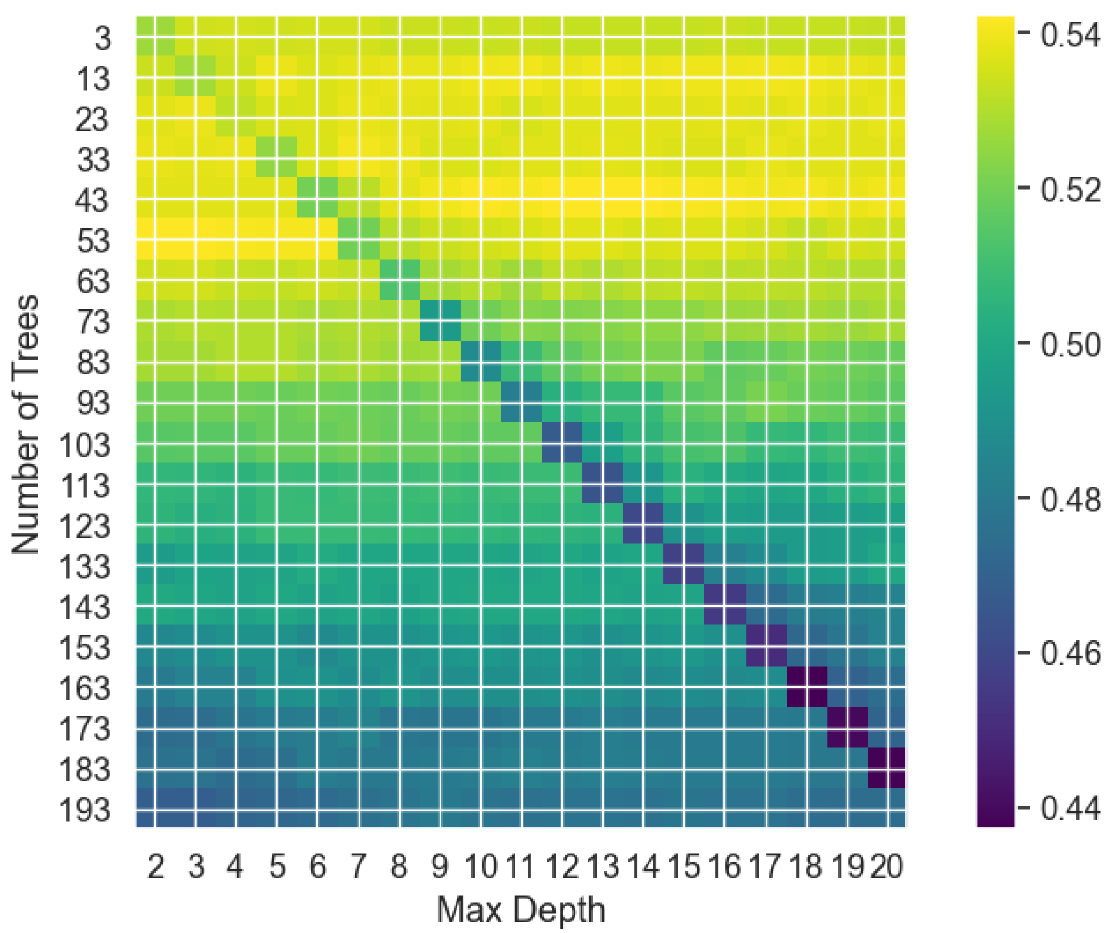
[133]:

```
# define the range of parameter values
param_grid = {
    'max_depth': range(2, 21),
    'n_estimators': range(3, 201, 10)
}

# create the Random Forest classifier object
rf = RandomForestClassifier(random_state=42)

# perform the grid search with 5-fold cross validation
grid_search = GridSearchCV(rf, param_grid, cv=5, n_jobs=-1)

# fit the grid search to the data
grid_search.fit(X_wine_lda, y_wine)
```

```
# print the best parameters and mean accuracy
print("Best Parameters:", grid_search.best_params_)
print("Mean Accuracy:", grid_search.best_score_)
```

```
Best Parameters: {'max_depth': 6, 'n_estimators': 73}
Mean Accuracy: 0.5422585420737845
```

[134]:
```
mean_scores = np.array(grid_search.cv_results_['mean_test_score']).
 ↪reshape(len(param_grid['n_estimators']), len(param_grid['max_depth']))
plt.figure(figsize=(10, 6))
plt.imshow(mean_scores, cmap='viridis', interpolation='nearest')
plt.xticks(np.arange(len(param_grid['max_depth'])), param_grid['max_depth'])
plt.yticks(np.arange(len(param_grid['n_estimators'])),␣
 ↪param_grid['n_estimators'])
plt.xlabel('Max Depth')
plt.ylabel('Number of Trees')
plt.colorbar()
plt.show()
```



15.1 Assignment2 Question 5 implementation starts here

15.1.1 Question 5

5 Gradient Tree Boosting You will now do classification on your datasets using Gradient Tree Boosting, on sklearn one is GradientBoostingClassifier, but you can use other implementations if you prefer. Use your judgement and experience from the other methods to decide how to train this algorithm and choose it's settings. At a minimum, pick some good parameter settings, train the model and show some analysis of it's performance and runtime compared to Random Forests.

[135]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.preprocessing import StandardScaler, MinMaxScaler
from sklearn.decomposition import PCA
import warnings
warnings.filterwarnings('ignore')

# Load raw abalone dataset
abalone_df = pd.read_csv(r"C:
 ↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
 ↪csv", names = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_weight',
                          'Sucked_weight', 'Viscera_weight', 'Shell_weight',␣
 ↪'Rings'], sep = ',')

# Separate indep and dep features
X_abalone = abalone_df.iloc[:, 1:-1] # Removed the sex feature
y_abalone = abalone_df.iloc[:, -1]

# Normalize dataset
sc1 = StandardScaler()
X_abalone = sc1.fit_transform(X_abalone)
X_abalone
```

[135]:
```
array([[-0.57455813, -0.43214879, -1.06442415, …, -0.60768536,
         -0.72621157, -0.63821689],
        [-1.44898585, -1.439929  , -1.18397831, …, -1.17090984,
         -1.20522124, -1.21298732],
        [ 0.05003309,  0.12213032, -0.10799087, …, -0.4634999 ,
         -0.35668983, -0.20713907],
        …,
        [ 0.6329849 ,  0.67640943,  1.56576738, …,  0.74855917,
          0.97541324,  0.49695471],
        [ 0.84118198,  0.77718745,  0.25067161, …,  0.77334105,
          0.73362741,  0.41073914],
        [ 1.54905203,  1.48263359,  1.32665906, …,  2.64099341,
```

```
         1.78744868,  1.84048058]])
```

[136]:
```
# Apply PCA on abalone dataset
pca = PCA(n_components=3)
abalone_pca = pca.fit_transform(X_abalone)
abalone_pca_df = pd.DataFrame(data=abalone_pca, columns=['PC1', 'PC2', 'PC3'])
abalone_pca_df
```

[136]:
```
           PC1       PC2       PC3
0    -1.756019 -0.390532 -0.329928
1    -3.362734 -0.105153  0.252264
2    -0.482338  0.252055 -0.443918
3    -1.509041  0.207608 -0.000519
4    -3.654006 -0.272819  0.275035
…          …         …         …
4172  0.801361  0.385426 -0.064832
4173  0.719312 -0.329146 -0.293062
4174  2.167373  0.724010  0.402521
4175  1.647501 -0.305166 -0.306030
4176  4.894542 -0.705798  0.550942

[4177 rows x 3 columns]
```

[137]:
```
# Apply LDA on raw abalone dataset
X_abalone_lda = X_abalone
y_abalone_lda = y_abalone
lda = LinearDiscriminantAnalysis(n_components=3)
X_abalone_lda = lda.fit(X_abalone_lda, y_abalone_lda).transform(X_abalone_lda)
abalone_lda_df = pd.DataFrame(X_abalone_lda, y_abalone_lda)
abalone_lda_df
```

[137]:
```
              0         1         2
Rings
15    -0.791003 -0.235208  0.359351
7     -2.355522  0.336978  0.214024
9      0.766719 -0.246564  1.129422
10    -0.611434  0.098075  0.230542
7     -2.674301  0.527509  0.102575
…           …         …         …
11     0.921330 -0.612381 -0.272399
10     0.425796 -0.894428 -0.034727
9      1.064523 -0.385654 -0.787231
10     0.840757 -1.513723 -0.864217
12     0.843580  0.352389 -2.262564

[4177 rows x 3 columns]
```

[138]:
```python
wine_r = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_r["colour"]=1
wine_w = pd.read_csv(r"C:
↪\Users\15485\Desktop\UWaterloo_Academics\ECE657A\Assignments\Assignment2\Assignment2_Submis
↪csv", sep=';')
wine_w["colour"]=0
wine_raw = pd.concat([wine_w,wine_r], ignore_index=True)
wine_raw.head(100)
```

[138]:
```
    fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0             7.0             0.270         0.36            20.7      0.045
1             6.3             0.300         0.34             1.6      0.049
2             8.1             0.280         0.40             6.9      0.050
3             7.2             0.230         0.32             8.5      0.058
4             7.2             0.230         0.32             8.5      0.058
..            …                 …           …               …         …
95            7.1             0.260         0.29            12.4      0.044
96            6.0             0.340         0.66            15.9      0.046
97            8.6             0.265         0.36             1.2      0.034
98            9.8             0.360         0.46            10.5      0.038
99            6.0             0.340         0.66            15.9      0.046

    free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                  45.0                 170.0   1.0010  3.00       0.45
1                  14.0                 132.0   0.9940  3.30       0.49
2                  30.0                  97.0   0.9951  3.26       0.44
3                  47.0                 186.0   0.9956  3.19       0.40
4                  47.0                 186.0   0.9956  3.19       0.40
..                  …                     …       …     …         …
95                 62.0                 240.0   0.9969  3.04       0.42
96                 26.0                 164.0   0.9979  3.14       0.50
97                 15.0                  80.0   0.9913  2.95       0.36
98                  4.0                  83.0   0.9956  2.89       0.30
99                 26.0                 164.0   0.9979  3.14       0.50

    alcohol  quality  colour
0       8.8        6       0
1       9.5        6       0
2      10.1        6       0
3       9.9        6       0
4       9.9        6       0
..      …        …       …
95      9.2        6       0
96      8.8        6       0
97     11.4        7       0
```

```
98     10.1        4       0
99      8.8        6       0

[100 rows x 13 columns]
```

[139]:
```python
# Separate indep and dep features
X_wine1 = wine_raw.iloc[:, :-2]
y_wine = wine_raw.iloc[:, -2]
X_wine = pd.concat([X_wine1, wine_raw.iloc[:, -1]], axis=1)

# Normalize dataset
sc2 = StandardScaler()
X_wine = sc2.fit_transform(X_wine)
X_wine.shape, y_wine.shape

# Apply PCA on wine dataset for dimensionality reduction
pca = PCA(n_components=2)
wine_pca = pca.fit_transform(X_wine)
wine_pca_df = pd.DataFrame(data=wine_pca, columns=['PC1', 'PC2'])
wine_pca_df
```

[139]:
```
           PC1       PC2
0    -2.185179  3.529983
1    -0.247707 -0.553177
2    -0.380592  0.365447
3    -1.735882  0.929351
4    -1.735882  0.929351
…          …         …
6492  2.699833 -0.854172
6493  2.524458 -1.161039
6494  2.775507 -0.761733
6495  2.984356 -0.767021
6496  1.852698 -0.516246

[6497 rows x 2 columns]
```

[140]:
```python
# Apply LDA on raw wine dataset
X_wine_lda = X_wine
y_wine_lda = y_wine
lda = LinearDiscriminantAnalysis(n_components=2)
X_wine_lda = lda.fit(X_wine_lda, y_wine_lda).transform(X_wine_lda)
wine_lda_df = pd.DataFrame(X_wine_lda, y_wine_lda)
print(wine_lda_df.shape)
wine_lda_df
```

```
(6497, 2)
```

[140]:
```
                 0         1
quality
6         0.752078 -1.466209
6         1.445150  0.392049
6        -0.123015  0.911451
6         0.288961 -0.721769
6         0.288961 -0.721769
…              …         …
5         0.512278 -0.224430
6        -0.514707 -0.597340
6        -0.231160 -0.831907
5         0.630811  0.158871
6        -0.668993 -2.296580

[6497 rows x 2 columns]
```

16 Gradient Boosting on Abalone dataset

[141]:
```python
from sklearn.model_selection import GridSearchCV, train_test_split
from sklearn.metrics import accuracy_score
from sklearn.ensemble import GradientBoostingClassifier
```

[142]:
```python
X_train, X_test, y_train, y_test = train_test_split(X_abalone, y_abalone,␣
 ↪test_size=0.2, random_state=42)

model = GradientBoostingClassifier(n_estimators=153, learning_rate=0.1,␣
 ↪max_depth=8)

model.fit(X_train, y_train)

y_pred = model.predict(X_test)
acc_score = accuracy_score(y_test, y_pred)
print(f"Accuracy score: {acc_score:.4f}")
```

```
Accuracy score: 0.2380
```

[143]:
```python
from sklearn.metrics import classification_report, confusion_matrix
print('Classification Report: \n', classification_report(y_test, y_pred))
print('Confusion Matrix: \n', confusion_matrix(y_test, y_pred))
gdb_train_acc = model.score(X_train, y_train)
print('Training Score: ', gdb_train_acc)
gdb_test_acc = model.score(X_test, y_test)
print('Testing Score: ', gdb_test_acc)
```

```
Classification Report:
               precision    recall  f1-score   support
```

```
           1       0.00      0.00      0.00         0
           3       0.00      0.00      0.00         3
           4       0.25      0.23      0.24        13
           5       0.41      0.34      0.37        32
           6       0.30      0.27      0.29        48
           7       0.26      0.26      0.26        84
           8       0.27      0.33      0.30        99
           9       0.25      0.32      0.28       142
          10       0.30      0.30      0.30       139
          11       0.19      0.23      0.21        93
          12       0.12      0.10      0.11        51
          13       0.09      0.10      0.09        31
          14       0.20      0.04      0.06        26
          15       0.00      0.00      0.00        21
          16       0.00      0.00      0.00        13
          17       0.00      0.00      0.00         8
          18       0.00      0.00      0.00        12
          19       0.00      0.00      0.00         7
          20       0.00      0.00      0.00         4
          21       0.00      0.00      0.00         3
          22       0.00      0.00      0.00         3
          23       0.00      0.00      0.00         4
          24       0.00      0.00      0.00         0

    accuracy                           0.24       836
   macro avg       0.11      0.11      0.11       836
weighted avg       0.23      0.24      0.23       836

Confusion Matrix:
 [[ 0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 1  0  2  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  1  3  7  1  1  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  2  6 11  7  6  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  0  1  5 13 17  9  3  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  3 15 22 27 11  4  0  0  0  0  0  0  0  1  0  1  0  0  0  0]
 [ 0  0  0  1  3 15 33 28 11  4  2  0  0  0  0  0  0  0  0  0  2  0  0]
 [ 0  0  0  0  1 10 25 45 28 24  3  3  1  0  0  0  2  0  0  0  0  0  0]
 [ 0  0  0  0  2  6 13 42 42 19  8  2  1  0  2  2  0  0  0  0  0  0  0]
 [ 0  0  0  0  1  5  6 20 20 21  9  6  0  1  1  0  1  1  0  1  0  0  0]
 [ 0  0  0  0  0  1  3  9 13 11  5  3  0  2  2  0  1  0  0  0  0  0  1]
 [ 0  0  0  0  0  2  3  4  7  7  3  3  0  0  1  0  1  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  3  5  5  5  1  3  1  1  2  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  4  5  3  1  7  1  0  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  1  1  3  4  1  1  0  0  0  1  0  0  1  0  0  0]
 [ 0  0  0  0  0  0  0  3  2  2  0  0  0  0  0  0  1  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  0  2  6  2  1  0  1  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  0  1  2  0  2  0  1  0  0  0  0  1  0  0  0  0]
 [ 0  0  0  0  0  0  0  1  0  1  1  1  0  0  0  0  0  0  0  0  0  0  0]
```

```
 [ 0  0  0  0  0  0  0  0  1  0  0  1  0  1  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  1  0  0  1  0  0  0  1  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  0  0  1  1  1  0  0  1  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]]
Training Score:  1.0
Testing Score:  0.23803827751196172
```

The accuracy on the abalone raw dataset using Gradient Boosting classifier is less than Random Forests when using similar parameters, possibly due to the effect of outliers. It takes longer to train with Gradient Boosting than Random Forests.

[144]:
```
model = GradientBoostingClassifier(n_estimators=100, learning_rate=0.1,
 ↪max_depth=3)

model.fit(X_train, y_train)

y_pred = model.predict(X_test)
acc_score = accuracy_score(y_test, y_pred)
print(f"Accuracy score: {acc_score:.4f}")
```

```
Accuracy score: 0.2584
```

[145]:
```
from sklearn.metrics import classification_report, confusion_matrix
print('Classification Report: \n', classification_report(y_test, y_pred))
print('Confusion Matrix: \n', confusion_matrix(y_test, y_pred))
gdb_train_acc = model.score(X_train, y_train)
print('Training Score: ', gdb_train_acc)
gdb_test_acc = model.score(X_test, y_test)
print('Testing Score: ', gdb_test_acc)
```

```
Classification Report:
               precision    recall  f1-score   support

           3       0.40      0.67      0.50         3
           4       0.32      0.46      0.37        13
           5       0.45      0.41      0.43        32
           6       0.27      0.23      0.25        48
           7       0.34      0.36      0.35        84
           8       0.28      0.36      0.31        99
           9       0.31      0.37      0.33       142
          10       0.26      0.28      0.27       139
          11       0.25      0.20      0.22        93
          12       0.03      0.02      0.02        51
          13       0.06      0.06      0.06        31
          14       0.25      0.15      0.19        26
          15       0.10      0.05      0.06        21
          16       0.00      0.00      0.00        13
          17       0.00      0.00      0.00         8
          18       0.00      0.00      0.00        12
```

```
          19       0.00      0.00      0.00         7
          20       0.00      0.00      0.00         4
          21       0.00      0.00      0.00         3
          22       0.00      0.00      0.00         3
          23       0.00      0.00      0.00         4
          24       0.00      0.00      0.00         0

    accuracy                           0.26       836
   macro avg       0.15      0.16      0.15       836
weighted avg       0.24      0.26      0.25       836

Confusion Matrix:
 [[ 2  1  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 2  6  4  1  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 1  8 13  7  3  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  4  6 11 17  7  3  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  0  5 14 30 21 10  1  0  0  1  0  0  1  0  0  0  1  0  0  0  0]
 [ 0  0  1  2 16 36 25 12  1  1  1  0  1  0  0  0  0  0  0  2  1  0]
 [ 0  0  0  2  8 29 52 34  9  5  1  1  0  0  0  1  0  0  0  0  0  0]
 [ 0  0  0  2  6 21 34 39 17  7  4  1  2  2  1  0  2  1  0  0  0  0]
 [ 0  0  0  0  5  7 21 27 19  4  5  2  1  0  0  2  0  0  0  0  0  0]
 [ 0  0  0  1  1  5  8 13 12  1  5  1  1  0  1  0  1  0  0  0  0  1]
 [ 0  0  0  1  1  2  5  5  7  5  2  0  1  1  0  1  0  0  0  0  0  0]
 [ 0  0  0  0  0  2  6  6  3  1  2  4  0  1  0  0  0  1  0  0  0  0]
 [ 0  0  0  0  0  0  2  6  1  1  5  2  1  1  0  0  0  1  0  0  1  0]
 [ 0  0  0  0  0  0  0  2  1  2  2  2  0  0  1  0  1  2  0  0  0  0]
 [ 0  0  0  0  0  0  2  2  2  0  1  1  0  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  1  1  3  2  3  0  1  0  0  0  1  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  1  1  1  2  0  0  0  1  0  0  1  0  0  0  0]
 [ 0  0  0  0  0  0  0  1  0  0  2  0  0  0  1  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  0  0  0  0  0  1  0  2  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  1  1  0  0  0  0  1  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  0  0  1  0  2  0  1  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]]
Training Score:  0.692008380724334
Testing Score:  0.2583732057416268
```

Upon using more optimum parameters for Gradient Boosting, the accuracy increases. This low accuracy may be due to the fact that the features are highly correlated.

17 Gradient Boosting on Wine dataset

[146]:
```
X_train, X_test, y_train, y_test = train_test_split(X_wine, y_wine, test_size=0.
 ↪2, random_state=42)

model = GradientBoostingClassifier(n_estimators=100, learning_rate=0.5,␣
 ↪max_depth=3)
```

```
model.fit(X_train, y_train)

y_pred = model.predict(X_test)
acc_score = accuracy_score(y_test, y_pred)
print(f"Accuracy score: {acc_score:.4f}")
```

```
Accuracy score: 0.6008
```

The accuracy of Gradient boosting on the wine - raw dataset is more than that of Random forests and this may be due to the fact that the dataset has outliers and is not balanced. When the dataset contains imbalanced classes, Random Forests may produce biased predictions towards the majority class, as each tree is built independently and can be influenced by the class imbalance, while Gradient Boosting Classifier can adjust the weights of the samples to balance the classes

18 Gradient Boosting on Abalone - PCA dataset

[147]:
```
X_train, X_test, y_train, y_test = train_test_split(abalone_pca, y_abalone,␣
↪test_size=0.2, random_state=42)

model = GradientBoostingClassifier(n_estimators=100, learning_rate=0.5,␣
↪max_depth=3)

model.fit(X_train, y_train)

y_pred = model.predict(X_test)
acc_score = accuracy_score(y_test, y_pred)
print(f"Accuracy score: {acc_score:.4f}")
```

```
Accuracy score: 0.1148
```

[148]:
```
from sklearn.metrics import classification_report, confusion_matrix
print('Classification Report: \n', classification_report(y_test, y_pred))
print('Confusion Matrix: \n', confusion_matrix(y_test, y_pred))
gdb_train_acc = model.score(X_train, y_train)
print('Training Score: ', gdb_train_acc)
gdb_test_acc = model.score(X_test, y_test)
print('Testing Score: ', gdb_test_acc)
```

```
Classification Report:
               precision    recall  f1-score   support

           3       0.00      0.00      0.00         3
           4       0.29      0.15      0.20        13
           5       0.04      0.03      0.03        32
           6       0.05      0.04      0.05        48
           7       0.00      0.00      0.00        84
           8       0.10      0.01      0.02        99
```

```
           9       0.10      0.06      0.07       142
          10       0.18      0.54      0.27       139
          11       0.00      0.00      0.00        93
          12       0.25      0.02      0.04        51
          13       0.04      0.06      0.05        31
          14       0.00      0.00      0.00        26
          15       0.00      0.00      0.00        21
          16       0.03      0.15      0.05        13
          17       0.00      0.00      0.00         8
          18       0.03      0.17      0.05        12
          19       0.00      0.00      0.00         7
          20       0.00      0.00      0.00         4
          21       0.00      0.00      0.00         3
          22       0.00      0.00      0.00         3
          23       0.00      0.00      0.00         4

    accuracy                           0.11       836
   macro avg       0.05      0.06      0.04       836
weighted avg       0.08      0.11      0.07       836

Confusion Matrix:
 [[ 0  3  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  2  0  0  1  0  0 10  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  2  1  0  0  0  1 28  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  0  6  2  0  1 16 20  0  0  2  0  0  0  0  1  0  0  0  0  0]
 [ 0  0 11  9  0  2 26 28  0  1  2  0  0  0  0  5  0  0  0  0  0]
 [ 0  0  0  8  3  1 15 42  0  0 18  0  0  1  0 11  0  0  0  0  0]
 [ 0  0  6  6 14  3  8 79  0  1  8  0  0  2  0 15  0  0  0  0  0]
 [ 0  0  2  3 15  1  7 75  0  1 10  0  0 13  0 11  0  0  1  0  0]
 [ 0  0  1  3 18  1  4 39  0  0  0  0  0 19  0  6  0  0  2  0  0]
 [ 0  0  0  3  4  1  2 26  0  1  1  0  0  9  0  4  0  0  0  0  0]
 [ 0  0  0  0  2  0  3 16  0  0  2  0  0  6  0  2  0  0  0  0  0]
 [ 0  0  0  1  1  0  0 12  0  0  3  0  0  4  0  5  0  0  0  0  0]
 [ 0  0  0  1  0  0  0 16  0  0  0  0  0  2  0  2  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  9  0  0  1  0  0  2  0  0  0  0  1  0  0]
 [ 0  0  0  0  0  0  0  4  0  0  1  0  0  3  0  0  0  0  0  0  0]
 [ 0  0  0  0  3  0  0  7  0  0  0  0  0  0  0  2  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  4  0  0  0  0  0  3  0  0  0  0  0  0  0]
 [ 0  0  0  0  1  0  0  2  0  0  0  0  0  1  0  0  0  0  0  0  0]
 [ 0  0  0  1  0  0  0  0  0  0  0  0  0  1  0  1  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  2  0  0  0  0  0  0  0  0  0  0  1  0  0]
 [ 0  0  0  0  1  0  0  2  0  0  1  0  0  0  0  0  0  0  0  0  0]]
Training Score:  0.10356180784196349
Testing Score:  0.11483253588516747
```

The accuracy on PCA dataset upon using Gradient Boosting is lesser than Random forests. Overall it can be seen that PCA hurts the performance of a tree boosting classifier as data has been lost while reducing the number of dimensions.

19 Gradient Boosting on Wine - PCA dataset

[149]:
```
X_train, X_test, y_train, y_test = train_test_split(wine_pca, y_wine,␣
↪test_size=0.2, random_state=42)

model = GradientBoostingClassifier(n_estimators=100, learning_rate=0.5,␣
↪max_depth=3)

model.fit(X_train, y_train)

y_pred = model.predict(X_test)
acc_score = accuracy_score(y_test, y_pred)
print(f"Accuracy score: {acc_score:.4f}")
```

```
Accuracy score: 0.5392
```

[150]:
```
from sklearn.metrics import classification_report, confusion_matrix
print('Classification Report: \n', classification_report(y_test, y_pred))
print('Confusion Matrix: \n', confusion_matrix(y_test, y_pred))
gdb_train_acc = model.score(X_train, y_train)
print('Training Score: ', gdb_train_acc)
gdb_test_acc = model.score(X_test, y_test)
print('Testing Score: ', gdb_test_acc)
```

```
Classification Report:
               precision    recall  f1-score   support

           3       0.00      0.00      0.00         2
           4       0.32      0.22      0.26        46
           5       0.57      0.56      0.56       420
           6       0.55      0.63      0.59       579
           7       0.50      0.38      0.43       221
           8       0.35      0.25      0.29        32

    accuracy                           0.54      1300
   macro avg       0.38      0.34      0.36      1300
weighted avg       0.54      0.54      0.53      1300

Confusion Matrix:
 [[  0   0   2   0   0   0]
 [  1  10  10  21   2   2]
 [  2  10 236 159  10   3]
 [  3   7 141 362  61   5]
 [  1   3  24 103  85   5]
 [  0   1   3   8  12   8]]
Training Score:  0.8289397729459304
Testing Score:  0.5392307692307692
```

The training score is 82% whereas the same classifer has a training score of approximately 70% on raw data without PCA reduction. So in this case, PCA helps in improving the accuracy but there is a considerable amount of overfitting.

20 Gradient Boosting on Abalone - LDA dataset

[151]:
```
X_train, X_test, y_train, y_test = train_test_split(X_abalone_lda, y_abalone,␣
 ↪test_size=0.2, random_state=42)

model = GradientBoostingClassifier(n_estimators=100, learning_rate=0.5,␣
 ↪max_depth=3)

model.fit(X_train, y_train)

y_pred = model.predict(X_test)
acc_score = accuracy_score(y_test, y_pred)
print(f"Accuracy score: {acc_score:.4f}")
```

```
Accuracy score: 0.2165
```

[152]:
```
from sklearn.metrics import classification_report, confusion_matrix
print('Classification Report: \n', classification_report(y_test, y_pred))
print('Confusion Matrix: \n', confusion_matrix(y_test, y_pred))
gdb_train_acc = model.score(X_train, y_train)
print('Training Score: ', gdb_train_acc)
gdb_test_acc = model.score(X_test, y_test)
print('Testing Score: ', gdb_test_acc)
```

```
Classification Report:
               precision    recall  f1-score   support

           3       0.00      0.00      0.00         3
           4       0.00      0.00      0.00        13
           5       0.43      0.59      0.50        32
           6       0.34      0.31      0.33        48
           7       0.30      0.26      0.28        84
           8       0.22      0.32      0.26        99
           9       0.27      0.25      0.26       142
          10       0.18      0.19      0.18       139
          11       0.15      0.14      0.14        93
          12       0.17      0.14      0.15        51
          13       0.11      0.19      0.14        31
          14       0.00      0.00      0.00        26
          15       0.00      0.00      0.00        21
          16       0.36      0.31      0.33        13
          17       0.08      0.12      0.10         8
          18       0.00      0.00      0.00        12
          19       0.00      0.00      0.00         7
          20       0.00      0.00      0.00         4
```

```
          21       0.00      0.00      0.00         3
          22       0.00      0.00      0.00         3
          23       0.00      0.00      0.00         4

    accuracy                           0.22       836
   macro avg       0.12      0.14      0.13       836
weighted avg       0.21      0.22      0.21       836

Confusion Matrix:
 [[ 0  0  3  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  0 13  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  2 19  6  4  0  1  0  0  0  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  2  4 15 12  9  2  1  0  1  0  0  1  0  0  0  0  0  0  0  1]
 [ 0  0  4 13 22 33  6  0  2  2  0  1  0  0  0  0  1  0  0  0  0]
 [ 0  0  1  4 15 32 25 13  2  2  1  2  2  0  0  0  0  0  0  0  0]
 [ 0  0  0  2 15 30 36 28 21  3  4  1  1  0  0  0  0  1  0  0  0]
 [ 0  0  0  1  3 25 32 26 23  3 14  5  1  1  4  0  0  0  0  0  1]
 [ 0  0  0  0  1  5 26 30 13  4  6  1  3  2  1  0  0  1  0  0  0]
 [ 0  0  0  1  0  6  0 10 12  7  9  2  1  0  3  0  0  0  0  0  0]
 [ 0  0  0  1  1  3  1 13  2  0  6  2  1  1  0  0  0  0  0  0  0]
 [ 0  0  0  1  0  0  0  8  2  6  5  0  1  2  0  0  0  0  0  0  1]
 [ 0  0  0  0  0  2  0  5  3  2  6  0  0  1  1  0  1  0  0  0  0]
 [ 0  0  0  0  0  0  0  3  1  1  1  3  0  4  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  1  1  1  1  1  0  0  0  1  1  0  1  0  0  0]
 [ 0  0  0  0  0  0  1  1  4  2  1  1  0  0  1  0  0  0  0  0  1]
 [ 0  0  0  0  0  0  0  2  1  2  1  1  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  1  0  1  1  0  0  0  1  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  0  1  2  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  1  0  2  0  0  0  0  0  0  0  0  0  0  0]
 [ 0  0  0  0  0  0  0  1  0  0  0  1  1  0  0  0  0  1  0  0  0]]
Training Score:  0.6049087099670757
Testing Score:  0.21650717703349281
```

Training score is high as when the dataset has a small number of samples, Gradient boosting can overfit and since most features in the abalone dataset is highly correlated, dimensionality reduction has a positive effect on efficient computation. But testing score is very low as there is considerable loss of data and Gradient boosting works better with more features. The mean accuracy using Random Forests is 0.27 whereas for Gradient boosting, it is lower. This is possible if there are too many outliers/high correlation in the dataset, which is true for this case.

21 Gradient Boosting on Wine - LDA dataset

[153]:
```
X_train, X_test, y_train, y_test = train_test_split(X_wine_lda, y_wine,␣
 ↪test_size=0.2, random_state=42)

model = GradientBoostingClassifier(n_estimators=100, learning_rate=0.1,␣
 ↪max_depth=3)
```

```
model.fit(X_train, y_train)

y_pred = model.predict(X_test)
acc_score = accuracy_score(y_test, y_pred)
print(f"Accuracy score: {acc_score:.4f}")
```

```
Accuracy score: 0.5531
```

[154]:
```
from sklearn.metrics import classification_report, confusion_matrix
print('Classification Report: \n', classification_report(y_test, y_pred))
print('Confusion Matrix: \n', confusion_matrix(y_test, y_pred))
gdb_train_acc = model.score(X_train, y_train)
print('Training Score: ', gdb_train_acc)
gdb_test_acc = model.score(X_test, y_test)
print('Testing Score: ', gdb_test_acc)
```

```
Classification Report:
               precision    recall  f1-score   support

           3       0.00      0.00      0.00         2
           4       0.33      0.09      0.14        46
           5       0.60      0.66      0.63       420
           6       0.54      0.64      0.59       579
           7       0.49      0.29      0.37       221
           8       0.20      0.03      0.05        32

    accuracy                           0.55      1300
   macro avg       0.36      0.29      0.30      1300
weighted avg       0.54      0.55      0.53      1300

Confusion Matrix:
 [[  0   0   2   0   0   0]
 [  0   4  26  15   1   0]
 [  2   4 279 131   4   0]
 [  1   3 152 370  49   4]
 [  2   1   5 148  65   0]
 [  0   0   0  18  13   1]]
Training Score:  0.6492207042524534
Testing Score:  0.553076923076923
```

There is less overfitting in the training data after using LDA and Gradient boosting techniques. The test accuracy is also close but not very high. Compared to random forests, the accuracy is similar on Wine - LDA dataset.

[ ]:
```

```