Out[158]: Click here to toggle on/off the raw code.

Out[5]:		Sex	Length	Diameter	Height	Whole_we	ight Suck	ced_weight	Viscera_v	veight	Shell_w	eight
	0	М	0.455	0.365	0.095	0.5	5140	0.2245	(0.1010	().150
	1	М	0.350	0.265	0.090	0.2	255	0.0995	(0.0485	(0.070
	2	F	0.530	0.420	0.135	0.6	3770	0.2565	(0.1415	(0.210
	3	М	0.440	0.365	0.125	0.5	160	0.2155	(0.1140	().155
	4	1	0.330	0.255	0.080		2050	0.0895		0.0395		0.055
			0.550	0.233	0.000	0.2	.000	0.0093	,	J.0333		7.033
	4											•
	cou mea stc mir 25% 50% 75% max	an d n % % % c unt an	4177.00 0.52 0.12 0.07 0.45 0.61 0.81 Viscera 4177	23992 20093 75000 50000 15000 15000 a_weight 7.000000	4177 0	000 4177 881 6 240 6 000 6 000 6 000 6 000 1 _weight .000000	4177.000 9.933	0.4 0.0 0.4 0.7 1.1 2.8 ings 0000	•	4177 0 0 0 0 0	_weight .000000 .359367 .221963 .001000 .186000 .336000 .502000	
	sto			0.109614		.139203	3.224					
	mir			0.000500		.001500	1.000					
	25% 50%			0.093500 0.171000		.130000 .234000	8.000 9.000					
	75%			3.171000 3.253000		.329000	11.000					
	max			7.760000		.005000	29.000					
				mean	median	variance	skew	ı kurtosi:	S			

	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

```
Sex
Length
Diameter
                   0
Height
Whole_weight
Sucked_weight
                   0
                   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.

there are no missing data

```
count
                 4177
        unique
                    3
        top
                    Μ
                1528
        freq
        Name: Sex, dtype: object
        Total Unique Sex: ['M' 'F' 'I']
Out[9]: M
             1528
        Ι
             1342
             1307
        Name: Sex, dtype: int64
```

Finding correlations between 2 variables/columns in abalone dataset

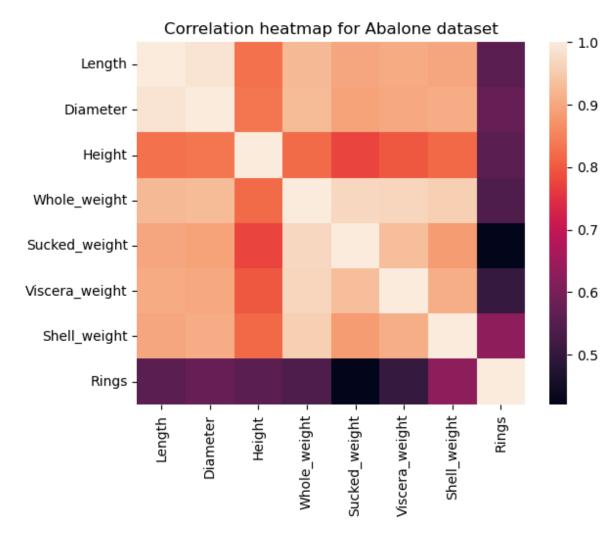
	Length	Diameter	Height	Whole_weight	Sucked_weight	\
Length	1.000000	0.986812	0.827554	0.925261	0.897914	
Diameter	0.986812	1.000000	0.833684	0.925452	0.893162	
Height	0.827554	0.833684	1.000000	0.819221	0.774972	
Whole_weight	0.925261	0.925452	0.819221	1.000000	0.969405	
Sucked_weight	0.897914	0.893162	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_w	eight She	ll_weight	Rings		
Length	0.9	03018	0.897706	0.556720		
Diameter						
Diameter	0.8	99724	0.905330	0.574660		
Height		99724 98319	0.905330 0.817338			
	0.7			0.574660		
Height	0.7 0.9	98319	0.817338	0.574660 0.557467		
Height Whole_weight	0.7 0.9 0.9	98319 66375	0.817338 0.955355	0.574660 0.557467 0.540390		
Height Whole_weight Sucked_weight	0.7 0.9 0.9 1.0	98319 66375 31961	0.817338 0.955355 0.882617	0.574660 0.557467 0.540390 0.420884		
Height Whole_weight Sucked_weight Viscera_weight	0.7 0.9 0.9 1.0 0.9	98319 66375 31961 00000	0.817338 0.955355 0.882617 0.907656	0.574660 0.557467 0.540390 0.420884 0.503819		

finding the correlation w.r.t to rings

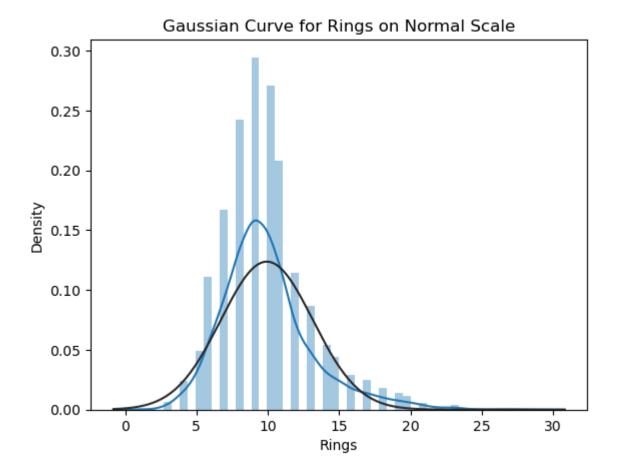
Length 0.556720 0.574660 Diameter Height 0.557467 Whole_weight 0.540390 Sucked_weight 0.420884 Viscera_weight 0.503819 Shell_weight 0.627574 Rings 1.000000 Name: Rings, dtype: float64

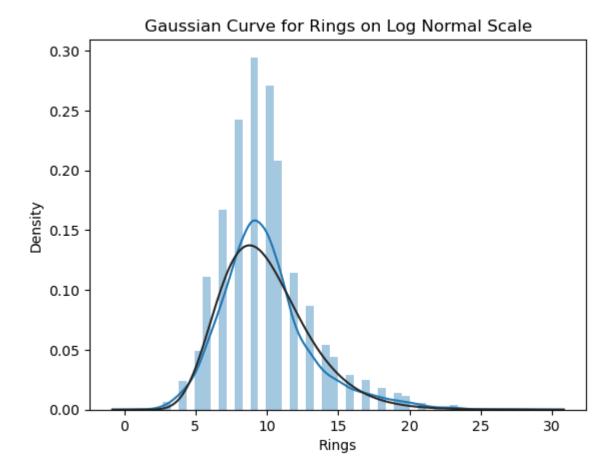
from the above block, we can see that only shell weight is somewhat correlated with rings columns. apart from this all other columns/parameters are not that much correlated with the rings. this would cause problem in the ring classification. 1 represents that the variables are highly correlated and 0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

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

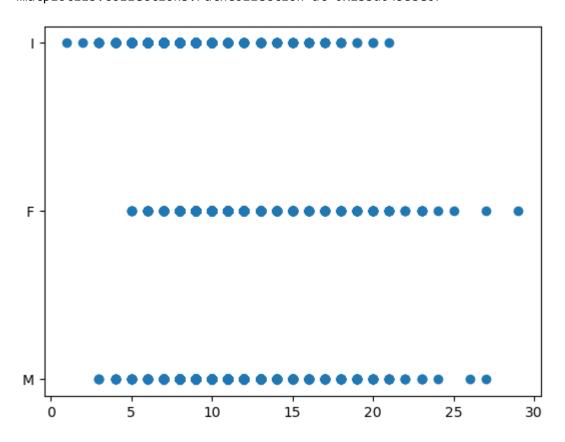


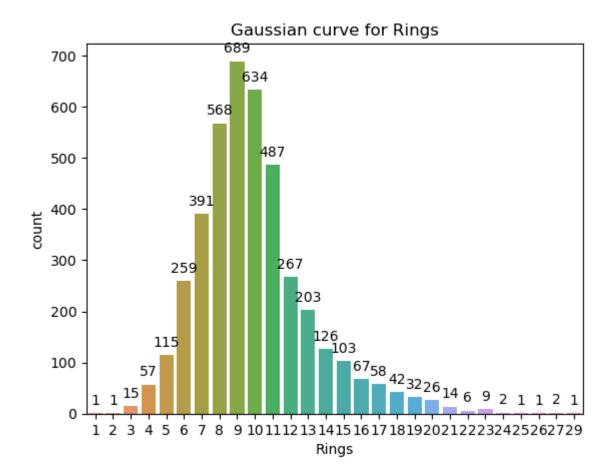
Out[13]: <AxesSubplot:title={'center':'Gaussian Curve for Rings on Log Normal Scale'},</pre> xlabel='Rings', ylabel='Density'>

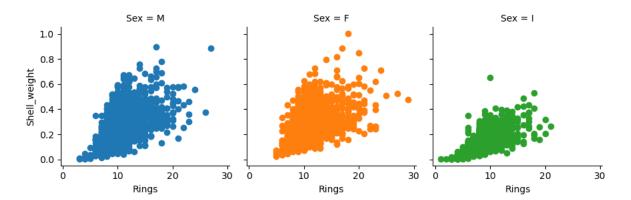




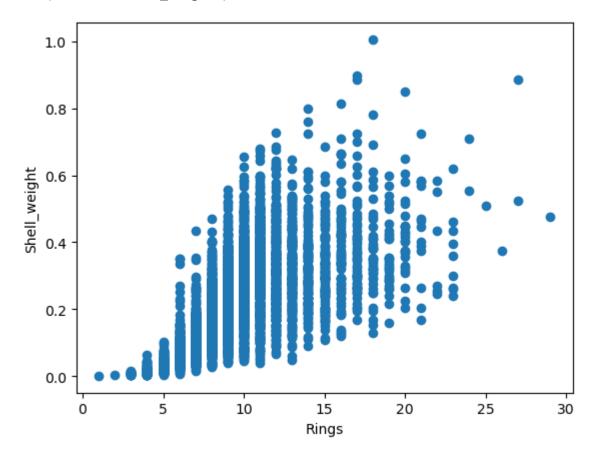
Out[14]: <matplotlib.collections.PathCollection at 0x1bbd045bbe0>



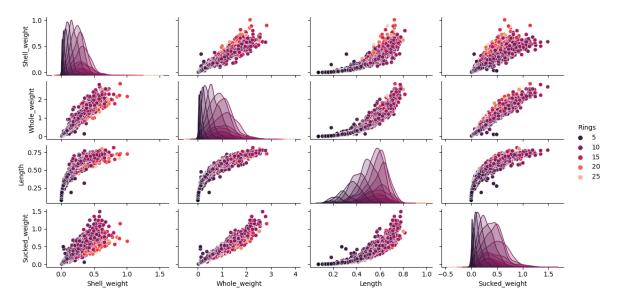




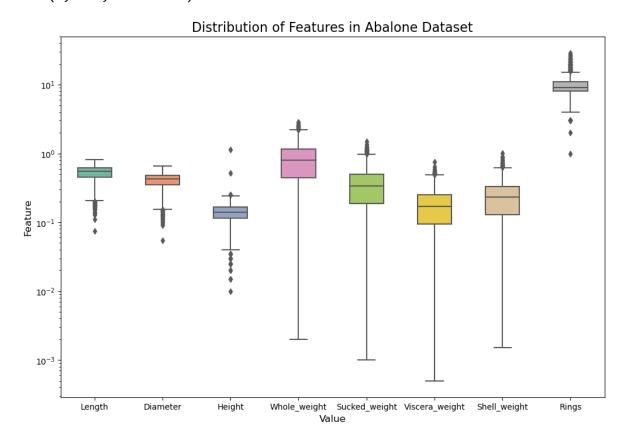
Out[17]: Text(0, 0.5, 'Shell_weight')



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



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



Starting Normalization from here

	Sex	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight
\							
0	М	0.455	0.365	0.095	0.5140	0.2245	0.1010
1	М	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	М	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
	She	ll_weigh	t Rings				
0		0.15	1 5				
1		0.07	9 7				
2		0.21	9				
3		0.15	5 10				
4		0.05	5 7				

'Training Data Original'

	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	Shell_weight
1794	0.575	0.450	0.130	0.8145	0.4030	0.1715	0.2130
1466	0.515	0.425	0.145	0.9365	0.4970	0.1810	0.2185
2275	0.655	0.525	0.185	1.2590	0.4870	0.2215	0.4450
3929	0.650	0.515	0.215	1.4980	0.5640	0.3230	0.4250
1955	0.645	0.510	0.180	1.6195	0.7815	0.3220	0.4675
	1 4	enath l	Diameter	Height	Whole weight S	Sucked weight \	iscera weight

	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	SI
count	3341.000000	3341.000000	3341.000000	3341.000000	3341.000000	3341.000000	3
mean	0.523590	0.407685	0.139397	0.829025	0.360037	0.180496	
std	0.120856	0.099806	0.042632	0.493738	0.223379	0.110090	
min	0.075000	0.055000	0.000000	0.002000	0.001000	0.000500	
25%	0.450000	0.350000	0.115000	0.438500	0.184500	0.092500	
50%	0.545000	0.425000	0.140000	0.797000	0.336000	0.170500	
75%	0.615000	0.480000	0.165000	1.153000	0.505500	0.253000	
max	0.815000	0.650000	1.130000	2.825500	1.488000	0.760000	

^{&#}x27;Testing Data Original'

	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	Shell_weight
341	0.62	0.510	0.205	1.3475	0.4775	0.2565	0.480
3413	0.49	0.395	0.120	0.6740	0.3325	0.1235	0.185
1088	0.45	0.340	0.120	0.4925	0.2410	0.1075	0.120
98	0.47	0.370	0.130	0.5225	0.2010	0.1330	0.165
3661	0.55	0.415	0.150	0.7915	0.3535	0.1760	0.236

	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	Shell ₋
count	836.000000	836.000000	836.000000	836.000000	836.000000	836.000000	836
mean	0.525598	0.408666	0.139994	0.827610	0.356690	0.180982	0
std	0.117049	0.096998	0.038462	0.477058	0.216322	0.107758	0
min	0.160000	0.110000	0.015000	0.014500	0.005500	0.002500	0
25%	0.453750	0.350000	0.115000	0.451500	0.190500	0.095375	0
50%	0.545000	0.425000	0.140000	0.806000	0.336750	0.171000	0
75%	0.615000	0.481250	0.165000	1.157125	0.492625	0.252875	0
max	0.800000	0.630000	0.240000	2.526000	1.351000	0.590000	0
,							

^{&#}x27;Training Data Z Normalized'

	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	Shell_weigh
1794	0.424788	0.424464	-0.227545	-0.029046	0.196599	-0.082970	-0.18558
1466	-0.074885	0.172519	0.131117	0.219766	0.620144	0.003708	-0.14607
2275	1.091018	1.180300	1.087551	0.877486	0.575086	0.373230	1.48124
3929	1.049379	1.079522	1.804876	1.364912	0.922032	1.299315	1.33755
1955	1.007740	1.029133	0.967997	1.612704	1.902043	1.290191	1.64290
4							

	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	SI
count	3341.000000	3341.000000	3341.000000	3341.000000	3341.000000	3341.000000	3
mean	-0.003347	-0.001980	-0.002858	0.000578	0.003019	-0.000887	
std	1.006478	1.005828	1.019371	1.006950	1.006500	1.004457	
min	-3.739154	-3.556267	-3.335953	-1.686092	-1.614731	-1.643173	
25%	-0.616198	-0.583316	-0.586208	-0.795876	-0.787917	-0.803766	
50%	0.174951	0.172519	0.011563	-0.064736	-0.105289	-0.092094	
75%	0.757903	0.726798	0.609334	0.661305	0.658443	0.660635	
max	2.423480	2.440025	23.683287	4.072271	5.085388	5.286500	
4						_	

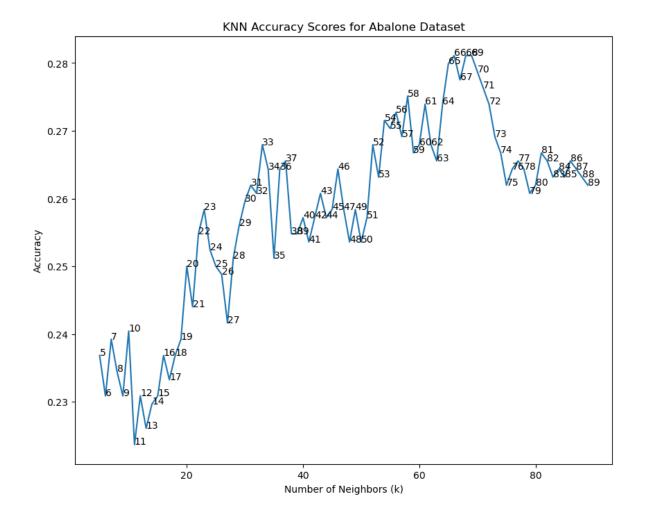
^{&#}x27;Testing Data Z Normalized'

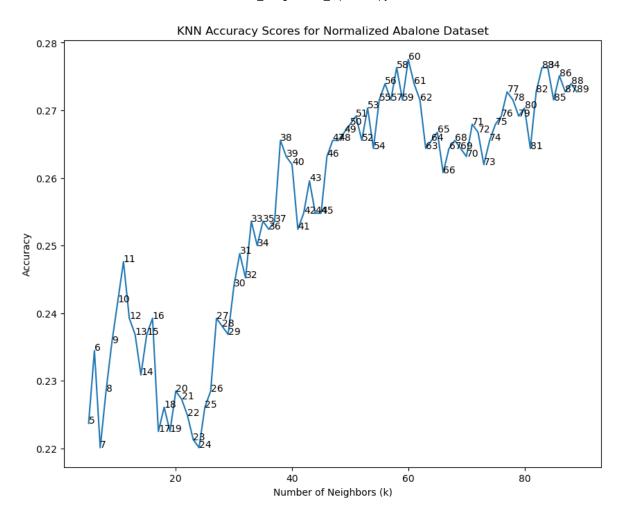
	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	Shell_weigl
341	0.799543	1.029133	1.565767	1.057976	0.532281	0.692569	1.73271
3413	-0.283082	-0.129815	-0.466653	-0.315588	-0.121059	-0.520922	-0.38675
1088	-0.616198	-0.684094	-0.466653	-0.685746	-0.533340	-0.666906	-0.85375
98	-0.449640	-0.381760	-0.227545	-0.624563	-0.713572	-0.434244	-0.53044
3661	0.216591	0.071741	0.250672	-0.075953	-0.026438	-0.041912	-0.02033

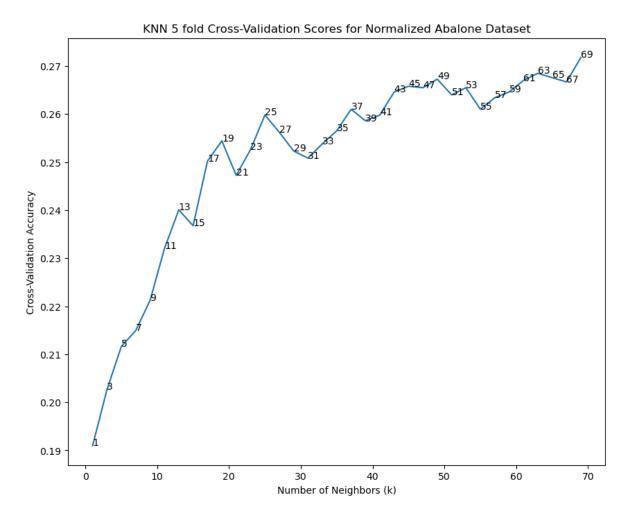
							1
	Length	Diameter	Height	Whole_weight	Sucked_weight	Viscera_weight	Shell _.
count	836.000000	836.000000	836.000000	836.000000	836.000000	836.000000	836
mean	0.013374	0.007911	0.011420	-0.002309	-0.012063	0.003544	0
std	0.974773	0.977526	0.919654	0.972932	0.974702	0.983182	0
min	-3.031284	-3.001988	-2.977291	-1.660599	-1.594455	-1.624925	-1
25%	-0.584968	-0.583316	-0.586208	-0.769363	-0.760882	-0.777534	-0
50%	0.174951	0.172519	0.011563	-0.046381	-0.101910	-0.087532	-0
75%	0.757903	0.739396	0.609334	0.669718	0.600431	0.659495	0
max	2.298562	2.238469	2.402646	3.461458	4.468094	3.735421	4
4							•

Out[23]: 0.20334928229665072

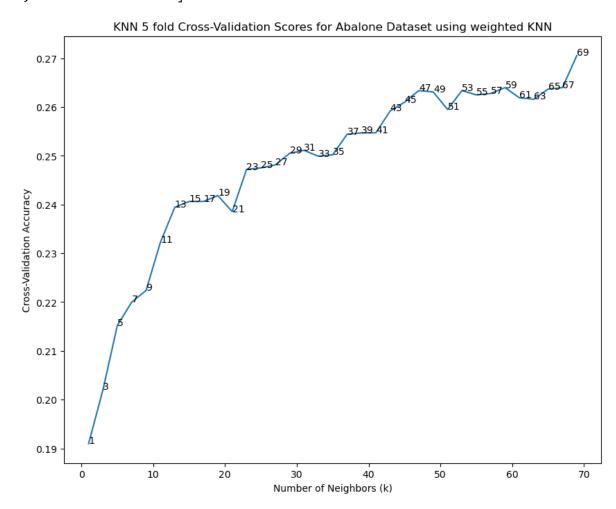
Out[24]: 0.215311004784689







[0.19096604996285454, 0.20203807631374024, 0.2152068061187043, 0.219991854855 31178, 0.22238706443615014, 0.2322668564216858, 0.23945248516420076, 0.240649 64241919745, 0.2406478522775078, 0.2418432193908148, 0.2385533865005415, 0.24 723467862481313, 0.24753139460988338, 0.24813064454051537, 0.2505231689088191 5, 0.25112197130402875, 0.249924814049032, 0.25022421524663674, 0.25441314680 05693, 0.2547147856752862, 0.2547147856752862, 0.25920267089140103, 0.2609946 027228055, 0.2633902598390663, 0.2630922012477287, 0.25950117701816094, 0.263 3916024453335, 0.2624969791358986, 0.2627945901918137, 0.2639917474468104, 0.2618968341344218, 0.2615983280076618, 0.26369324132005045, 0.2639926425176552 5, 0.2705758885815812]



Assignment 2 Question 1 implementation starts here

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.

- 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.

Using Abalone Dataset

[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.

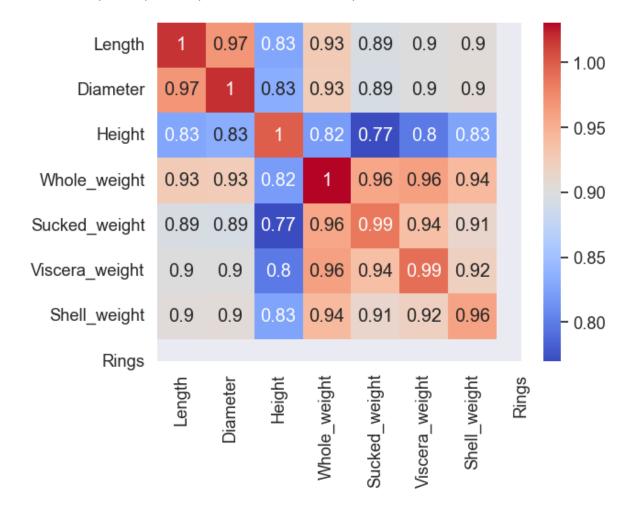
Using PCA as a preprocessing step for abalone dataset

Variance explained by each principal component:

[0.9078731478516083, 0.03991890899342265, 0.023906381975154992, 0.0162959778 83821613, 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
```

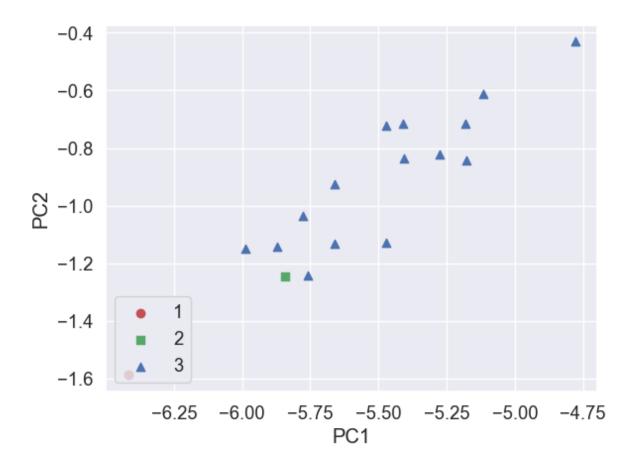
Eigenvalues of the principal components:

6.3566

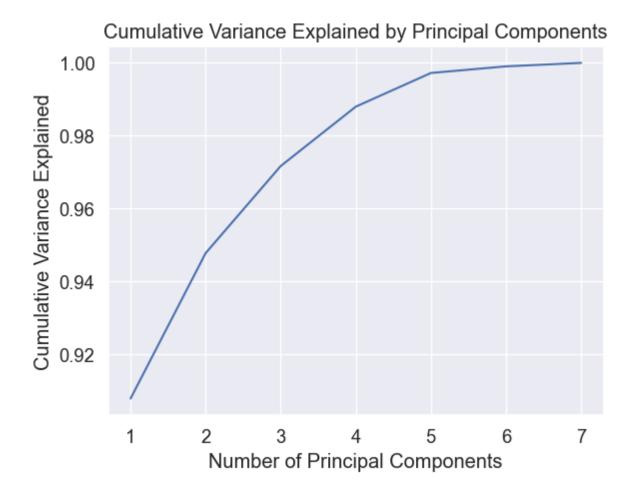
0.2795

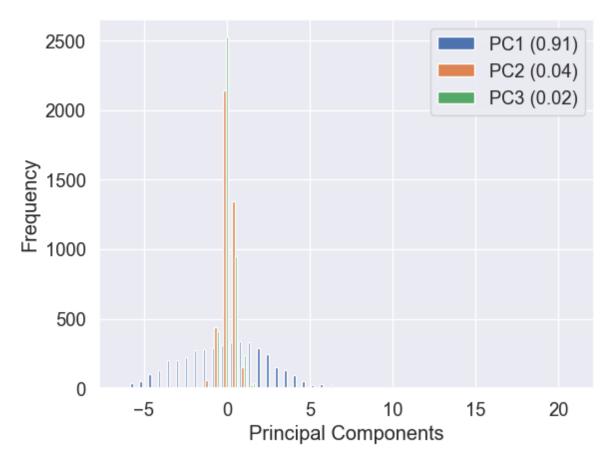
0.1674

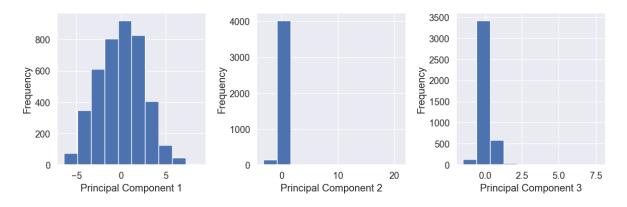
Eigenvectors of the principal components: 0.3833 0.3836 0.3481 0.3907 0.3782 0.3815 0.3789 -0.5933 -0.5854 0.3149 0.2308 0.2316 0.2703 0.1621

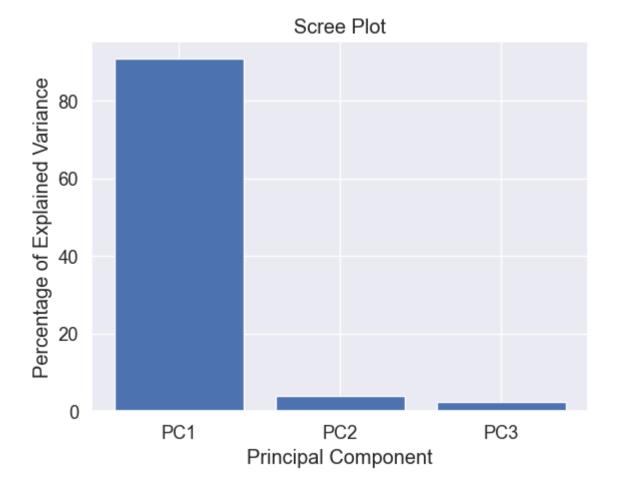


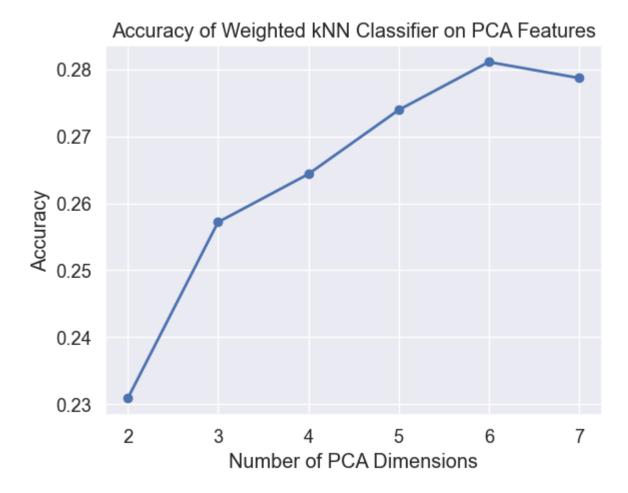
from the eigen values, we can see that the first principal components captures most variance.











Accuracy: 0.25717703349282295

Using LDA as a preprocessing step for abalone dataset

```
['old', 'young', 'middle-aged', 'middle-aged', 'young', ..., 'middle-aged',
'middle-aged', 'middle-aged', 'old']
```

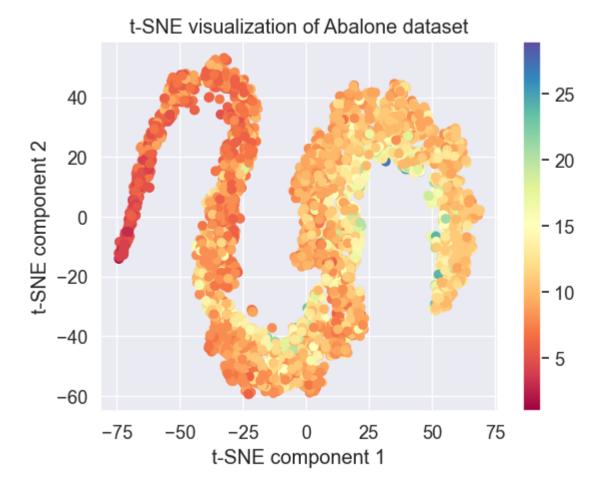
Length: 4177

Categories (3, object): ['young' < 'middle-aged' < 'old']</pre>

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



- 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.

Using Wine Dataset

Out[39]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alco
	7.0	0.270	0.36	20.7	0.045	45.0	170.0	1.00100	3.00	0.45	
•	6.3	0.300	0.34	1.6	0.049	14.0	132.0	0.99400	3.30	0.49	
2	8.1	0.280	0.40	6.9	0.050	30.0	97.0	0.99510	3.26	0.44	
3	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.99560	3.19	0.40	
4	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.99560	3.19	0.40	
6492	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	
6493	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	
6494	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	
649	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	
6496	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	

6497 rows × 13 columns

<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	рН	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

Out[41]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sul dioxi
count	6497.000000	6497.000000	6497.000000	6497.000000	6497.000000	6497.000000	6497.0000
mean	7.215307	0.339666	0.318633	5.443235	0.056034	30.525319	115.7445
std	1.296434	0.164636	0.145318	4.757804	0.035034	17.749400	56.5218
min	3.800000	0.080000	0.000000	0.600000	0.009000	1.000000	6.0000
25%	6.400000	0.230000	0.250000	1.800000	0.038000	17.000000	77.0000
50%	7.000000	0.290000	0.310000	3.000000	0.047000	29.000000	118.0000
75%	7.700000	0.400000	0.390000	8.100000	0.065000	41.000000	156.0000
max	15.900000	1.580000	1.660000	65.800000	0.611000	289.000000	440.0000
4							•

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.

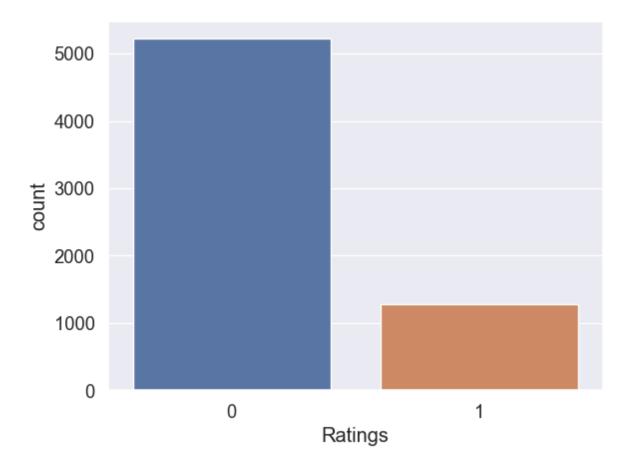
Out[42]: (6497, 13)

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).

Out[43]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alco
0	7.0	0.270	0.36	20.7	0.045	45.0	170.0	1.00100	3.00	0.45	
1	6.3	0.300	0.34	1.6	0.049	14.0	132.0	0.99400	3.30	0.49	
2	8.1	0.280	0.40	6.9	0.050	30.0	97.0	0.99510	3.26	0.44	
3	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.99560	3.19	0.40	
4	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.99560	3.19	0.40	
6492	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	
6493	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	
6494	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	
6495	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	
6496	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	

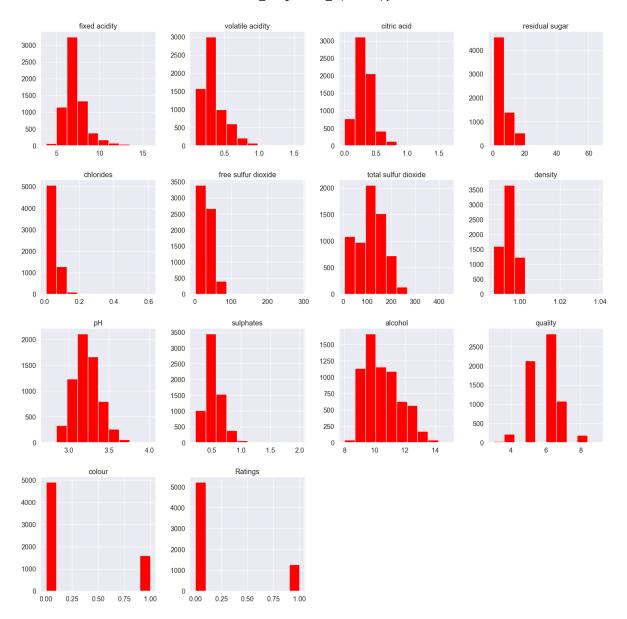
6497 rows × 14 columns



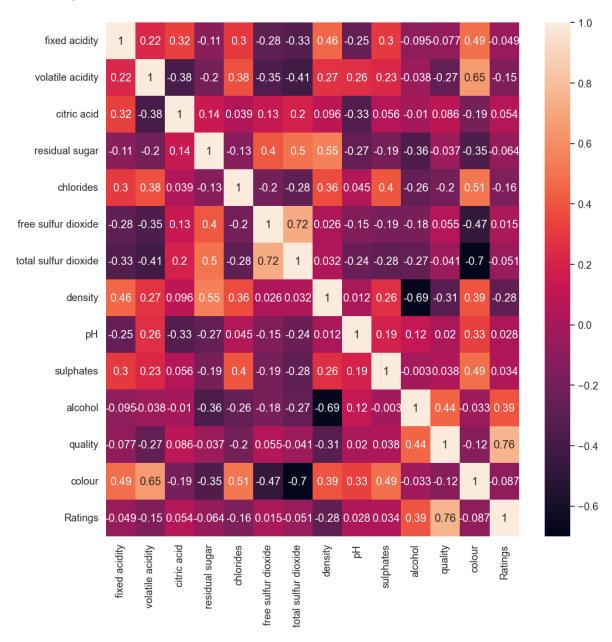
Almost 5200 of the total number of wines seem to be "Bad" and the remaining 1297 wines "Good".

count mean std min 25% 50% 75% max	fixed acidity 6497.000000 7.215307 1.296434 3.800000 6.4000000 7.0000000 7.7000000	6497. 7 0. 4 0. 9 0. 9 0.	-	6497. 0. 0. 0. 0. 0.	c acid 000000 318633 145318 000000 250000 310000 390000 660000	5.4 4.7 0.6 1.8 3.6 8.3	sugar \ 2000000 443235 757804 500000 800000 100000		
count mean std min 25% 50% 75% max	chlorides 6497.000000 0.056034 0.035034 0.009000 0.038000 0.047000 0.065000 0.611000	36 17 1 17 29 41	dioxide 7.000000 0.525319 7.749400 0.000000 0.000000 0.000000 0.000000	tota	11! 50 7 11: 15:	dioxide 7.000000 5.744574 6.521855 6.000000 7.000000 8.000000 6.000000	dens 6497.000 0.994 0.002 0.987 0.992 0.994 0.996 1.038	000 697 999 1110 340 890	\
count mean std min 25% 50% 75% max	pH 6497.000000 3.218501 0.160787 2.720000 3.110000 3.210000 3.320000 4.010000	sulphates 6497.000000 0.531268 0.148806 0.220000 0.430000 0.510000 0.600000 2.0000000	alc 6497.00 10.49 1.19 8.00 9.50 10.30 11.30	1801 2712 0000 0000 0000 0000	qua: 6497.000 5.81: 0.87: 3.000 5.000 6.000 9.000	8378 3255 3000 3000 3000 3000	colour 97.00000 0.246114 0.430779 0.000000 0.000000 0.000000 0.000000 1.000000	\	
count mean std min 25% 50% 75% max	Ratings 6497.000000 0.196552 0.397421 0.000000 0.000000 0.000000 0.000000								

	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
рН	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



Out[47]: <AxesSubplot:>



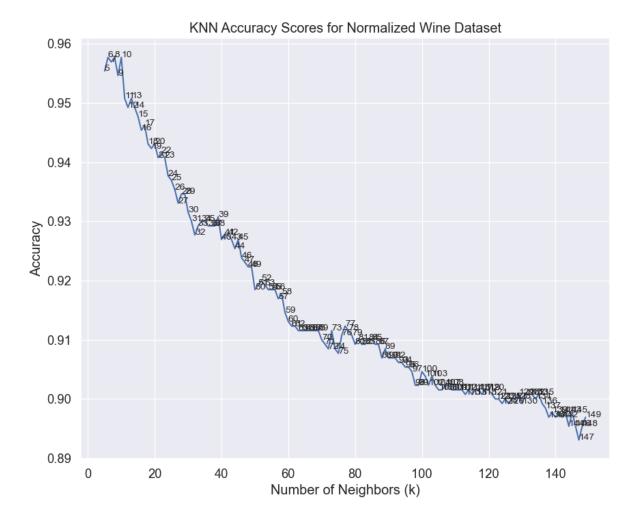
Alcohol has the maximum correlation with quality followed by sulphates and citric acid and then fixed acidity. We can also observe that residual sugar has a significant positive correlation with density and total sulfur dioxide is strongly correlated with the type of wine.

Apply Z-score Normalization on wine dataset:

```
6
1
      6
2
      6
3
      6
4
      6
6492
      5
6493
6494
      6
6495
      5
6496
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]
1.75018984]
1.75018984]
[-0.93749534 -0.1802048
                     1.04170561 ... 0.42611996 0.20799905
  1.75018984]]
```

Covariance Matrix Calculated using numpy:

```
1.0002 0.2190 0.3245 -0.1120 0.2982 -0.2828 -0.3291 0.4590 -0.2527 0.299
       -0.0955 -0.0768 0.4868
0.2190 1.0002 -0.3780 -0.1960 0.3772 -0.3526 -0.4145 0.2713 0.2615 0.226
       -0.0376 -0.2657 0.6531
0.3245
       -0.3780 1.0002 0.1425 0.0390 0.1331 0.1953 0.0962 -0.3299 0.056
       -0.0105 0.0855
                      -0.1874
-0.1120 -0.1960 0.1425 1.0002
                              -0.1290 0.4029 0.4956 0.5526 -0.2674 -0.18
60
       -0.3595 -0.0370 -0.3489
0.2982 0.3772 0.0390 -0.1290 1.0002 -0.1951 -0.2797 0.3627 0.0447 0.395
       -0.2570 -0.2007 0.5128
-0.2828 -0.3526 0.1331 0.4029 -0.1951 1.0002 0.7210 0.0257 -0.1459 -0.18
       -0.1799 0.0555
                      -0.4717
-0.3291 -0.4145 0.1953 0.4956 -0.2797 0.7210 1.0002
                                                     0.0324 -0.2384 -0.27
       -0.2658 -0.0414 -0.7005
58
0.4590
       0.2713 0.0962 0.5526 0.3627 0.0257 0.0324
                                                    1.0002 0.0117 0.259
       -0.6869 -0.3059 0.3907
-0.2527 0.2615 -0.3299 -0.2674 0.0447 -0.1459 -0.2384 0.0117
                                                             1.0002
                                                                    0.192
2
       0.1213 0.0195 0.3292
0.2996 0.2260 0.0562 -0.1860 0.3957 -0.1885 -0.2758 0.2595 0.1922 1.000
       -0.0030 0.0385 0.4873
-0.0955 -0.0376 -0.0105 -0.3595 -0.2570 -0.1799 -0.2658 -0.6869 0.1213
       1.0002 0.4444 -0.0330
-0.0768 -0.2657 0.0855 -0.0370 -0.2007 0.0555 -0.0414 -0.3059 0.0195
                                                                   0.038
       0.4444 1.0002 -0.1193
0.4868
       0.6531 -0.1874 -0.3489 0.5128 -0.4717 -0.7005 0.3907 0.3292 0.487
       -0.0330 -0.1193 1.0002
```



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

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

PCA preprocessing on Wine dataset

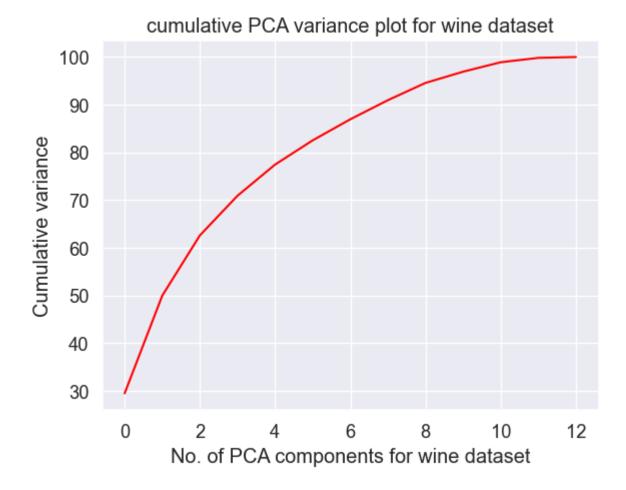
```
Out[52]: array([[-2.06707183, 3.48606943, -0.12160483, ..., 0.355487 ,
                  0.09523024, 0.03915981],
                [-0.27234588, -0.50787251, -0.41460196, ..., -0.14436514,
                  0.04905848, 0.16266364],
                [-0.38931517, 0.29383078, 0.53340294, ..., -0.20948338,
                 -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]])
```

Out[53]:		component1	component2	component3	component4	component5	component6	component7
	0	-2.067072	3.486069	-0.121605	0.225732	1.926477	0.354486	-0.672678
	1	-0.272346	-0.507873	-0.414602	-0.251146	-0.448951	-0.855633	-0.837531
	2	-0.389315	0.293831	0.533403	-0.253599	0.420879	-0.646033	-0.108228
	3	-1.708927	0.968794	-0.219406	0.149823	0.055460	0.226626	-0.012470
	4	-1.708927	0.968794	-0.219406	0.149823	0.055460	0.226626	-0.012470
	4							•

```
Out[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])
Out[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. ])
```

```
Out[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],
                              0.40294671, 0.10595656, -0.13885955, -0.45217669,
                [ 0.3868432 ,
                  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])
```

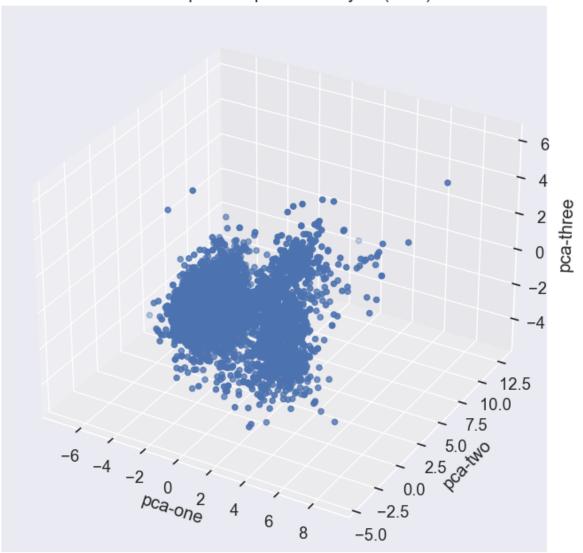
Out[157]: Text(0.5, 1.0, 'cumulative PCA variance plot for wine dataset')

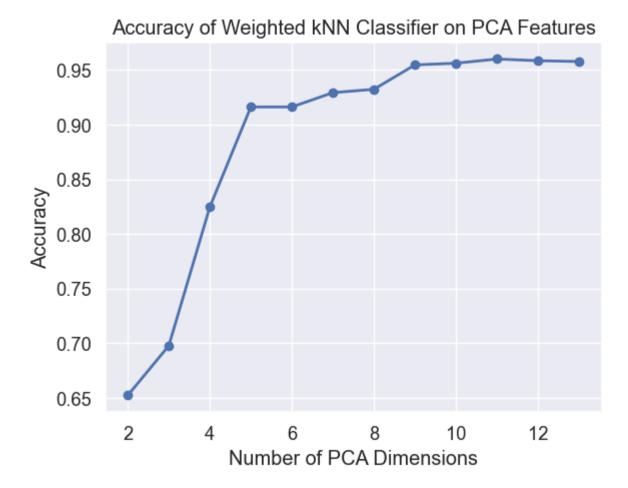


Our problem suggests to use the first 3 principal components.

Out[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

3D Principal Component Analysis (PCA)





Test Accuracy: 0.7115384615384616

CV Accuracy scores: [0.67980769 0.70865385 0.67853705 0.68046198 0.70452358]

CV Average accuracy: 0.6903968312726734

Mean CV accuracy: 1.0 Test Accuracy: 1.0

CV Accuracy scores: [1. 1. 1. 1.]

CV Average accuracy: 1.0

Assignment 2 Question 2 implementation starts here

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.

```
Out[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]])
Out[66]:
                   PC1
                            PC2
                                    PC3
```

		101	1 02	1 03
4	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
41	72	0.100632	-0.034549	-0.011468
41	73	0.128141	-0.023082	-0.028686
41	74	0.273938	0.019037	-0.025086
41	75	0.262282	-0.027659	-0.045737
41	76	0.739028	0.130322	-0.046922

4177 rows × 3 columns

Out[67]: 0 1

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 × 3 columns

Wine Datasets

_			_	o -	
()	11	1	IЬ	×	
$\mathbf{\circ}$	u		ıv	o	

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alcoho
0	7.0	0.270	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.
1	6.3	0.300	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.
2	8.1	0.280	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.
3	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
4	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
95	7.1	0.260	0.29	12.4	0.044	62.0	240.0	0.9969	3.04	0.42	9.
96	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.
97	8.6	0.265	0.36	1.2	0.034	15.0	80.0	0.9913	2.95	0.36	11.
98	9.8	0.360	0.46	10.5	0.038	4.0	83.0	0.9956	2.89	0.30	10.
99	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.
100 rows × 13 columns											

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

Out[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 r	rows × 2 co	olumns
	(6497	, 2)	
Out[71]:			0 1
	qualit	у	
		6 0.75207	8 -1.466209
		6 1.44515	0 0.392049
		6 -0.12301	5 0.911451
		6 0.28896	1 -0.721769
		6 0.28896	1 -0.721769

9 0.512278 -0.224430 6 -0.514707 -0.597340 -0.231160 -0.831907 0.630811 0.158871 -0.668993 -2.296580

6497 rows × 2 columns

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.

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

Wine - Raw dataset - Multinomial Naive **Bayes:**

Out[73]: 0.46159223071001365

Out[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 5folds. A combination of Standardisation and then KNN has no significant effect on the accuracy improvement.

Abalone - Raw - Complement NB

Out[76]: 0.17500329484571525

Wine dataset - raw - complement NB

Out[77]: 0.38971090187718366

Cross-validation accuracy of Raw abalone using Multinomial Naive Bayes classi

fier: 16.37%

Cross-validation accuracy of Raw abalone using Complement Naive Bayes classif

ier: 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%

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 c lassifier with PCA: 18.26%

Test accuracy of processed abalone using Multinomial Naive Bayes classifier w ith PCA: 16.99%

Test accuracy of processed abalone using Complement Naive Bayes classifier wi th PCA: 17.22%

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 c lassifier with LDA: 23.97%

Test accuracy of processed abalone using Multinomial Naive Bayes classifier L

Test accuracy of processed abalone using Complement Naive Bayes classifier LD A: 21.53%

Using Wine Dataset

Out[81]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alcoho
0	7.0	0.270	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.
1	6.3	0.300	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.
2	8.1	0.280	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.
3	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
4	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
95	7.1	0.260	0.29	12.4	0.044	62.0	240.0	0.9969	3.04	0.42	9.
96	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.
97	8.6	0.265	0.36	1.2	0.034	15.0	80.0	0.9913	2.95	0.36	11.
98	9.8	0.360	0.46	10.5	0.038	4.0	83.0	0.9956	2.89	0.30	10.
99	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.

100 rows × 13 columns

```
15
1
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]]
```

Cross-validation accuracy of raw wine using Multinomial Naive Bayes classifie r: 43.54%

Cross-validation accuracy of raw wine using Complement Naive Bayes classifie r: 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%

Cross-validation accuracy of processed wine using Multinomial Naive Bayes cla ssifier with PCA: 43.43%

Cross-validation accuracy of processed wine using Complement Naive Bayes clas sifier 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%

Cross-validation accuracy of processed wine using Multinomial Naive Bayes cla ssifier with LDA: 43.43%

Cross-validation accuracy of processed wine using Complement Naive Bayes clas sifier with LDA: 0.54%

Test accuracy of processed wine using Multinomial Naive Bayes classifier with

Test accuracy of processed wine using Complement Naive Bayes classifier with

LDA: 0.15%

Assignment 2 Question 3 implementation starts here

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.
- 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 builtin 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.

Using Abalone Dataset

```
Out[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,
                 0.4917787711)
```

Out[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 × 3 columns

Out[90]:

Rings	i		
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 × 3 columns

2

Wine Dataset

Out	[91]
ouc	レンエコ

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alcoho
0	7.0	0.270	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.
1	6.3	0.300	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.
2	8.1	0.280	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.
3	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
4	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
95	7.1	0.260	0.29	12.4	0.044	62.0	240.0	0.9969	3.04	0.42	9.
96	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.
97	8.6	0.265	0.36	1.2	0.034	15.0	80.0	0.9913	2.95	0.36	11.
98	9.8	0.360	0.46	10.5	0.038	4.0	83.0	0.9956	2.89	0.30	10.
99	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.
100	rowe v	12 oolum	no								

100 rows × 13 columns

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

Out[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 × 2 columns

(6497, 2)

0	u	t	۲9	4]	Ŀ

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			

0

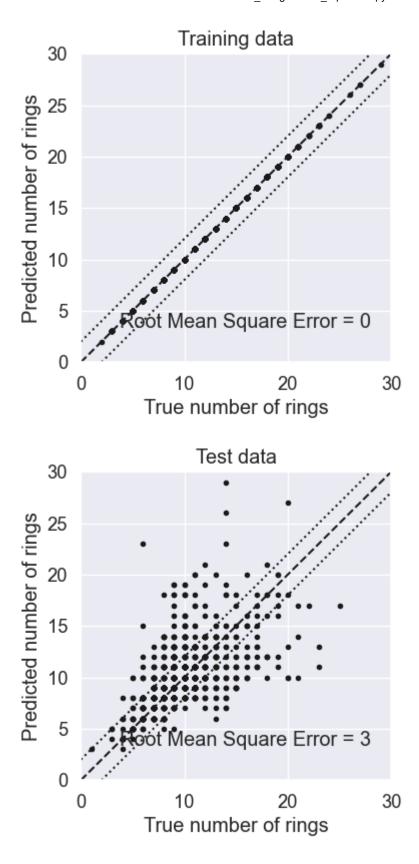
6497 rows × 2 columns

Decision Tree on Abalone dataset

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

```
Testing score: [-0.029170677339277695, 0.1593988145639289, 0.075667370095526
04, 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.



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.

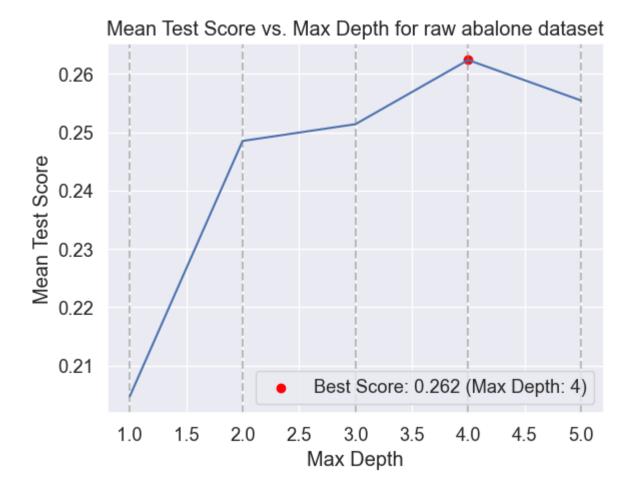
```
Out[99]: [0.2743675926265253,
           0.32115270603998214,
           0.3433132428439525,
           0.40126800234349214,
           0.4278684960176351,
           0.4340850300095299,
           0.4390516759870713,
           0.35617530225868343,
           0.3674679511109248]
```

Using GridSearchCV

Best parameters: {'max_depth': 4}

Best accuracy score: 0.26238260321462337

```
--- 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
```



<graphviz.sources.Source at 0x1bbcb49b340>

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

```
Best parameters: {'max_depth': 4, 'max_features': 'sqrt', 'max_leaf_nodes': 1
0, 'min_samples_leaf': 1, 'min_weight_fraction_leaf': 0.0, 'splitter': 'bes
t'}
```

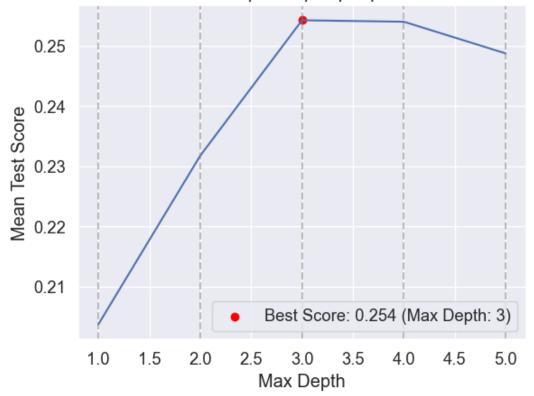
Best accuracy score: 0.2688488095579177

Best parameters: {'max depth': 3}

Best accuracy score: 0.2542440477895883

```
- 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
        -0.25
-- PC2 >
  --- 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
```

Mean Test Score vs. Max Depth for pca pre-processed abalone dataset



<graphviz.sources.Source at 0x1bbd5038ca0>

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

```
Best parameters: {'max_depth': 5, 'max_features': 'sqrt', 'max_leaf_nodes': 2
0, 'min_samples_leaf': 5, 'min_weight_fraction_leaf': 0.0, 'splitter': 'bes
t'}
```

Best accuracy score: 0.25376471936509754

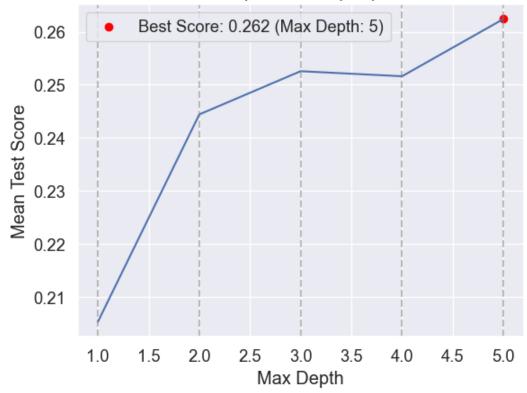
Best parameters: {'max_depth': 5}

Best accuracy score: 0.2623840357562387

```
|--- 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
```

Mean Test Score vs. Max Depth for LDA pre-processed abalone dataset



<graphviz.sources.Source at 0x1bbd42f9a60>

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

```
Best parameters: {'max_depth': 5, 'max_features': 'sqrt', 'max_leaf_nodes': 2
0, 'min_samples_leaf': 5, 'min_weight_fraction_leaf': 0.0, 'splitter': 'bes
Best accuracy score: 0.2583127524854597
Best parameters: {'max depth': 5, 'max features': 'log2', 'max leaf nodes': 1
5, 'min_samples_leaf': 2, 'min_weight_fraction_leaf': 0.0, 'splitter': 'bes
t'}
Best accuracy score: 0.5314768757032037
Best parameters: {'max depth': 5, 'max features': 'log2', 'max leaf nodes': N
one, 'min_samples_leaf': 3, 'min_weight_fraction_leaf': 0.0, 'splitter': 'bes
Best accuracy score: 0.5023857405104518
Best parameters: {'max_depth': 5, 'max_features': 'sqrt', 'max_leaf_nodes': N
one, 'min samples leaf': 3, 'min weight fraction leaf': 0.0, 'splitter': 'bes
t'}
Best accuracy score: 0.5411726179901699
```

Assignment 2 Question 4

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.

```
Out[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]])
```

Out[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 × 3 columns

Out[118]:

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 × 3 columns

2

Out[119]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alcoho
0	7.0	0.270	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.
1	6.3	0.300	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.
2	8.1	0.280	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.
3	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
4	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
95	7.1	0.260	0.29	12.4	0.044	62.0	240.0	0.9969	3.04	0.42	9.
96	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.
97	8.6	0.265	0.36	1.2	0.034	15.0	80.0	0.9913	2.95	0.36	11.
98	9.8	0.360	0.46	10.5	0.038	4.0	83.0	0.9956	2.89	0.30	10.
99	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.

100 rows × 13 columns

Out[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 × 2 columns

(6497, 2)

Out[121]]:	0
----------	----	---

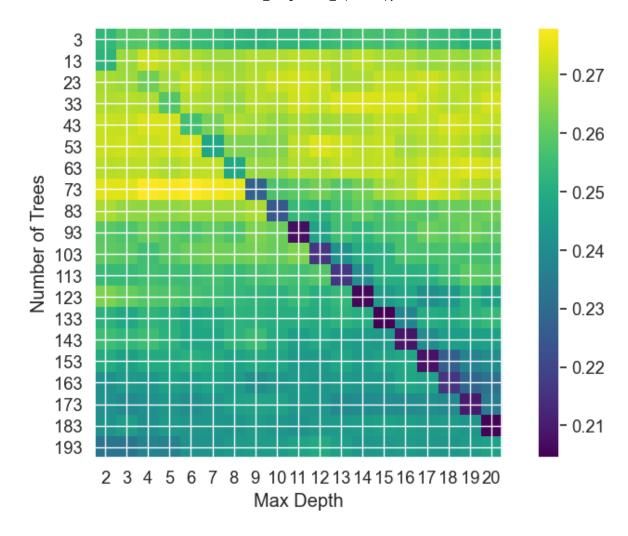
quality		
6	0.752078	-1.466209
6	1.445150	0.392049
6	-0.123015	0.911451
6	0.288961	-0.721769
6	0.288961	-0.721769
5	0.512278	-0.224430
6	-0.514707	-0.597340
6	-0.231160	-0.831907
5	0.630811	0.158871
6	-0.668993	-2.296580

6497 rows × 2 columns

Random Forest on Abalone dataset

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

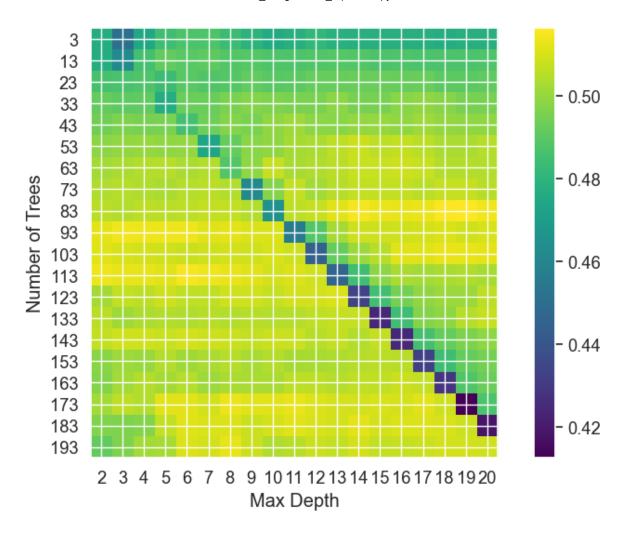
To produce a plot showing the mean accuracy vs. the above parameter settings, we can use the following code:



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

Random Forest on Wine - raw dataset:

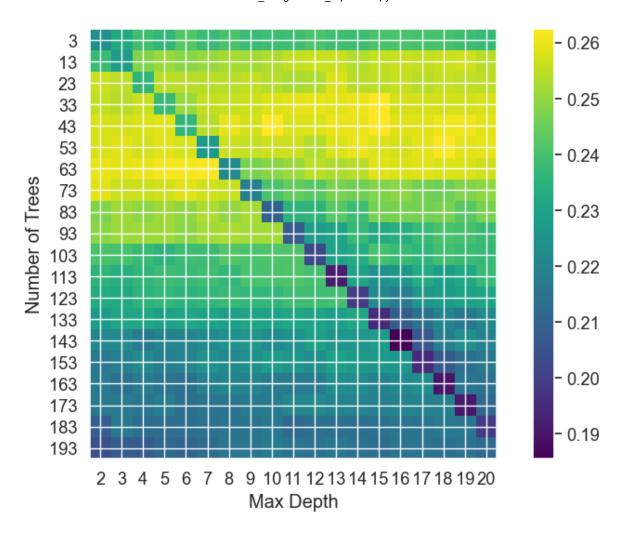
Best Parameters: {'max_depth': 10, 'n_estimators': 93}



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

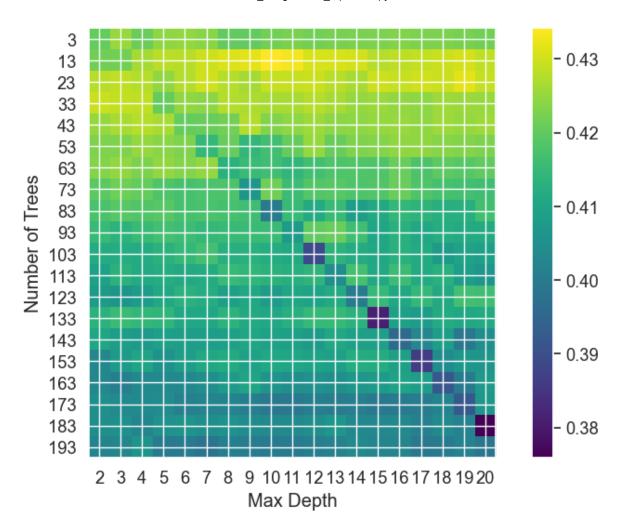
Random Forest - Abalone PCA dataset

Best Parameters: {'max_depth': 6, 'n_estimators': 43}



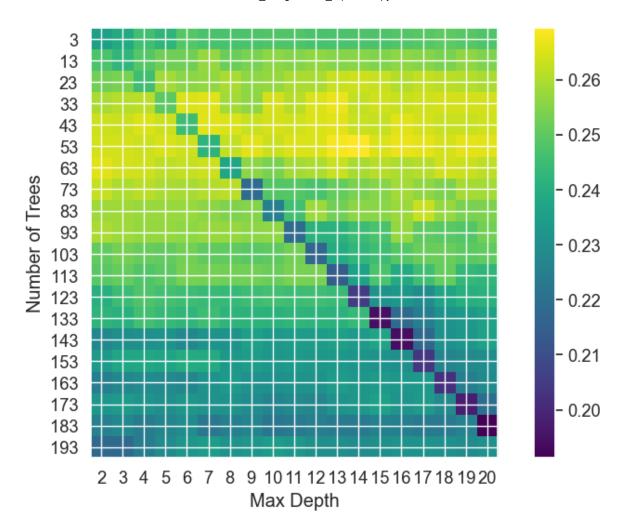
Random Forest - Wine PCA dataset

Best Parameters: {'max_depth': 3, 'n_estimators': 73}



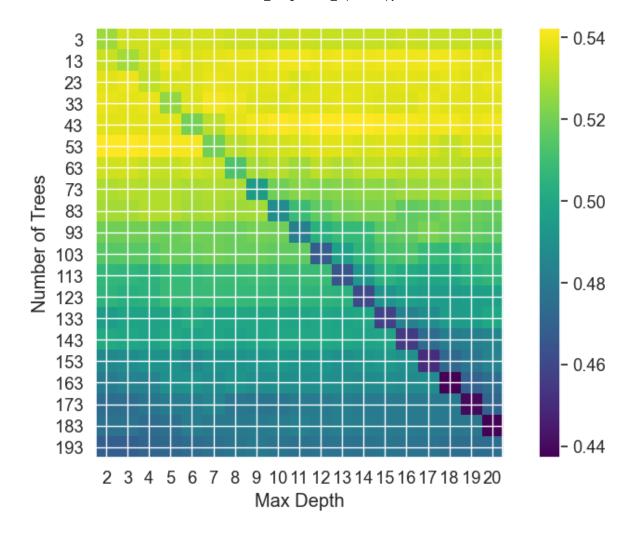
Random Forest - Abalone LDA dataset

Best Parameters: {'max_depth': 7, 'n_estimators': 73}



Random Forest - Wine LDA dataset

Best Parameters: {'max_depth': 6, 'n_estimators': 73}



Assignment2 Question 5 implementation starts here

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.

```
Out[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]])
```

Out[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 × 3 columns

2

Out[137]:

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 × 3 columns

Out[138]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pН	sulphates	alcoho
0	7.0	0.270	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.
1	6.3	0.300	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.
2	8.1	0.280	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.
3	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
4	7.2	0.230	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.
95	7.1	0.260	0.29	12.4	0.044	62.0	240.0	0.9969	3.04	0.42	9.
96	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.
97	8.6	0.265	0.36	1.2	0.034	15.0	80.0	0.9913	2.95	0.36	11.
98	9.8	0.360	0.46	10.5	0.038	4.0	83.0	0.9956	2.89	0.30	10.
99	6.0	0.340	0.66	15.9	0.046	26.0	164.0	0.9979	3.14	0.50	8.

100 rows × 13 columns

Out[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 rd	ows × 2 co	lumns
	(6497)	, 2)	
Out[140]:		(0 .
	quality	1	
	6	0.752078	3 -1.466209

quanty		
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 × 2 columns

Gradient Boosting on Abalone dataset

Accuracy score: 0.2380

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	6) (9 6	9 6	9 (9 6	9 6	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]
Ĺ	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.

Accuracy score: 0.2584

		- F			
		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
aco	curacy			0.26	836
macr	ro avg	0.15	0.16	0.15	836
weighte	ed avg	0.24	0.26	0.25	836

Confusion Matrix:

0] 0] 8 13 0] 11 17 0] 14 30 21 10 0] 2 16 36 25 12 0] 29 52 34 21 34 39 0] 21 27 19 0] 8 13 1] 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.

Gradient Boosting on Wine dataset

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

Gradient Boosting on Abalone - PCA dataset

Accuracy score: 0.1148

		- F			
		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
aco	uracy			0.11	836
macr	o avg	0.05	0.06	0.04	836
weighte	ed avg	0.08	0.11	0.07	836

Confusion Matrix:

[[0	3	8 0	(0	6	9 6	9 0	0	6	0	0	6	0	6	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.

Gradient Boosting on Wine - PCA dataset

Accuracy score: 0.5392

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	6) 2	2 6	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.

Gradient Boosting on Abalone - LDA dataset

Accuracy score: 0.2165

Classi	fication.	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
aco	uracy			0.22	836
macr	ro avg	0.12	0.14	0.13	836
weighte	ed avg	0.21	0.22	0.21	836

Confusion Matrix:

[[0	6	3	3 (9 (9 6) () (0	6	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.

Gradient Boosting on Wine - LDA dataset

Accuracy score: 0.5531

Classification	Report:
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	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	9) 2	20	0	0]
[0	4	26	15		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.