[521	<pre>import pandas as pd import matplotlib.pyplot as plt import seaborn as sns IMPORTING THE DATASET Here, we have used 'read_csv' to read the dataset into the notebook, then we have used 'head()' function to get a taste of the dataset</pre>				
	which shows us the top 5 rows, then we used 'info()' function to actually check if there are any missing values, fortunately there are no missing values, so cleaning missing values need not be done data = pd.read_csv('epoch.csv') print(data.head()) print(data.info()) fixed acidity volatile acidity citric acid residual sugar chlorides \ 0				
	4 7.4 0.70 0.00 1.9 0.076 free sulfur dioxide total sulfur dioxide density pH sulphates \				
	3 9.8 1 11.48 5.74 0.655 35.294118 4 9.4 0 8.10 4.05 0.636 30.909091 n_value 0 0.6080 1 0.8290 2 0.7440 3 0.7195 4 0.6080 <class 'pandas.core.frame.dataframe'=""> RangeIndex: 1599 entries, 0 to 1598 Data columns (total 17 columns):</class>				
	# Column Non-Null Count Dtype				
	10 alcohol 1599 non-null float64 11 quality 1599 non-null int64 12 k_value 1599 non-null float64 13 l_value 1599 non-null float64 14 m_value 1599 non-null float64 15 percentage_free_sulphur 1599 non-null float64 16 n_value 1599 non-null float64 16 n_value 1599 non-null float64 16 n_value 1599 non-null float64 1700 non-null float64 1800 non-null float64 1900 non-null float				
[508	fixed acidity volatile acidity citric acid residual sugar \ count 1599.000000 1599.000000 1599.000000				
	mean 8.319637 0.527821 0.270976 2.538806 std 1.741096 0.179060 0.194801 1.409928 min 4.600000 0.120000 0.000000 0.900000 25% 7.100000 0.390000 0.090000 1.900000 50% 7.900000 0.520000 0.260000 2.200000 75% 9.200000 0.640000 0.420000 2.600000 max 15.900000 1.580000 1.000000 15.500000 count 1599.000000 1599.000000 1599.000000 1599.000000 mean 0.087467 15.874922 46.467792 0.996747 std 0.047065 10.460157 32.895324 0.001887				
	min 0.012000 1.000000 6.000000 0.990070 25% 0.070000 7.000000 22.000000 0.995600 50% 0.079000 14.000000 38.000000 0.996750 75% 0.090000 21.000000 62.000000 0.997835 max 0.611000 72.000000 289.000000 1.003690 pH sulphates alcohol quality k_value \ count 1599.000000 1599.000000 1599.00000 1599.00000 mean 3.311113 0.658149 10.422983 0.534709 8.847458 std 0.154386 0.169507 1.065668 0.498950 1.704047 min 2.740000 0.330000 8.400000 0.000000 7.680000 25% 3.210000 0.550000 9.500000 0.000000 7.680000				
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[509	FINDING CORRELATION BETWEEN FEATURES 'corr()' function provides us the correlation dataframe where the rows and columns are both the features, hence we get to know the correlation between the features, next to visualize it we have implemented the heatmap of the correlation data, this a very good method improve our feature selction corr = data.corr() sns.heatmap(corr)				
[509	<pre> <matplotlib.axessubplots.axessubplot 0x7f06f5eab110="" at=""> fixed acidity volatile acidity citric acid residual sugar chlorides free sulfur dioxide total sulfur dioxide density pH sulphates sulphates - 0.2 </matplotlib.axessubplots.axessubplot></pre>				
	alcohol quality k value citric acid density m value n				
[510	So, as we see from the heatmap above, we are going to eliminate one of 2 features which lie in the correlation value region of white color which implies that both those features are strongly corelated and hence increase the redundancy in the model, the pairs which we found out are (fixed acidity, k value, I value); (residual sugar, n value); (sulphates, m value). Interestingly k value and I value have the same correlation with every feature, hence we directly opt out one of them i.e we are going to eliminate I value, now among the remaining pair to decide upon what to drop we are using the dataframe of correlation values which is exactly what print(corr) will do				
	fixed acidity volatile acidity citric acid \ fixed acidity 1.000000 -0.256131 0.671703 \ volatile acidity -0.256131 1.000000 -0.552496 \ citric acid 0.671703 -0.552496 1.000000 \ residual sugar 0.114777 0.001918 0.143577 \ chlorides 0.093705 0.061298 0.203823 \ free sulfur dioxide -0.153794 -0.010504 -0.060978 \ total sulfur dioxide -0.113181 0.076470 0.035533 \ density 0.668047 0.022026 0.364947 \ pH -0.682978 0.234937 -0.541904				
	alcohol				
	citric acid 0.143577 0.203823 -0.060978 residual sugar 1.000000 0.055610 0.187049 chlorides 0.055610 1.000000 0.005562 free sulfur dioxide 0.187049 0.005562 1.000000 total sulfur dioxide 0.203028 0.047400 0.667666 density 0.355283 0.200632 -0.021946 pH -0.085652 -0.265026 0.070377 sulphates 0.005527 0.371260 0.051658 alcohol 0.042075 -0.221141 -0.069408 quality -0.002160 -0.109494 -0.061757 k_value 0.117474 0.102184 -0.158242 1_value 0.018509 0.572840 0.046965				
	percentage_free_sulphur				
	pH				
	volatile acidity -0.202288 -0.321441 -0.156621 -0.156621 -0.215364 citric acid 0.109903 0.159129 0.628252 0.628252 0.326059 residual sugar 0.042075 -0.002160 0.117474 0.117474 0.018509 chlorides -0.221141 -0.109494 0.102184 0.102184 0.572840 free sulfur dioxide -0.069408 -0.061757 -0.158242 -0.158242 0.046965 total sulfur dioxide -0.205654 -0.231963 -0.107607 -0.107607 0.049530 density -0.496180 -0.159110 0.684886 0.684886 0.180272 pH 0.205633 -0.003264 -0.673141 -0.673141 -0.238552 sulphates 0.093595 0.218072 0.159560 0.159560 0.973757 alcohol 1.000000 0.434751 -0.084265 -0.084265 0.028419 quality 0.434751 1.000000 0.063384 0.063384 0.165667				
	1_value				
	free sulfur dioxide				
	Here, we have eliminated fixed acidity from (fixed acidity, k value) as clearky fixed acidity has a lot of correlation with other features, now we are eliminating both residual sugar and n value from their pair as both of them are strongly correlated with 0.993575 and have very minimum correlation with our target variable quality, from the pair of (sulphates, m value), we are eliminating m value, as it has higher correlation values with other features when compared with sulphates, interesting we found that quality has very minimum correlation with free sulphur dioxide and pH and also total sulphur dioxide accounts for free sulphur dioxide, and all the acid features account for pH, so we can remove these 2 features too VISUALIZING THE FEATURES				
[511	Here we have implemented a for loop where each iteration plots a histogram of a feature from our dataset, to implement this'distplot' is used from seaborn module and 'subplot()' does dimensioning of the space so that the histograms can be drawn as per our requirements, here too we can see the similarity between the histograms of the features which had high correlation values with each other, this just to confirm our feature elimination and to visualize each feature plt.figure(figsize = (20, 20)) num = 1 for columns in data: if num <= 17:				
	<pre>plt.subplot(5, 4, num) sns.distplot(data[columns]) plt.xlabel(columns) num += 1 plt.show() /usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureWarning: `distplot` is a deprecation and will be removed in a future version. Please adapt your code to use either `displot` (a figure-label) function with similar flexibility) or `histplot` (an axes-level function for histograms).</pre>				
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