

Import Libraries

INFO 5502- PRINCIPLES AND TECHNIQUES OF DATA SCIENCE

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Group 6

WINE QUALITY PREDICTION

```
In [1]: import pandas as pd
import numpy as np
import sklearn
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, accuracy_score
```

Load Dataset

```
In [2]: data = pd.read_csv("winequality-red.csv")
data.head()
```

```
Out[2]:
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quali
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	

Check the correlation for each of the fields

```
In [3]: data.corr
```

```
Out[3]: <bound method DataFrame.corr of
dual sugar chlorides \
0          7.4          0.700          0.00          1.9          0.076
1          7.8          0.880          0.00          2.6          0.098
2          7.8          0.760          0.04          2.3          0.092
3         11.2          0.280          0.56          1.9          0.075
4          7.4          0.700          0.00          1.9          0.076
...          ...          ...          ...          ...          ...
```

1594	6.2	0.600	0.08	2.0	0.090
1595	5.9	0.550	0.10	2.2	0.062
1596	6.3	0.510	0.13	2.3	0.076
1597	5.9	0.645	0.12	2.0	0.075
1598	6.0	0.310	0.47	3.6	0.067

	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates \
0	11.0	34.0	0.99780	3.51	0.56
1	25.0	67.0	0.99680	3.20	0.68
2	15.0	54.0	0.99700	3.26	0.65
3	17.0	60.0	0.99800	3.16	0.58
4	11.0	34.0	0.99780	3.51	0.56
...
1594	32.0	44.0	0.99490	3.45	0.58
1595	39.0	51.0	0.99512	3.52	0.76
1596	29.0	40.0	0.99574	3.42	0.75
1597	32.0	44.0	0.99547	3.57	0.71
1598	18.0	42.0	0.99549	3.39	0.66

	alcohol	quality
0	9.4	5
1	9.8	5
2	9.8	5
3	9.8	6
4	9.4	5
...
1594	10.5	5
1595	11.2	6
1596	11.0	6
1597	10.2	5
1598	11.0	6

[1599 rows x 12 columns]>

In [4]: data.columns

Out[4]: Index(['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar', 'chlorides', 'free sulfur dioxide', 'total sulfur dioxide', 'density', 'pH', 'sulphates', 'alcohol', 'quality'], dtype='object')

In [5]: data.info()

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1599 entries, 0 to 1598
Data columns (total 12 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   fixed acidity                         1599 non-null   float64
1   volatile acidity                     1599 non-null   float64
2   citric acid                          1599 non-null   float64
3   residual sugar                       1599 non-null   float64
4   chlorides                           1599 non-null   float64
5   free sulfur dioxide                  1599 non-null   float64
6   total sulfur dioxide                 1599 non-null   float64
7   density                             1599 non-null   float64
8   pH                                  1599 non-null   float64
9   sulphates                           1599 non-null   float64
10  alcohol                             1599 non-null   float64
```

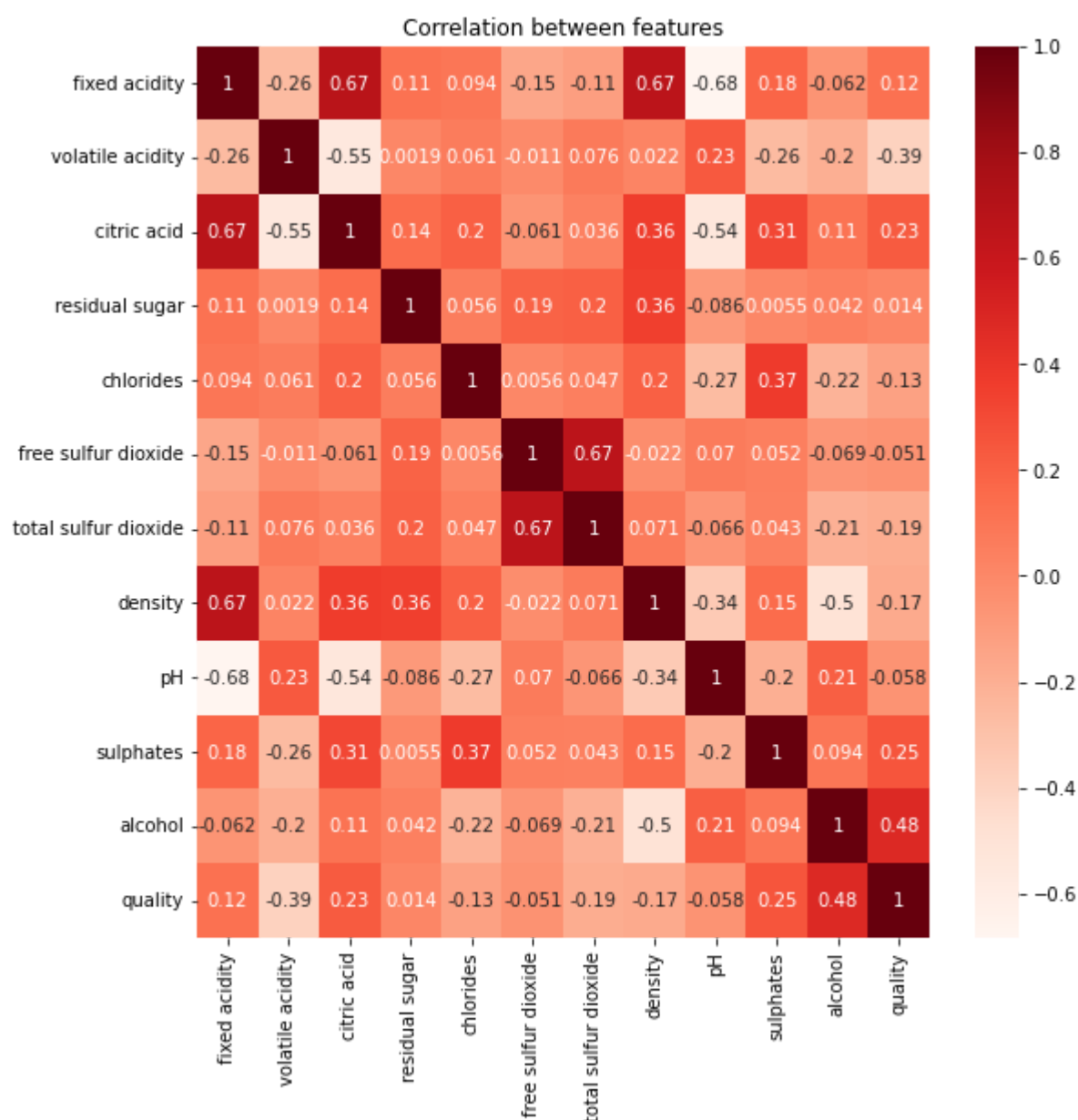
```
11 quality 1599 non-null int64
dtypes: float64(11), int64(1)
memory usage: 150.0 KB
```

```
In [6]: data['quality'].unique()
```

```
Out[6]: array([5, 6, 7, 4, 8, 3], dtype=int64)
```

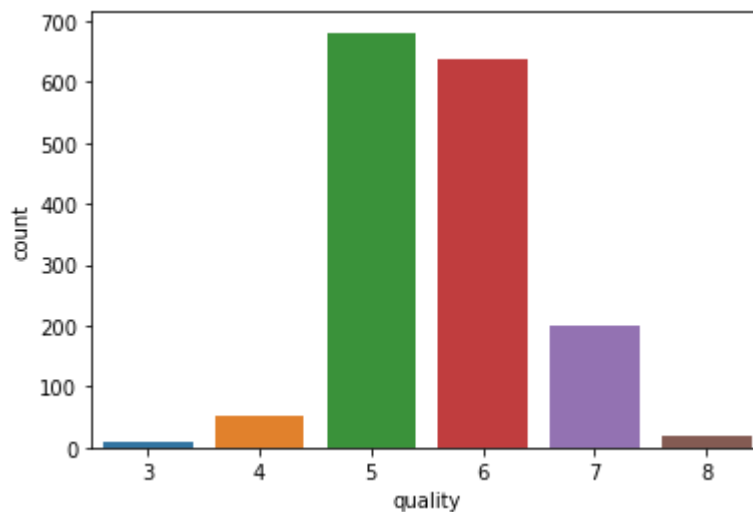
Check correlation between the attributes using heatmap

```
In [7]: plt.figure(figsize=(9, 9))
correlation = data.corr()
heatmap = sns.heatmap(correlation, annot=True, cmap="Reds")
plt.title("Correlation between features")
plt.show()
```



```
In [8]: sns.countplot(x='quality', data=data)
```

```
Out[8]: <AxesSubplot:xlabel='quality', ylabel='count'>
```



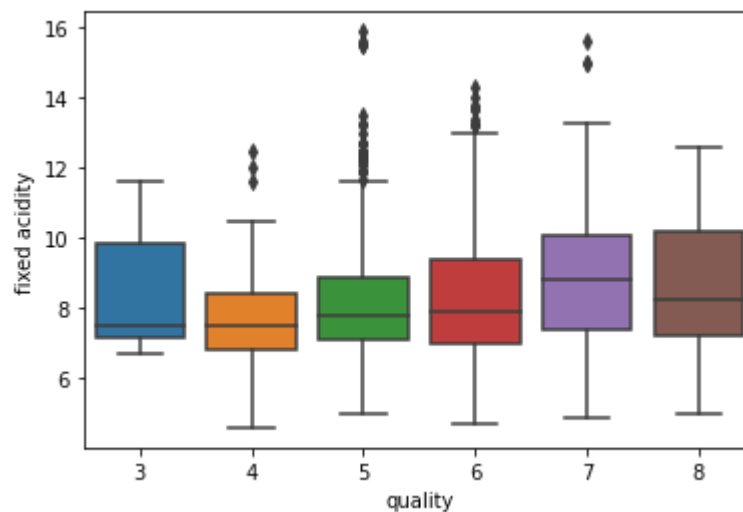
Plot a boxplot to check for Outliers

```
In [9]: sns.boxplot('quality', 'fixed acidity', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

warnings.warn(

```
Out[9]: <AxesSubplot:xlabel='quality', ylabel='fixed acidity'>
```

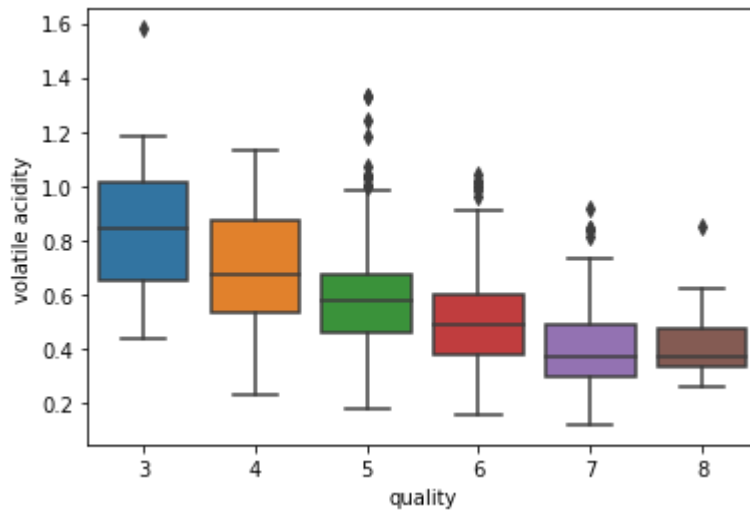


```
In [10]: sns.boxplot('quality', 'volatile acidity', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

warnings.warn(

```
Out[10]: <AxesSubplot:xlabel='quality', ylabel='volatile acidity'>
```

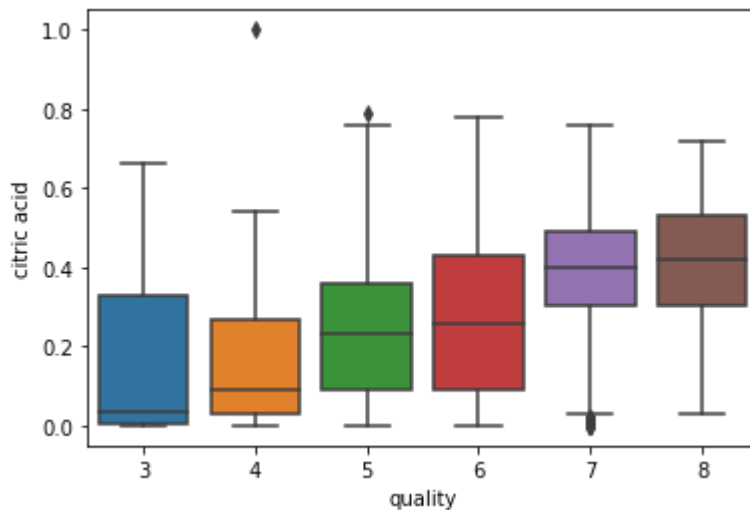


```
In [11]: sns.boxplot('quality', 'citric acid', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

warnings.warn(

```
Out[11]: <AxesSubplot:xlabel='quality', ylabel='citric acid'>
```

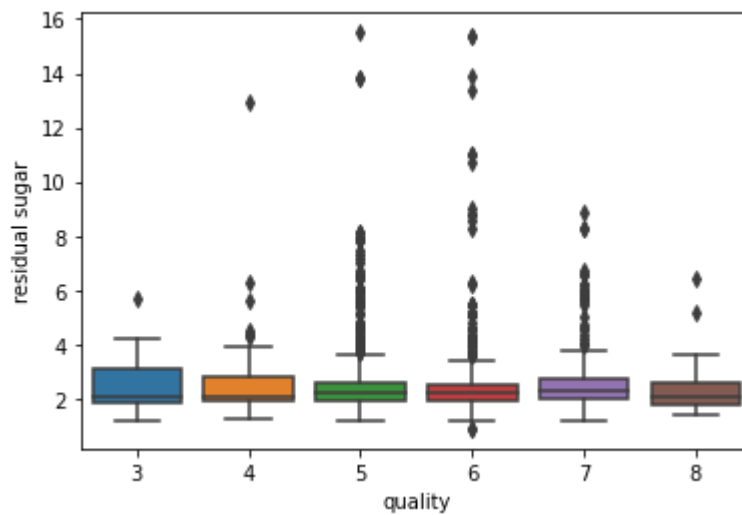


```
In [12]: sns.boxplot('quality', 'residual sugar', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

warnings.warn(

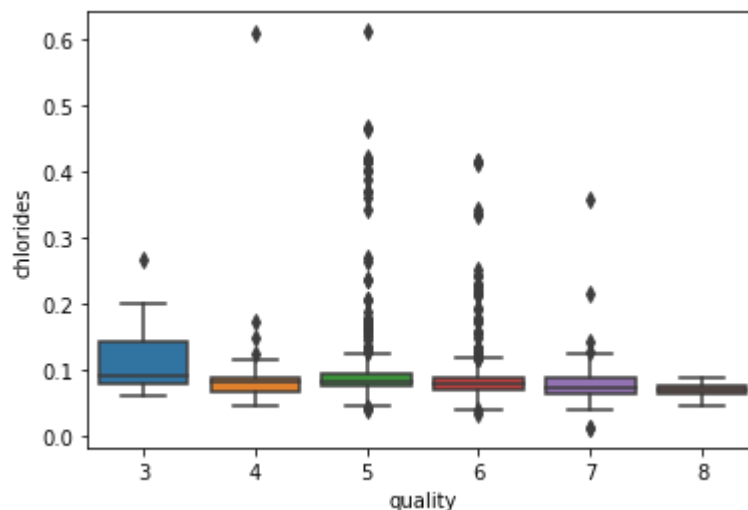
```
Out[12]: <AxesSubplot:xlabel='quality', ylabel='residual sugar'>
```



```
In [13]: sns.boxplot('quality', 'chlorides', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

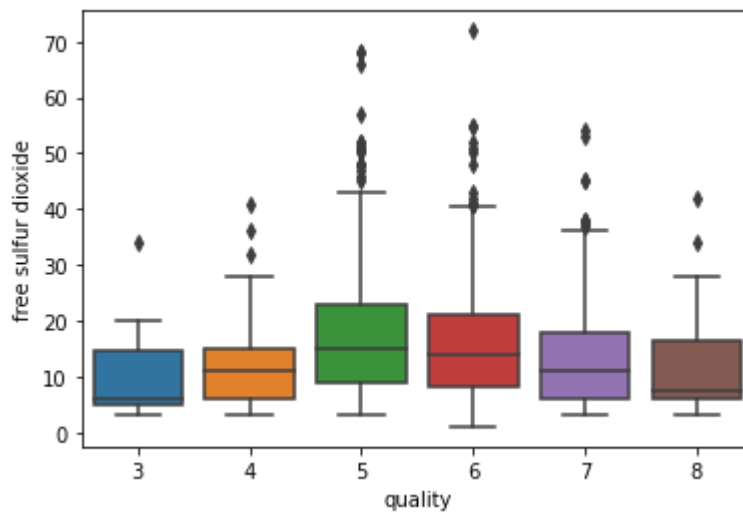
```
Out[13]: <AxesSubplot:xlabel='quality', ylabel='chlorides'>
```



```
In [14]: sns.boxplot('quality', 'free sulfur dioxide', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

```
Out[14]: <AxesSubplot:xlabel='quality', ylabel='free sulfur dioxide'>
```

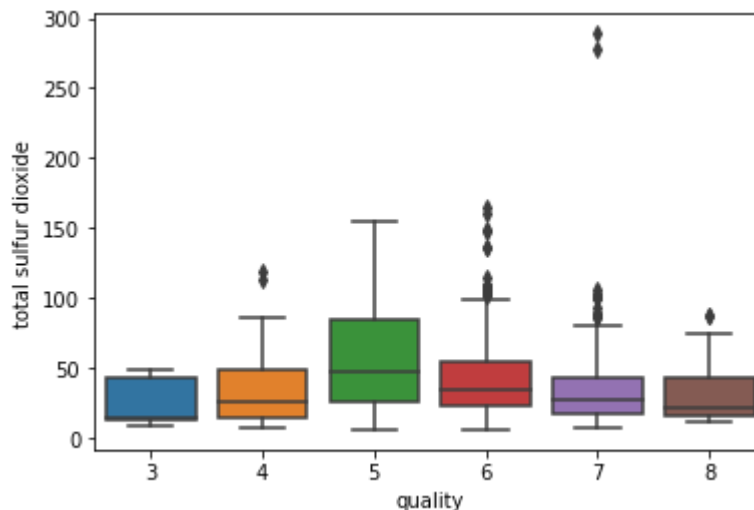


```
In [15]: sns.boxplot('quality', 'total sulfur dioxide', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

```
warnings.warn(
```

```
Out[15]: <AxesSubplot:xlabel='quality', ylabel='total sulfur dioxide'>
```

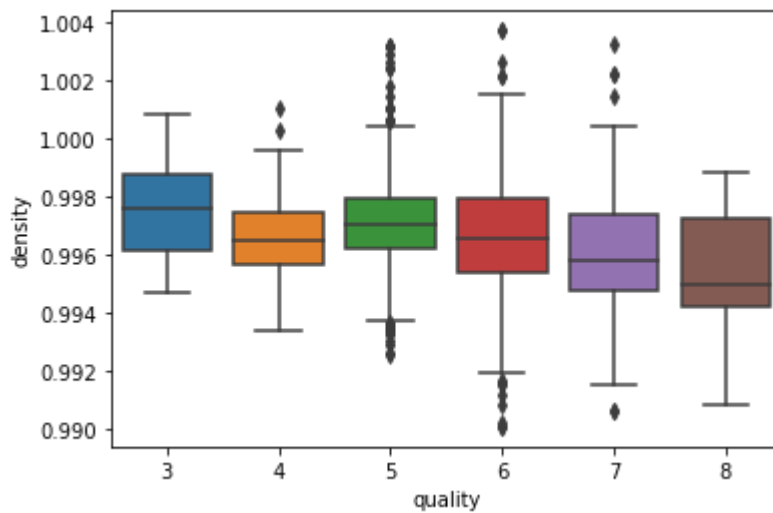


```
In [16]: sns.boxplot('quality', 'density', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

```
warnings.warn(
```

```
Out[16]: <AxesSubplot:xlabel='quality', ylabel='density'>
```

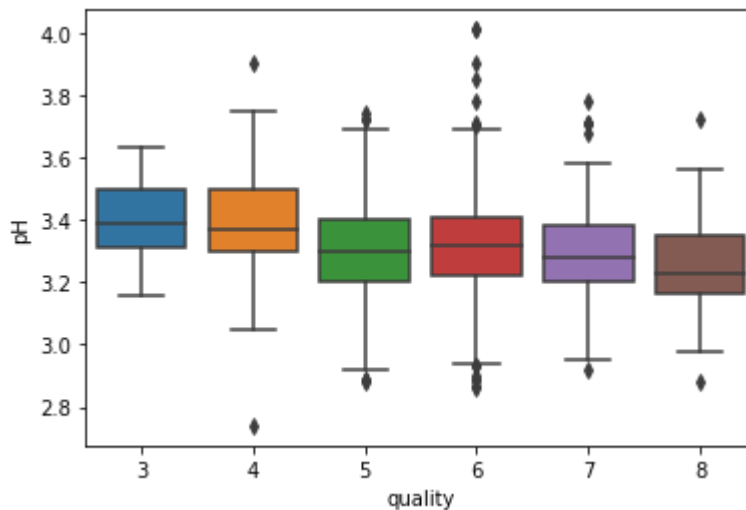


```
In [17]: sns.boxplot('quality', 'pH', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

warnings.warn(

```
Out[17]: <AxesSubplot:xlabel='quality', ylabel='pH'>
```

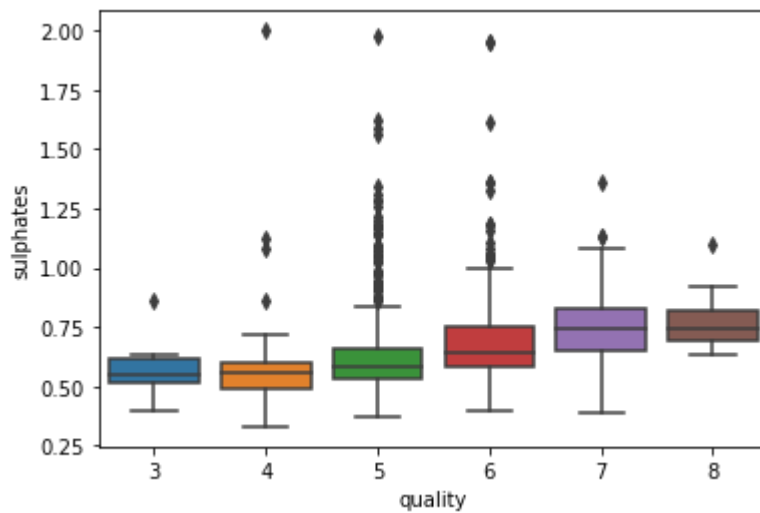


```
In [18]: sns.boxplot('quality', 'sulphates', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

warnings.warn(

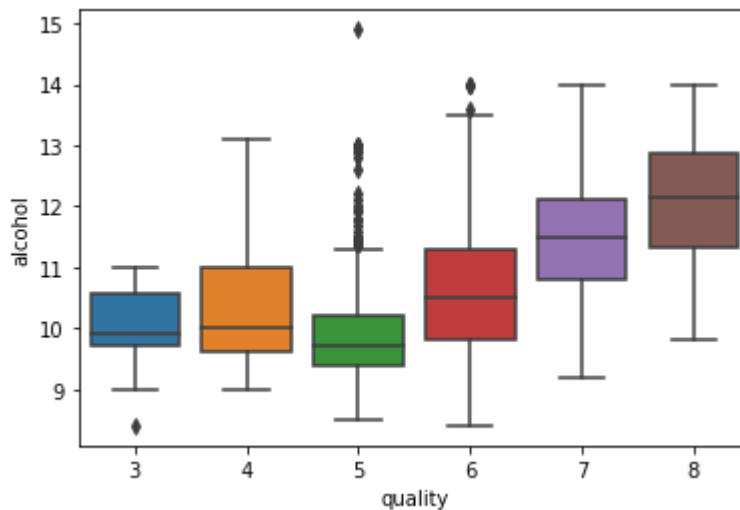
```
Out[18]: <AxesSubplot:xlabel='quality', ylabel='sulphates'>
```

```
In [19]: sns.boxplot('quality', 'alcohol', data = data)
```

C:\Users\LaptopCheckout\software\anaconda\lib\site-packages\seaborn_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

```
Out[19]: <AxesSubplot:xlabel='quality', ylabel='alcohol'>
```



```
In [20]: data.describe()
```

```
Out[20]:
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	quality
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.467792	5.436991
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	1.065959
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	3.000000
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	4.000000
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	5.000000

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	(
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1

Categorizing the values into high or low quality

```
In [21]: data['quality']=data.quality.apply(lambda x: "High Quality" if x>= 7 else "Low Quality")
data.head()
```

```
Out[21]:
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	Low Quality
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	Low Quality
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	Low Quality
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	Low Quality
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	Low Quality

Splitting the target and independent variable

```
In [22]: x=data.iloc[:, 0:11].values
y=data['quality']
```

Label encoder

```
In [23]: from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
y = le.fit_transform(y)
```

Split train and test data

```
In [24]: x_train, x_test, y_train, y_test = train_test_split(x,y,test_size=0.20,random_state=1)
```

```
In [25]: print(x_train.shape, y_train.shape)
print(x_test.shape, y_test.shape)
```

```
(1279, 11) (1279,)
```

```
(320, 11) (320,)
```

Standardization of features

```
In [26]: scale=StandardScaler()
x_train= scale.fit_transform(x_train)
x_test= scale.transform(x_test)
```

Logistic regression

```
In [27]: lm = LogisticRegression(random_state=1)
lm.fit(x_train,y_train)
lm_predict = lm.predict(x_test)
```

Accuracy score

```
In [28]: acc_score = accuracy_score(y_test,lm_predict)
print("Accuracy ",acc_score*100)
```

Accuracy 88.4375

Confusion matrix

```
In [29]: lm_confusion_matrix = confusion_matrix(y_test,lm_predict)
print("Confusion Matrix \n",lm_confusion_matrix)
```

Confusion Matrix
[[7 25]
[12 276]]

Decision Tree

```
In [30]: from sklearn.tree import DecisionTreeClassifier

dt = DecisionTreeClassifier()
dt.fit(x_train,y_train)
dt_predict = dt.predict(x_test)
```

Accuracy score

```
In [31]: dt_acc_score = accuracy_score(y_test, dt_predict)
print(dt_acc_score*100)
```

89.375

Confusion matrix

```
In [32]: dt_conf_matrix = confusion_matrix(y_test, dt_predict)
dt_conf_matrix
```

```
Out[32]: array([[ 19,  13],
               [ 21, 267]], dtype=int64)
```

NaiveBayes

```
In [33]: from sklearn.naive_bayes import GaussianNB

nb = GaussianNB()
nb.fit(x_train,y_train)
nb_predict=nb.predict(x_test)
```

Accuracy score

```
In [34]: nb_acc_score = accuracy_score(y_test, nb_predict)
print(nb_acc_score*100)
```

81.875

confusion matrix

```
In [35]: nb_conf_matrix = confusion_matrix(y_test, nb_predict)
nb_conf_matrix
```

```
Out[35]: array([[ 22,  10],
               [ 48, 240]], dtype=int64)
```

RandomForest classifier

```
In [36]: from sklearn.ensemble import RandomForestClassifier

rf = RandomForestClassifier()
rf.fit(x_train, y_train)
rf_predict=rf.predict(x_test)
```

Accuracy score

```
In [37]: rf_acc_score = accuracy_score(y_test, rf_predict)
print(rf_acc_score*100)
```

91.875

Confusion matrix

```
In [38]: rf_conf_matrix = confusion_matrix(y_test, rf_predict)
rf_conf_matrix
```

```
Out[38]: array([[ 15,  17],
               [  9, 279]], dtype=int64)
```

SVM Classifier

```
In [39]: from sklearn.svm import SVC

lin_svc = SVC()
```

```
lin_svc.fit(x_train, y_train)
lin_svc=rf.predict(x_test)
```

Accuracy score

```
In [40]: lin_svc_acc_score = accuracy_score(y_test, rf_predict)
print(lin_svc_acc_score*100)
```

91.875

Confusion matrix

```
In [41]: lin_svc_conf_matrix = confusion_matrix(y_test, rf_predict)
lin_svc_conf_matrix
```

```
Out[41]: array([[ 15,  17],
               [  9, 279]], dtype=int64)
```