Red-Wine Analysis

In this project I will analyse Wine quality by means of kNeighborsClassification (machine learning algorithm).
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ABSTRACT :

Wine classification is a difficult task since taste is the least understood of the human senses. A good wine quality prediction can be very useful in the certification phase, since currently the sensory analysis is performed by human tasters, being clearly a subjective approach. An automatic predictive system can be integrated into a decision support system, helping the speed and quality of the performance. Furthermore, a feature selection process can help to analyze the impact of the analytical tests. If it is concluded that several input variables are highly relevant to predict the wine quality, since in the production process some variables can be controlled, this information can be used to improve the wine quality. Classification models used here is kNeighborsClassification.

KEYWORDS :

Machine Learning, Classification,kNeighborsClassification,Prediction.

Instructions:

1.Import the dataset.

2.Data quality check:

```
* Check if null values are present. If there are, drop those rows.
```

3.Exploratory Data Analysis:

```
* Univariate Analysis:
    i. Draw a minimum of 5 histograms .
    ii. Draw boxplots for each numerical columns.
* Bivariate analysis:
    i. Draw a minimum of 5 scatter plots
```

4.Modelling:

```
* Split the dataset using “train-test-split” function.
* Apply KNN classification on “quality” column of the dataset. Select the appropriate
features
* Predict on the test set.
* Find out the accuracy.
```

Step : Import Prerequisite Modules

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score
%matplotlib inline

sns.set()
```

In [ ]:

Step : Now we will load the Dataset

Dataset used here is [https://www.kaggle.com/uciml/red-wine-quality-cortez-et-al-2009 (https://www.kaggle.com/uciml/red-wine-quality-cortez-et-al-2009)](https://www.kaggle.com/uciml/red-wine-quality-cortez-et-al-2009)

In [2]:
```
#Loading data

data = pd.read_csv("./winequality-red.csv")

#Displaying Data

data.head()
```

Out[2]:

	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	5
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5

Step: Preliminary Checks

In [3]:
```
data.describe()
```

Out[3]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	densi
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.00000
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.467792	0.99674
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	0.00188
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.99007
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.99560
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.99675
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.99783
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1.00369

Step : Data Quality Check

Check if null values are present.

In [4]:
```
data.isnull().any()
```

Out[4]:
```
fixed acidity           False
volatile acidity        False
citric acid             False
residual sugar          False
chlorides               False
free sulfur dioxide     False
total sulfur dioxide    False
density                 False
pH                      False
sulphates               False
alcohol                 False
quality                 False
dtype: bool
```

So We Don't Have Any Missing Values ......

Examine the features in the data-set and their data types

In [5]:
```
display(data.info)
```

```
<bound method DataFrame.info of       fixed acidity  volatile acidity  citric ac
id  residual 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]>
```

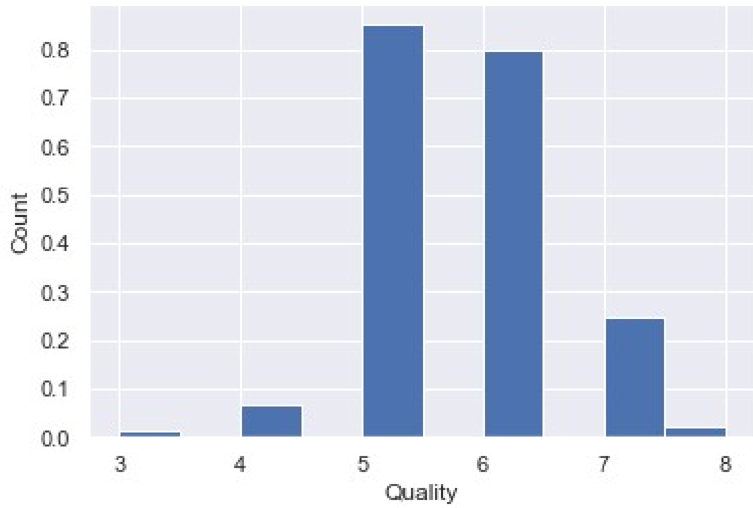
Step : Exploratory Data Analysis

Univariate Analysis :

Quality frequency Histogram

In [6]:
```
_ = plt.hist(data['quality'],normed=True)
_ = plt.xlabel('Quality')
_ = plt.ylabel('Count')
plt.show()
```

```
D:\pran\anaconda3\lib\site-packages\ipykernel_launcher.py:1: MatplotlibDeprecati
onWarning:
The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1.
Use 'density' instead.
  """Entry point for launching an IPython kernel.
```

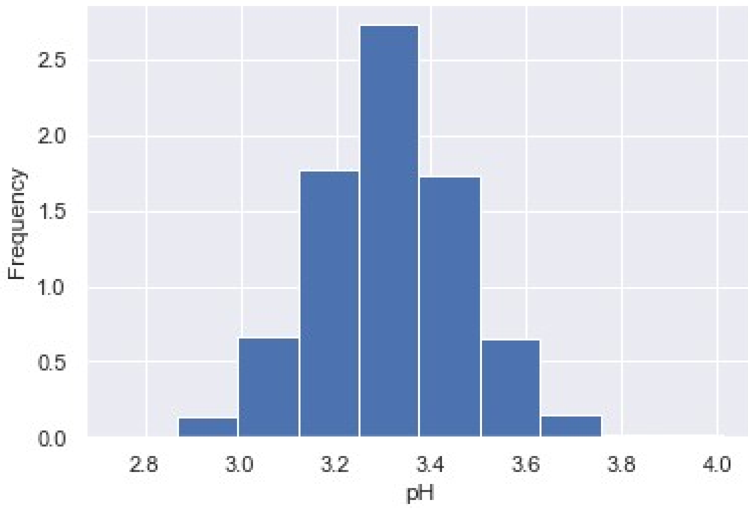


This shows quality ratings of 5,6 are high. Indicating most of the produce has been of good quality

pH Frequency Histogram

In [7]:
```
_ = plt.hist(data['pH'],normed=True)
_ = plt.xlabel('pH')
_ = plt.ylabel('Frequency')
plt.show()
```

```
D:\pran\anaconda3\lib\site-packages\ipykernel_launcher.py:1: MatplotlibDeprecati
onWarning:
The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1.
Use 'density' instead.
  """Entry point for launching an IPython kernel.
```

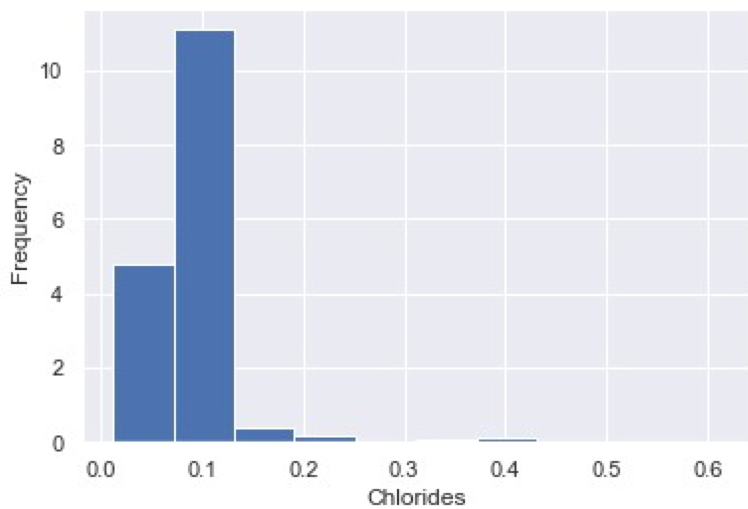


This Graph indicates pH of 3.3 was found in most test samples

Chloride Content in samples found

In [8]:
```
_ = plt.hist(data['chlorides'],normed=True)
_ = plt.xlabel('Chlorides')
_ = plt.ylabel('Frequency')
plt.show()
```

```
D:\pran\anaconda3\lib\site-packages\ipykernel_launcher.py:1: MatplotlibDeprecati
onWarning:
The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1.
Use 'density' instead.
  """Entry point for launching an IPython kernel.
```

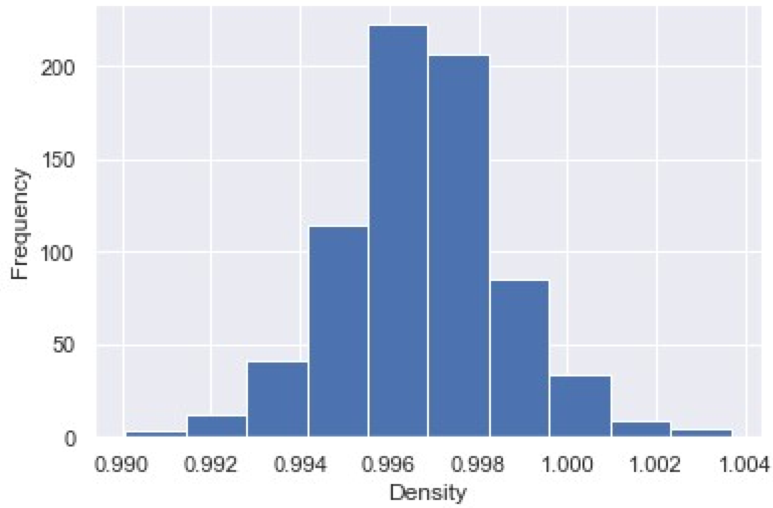


This indicates 0.1% of chlorides was found in most test Samples

Density frequency Histogram

In [9]:
```
_ = plt.hist(data['density'],normed=True)
_ = plt.xlabel('Density')
_ = plt.ylabel('Frequency')
plt.show()
```

```
D:\pran\anaconda3\lib\site-packages\ipykernel_launcher.py:1: MatplotlibDeprecati
onWarning:
The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1.
Use 'density' instead.
  """Entry point for launching an IPython kernel.
```

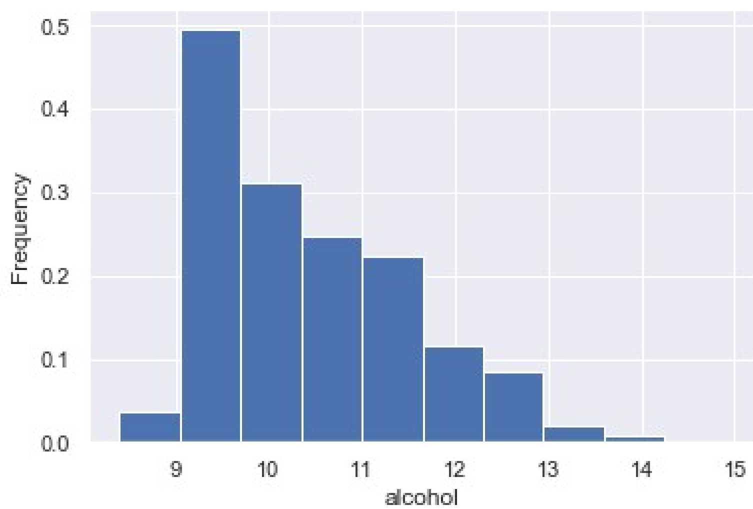


This shows 0.996-0.998 g/cm^3 density was found in most wine Samples

Alcohol content histogram

In [10]:
```
_ = plt.hist(data['alcohol'],normed=True)
_ = plt.xlabel('alcohol')
_ = plt.ylabel('Frequency')
plt.show()
```

```
D:\pran\anaconda3\lib\site-packages\ipykernel_launcher.py:1: MatplotlibDeprecati
onWarning:
The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1.
Use 'density' instead.
  """Entry point for launching an IPython kernel.
```

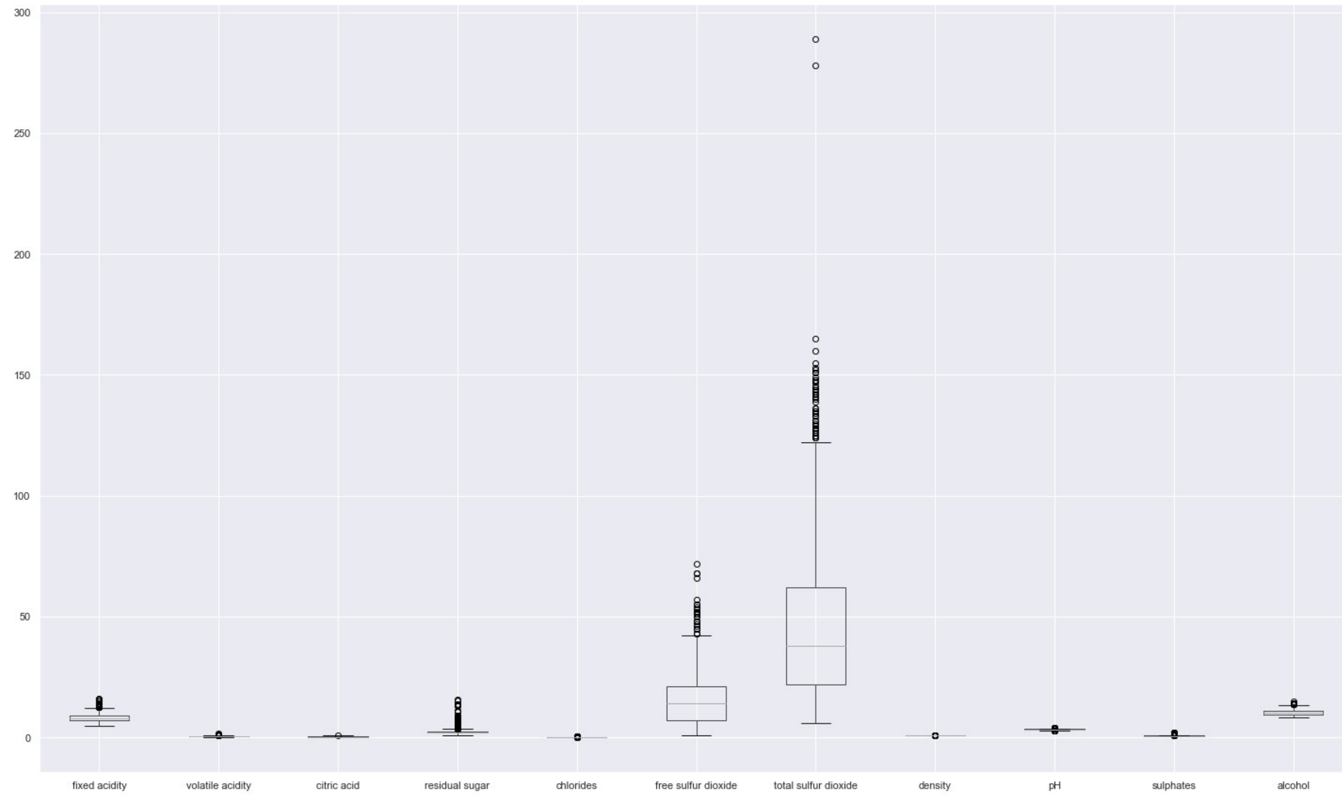


This graph indicates most red wine samples contained 9%-10% alcohol content

Boxplot analysis

All features

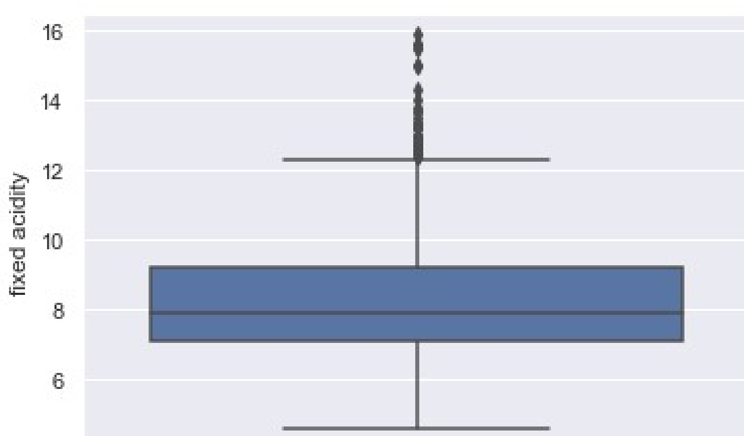
In [11]:
```
plt.figure(figsize=(25,15))
data.drop(['quality'],axis = 1).boxplot()
plt.show()
```



It can percieved that there are outliers in each feature which may cause trouble in predicting outcome

Fixed Acidity boxplot

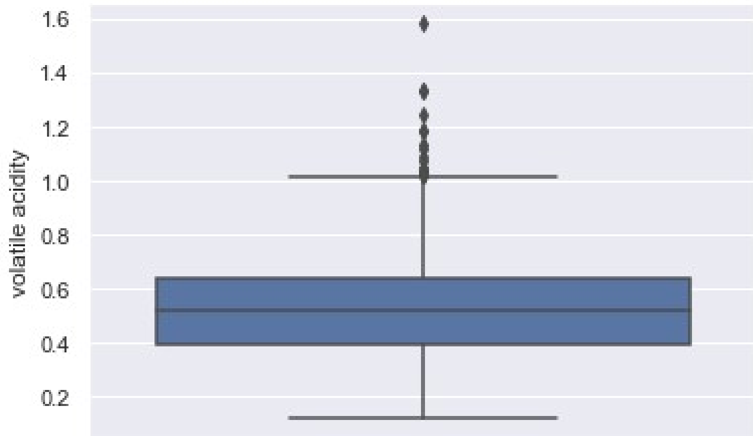
In [12]:
```
sns.boxplot(y = data['fixed acidity'])
plt.show()
```



This shows there are a few outliers above the value 14.3

Volatile acidity

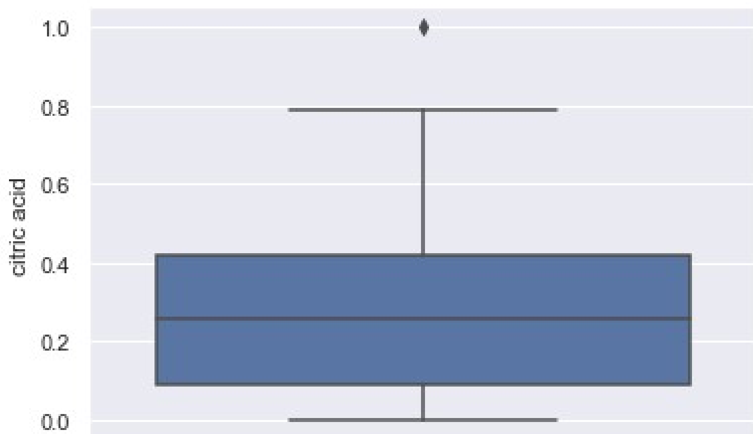
In [13]:
```
sns.boxplot(y = data['volatile acidity'])
plt.show()
```



We have outliers above 1.6

Citric acid

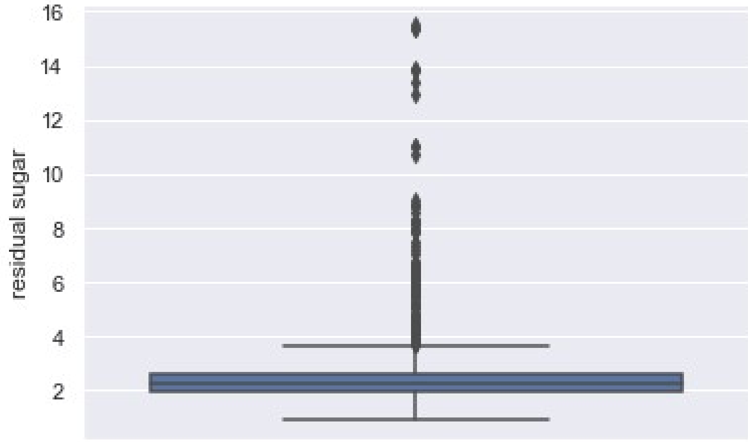
In [14]:
```
sns.boxplot(y = data['citric acid'])
plt.show()
```



Outliers are negligible

Residual Sugar

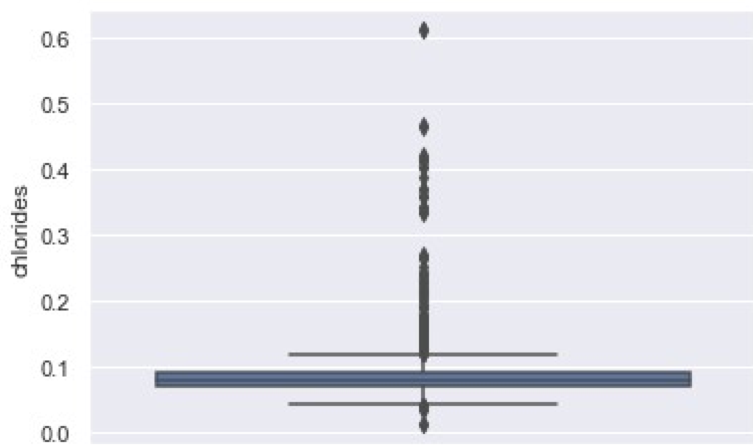
In [15]:
```
sns.boxplot(y = data['residual sugar'])
plt.show()
```



Outlier above 13

Chlorides

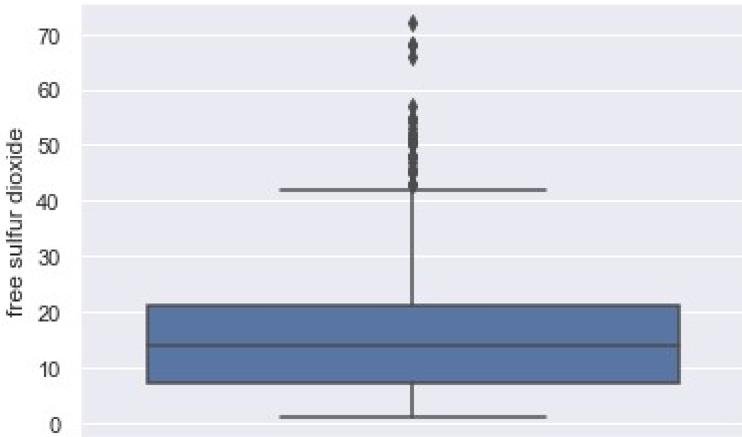
In [16]:
```
sns.boxplot(y = data['chlorides'])
plt.show()
```



Outliers above 0.6

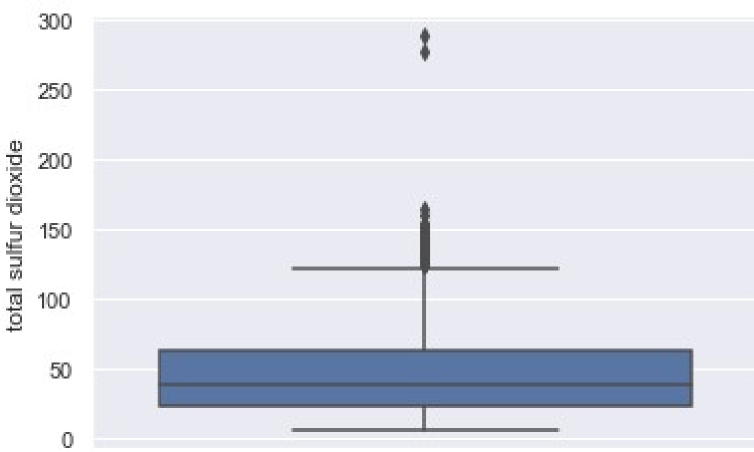
Free Sulfur Dioxides

In [17]:
```
sns.boxplot(y = data['free sulfur dioxide'])
plt.show()
```



Total Sulfur Dioxide

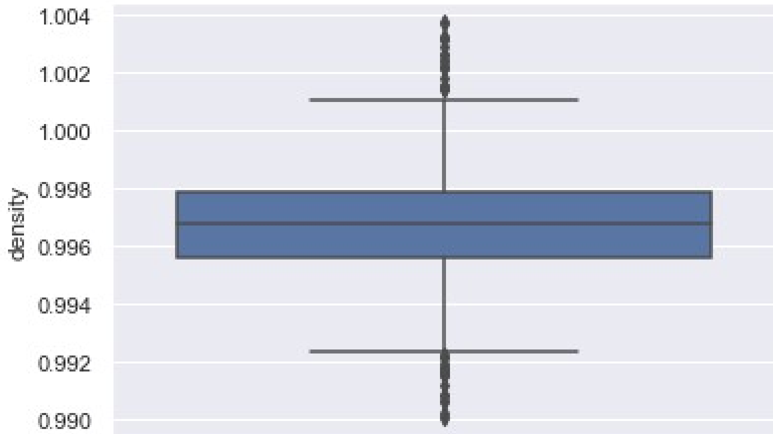
In [18]:
```
sns.boxplot(y = data['total sulfur dioxide'])
plt.show()
```



Outliers above 250

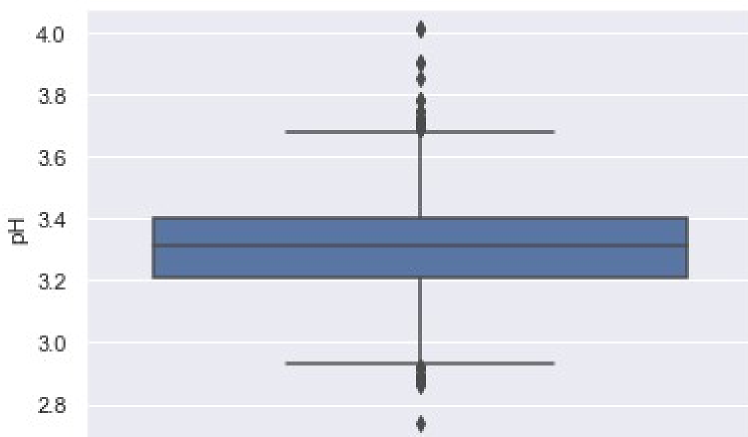
Density

In [19]:
```
sns.boxplot(y = data['density'])
plt.show()
```



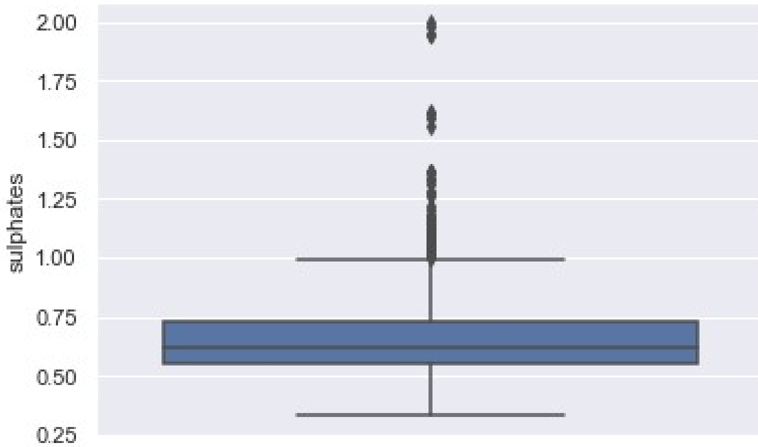
pH

In [20]:
```
sns.boxplot(y = data['pH'])
plt.show()
```



Sulphates

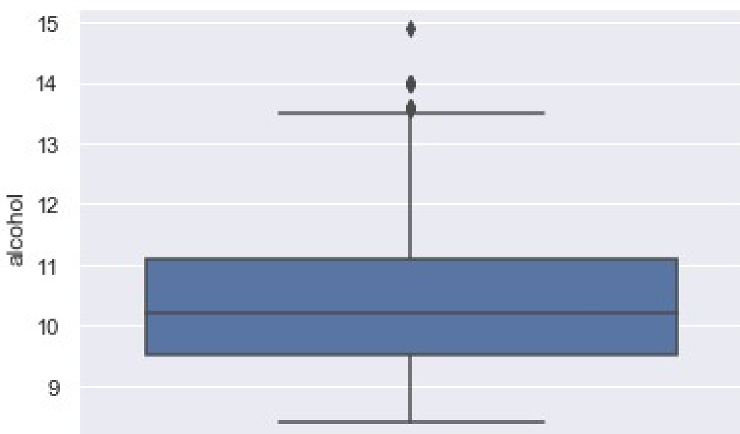
In [21]:
```
sns.boxplot(y = data['sulphates'])
plt.show()
```



Outliers above 1.75

Alcohol

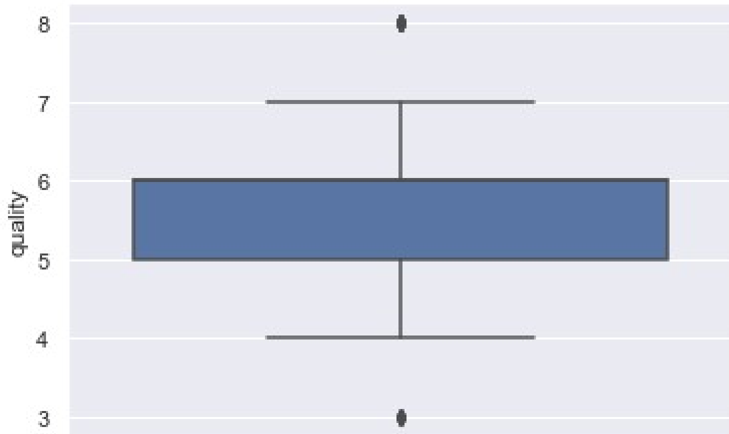
In [22]:
```
sns.boxplot(y = data['alcohol'])
plt.show()
```



Outlier at 15

Brief Quality analysis via boxplot

In [23]:
```
sns.boxplot(y = data['quality'])
plt.show()
```

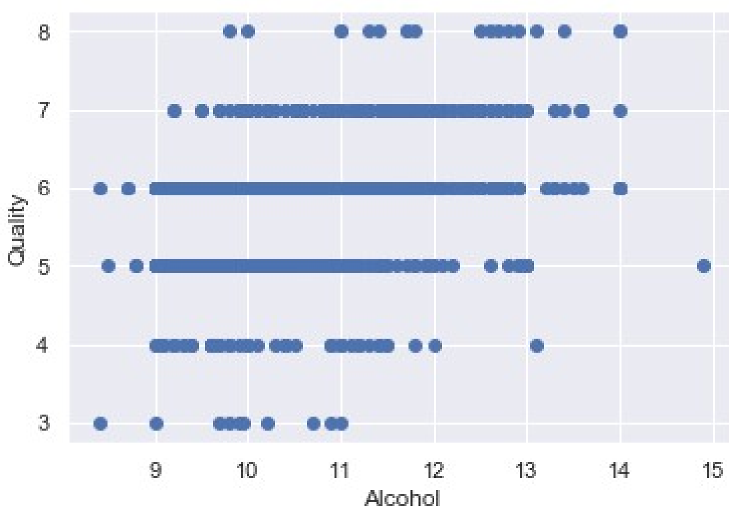


This indicates major chunk of observations had quality rating between 5-6

Bivariate Analysis

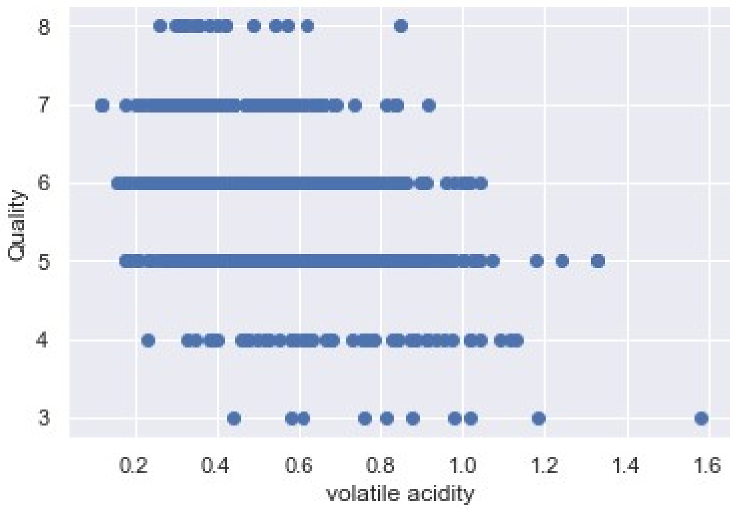
Alcohol VS quality

In [24]:
```
plt.scatter(data['alcohol'],data['quality'])
plt.xlabel('Alcohol')
plt.ylabel('Quality')
plt.show()
```



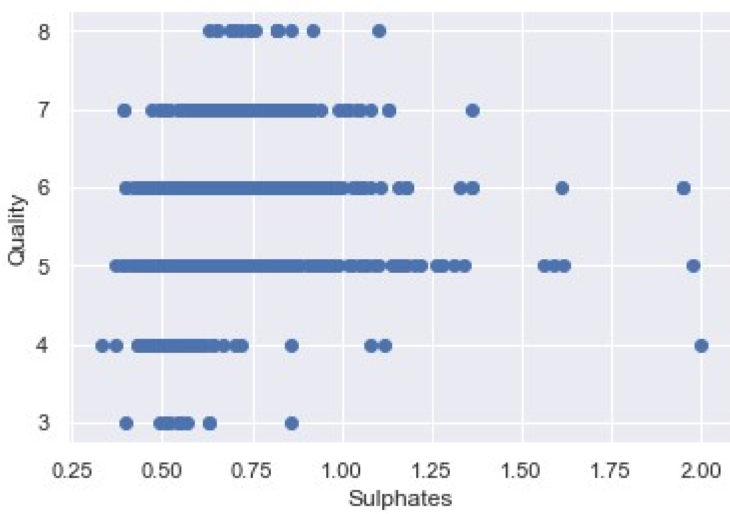
Volatile Acidity VS Quality

In [25]:
```
plt.scatter(data['volatile acidity'],data['quality'])
plt.xlabel('volatile acidity')
plt.ylabel('Quality')
plt.show()
```



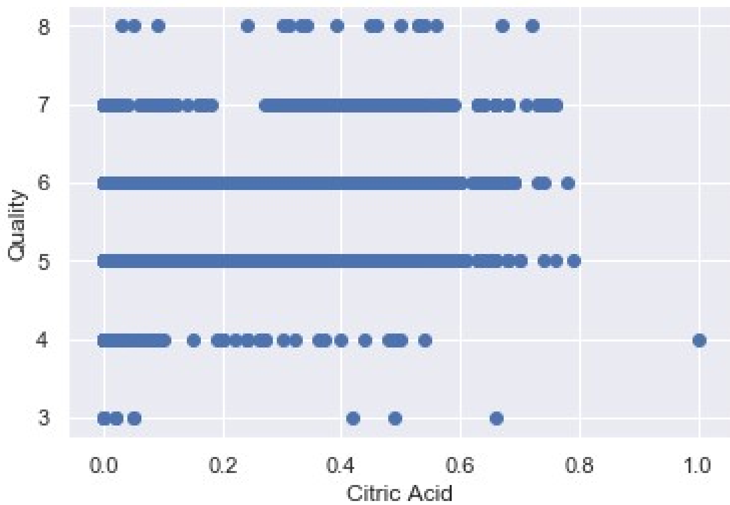
Sulphates VS Quality

In [26]:
```
plt.scatter(data['sulphates'],data['quality'])
plt.xlabel('Sulphates')
plt.ylabel('Quality')
plt.show()
```



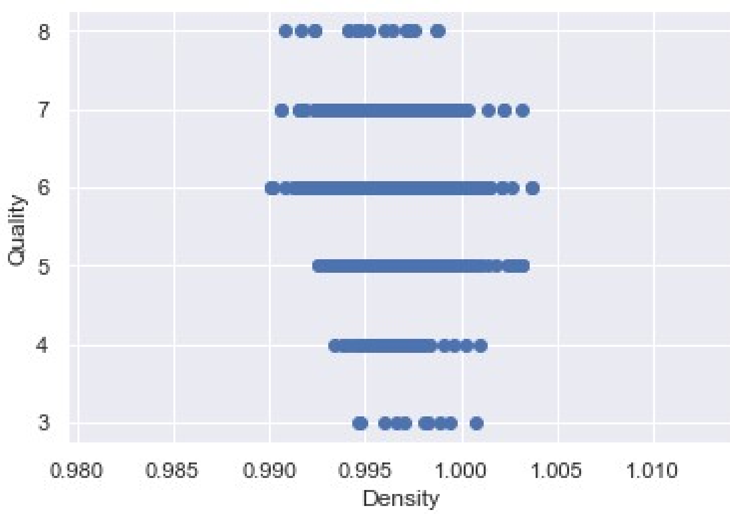
Citric Acid VS Quality

In [27]:
```
plt.scatter(data['citric acid'],data['quality'])
plt.xlabel('Citric Acid')
plt.ylabel('Quality')
plt.show()
```



Density VS Quality

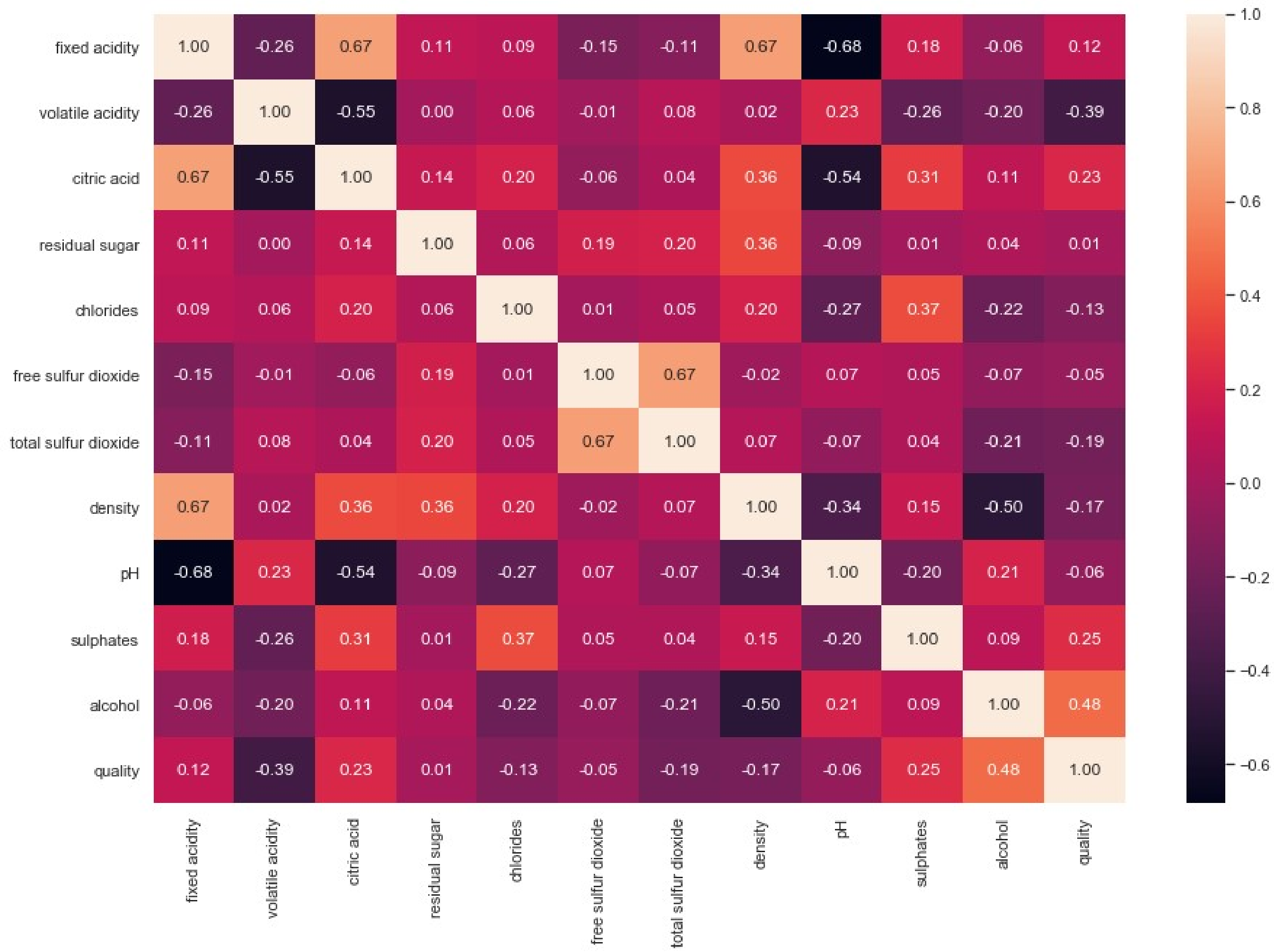
In [28]:
```
plt.scatter(data['density'],data['quality'])
plt.xlabel('Density')
plt.ylabel('Quality')
plt.show()
```



Correlation Heat-Map

In [29]:
```
plt.figure(figsize=(15,10))
sns.heatmap(data.corr(),annot = True, fmt=".2f")
```

Out[29]: <matplotlib.axes._subplots.AxesSubplot at 0x20cf12fbe08>



This suggests Quality of Wine is more dependant on alcohol and acidity than other stuff

Feature Selection :

Inferring from the above correlation matrix we can conclude that residual sugar does not play a good role the determination of quality of red Wine.

Step : Modelling

Removing Outliers

In [30]:
```
# For each feature find the data points with extreme high or low values
for feature in data.keys():
    # TODO: Calculate Q1 (25th percentile of the data) for the given feature
    Q1 = np.percentile(data[feature], q=25)

    # TODO: Calculate Q3 (75th percentile of the data) for the given feature
    Q3 = np.percentile(data[feature], q=75)

    # TODO: Use the interquartile range to calculate an outlier step (1.5 times the
interquartile range)
    interquartile_range = Q3 - Q1
    step = 1.5 * interquartile_range

    # Display the outliers
#     print("Data points considered outliers for the feature '{}':".format(featur
e))
#     display(data[~((data[feature] >= Q1 - step) & (data[feature] <= Q3 + step))])

    # OPTIONAL: Select the indices for data points you wish to remove
    outliers = []
    # Remove the outliers, if any were specified
    good_data = data.drop(data.index[outliers]).reset_index(drop = True)
```

In [31]:
```
X = good_data.drop(['quality','residual sugar'], axis = 1)
y = good_data['quality']
```

Train-test-split

In [32]:
```
X_features = X
X = StandardScaler().fit_transform(X)
```

In [33]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=.21, random_sta
te=0)
```

In [34]:
```
knn = KNeighborsClassifier(n_neighbors=90)
knn.fit(X_train,y_train)
y_pred = knn.predict(X_test)
print(y_pred)
print(classification_report(y_test, y_pred, zero_division=1))
```

```
[6 5 7 5 6 5 5 6 5 5 5 5 6 6 6 6 7 6 6 5 6 5 6 5 5 5 5 6 5 6 6 6 6 5 6 6 5
 5 6 6 5 6 6 6 6 5 5 6 5 6 5 5 5 6 6 5 5 5 7 5 5 6 6 6 5 6 5 6 6 6 5 5 5 5
 6 6 5 5 5 6 6 5 6 6 6 5 6 5 6 5 5 5 6 5 6 5 7 5 5 6 7 6 6 6 6 5 6 6 6 5 6
 5 6 5 6 6 6 7 6 6 5 6 5 5 6 7 5 5 6 7 5 5 6 6 6 5 6 5 6 5 6 5 5 5 6 6 6 6
 6 5 6 6 6 5 5 6 6 5 6 6 6 6 6 5 6 5 6 6 5 6 6 6 5 7 6 6 6 7 6 5 5 7 5 6 6
 5 5 6 5 6 6 6 5 5 5 5 5 5 5 5 5 6 5 5 5 5 5 6 6 5 6 5 5 6 5 6 6 6 6 5 5 6
 6 6 6 6 6 6 5 5 5 6 5 6 6 6 6 7 6 6 5 5 5 5 6 5 5 5 5 6 5 5 5 5 6 6 5 5 5
 6 5 6 5 6 5 5 5 5 6 6 5 6 5 6 6 6 6 5 7 6 5 6 6 6 6 5 5 5 6 6 6 6 6 5 5 6
 5 5 5 5 6 5 5 5 6 6 5 5 5 5 5 6 5 5 5 7 6 6 5 7 5 6 6 6 5 5 7 5 5 5 7 5 5
 6 5 6]
              precision    recall  f1-score   support

           3       1.00      0.00      0.00         2
           4       1.00      0.00      0.00        11
           5       0.66      0.73      0.69       144
           6       0.59      0.64      0.61       146
           7       0.47      0.28      0.35        29
           8       1.00      0.00      0.00         4

    accuracy                           0.62       336
   macro avg       0.79      0.27      0.28       336
weighted avg       0.63      0.62      0.59       336
```

In [35]:
```
print('Accuracy of the model is :      ' + str(accuracy_score(y_test, y_pred)))
```

```
Accuracy of the model is :      0.6160714285714286
```

Using Binary Quality Analysis

Here for every rating above 7 will be treated as Good Wine and rest as Bad Wine

In [36]:
```
#Create Classification version of target variable
good_data['goodquality'] = [1 if x >= 7 else 0 for x in data['quality']]
# Separate feature variables and target variable

y = good_data['goodquality']
```

In [37]:
```python
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=.21, random_sta
te=0)
knn = KNeighborsClassifier(n_neighbors=90)
knn.fit(X_train,y_train)
y_pred = knn.predict(X_test)
print(y_pred)
print(classification_report(y_test, y_pred, zero_division=1))
```

```
[0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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 0 0 0]
              precision    recall  f1-score   support

           0       0.93      0.99      0.96       303
           1       0.77      0.30      0.43        33

    accuracy                           0.92       336
   macro avg       0.85      0.65      0.70       336
weighted avg       0.91      0.92      0.91       336
```

In [38]:
```python
print('Accuracy of the model is :      ' + str(accuracy_score(y_test, y_pred)))
```

```
Accuracy of the model is :      0.9226190476190477
```

Conclusion :

Based on the box plots plotted we come to an conclusion that not all input features are essential and affect the data, for example from the bar plot against quality and residual sugar we see that as the quality increases residual sugar is moderate and does not have change drastically. So this feature is not so essential as compared to others like alcohol and citric acid, so we can drop this feature while feature selection.

For classifying the wine quality, we have implemented algorith namely, **kNeighborsClassification** We were able to achieve maximum accuracy using of **92%** when Quality was predicted as either good or bad, while accuracy of 62% was achieved when Quality was predicted with range 0-10