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ASSIGNMENT – 4

Artificial Intelligence & Machine Learning in collaboration with Google (Applied Data Science)

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#Grapes to Greatness: Machine Learning in Wine Quality Prediction

0.0.1 Task 1 : Load the Dataset

[1]:
```
# import required libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

[2]:
```
df = pd.read_csv('/content/winequality-red.csv')
df.head()
```

[2]:
```
 fixed_acidity volatile_acidity citric_acid residual_sugar chlorides \
0            7.4              0.70        0.00             1.9     0.076
1            7.8              0.88        0.00             2.6     0.098
2            7.8              0.76        0.04             2.3     0.092
3           11.2              0.28        0.56             1.9     0.075
4            7.4              0.70        0.00             1.9     0.076
 free_sulfur_dioxide total_sulfur_dioxide density pH sulphates \
0                 11.0   34.0 0.9978 3.51 0.56
1                 25.0   67.0 0.9968 3.20 0.68
2                 15.0   54.0 0.9970 3.26 0.65
3                 17.0   60.0 0.9980 3.16 0.58
4                 11.0   34.0 0.9978 3.51 0.56

   alcohol quality
0     9.4   5 1
      9.8   5 2
      9.8   5 3
      9.8   6
 4     9.4       5
```

0.0.2 Task 2 : Data preprocessing including visualization

[3]:
```
df.shape
```

[3]:
```
(1599, 12)
```

[4]:
```
df.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-nullfloat64
 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
```

```
[5]: df.isnull().sum() # There are no null values in the dataset.
```

```
[5]:  fixed_acidity        0
      volatile_acidity     0
      citric_acid          0
      residual_sugar       0
      chlorides            0
    free_sulfur_dioxide    0
    total_sulfur_dioxide   0
      density              0
      pH                   0
      sulphates            0
      alcohol              0
      quality              0
      dtype:
      int64
```

```
[6]: df.describe() # Descriptive Statistics
```

```
[6]:        fixed_acidity      volatile_acidity      citric_acid
            residual_sugar  \
      count   1599.000000    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
           chlorides  free_sulfur_dioxide  total_sulfur_dioxide   density  \
      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
count    1599.000000    1599.000000    1599.000000
1599.000000  mean   3.311113  0.658149  10.422983
5.636023 std 0.154386 0.169507 1.065668 0.807569
min   2.740000  0.330000  8.400000  3.000000  25%
3.210000 0.550000 9.500000 5.000000
50%   3.310000   0.620000   10.200000  6.000000 75%
      3.400000   0.730000   11.100000  6.000000 max
      4.010000   2.000000   14.900000  8.000000
```

[7]:
```
df.corr()
```

[7]:
```
                       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
sulphates                  0.183006      -0.260987   0.312770
alcohol                   -0.061668      -0.202288   0.109903
quality                    0.124052      -0.390558   0.226373
                      residual_sugar chlorides free_sulfur_dioxide \
fixed_acidity               0.114777 0.093705          -0.153794
volatile_acidity            0.001918 0.061298          -0.010504
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                      0.013732 -0.128907   -0.050656
                        total_sulfur_dioxide density    pH sulphates
                        \
fixed_acidity                  -0.113181 0.668047 -0.682978 0.183006
```

```
volatile_acidity                0.076470 0.022026 0.234937 -
                                0.260987
citric_acid                    0.035533 0.364947 -0.541904 0.312770
residual_sugar                 0.203028 0.355283 -0.085652 0.005527
chlorides                      0.047400 0.200632 -0.265026 0.371260
free_sulfur_dioxide            0.667666 -0.021946 0.070377 0.051658
total_sulfur_dioxide           1.000000 0.071269 -0.066495 0.042947
density                        0.071269 1.000000 -0.341699 0.148506
pH                              -0.066495 -0.341699 1.000000 -
                                0.196648
sulphates                      0.042947 0.148506 -0.196648 1.000000
alcohol                       -0.205654 -0.496180 0.205633 0.093595
quality                      -0.185100 -0.174919 -0.0577310.251397

                    alcohol   quality
fixed_acidity       -0.061668 0.124052
volatile_acidity    -0.202288 -0.390558
citric_acid          0.109903 0.226373
residual_sugar       0.042075 0.013732
chlorides           -0.221141 -0.128907
free_sulfur_dioxide -0.069408 -0.050656
total_sulfur_dioxide -0.205654 -0.185100
density            -0.496180       -
                   0.174919
pH                  0.205633       -
                    0.057731
sulphates           0.093595
                    0.251397
alcohol             1.000000
                    0.476166
quality             0.476166
                    1.000000
```

[8]:

```
# Correlation of dependent varriables with the target variable
df.corr().quality.sort_values(ascending = False)
```

[8]:

```
quality              1.000000
alcohol              0.476166
sulphates            0.251397
citric_acid          0.226373
fixed_acidity        0.124052
residual_sugar       0.013732
free_sulfur_dioxide -
                    0.050656
pH                  -
                    0.057731
chlorides           -
                    0.128907
```

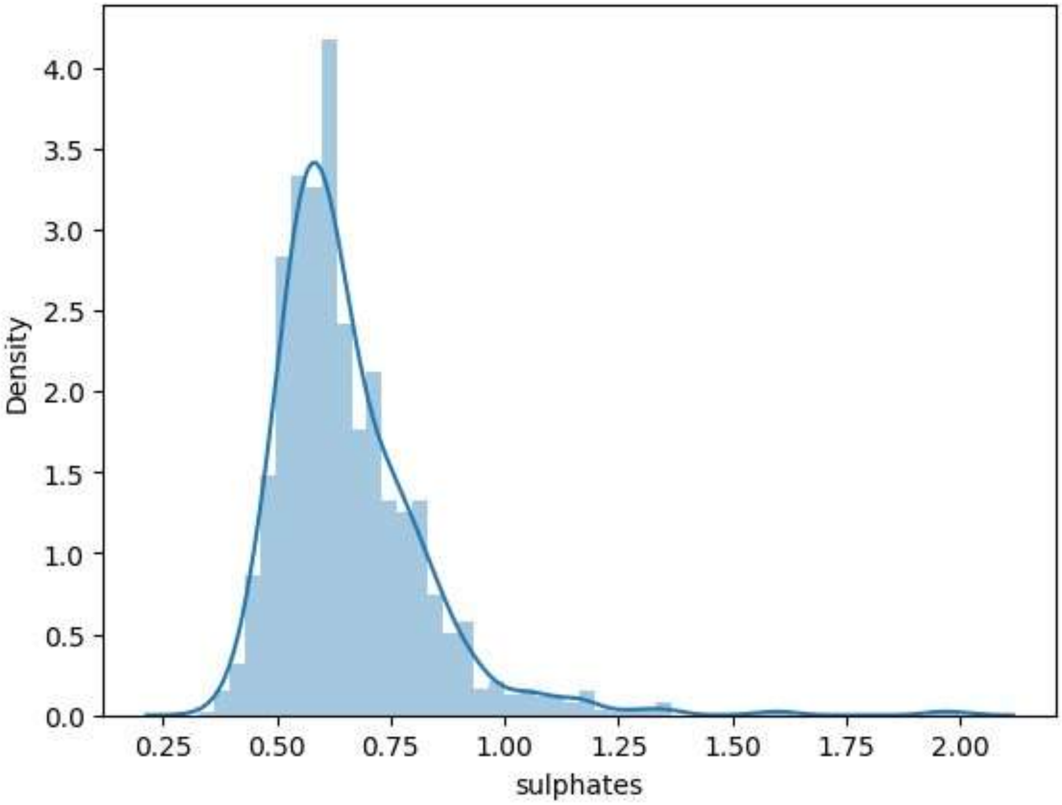
```
density              -
                     0.174919
total_sulfur_dioxide-
                     0.185100
volatile_acidity     -
                     0.390558
Name: quality, dtype: float64
```

Univariate Analysis

```
[9]: sns.distplot(df.sulphates)
```

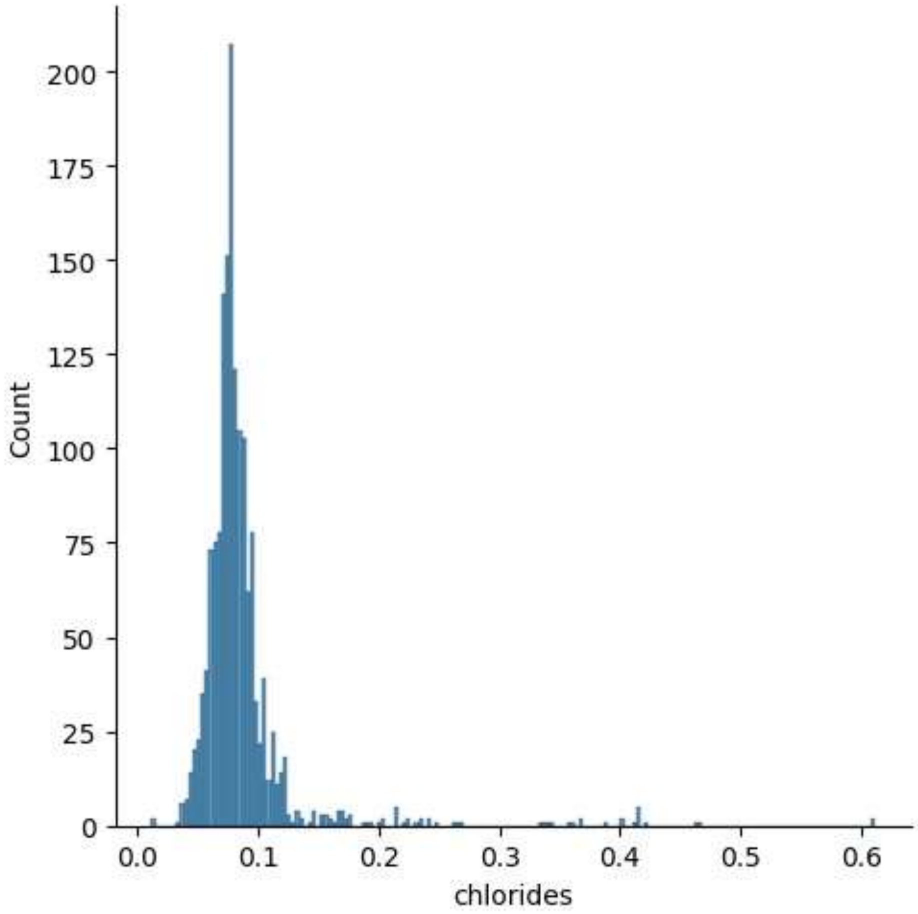
```
<ipython-input-9-8b271c44c149>:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn
v0.14.0.

Please adapt your code to use either `displot` (a figure-level function
with similar flexibility) or `histplot` (an axes-level function for
histograms).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751
  sns.distplot(df.sulphates)
```

```
[9]: <Axes: xlabel='sulphates', ylabel='Density'>
```



```
[10]: sns.displot(df.chlorides)
```

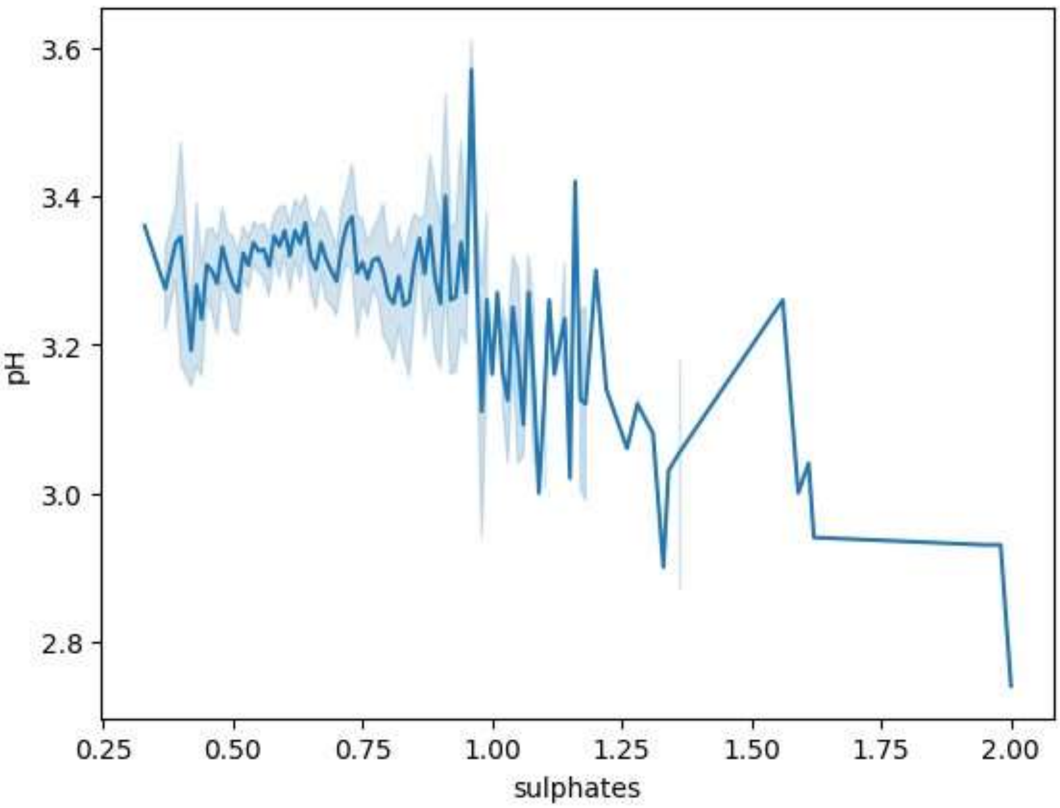
```
[10]: <seaborn.axisgrid.FacetGrid at 0x7ddd8a543160>
```



Bivariate Analysis

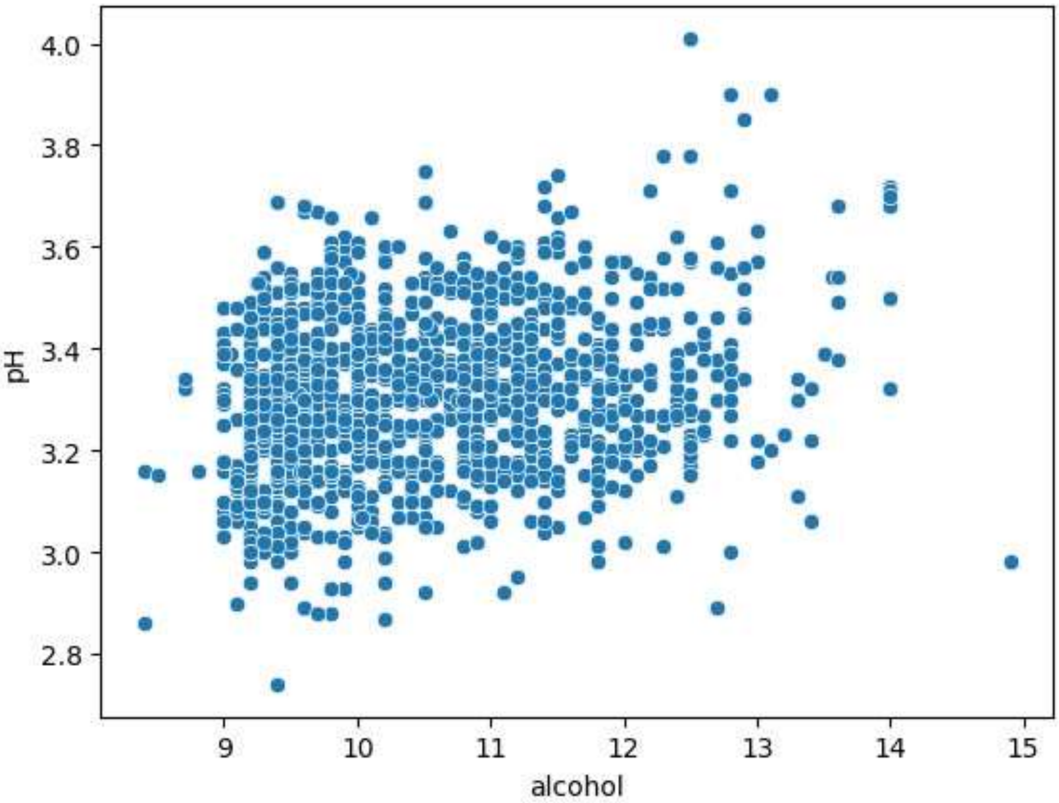
```
[11]: sns.lineplot(x=df.sulphates, y=df.pH)
```

```
[11]: <Axes: xlabel='sulphates', ylabel='pH'>
```



[12]:
```
sns.scatterplot(x=df.alcohol, y=df.pH)
```

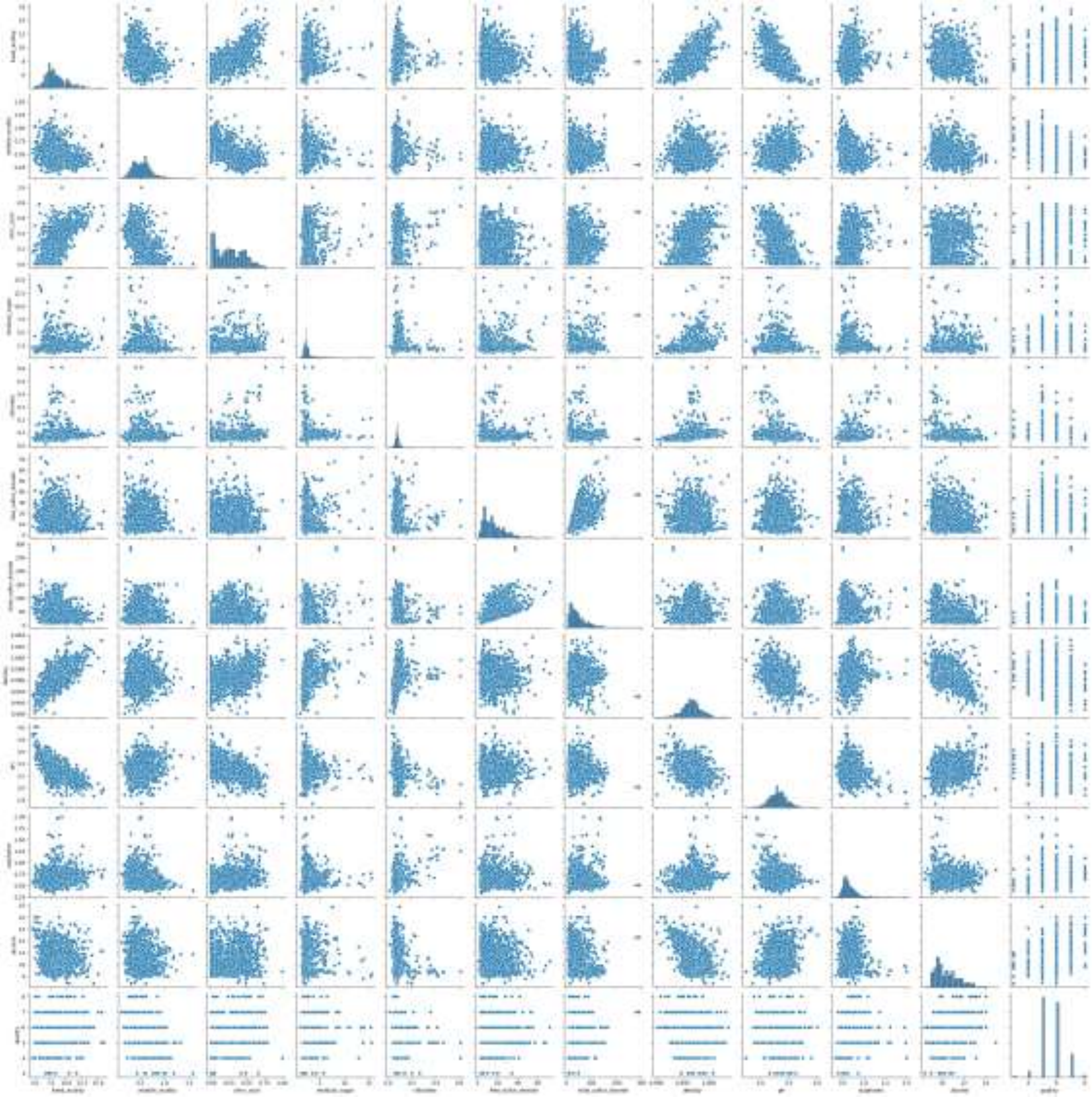
[12]:
```
<Axes: xlabel='alcohol', ylabel='pH'>
```



Multivariate Analysis

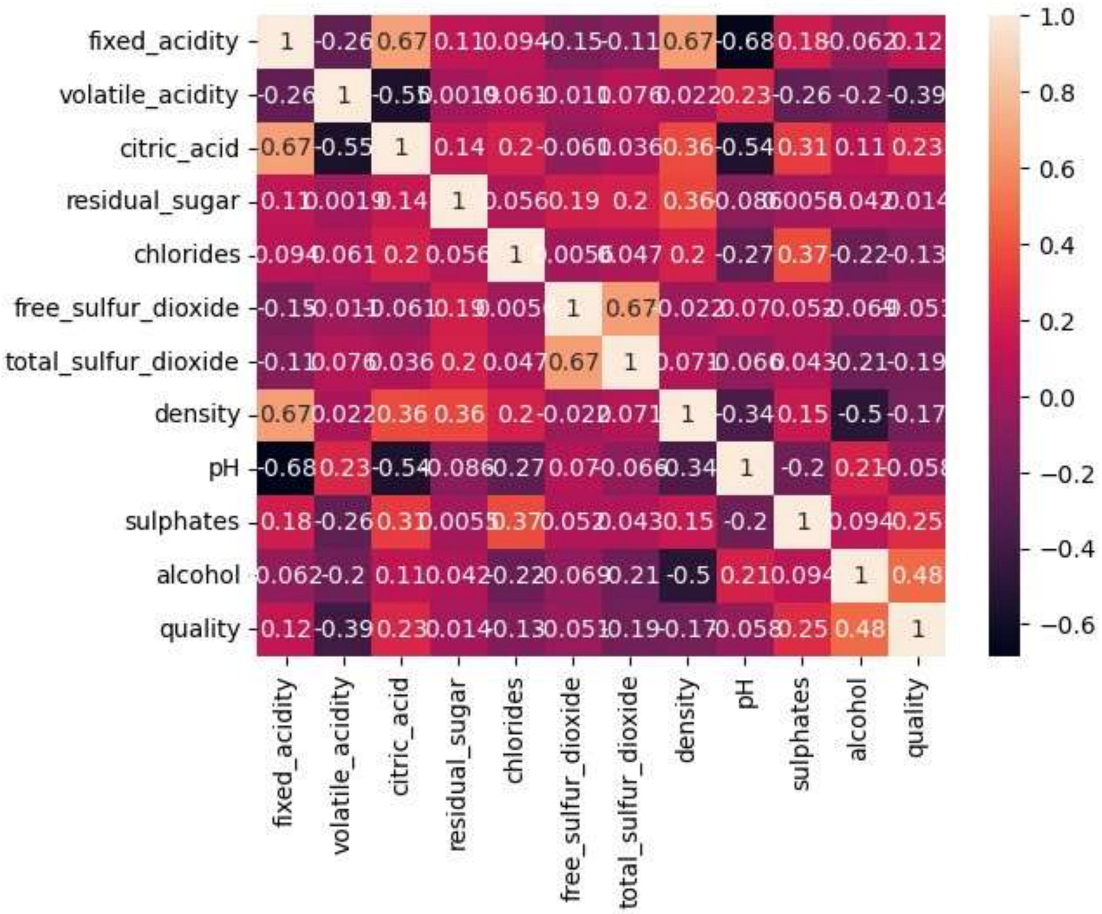
```
[13]:
sns.pairplot(df)
```

```
[13]: <seaborn.axisgrid.PairGrid at 0x7ddd4f583280>
```



```
[14]: # Correlation Heatmap

      sns.heatmap(df.corr(),annot=True)
```

```
[14]: <Axes: >
```



Outlier Detection and removal by percentile method & IQR MEthod

[16]:
```
df.head()
```

[16]:
```
 fixed_acidity volatile_acidity citric_acid residual_sugar chlorides \
0          7.4             0.70        0.00            1.9     0.076
1          7.8             0.88        0.00            2.6     0.098
2          7.8             0.76        0.04            2.3     0.092
3         11.2             0.28        0.56            1.9     0.075
4          7.4             0.70        0.00            1.9     0.076
 free_sulfur_dioxide total_sulfur_dioxide density pH sulphates \
0               11.0                 34.0 0.9978 3.51      0.56
1               25.0                 67.0 0.9968 3.20      0.68
2               15.0                 54.0 0.9970 3.26      0.65
3               17.0                 60.0 0.9980 3.16      0.58
4               11.0                 34.0 0.9978 3.51      0.56
   alcohol quality
0     9.4       5
```

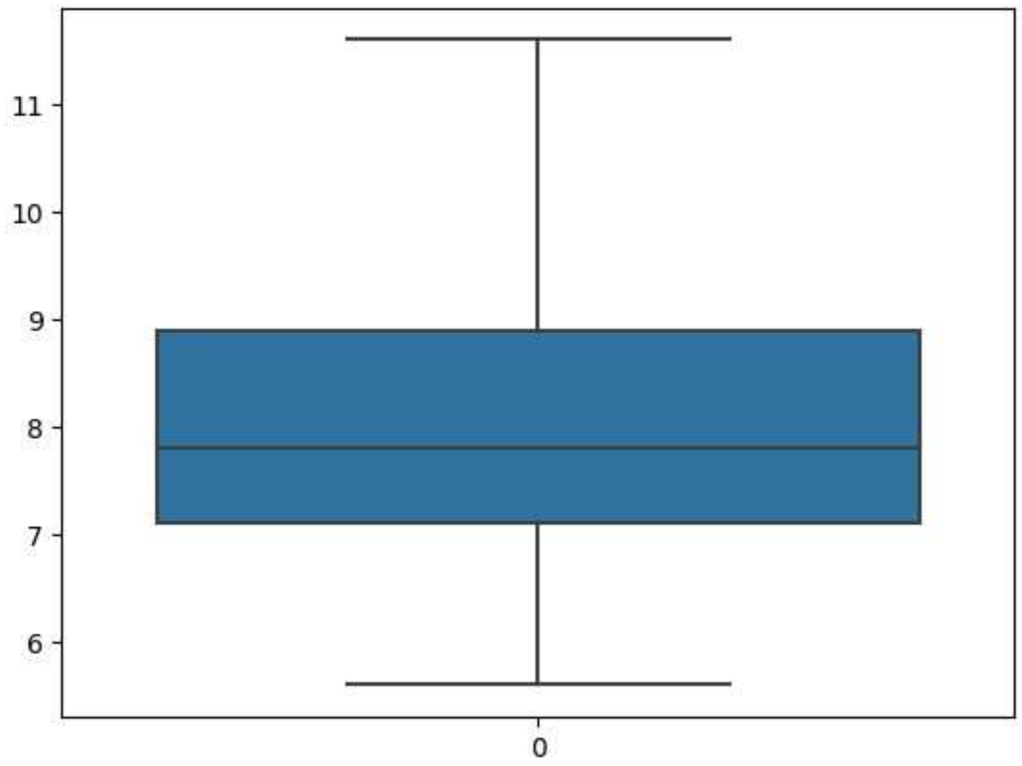
```
1      9.8       5
2      9.8       5
3      9.8       6
4      9.4       5
```

[49]:
```
# Removing outliers from fixed_acidity column

f1 = df.fixed_acidity.quantile(0.25) #Q1
f3 = df.fixed_acidity.quantile(0.75) #Q3
IQR_f = f3 - f1
upper_limit_f = f3+(1.5)*(IQR_f)
lower_limit_f = f1-(1.5)*(IQR_f)
print(f1)
print(f3)
print(IQR_f)
print(upper_limit_f)
print(lower_limit_f)
```

```
7.1
8.9
1.8000000000000007
11.600000000000001
4.3999999999999999
```

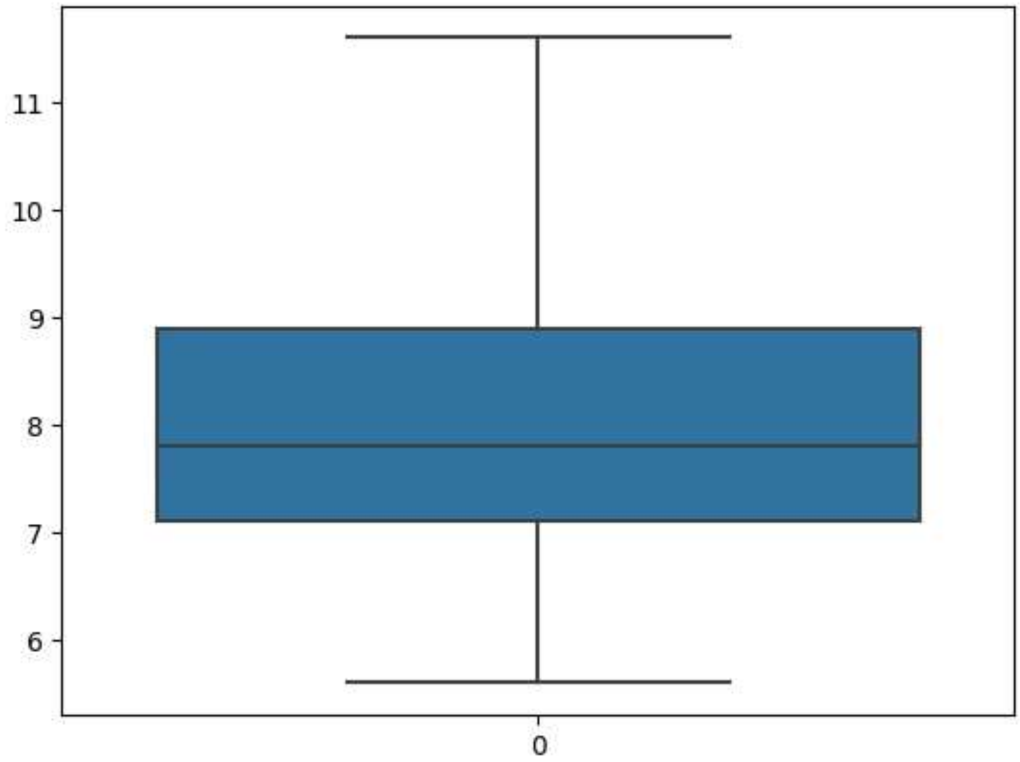
[51]:
```
df=df[(df.fixed_acidity<upper_limit_f) &
(df.fixed_acidity>lower_limit_f)] sns.boxplot(df.fixed_acidity)
```

[51]:
```
<Axes: >
```



```
[47]: fa_01=df.fixed_acidity.quantile(0.01)
      fa_9=df.fixed_acidity.quantile(0.98)
      print(fa_01)
      print(fa_98)

      5.6
      11.6
```

```
[48]: df=df[(df.fixed_acidity>=fa_01) & (df.fixed_acidity<=fa_98)]
      sns.boxplot(df.fixed_acidity)

[48]: <Axes: >
```

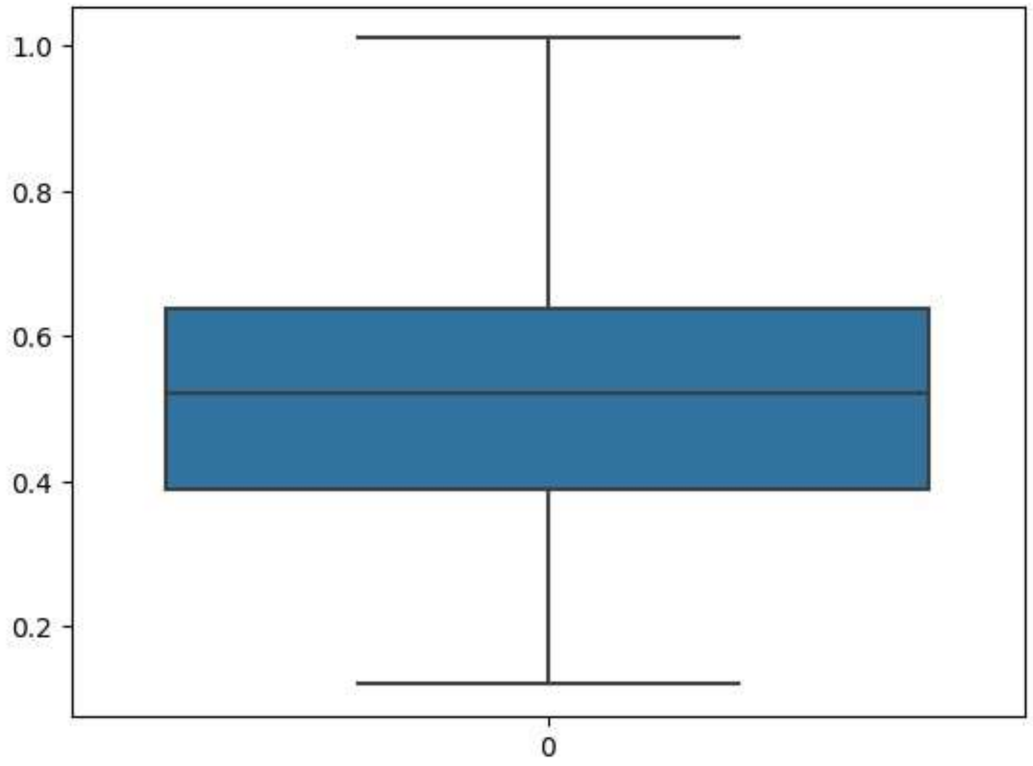


```
[22]: # Removing outliers from volatile_acidity column

      v1 = df.volatile_acidity.quantile(0.25) #Q1
      v3 = df.volatile_acidity.quantile(0.75) #Q3
      IQR_v = v3 - v1
      upper_limit_v = v3+(1.5)*(IQR_v)
      lower_limit_v = v1-(1.5)*(IQR_v)
      print(v1)
      print(v3)
      print(IQR_v)
      print(upper_limit_v)
      print(lower_limit_v)
```

```
0.3925
0.64
0.2475
1.01125

0.021250000000000047
```

```
[23]: df=df[(df.volatile_acidity<upper_limit_v) &
      (df.volatile_acidity>lower_limit_v)] sns.boxplot(df.volatile_acidity)
```

```
[23]: <Axes: >
```

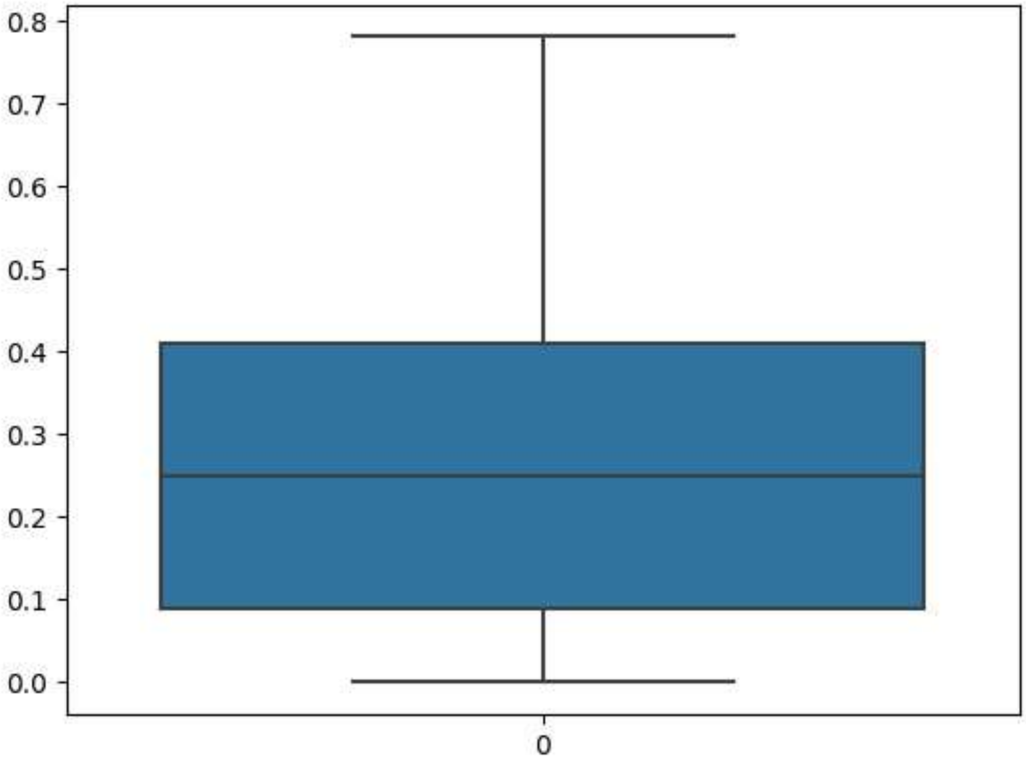


```
[24]: # Removing outliers from citric_acid column

      c1 = df.citric_acid.quantile(0.25) #Q1
      c3 = df.citric_acid.quantile(0.75) #Q3
      IQR_c = c3 - c1
      upper_limit_c = c3+(1.5)*(IQR_c)
      lower_limit_c = c1-(1.5)*(IQR_c)
      print(c1)
      print(c3)
      print(IQR_c)
      print(upper_limit_c)
      print(lower_limit_c)
```

```
      0.09
      0.41
      0.31999999999999995
      0.8899999999999999
     -0.3899999999999999
```

```
[25]: df=df[(df.citric_acid<upper_limit_c) &
      (df.citric_acid>lower_limit_c)] sns.boxplot(df.citric_acid)
```

```
[25]: <Axes: >
```

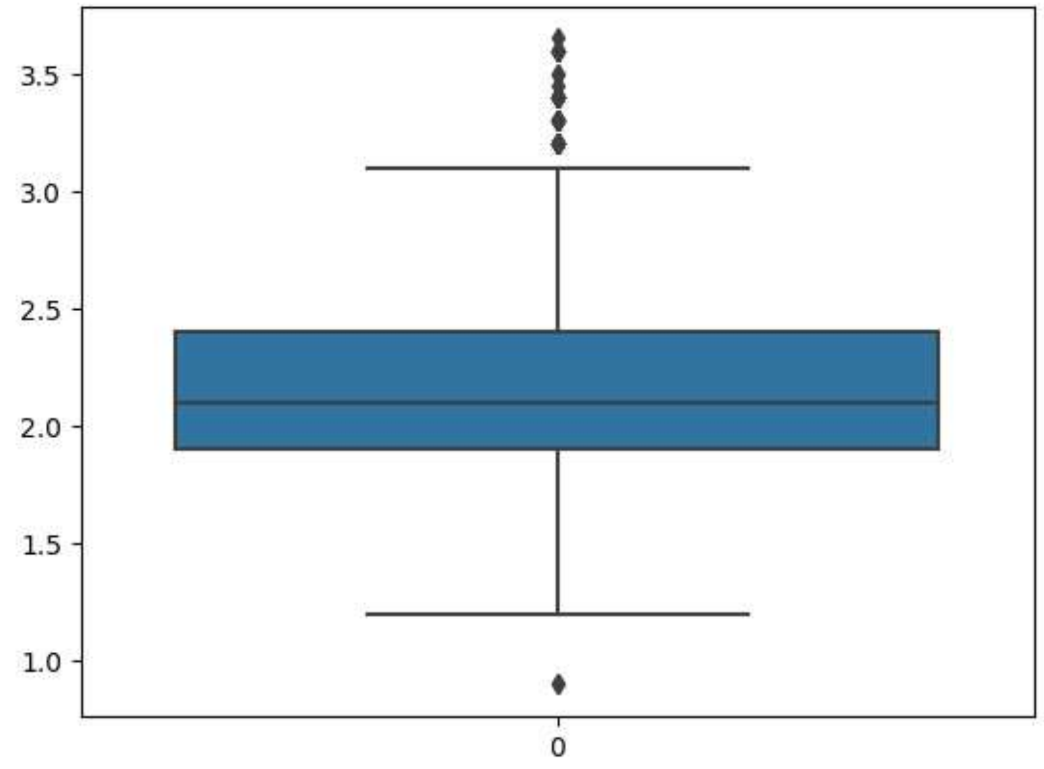


```
[26]: # Removing outliers from residual_sugar column

      r1 = df.residual_sugar.quantile(0.25) #Q1
      r3 = df.residual_sugar.quantile(0.75) #Q3
      IQR_r = r3 - r1
      upper_limit_r = r3+(1.5)*(IQR_r)
      lower_limit_r = r1-(1.5)*(IQR_r)
      print(r1)
      print(r3)
      print(IQR_r)
      print(upper_limit_r)
      print(lower_limit_r)
```

```
1.9
2.6
0.7000000000000002
3.6500000000000004
0.8499999999999996
```

```
[27]: df=df[(df.residual_sugar<upper_limit_r) &
      (df.residual_sugar>lower_limit_r)] sns.boxplot(df.residual_sugar)
```

```
[27]: <Axes: >
```

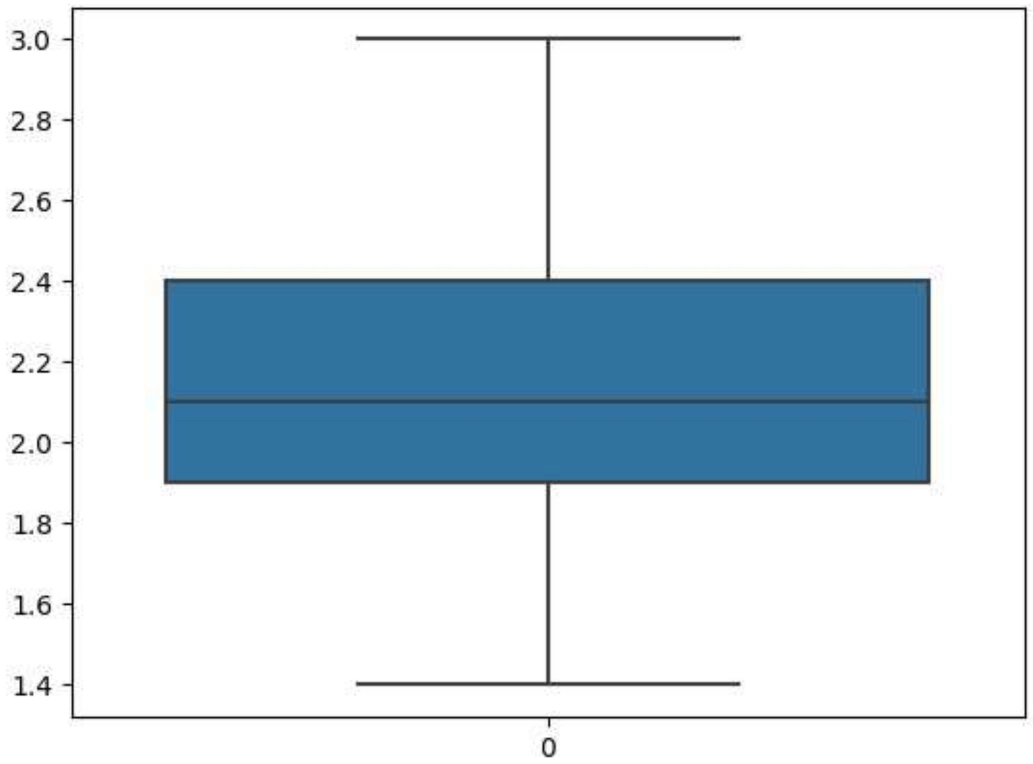


```
[34]: rs_02=df.residual_sugar.quantile(0.02)
      rs_96=df.residual_sugar.quantile(0.96)
      print(rs_02)
      print(rs_96)
```

```
1.4
3.0159999999999854
```

```
[35]: df=df[(df.residual_sugar>=rs_02) & (df.residual_sugar<=rs_96)]
      sns.boxplot(df.residual_sugar)
```

```
[35]: <Axes: >
```

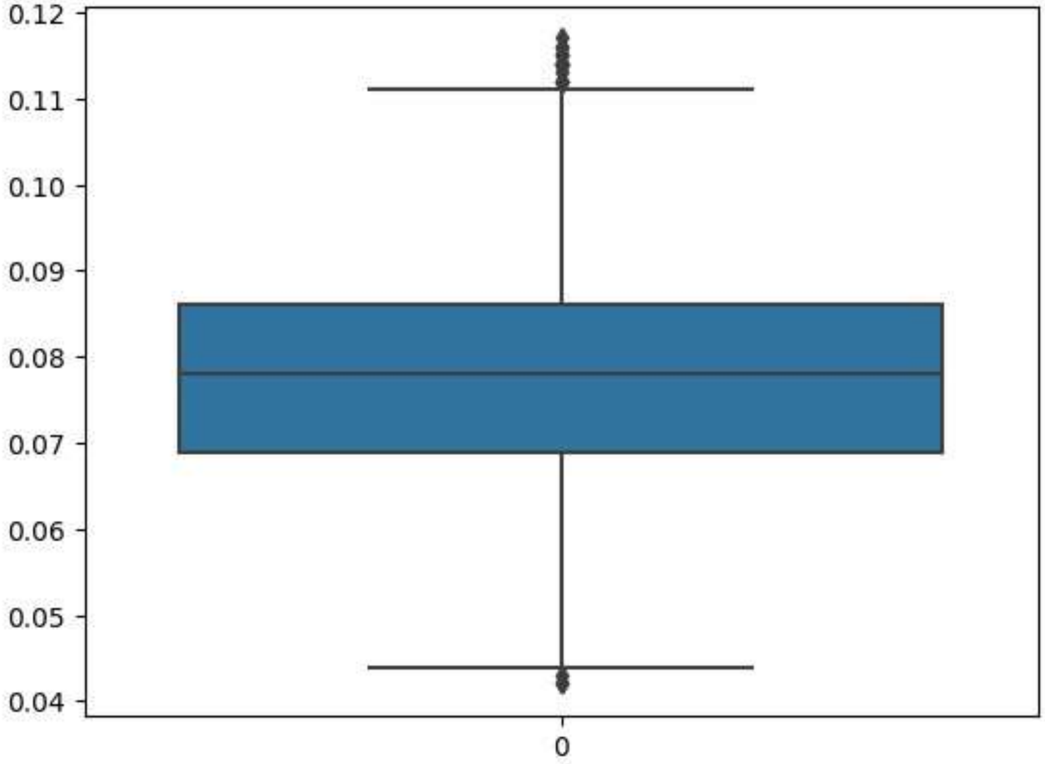


[36]:
```
# Removing outliers from chlorides column

ch1 = df.chlorides.quantile(0.25) #Q1
ch3 = df.chlorides.quantile(0.75) #Q3
IQR_ch = ch3 - ch1
upper_limit_ch = ch3+(1.5)*(IQR_ch)
lower_limit_ch = ch1-(1.5)*(IQR_ch)
print(ch1)
print(ch3)
print(IQR_ch)
print(upper_limit_ch)
print(lower_limit_ch)
```

```
0.07
0.089
0.018999999999999999
0.11749999999999998
0.04150000000000002
```

[37]:
```
df=df[(df.chlorides<upper_limit_ch) & (df.chlorides>lower_limit_ch)]
sns.boxplot(df.chlorides)
```

[37]:
```
<Axes: >
```

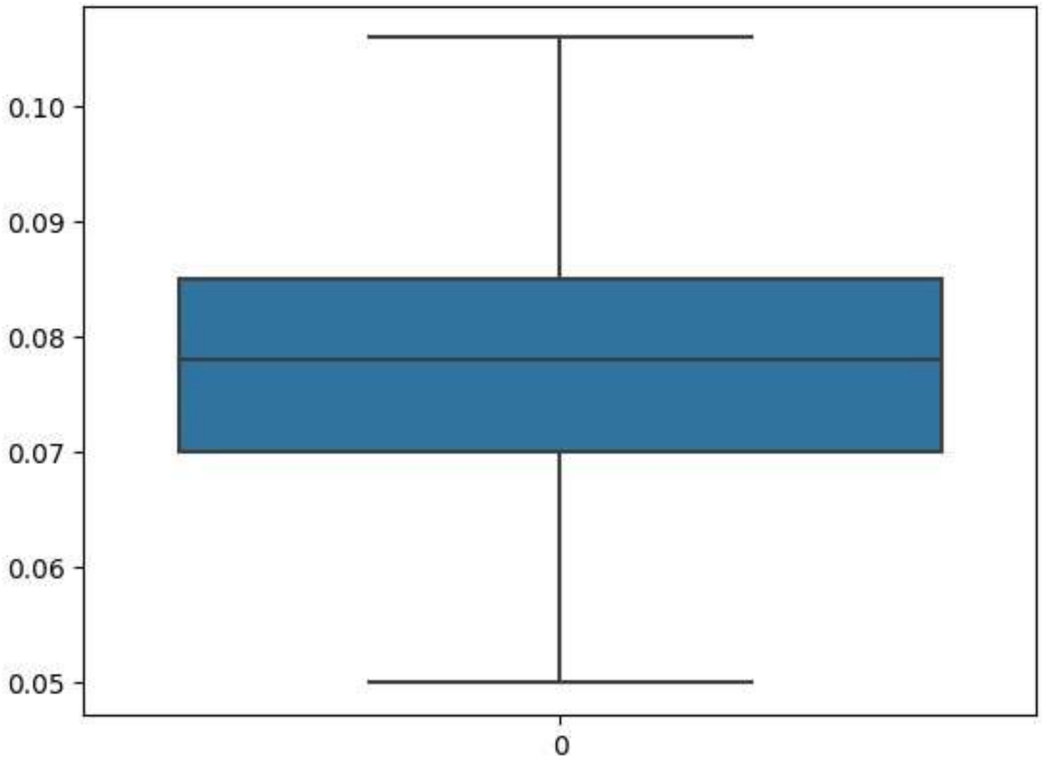


[44]:
```
ch_01=df.chlorides.quantile(0.01)
ch_97=df.chlorides.quantile(0.97)
print(ch_01)
print(ch_97)
```

```
0.049890000000000004
0.106
```

[45]:
```
 df=df[(df.chlorides>=ch_01) & (df.chlorides<=ch_97)]
sns.boxplot(df.chlorides)
```

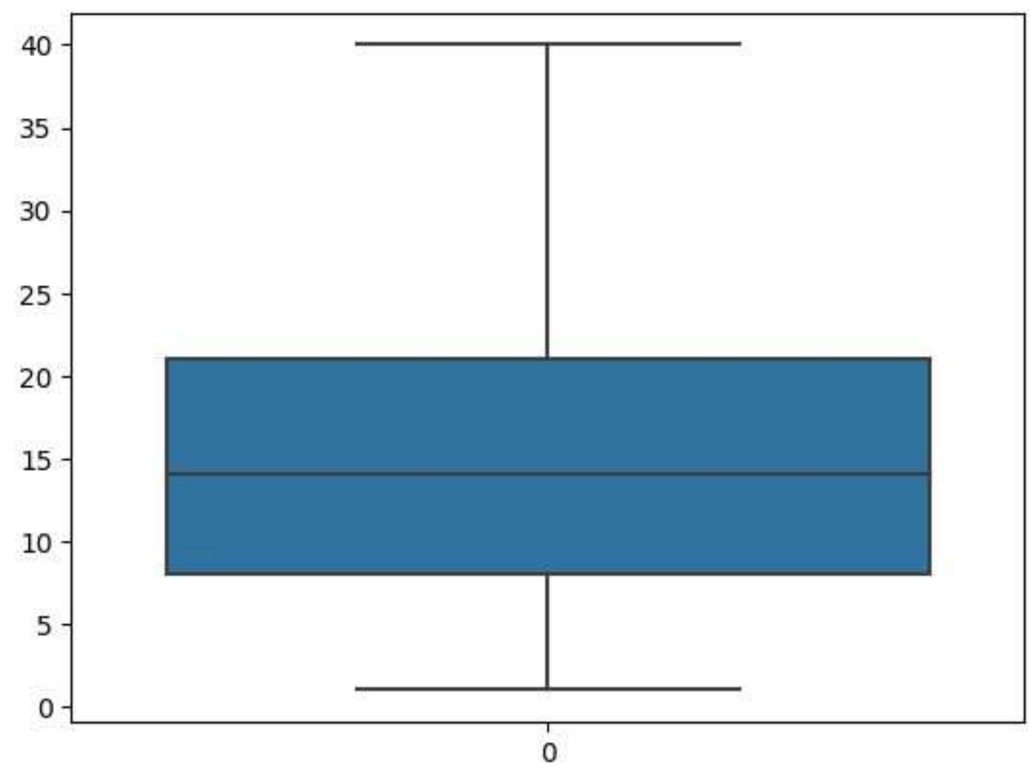
[45]:
```
<Axes: >
```



[52]:
```
# Removing outliers from free_sulfur_dioxide column

fs1 = df.free_sulfur_dioxide.quantile(0.25) #Q1
fs3 = df.free_sulfur_dioxide.quantile(0.75) #Q3
IQR_fs = fs3 - fs1
upper_limit_fs = fs3+(1.5)*(IQR_fs)
lower_limit_fs = fs1-(1.5)*(IQR_fs)
print(fs1)
print(fs3)
print(IQR_fs)
print(upper_limit_fs)
print(lower_limit_fs)
```

```
8.0
21.0
13.0
40.5 -
11.5
```

[53]:
```
df=df[(df.free_sulfur_dioxide<upper_limit_fs) & (df.
 ↪free_sulfur_dioxide>lower_limit_fs)]
sns.boxplot(df.free_sulfur_dioxide) [53]: <Axes: >
```



[54]:

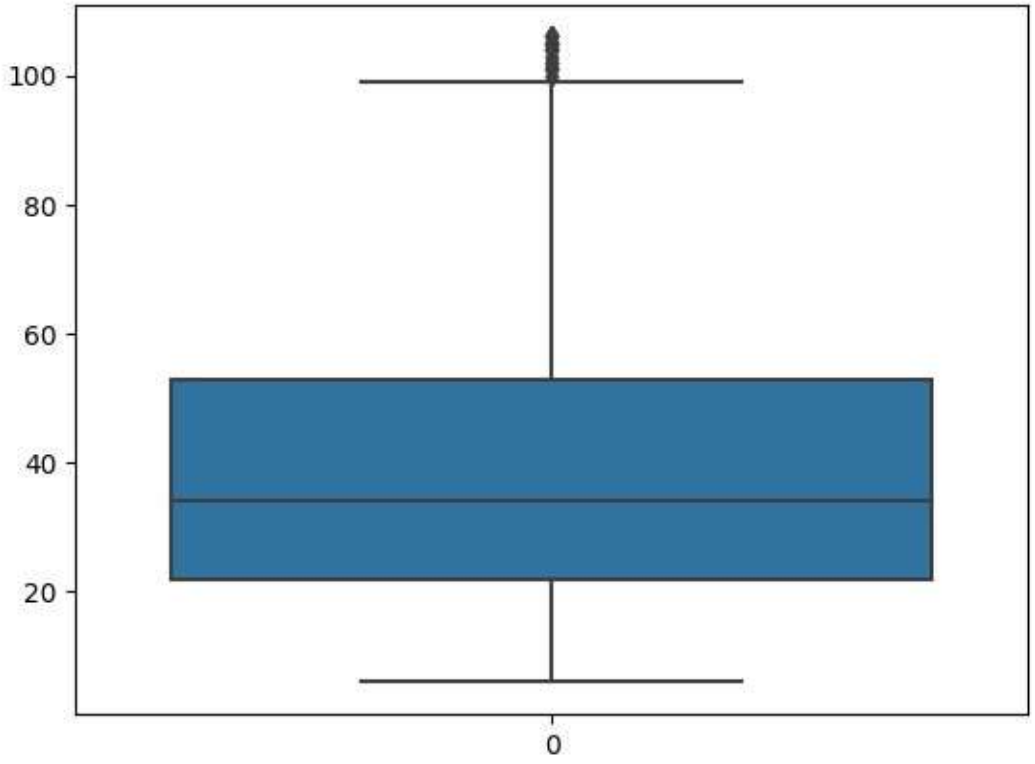
```
# Removing outliers from total_sulfur_dioxide column

ts1 = df.total_sulfur_dioxide.quantile(0.25) #Q1
ts3 = df.total_sulfur_dioxide.quantile(0.75) #Q3
IQR_ts = ts3 - ts1
upper_limit_ts = ts3+(1.5)*(IQR_ts)
lower_limit_ts = ts1-(1.5)*(IQR_ts)
print(ts1)
print(ts3)
print(IQR_ts)
print(upper_limit_ts)
print(lower_limit_ts)
```

```
23.0
57.0
34.0
108.0
-28.0
```

[55]:

```
df=df[(df.total_sulfur_dioxide<upper_limit_ts) & (df.
 ↪total_sulfur_dioxide>lower_limit_ts)]
sns.boxplot(df.total_sulfur_dioxide)
```

```
[55]: <Axes: >
```

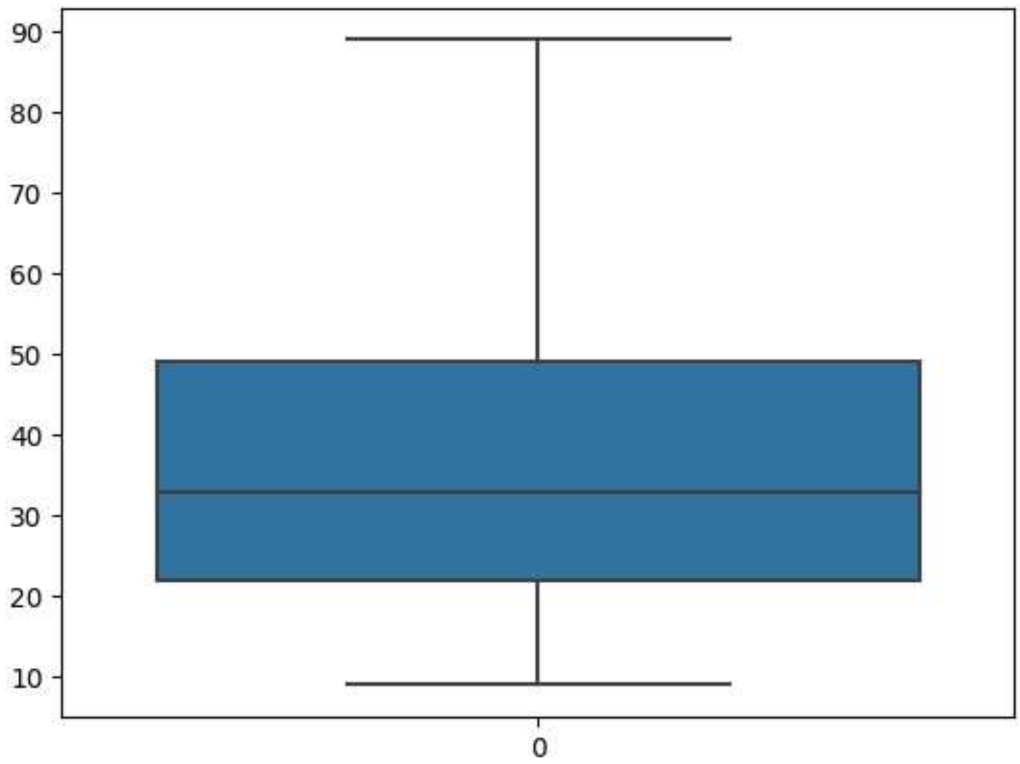


```
[60]: ts_01=df.total_sulfur_dioxide.quantile(0.01)
      ts_97=df.total_sulfur_dioxide.quantile(0.97)
      print(ts_01)
      print(ts_97)
```

```
9.0
89.0
```

```
[61]: df=df[(df.total_sulfur_dioxide>=ts_01) &
      (df.total_sulfur_dioxide<=ts_97)] sns.boxplot(df.total_sulfur_dioxide)
```

```
[61]: <Axes: >
```

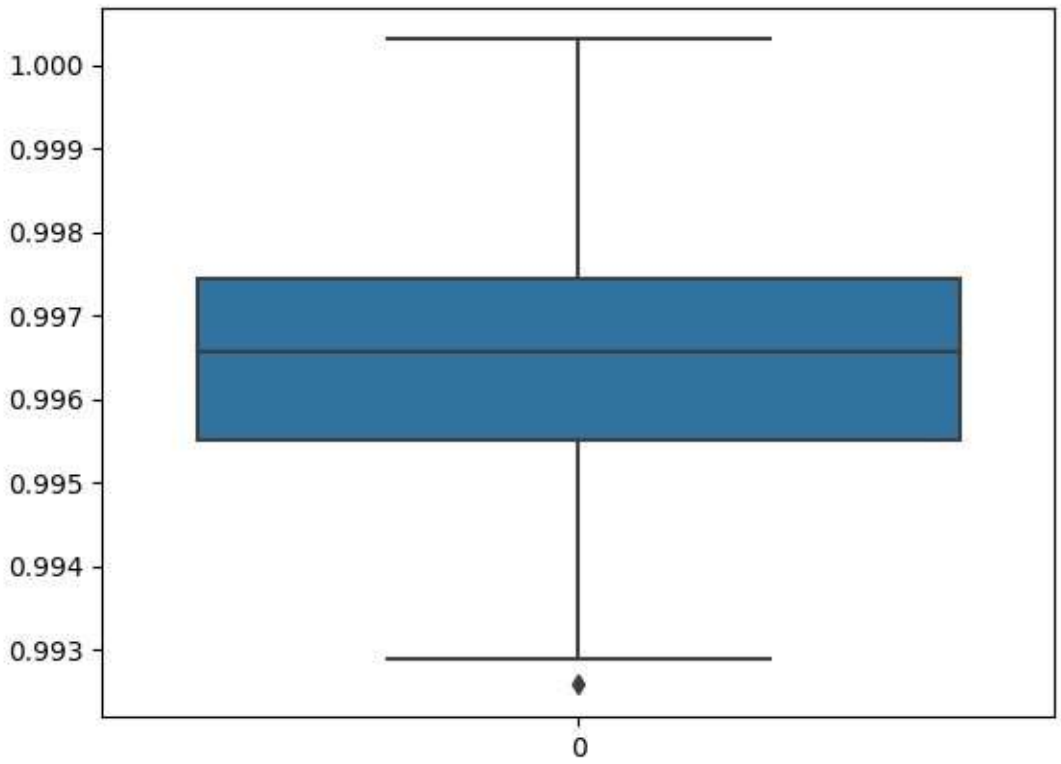


```
[62]: # Removing outliers from density column

      d1 = df.density.quantile(0.25) #Q1
      d3 = df.density.quantile(0.75) #Q3
      IQR_d = d3 - d1
      upper_limit_d = d3+(1.5)*(IQR_d)
      lower_limit_d = d1-(1.5)*(IQR_d)
      print(d1)
      print(d3)
      print(IQR_d)
      print(upper_limit_d)
      print(lower_limit_d)
```

```
0.9955
0.99745
0.0019499999999998963
1.0003749999999998
0.9925750000000002
```

```
[63]: df=df[(df.density<upper_limit_d) & (df.density>lower_limit_d)]
      sns.boxplot(df.density)
```

```
[63]: <Axes: >
```



[64]:

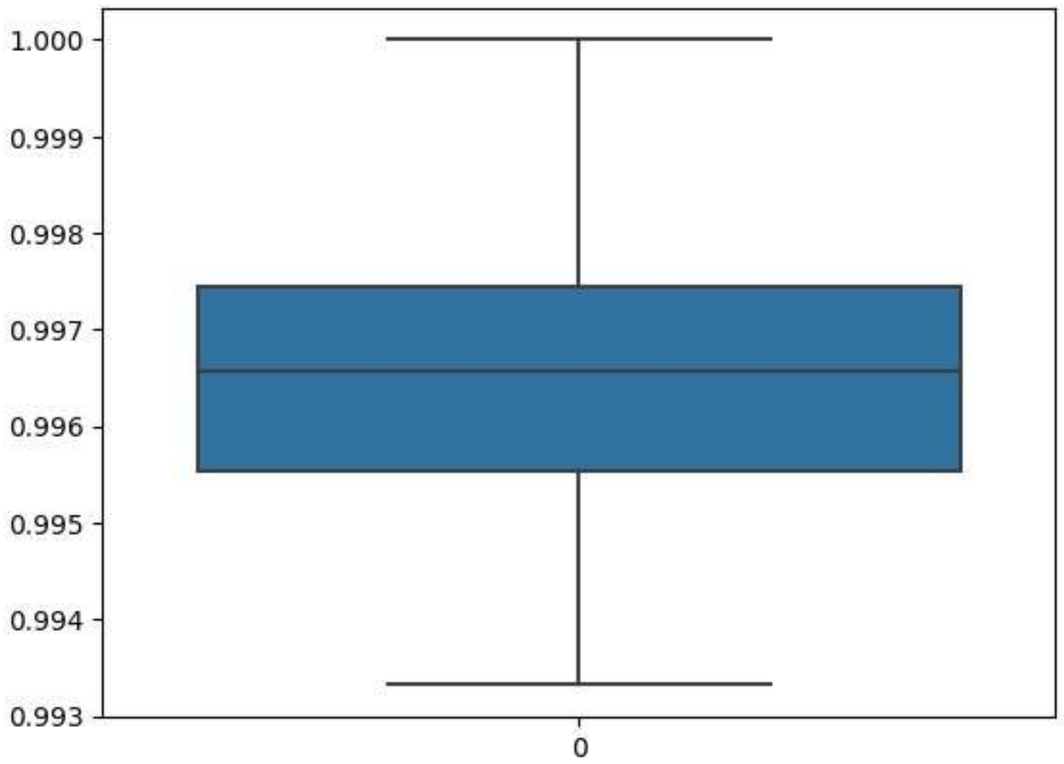
```
d_01=df.density.quantile(0.01)
d_99=df.density.quantile(0.99)
print(d_01)
print(d_99)
```

```
0.9933132
1.0
```

[65]:

```
df=df[(df.density>=d_01) & (df.density<=d_99)]
sns.boxplot(df.density)
```

```
[65]: <Axes: >
```

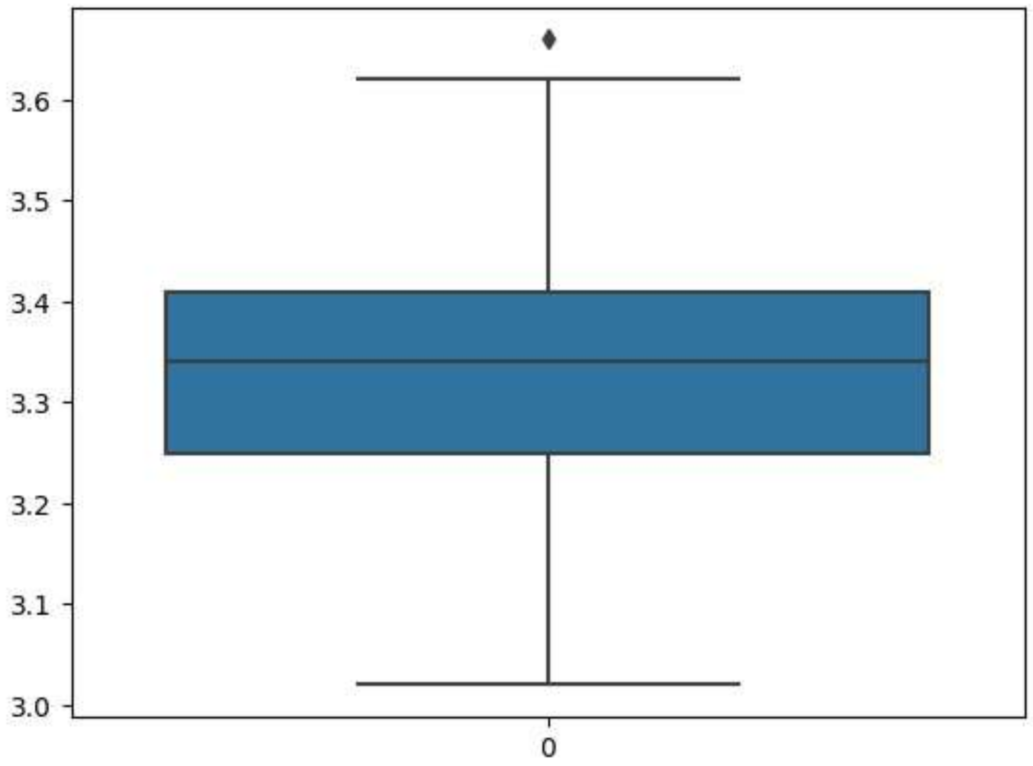


[66]:
```
# Removing outliers from pH column

pH1 = df.pH.quantile(0.25) #Q1
pH3 = df.pH.quantile(0.75) #Q3
IQR_pH = pH3 - pH1
upper_limit_pH = pH3+(1.5)*(IQR_pH)
lower_limit_pH = pH1-(1.5)*(IQR_pH)
print(pH1)
print(pH3)
print(IQR_pH)
print(upper_limit_pH)
print(lower_limit_pH)
```

```
3.2425
3.41
0.16749999999999998
3.66125
2.99125
```

[67]:
```
df=df[(df.pH<upper_limit_pH) & (df.pH>lower_limit_pH)]
sns.boxplot(df.pH)
```

[67]:
```
<Axes: >
```

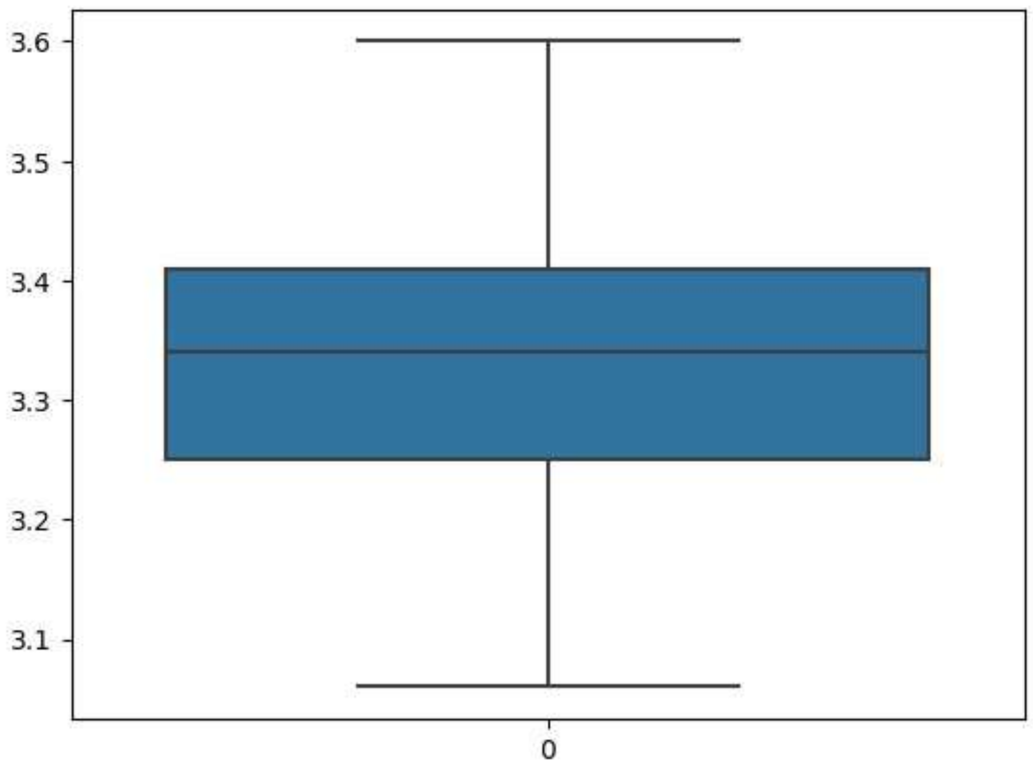


[68]:
```
pH_01=df.pH.quantile(0.01)
pH_99=df.pH.quantile(0.99)
print(pH_01)
print(pH_99)
```

```
3.06
3.6066
```

[69]:
```
df=df[(df.pH>=pH_01) & (df.pH<=pH_99)]
sns.boxplot(df.pH)
```

[69]:
```
<Axes: >
```

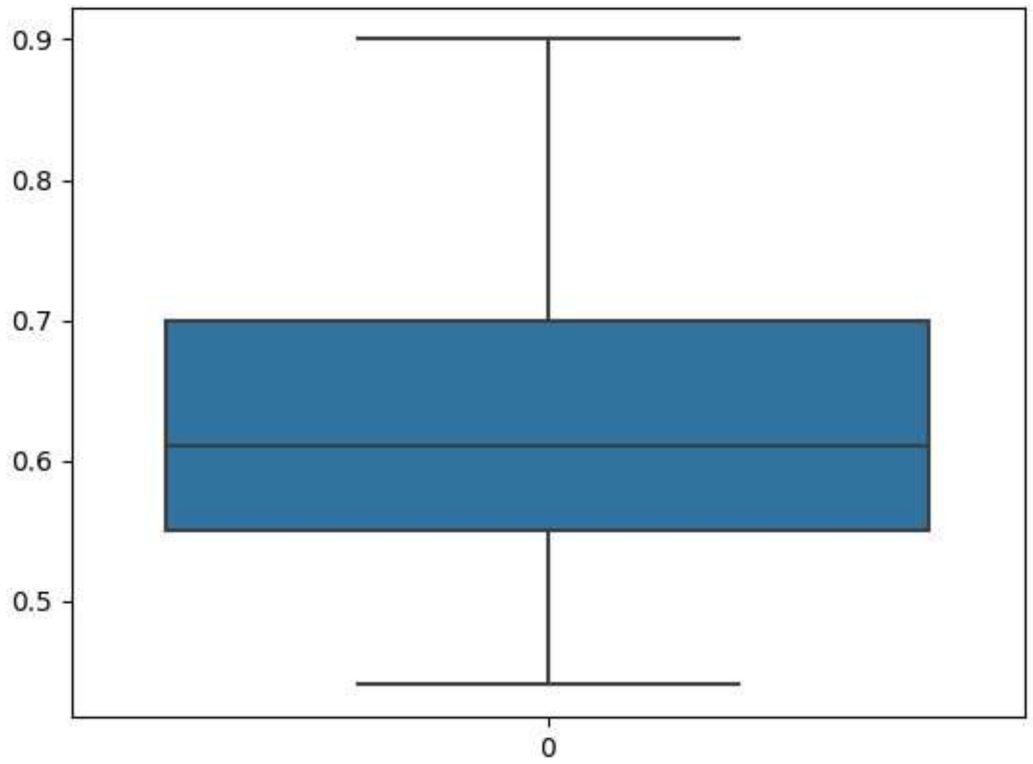


[74]:
```
# Removing outliers from fixed_acidity column

su_01=df.sulphates.quantile(0.01)
su_98=df.sulphates.quantile(0.98)
print(su_01)
print(su_98)
```

```
0.44
0.9
```

[75]:
```
df=df[(df.sulphates>=su_01) & (df.sulphates<=su_98)]
sns.boxplot(df.sulphates)
```

[75]:
```
<Axes: >
```

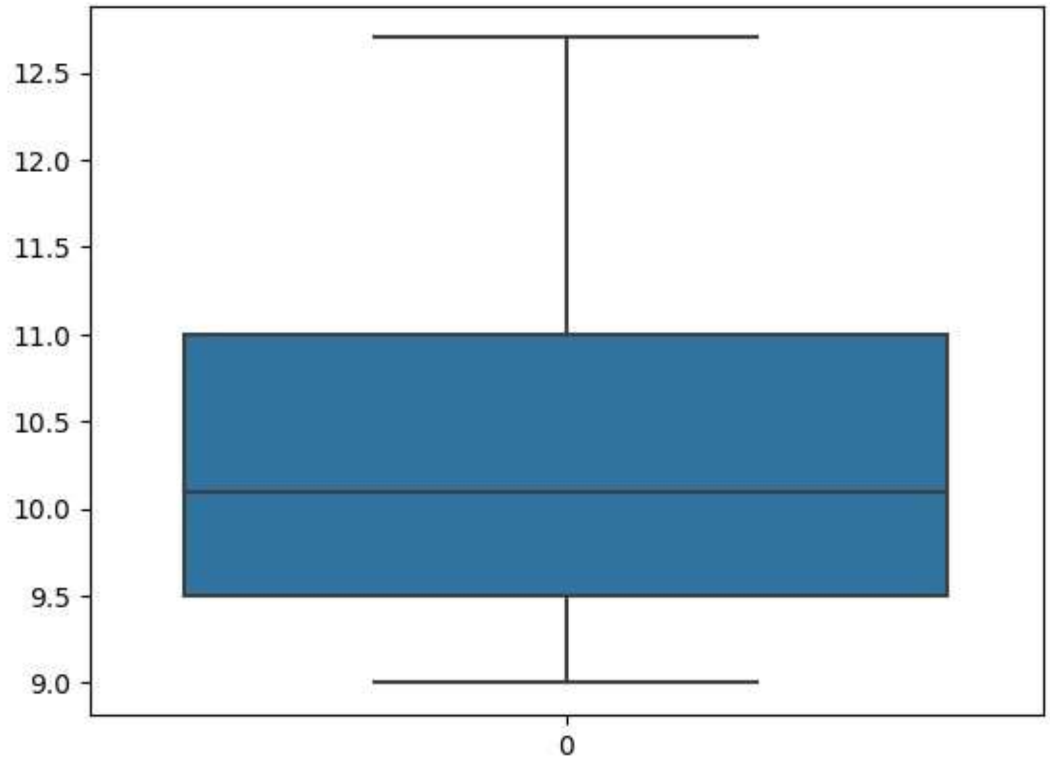


[76]:
```
# Removing outliers from alcohol column

a_01=df.alcohol.quantile(0.01)
a_99=df.alcohol.quantile(0.99)
print(a_01)
print(a_99)
```

```
9.0
12.724
```

[77]:
```
df=df[(df.alcohol>=a_01) & (df.alcohol<=a_99)]
sns.boxplot(df.alcohol)
```

[77]:
```
<Axes: >
```



Therefore all the outliers are removed

0.0.3 Task - 3 : Machine Learning Model Building

```
[233]: # split into X and y

       X =df.iloc[:,:-1]
       X.head()
```

```
[233]: fixed_acidity volatile_acidity citric_acid residual_sugar chlorides \
0          7.4  0.70  0.00  1.9   0.076

1          7.8  0.88  0.00  2.6   0.098

2          7.8  0.76  0.04  2.3   0.092

3          11.2 0.28  0.56  1.9   0.075

4          7.4  0.70  0.00  1.9   0.076

       free_sulfur_dioxide total_sulfur_dioxide density pH sulphates \
       0                 11.0                 34.0 0.9978 3.51      0.56
       1                 25.0                 67.0 0.9968 3.20      0.68
       2                 15.0                 54.0 0.9970 3.26      0.65
```

```
 3                 17.0                     60.0 0.9980 3.16       0.58
 4                 11.0                     34.0 0.9978 3.51       0.56
    alcohol
0      9.4
1      9.8
2      9.8
3      9.8
 4      9.4
```

```
[234]: Y =df.quality
       Y.head()
```

```
[234]: 0   5

1    5

2    5

3    6

4    5

        Name: quality, dtype: int64
```

Label Binarisation (Conidering alcohol quality > 7 as good and assigning ‘1’ to it else assigning ‘0’)

```
[235]: Y = df['quality'].apply(lambda y_value: 1 if y_value>=7 else 0)
```

```
[236]: print(Y)
```

```
0       0
1       0
2       0
3       0
4       0
       ..
1593    0
1594    0
1595    0
1596    0
1597    0
```

```
Name: quality, Length: 866, dtype: int64
```

```
[237]: from sklearn.model_selection import train_test_split
       X_train, X_test, Y_train, Y_test  = train_test_split(X, Y, test_size=0.2,␣
        ↪random_state=3)
```

```
[238]: X_train.shape
```

```
[238]: (692, 11)
```

```
[239]: X_test.shape
```

```
[239]: (174, 11)
```

```
[240]: print(Y.shape, Y_train.shape, Y_test.shape)
```

```
(866,) (692,) (174,)
```

0.0.4 Decision Tree Classifier

```
[242]: from sklearn.tree import DecisionTreeClassifier model1 =
       DecisionTreeClassifier(max_depth=2,splitter='best',criterion='entropy
       ') model1.fit(X_train,Y_train)
```

```
[242]: DecisionTreeClassifier(criterion='entropy', max_depth=2)
```

```
[243]: d_y_predict = model1.predict(X_test)
       d_y_predict
```

```
 [243]: array([1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 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,
           1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,
           0,
           0, 0, 0, 0, 0, 1, 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, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
           0,
           0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 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, 0, 0, 0, 0, 1, 1,
           0, 0, 0, 0])
```

```
[245]: d_y_predict_train = model1.predict(X_train)
```

0.0.5 Task - 4 : Evaluating the model (Decision tree classifier)

```
[246]: from sklearn.metrics import␣
```

```
 ↪accuracy_score,classification_report,confusion_matrix
print('Testing Accuracy = ',
accuracy_score(Y_test,d_y_predict)) print('Training Accuracy =
', accuracy_score(Y_train,d_y_predict_train))
```

```
Testing Accuracy = 0.8793103448275862
Training Accuracy = 0.8916184971098265
```

0.0.6 Random Forest Classifier

```
[247]: from sklearn.ensemble import RandomForestClassifier model2
       =RandomForestClassifier(n_estimators=200,criterion='entrop
       y') model2.fit(X_train,Y_train)
```

```
[247]: RandomForestClassifier(criterion='entropy', n_estimators=200)
```

```
[248]: r_y_predict = model2.predict(X_test)
       r_y_predict_train = model2.predict(X_train)
```

0.0.7 Task - 4 : Evaluating Random Forest Model

```
[249]: print('Testing Accuracy = ', accuracy_score(Y_test,r_y_predict))
       print('Training Accuracy = ',
       accuracy_score(Y_train,r_y_predict_train))
```

```
Testing Accuracy = 0.9425287356321839
Training Accuracy = 1.0
```

0.0.8 Naive Bayesian Classification Model

```
[251]: from sklearn.naive_bayes import GaussianNB
       gnb = GaussianNB()
       gnb.fit(X_train,Y_train)
```

```
[251]: GaussianNB()
```

```
[252]: y_pred2 = gnb.predict(X_test)
       y_pred2
```

```
  [252]: array([1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1,
0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                                                              0, 0, 0,
           0, 0, 0, 1, 0, 0, 0, 0, 1, 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, 1, 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, 0,
           1,
           0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0,
           0,
           0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0,
           1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0,
           0, 0, 0, 0])
```

0.0.9 Task - 4 : Evaluating Naive Bayesian Classification Model

```
[254]: from sklearn.metrics import accuracy_score
       gnb_acc=accuracy_score(Y_test,y_pred2)
       gnb_acc
```

```
[254]: 0.8850574712643678
```

0.1 Accuracies of all the algorithms used in model nuilding phase :

Decision Tree Classification : 87.93 %

0.1.1 Random Forset Classification : 94.25 %

Naive Bayesian Classification : 88.50 %

0.1.2 Conclusion : Random Forest Classifier Model is best suited for the wine quality dataset.

0.1.3 Task - 5 : Test with random observation

```
[262]:  input_data = [7.9, 1.0, 0, 3.0, 0.08, 30, 100, 0.9562, 3.1,
       0.74, 11.5] prediction = model1.predict([input_data])
       prediction
```

```
       /usr/local/lib/python3.10/dist-packages/sklearn/base.py:439:
       UserWarning: X does not have valid feature names, but
       DecisionTreeClassifier was fitted with feature names
         warnings.warn(
```

```
[262]: array([0])
```

According to “decision tree classifier” model, the above random observation gives prediction “array([0])” i.e., bad quality alcohol

```
[263]:  input_data_2 = [7.9, 1.0, 0, 3.0, 0.08, 30, 100, 0.9562, 3.1,
       0.74, 11.5] prediction2 = model2.predict([input_data_2])
       prediction2
```

```
       /usr/local/lib/python3.10/dist-packages/sklearn/base.py:439:
       UserWarning: X does not have valid feature names, but
       RandomForestClassifier was fitted with feature names
         warnings.warn(
[263]: array([0])
```

According to "Random Forest classifier" model, the above random observation gives prediction "array([0])" i.e., bad quality alcohol

```
[264]: input_data_3 = [7.9, 1.0, 0, 3.0, 0.08, 30, 100, 0.9562, 3.1,
0.74, 11.5] prediction3 = gnb.predict([input_data_3])
prediction3
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/base.py:439:
UserWarning: X does not have valid feature names, but GaussianNB was
fitted with feature names
  warnings.warn(
```

```
[264]: array([0])
```

According to "Naive Bayesian classifier" model, the above random observation gives prediction "array([0])" i.e., bad quality alcohol

0.2 CONCLUSION : For the same random observation, all the three models gave the "alchohol quality is BAD"