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#Grapes to Greatness: Machine Learning in Wine Quality Prediction

Task 1 : Load the Dataset

In [1]:

```
# import required libraries

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

In [2]:

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

Out[2]:

	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_sulfur_dioxide	to
0	7.4	0.70	0.00	1.9	0.076	11.0	
1	7.8	0.88	0.00	2.6	0.098	25.0	
2	7.8	0.76	0.04	2.3	0.092	15.0	
3	11.2	0.28	0.56	1.9	0.075	17.0	
4	7.4	0.70	0.00	1.9	0.076	11.0	

Task 2 : Data preprocessing including visualization

In [3]:

```
df.shape
```

Out[3]:

```
(1599, 12)
```

In [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-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 [5]:

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

Out[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
```

In [6]:

```
df.describe() # Descriptive Statistics
```

Out[6]:

	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_sulfur_di
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.00
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.87
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.46
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.00
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.00
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.00
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.00
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.00

In [7]:

```
df.corr()
```

Out[7]:

	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_
fixed_acidity	1.000000	-0.256131	0.671703	0.114777	0.093705	
volatile_acidity	-0.256131	1.000000	-0.552496	0.001918	0.061298	
citric_acid	0.671703	-0.552496	1.000000	0.143577	0.203823	
residual_sugar	0.114777	0.001918	0.143577	1.000000	0.055610	
chlorides	0.093705	0.061298	0.203823	0.055610	1.000000	
free_sulfur_dioxide	-0.153794	-0.010504	-0.060978	0.187049	0.005562	
total_sulfur_dioxide	-0.113181	0.076470	0.035533	0.203028	0.047400	
density	0.668047	0.022026	0.364947	0.355283	0.200632	
pH	-0.682978	0.234937	-0.541904	-0.085652	-0.265026	
sulphates	0.183006	-0.260987	0.312770	0.005527	0.371260	
alcohol	-0.061668	-0.202288	0.109903	0.042075	-0.221141	
quality	0.124052	-0.390558	0.226373	0.013732	-0.128907	

In [8]:

```
# Correlation of dependent varriables with the target variable

df.corr().quality.sort_values(ascending = False)
```

Out[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

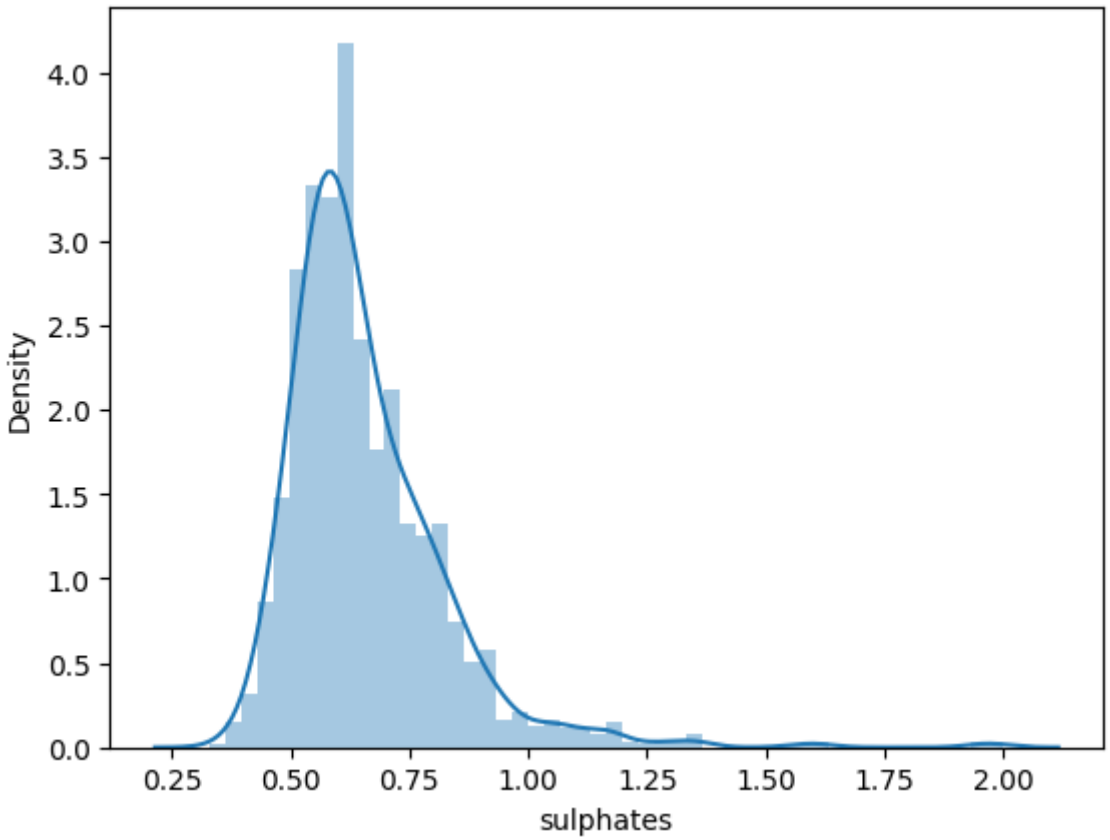
In [9]:

```
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 wi
th
similar flexibility) or `histplot` (an axes-level function for histogram
s).

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

  sns.distplot(df.sulphates)
```

Out[9]:

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

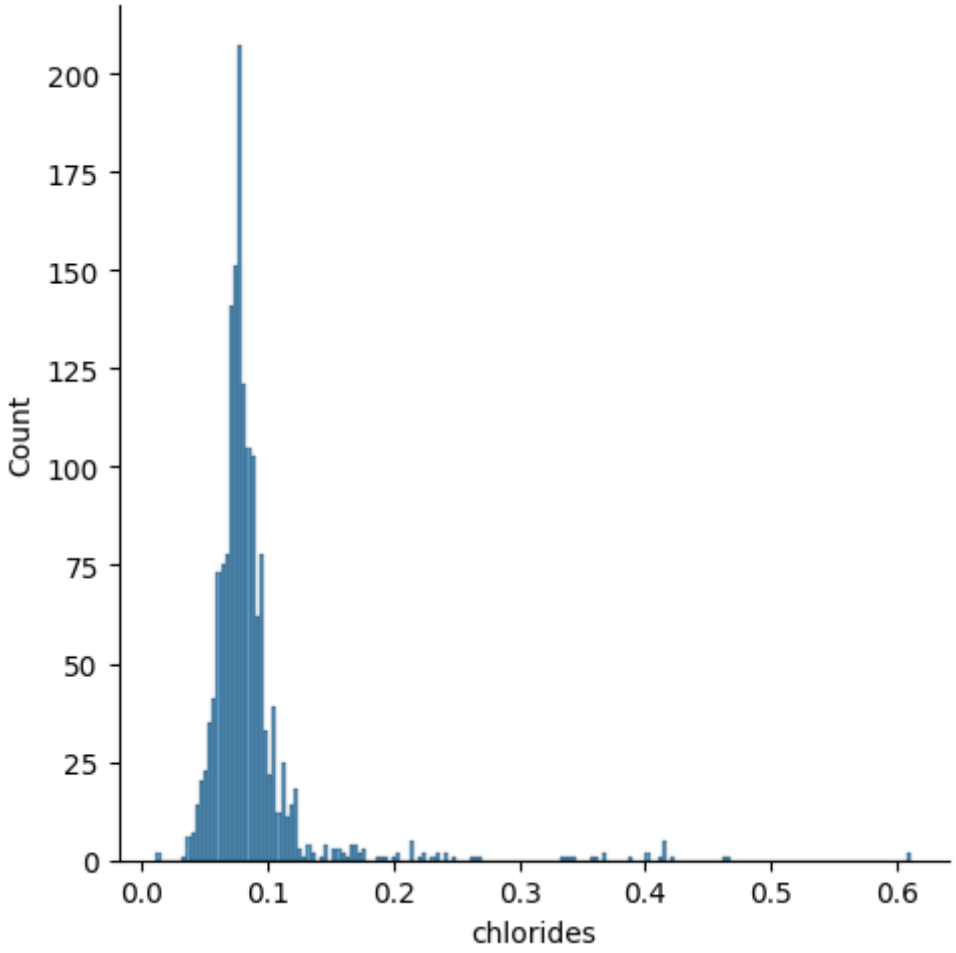


In [10]:

```
sns.displot(df.chlorides)
```

Out[10]:

```
<seaborn.axisgrid.FacetGrid at 0x7ddd8a543160>
```



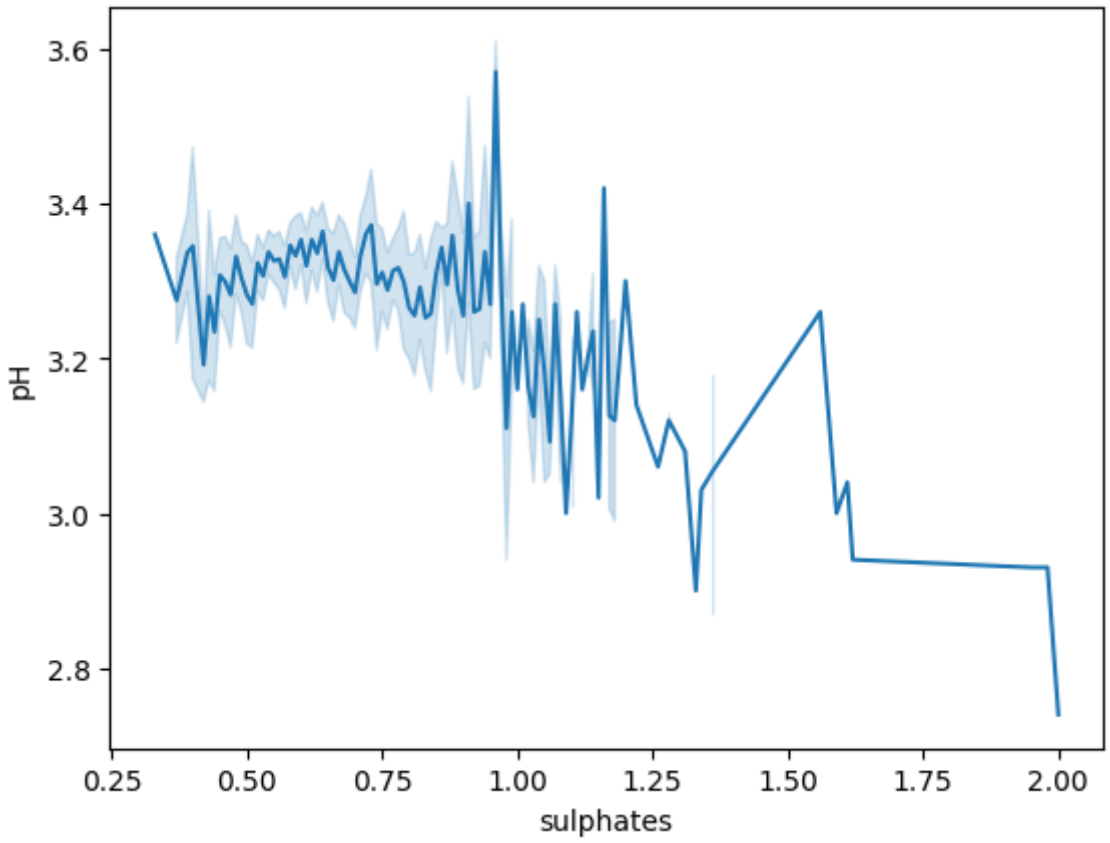
Bivariate Analysis

In [11]:

```
sns.lineplot(x=df.sulphates, y=df.pH)
```

Out[11]:

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

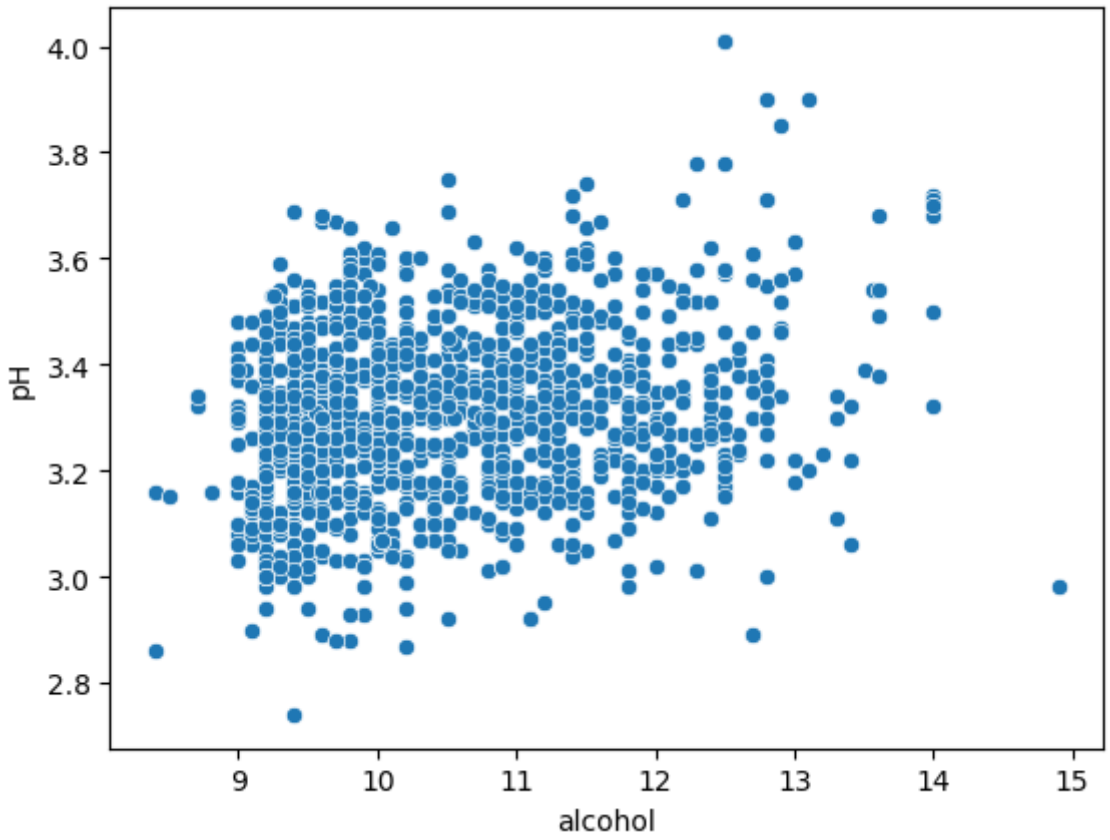


In [12]:

```
sns.scatterplot(x=df.alcohol, y=df.pH)
```

Out[12]:

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



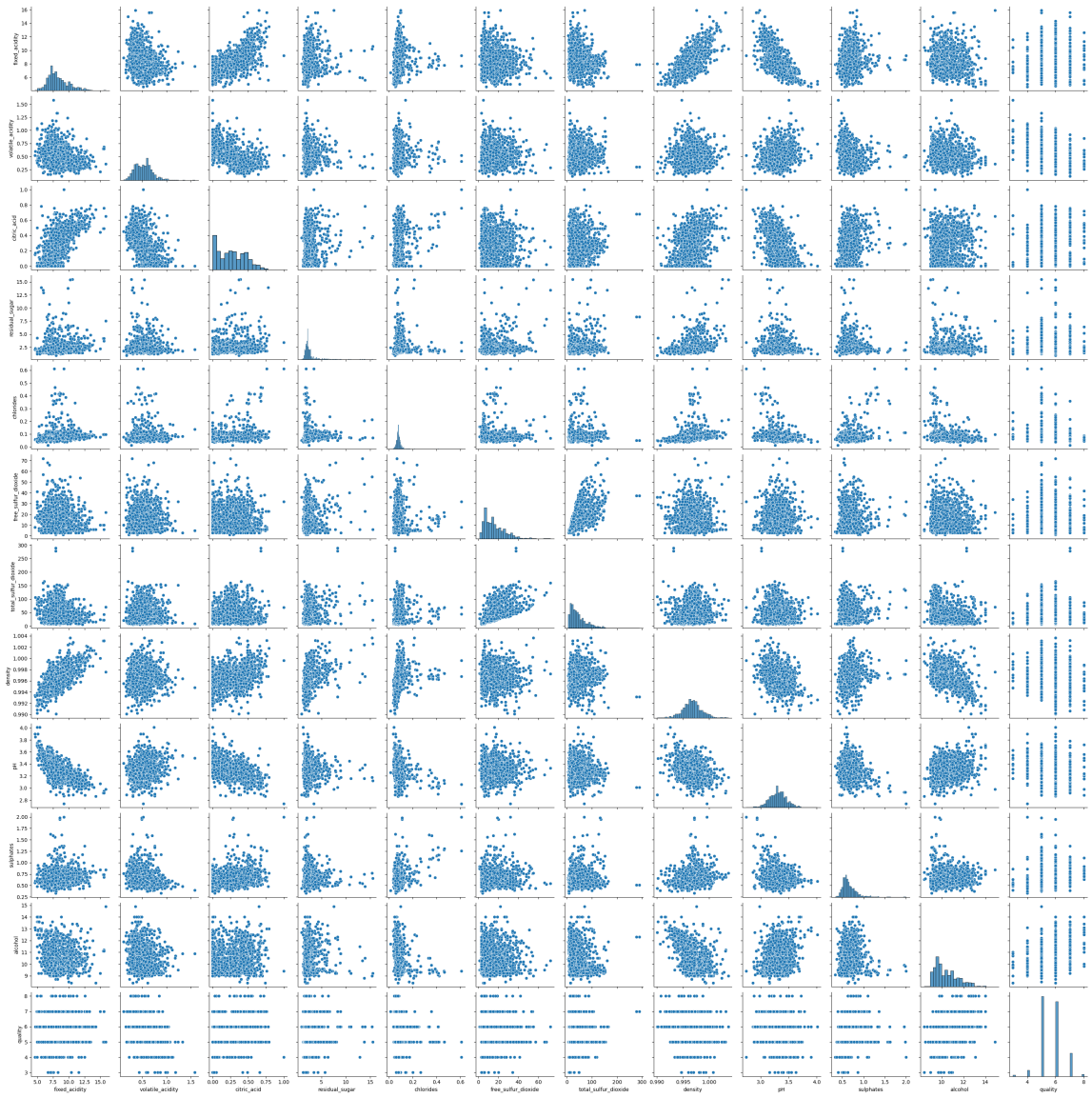
Multivariate Analysis

In [13]:

```
sns.pairplot(df)
```

Out[13]:

```
<seaborn.axisgrid.PairGrid at 0x7ddd4f583280>
```

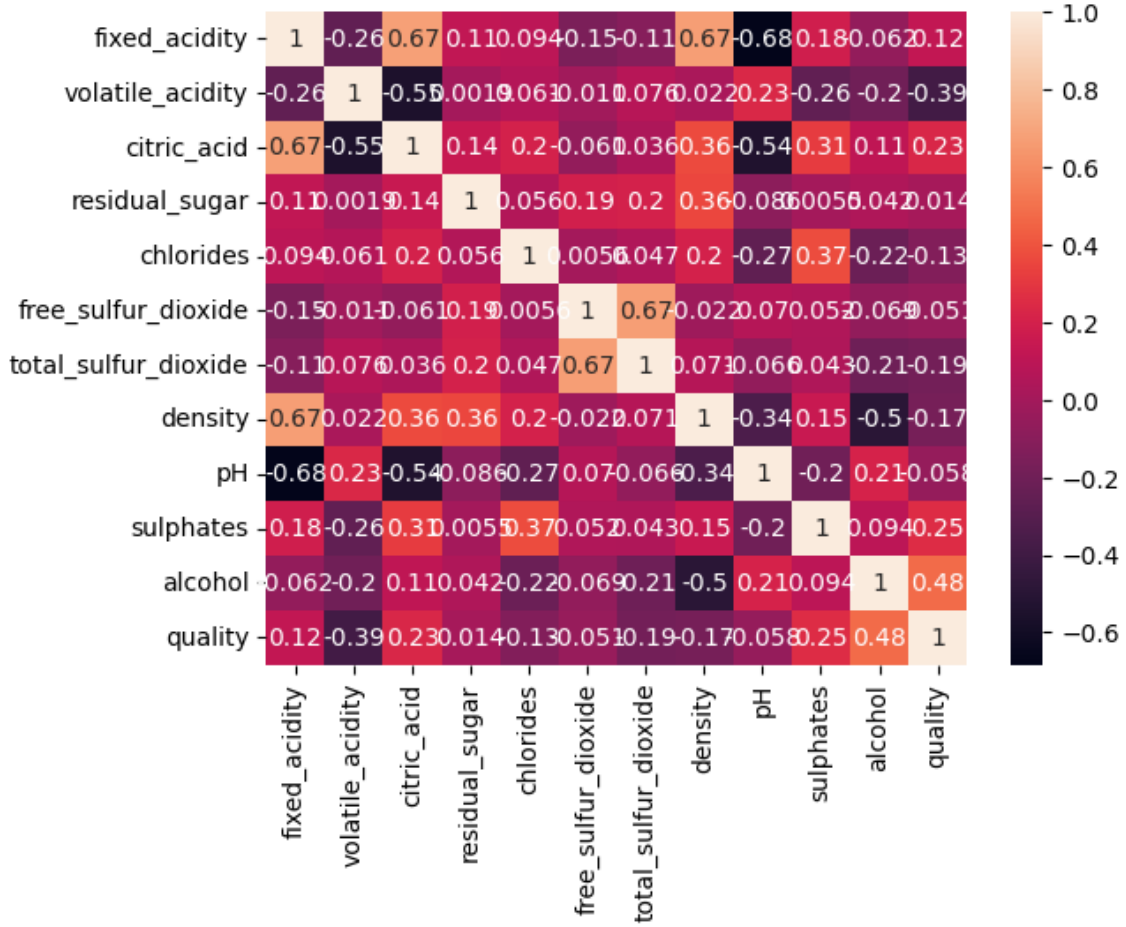


In [14]:

```
# Correlation Heatmap

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

Out[14]:

<Axes: >



Outlier Detection and removal by percentile method & IQR MEthod

In [16]:

```
df.head()
```

Out[16]:

	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_sulfur_dioxide	to
0	7.4	0.70	0.00	1.9	0.076	11.0	
1	7.8	0.88	0.00	2.6	0.098	25.0	
2	7.8	0.76	0.04	2.3	0.092	15.0	
3	11.2	0.28	0.56	1.9	0.075	17.0	
4	7.4	0.70	0.00	1.9	0.076	11.0	

In [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)
```

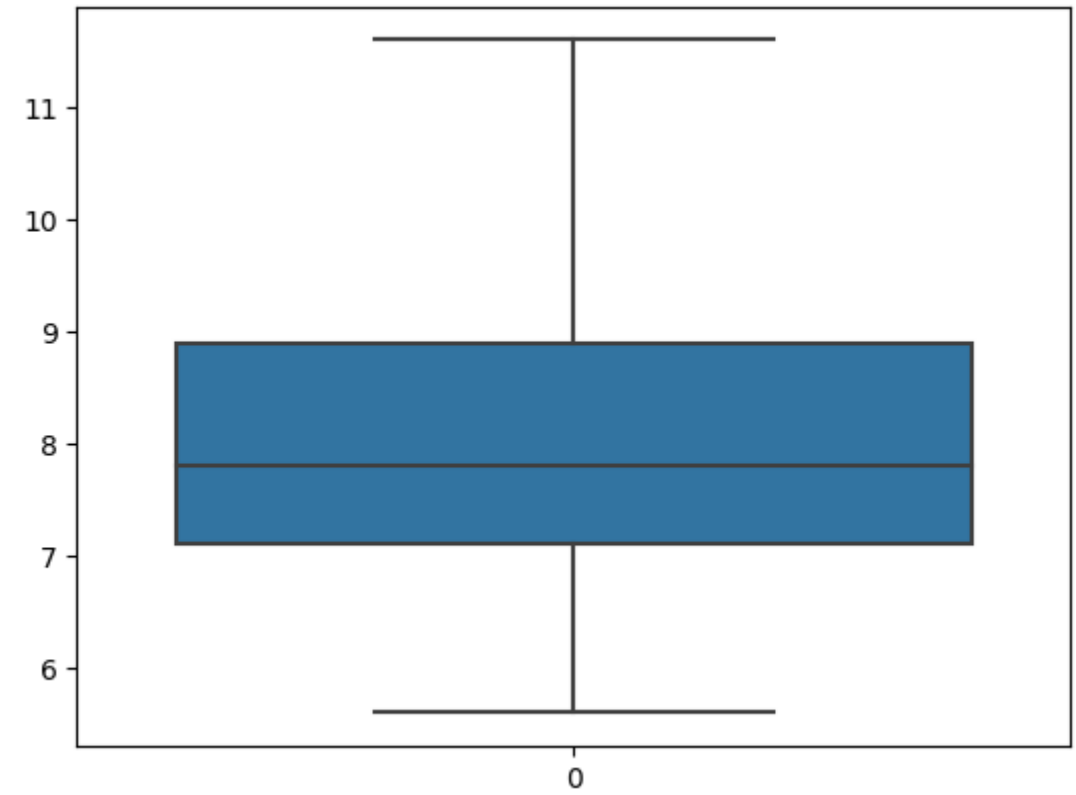
```
7.1
8.9
1.8000000000000007
11.600000000000001
4.399999999999999
```

In [51]:

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

Out[51]:

```
<Axes: >
```



In [47]:

```
fa_01=df.fixed_acidity.quantile(0.01)
fa_9=df.fixed_acidity.quantile(0.98)
print(fa_01)
print(fa_98)
```

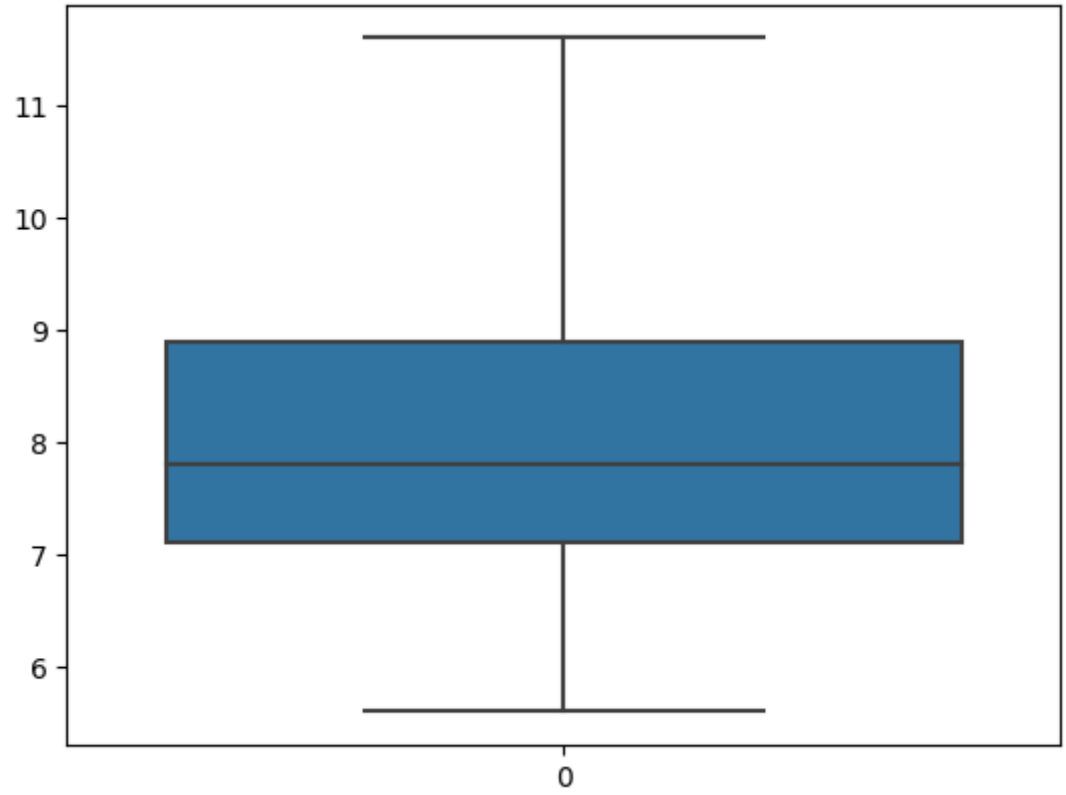
```
5.6
11.6
```

In [48]:

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

Out[48]:

```
<Axes: >
```



In [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)
```

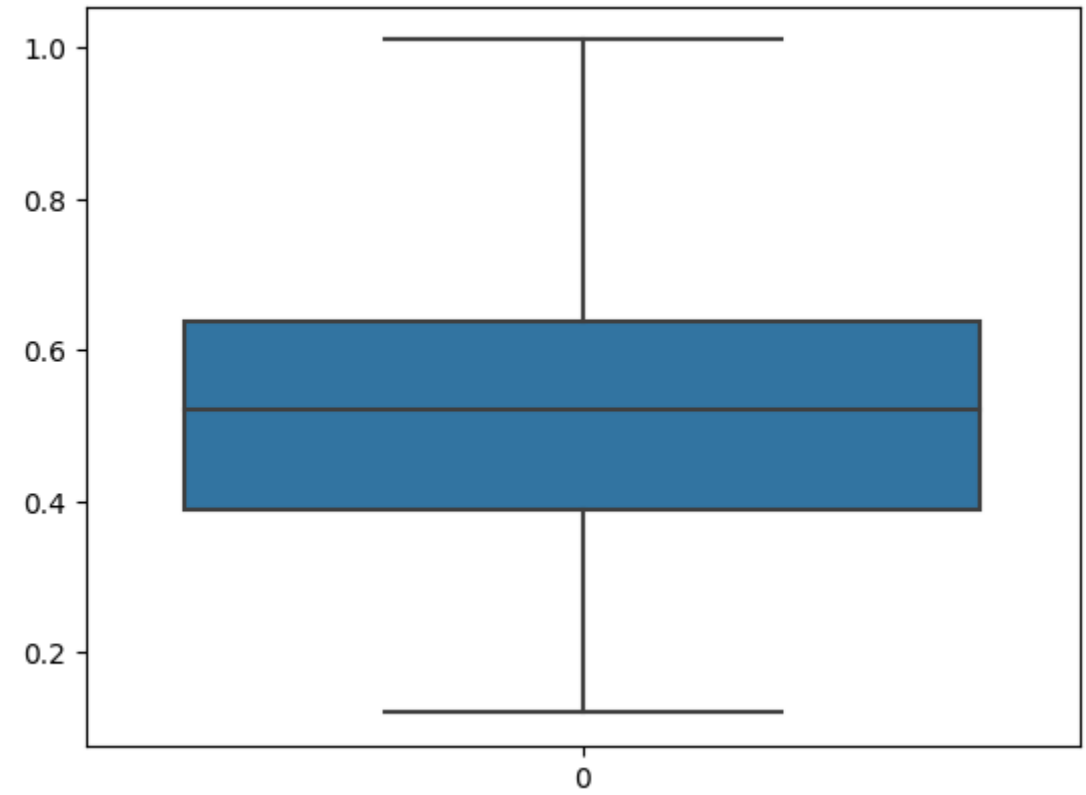
```
0.3925
0.64
0.2475
1.01125
0.021250000000000047
```

In [23]:

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

Out[23]:

```
<Axes: >
```



In [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)
```

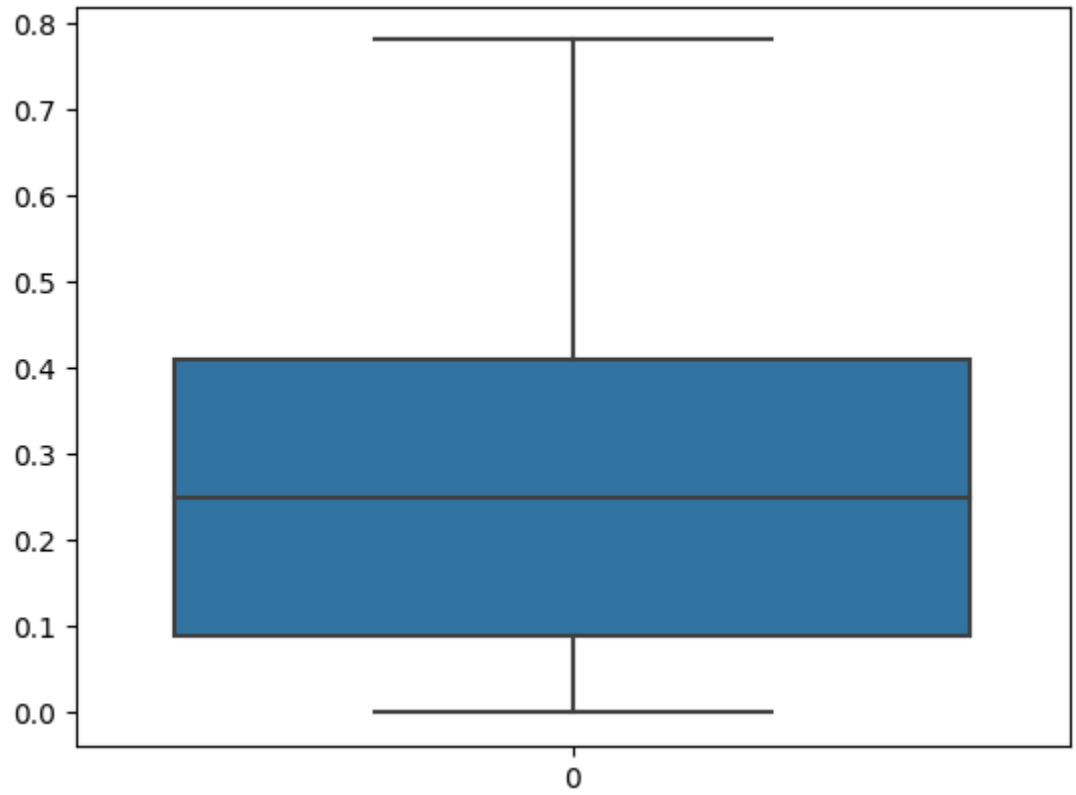
```
0.09
0.41
0.31999999999999995
0.8899999999999999
-0.3899999999999999
```

In [25]:

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

Out[25]:

```
<Axes: >
```



In [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)
```

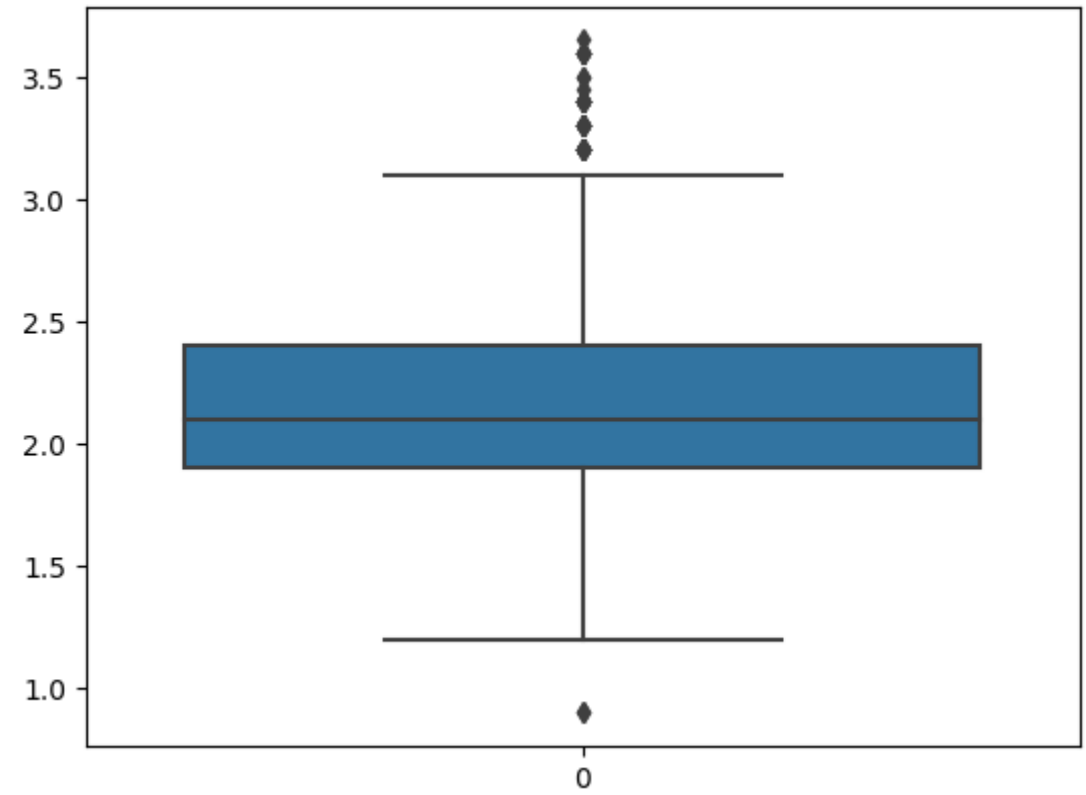
```
1.9
2.6
0.7000000000000002
3.6500000000000004
0.8499999999999996
```

In [27]:

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

Out[27]:

```
<Axes: >
```



In [34]:

```
rs_02=df.residual_sugar.quantile(0.02)
rs_96=df.residual_sugar.quantile(0.96)
print(rs_02)
print(rs_96)
```

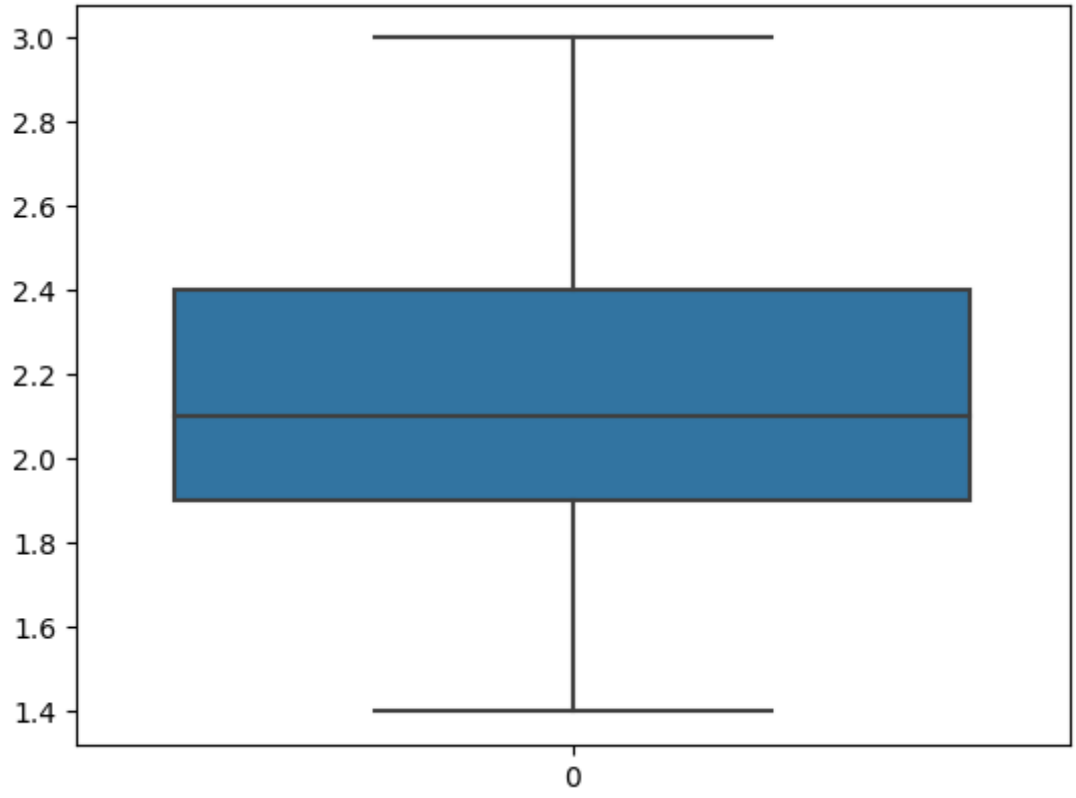
```
1.4
3.0159999999999854
```

In [35]:

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

Out[35]:

```
<Axes: >
```



In [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)
```

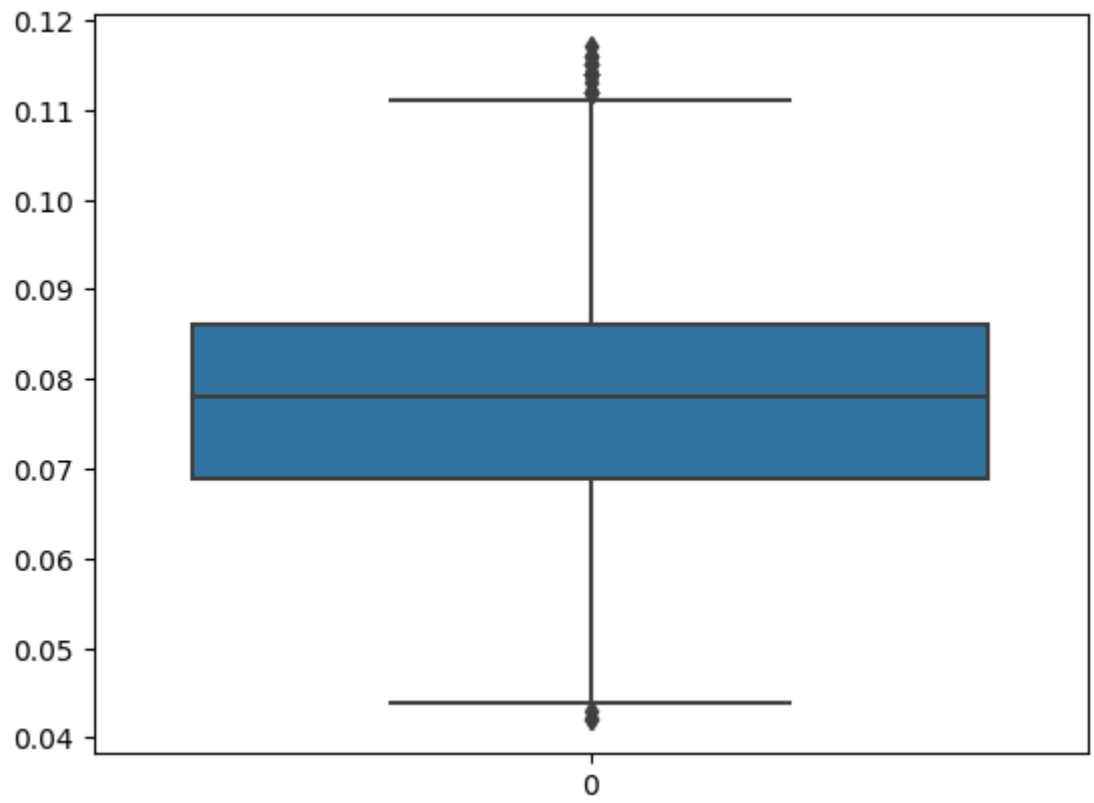
```
0.07
0.089
0.01899999999999999
0.11749999999999998
0.04150000000000002
```

In [37]:

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

Out[37]:

```
<Axes: >
```



In [44]:

```
ch_01=df.chlorides.quantile(0.01)
ch_97=df.chlorides.quantile(0.97)
print(ch_01)
print(ch_97)
```

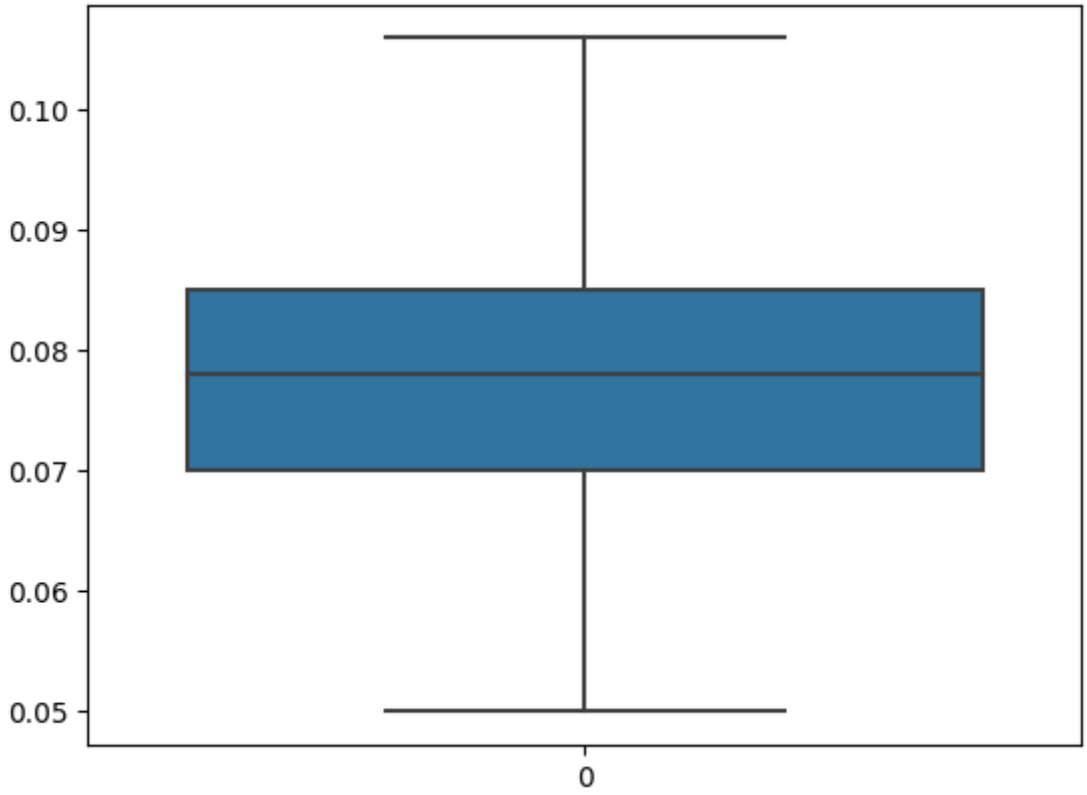
```
0.049890000000000004
0.106
```

In [45]:

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

Out[45]:

```
<Axes: >
```



In [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)
```

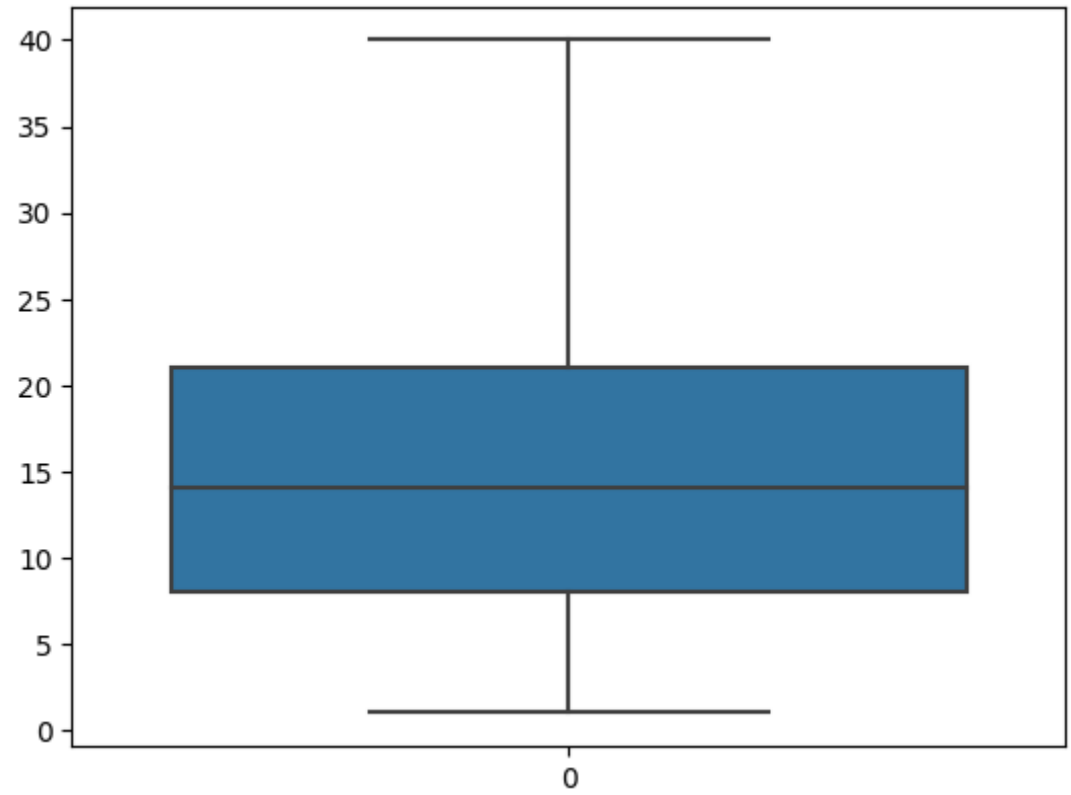
```
8.0
21.0
13.0
40.5
-11.5
```

In [53]:

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

Out[53]:

```
<Axes: >
```



In [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)
```

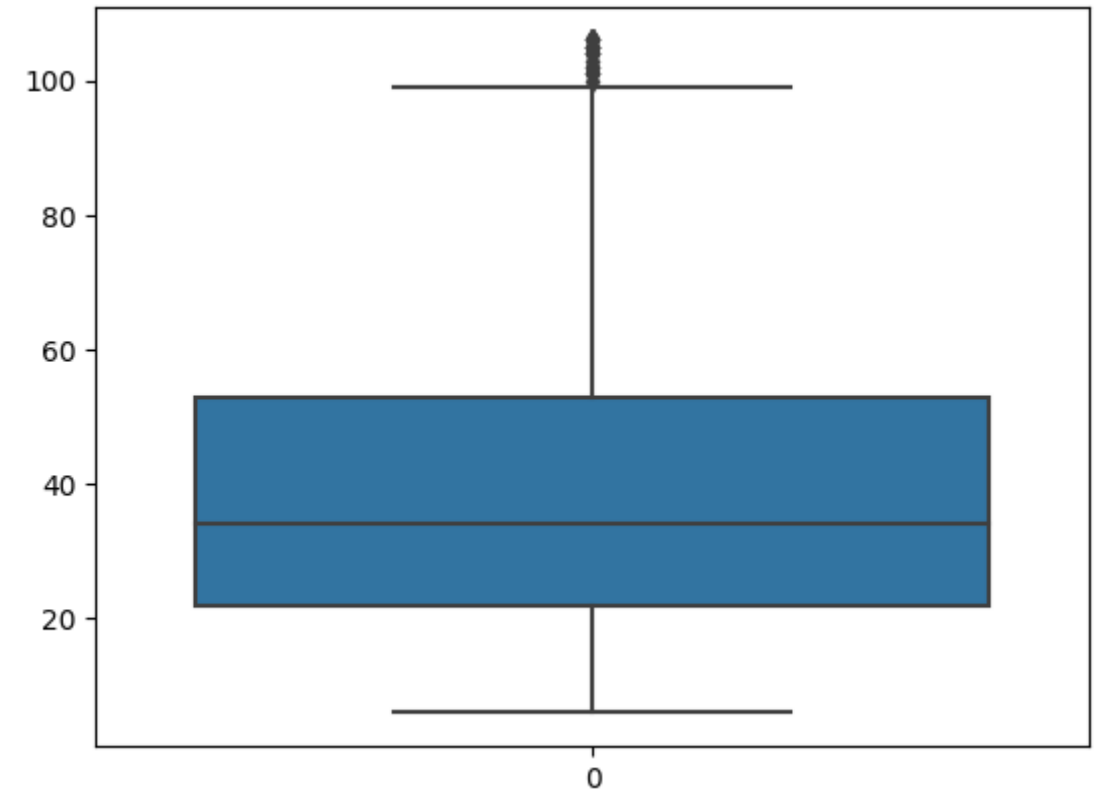
```
23.0
57.0
34.0
108.0
-28.0
```

In [55]:

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

Out[55]:

```
<Axes: >
```



In [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)
```

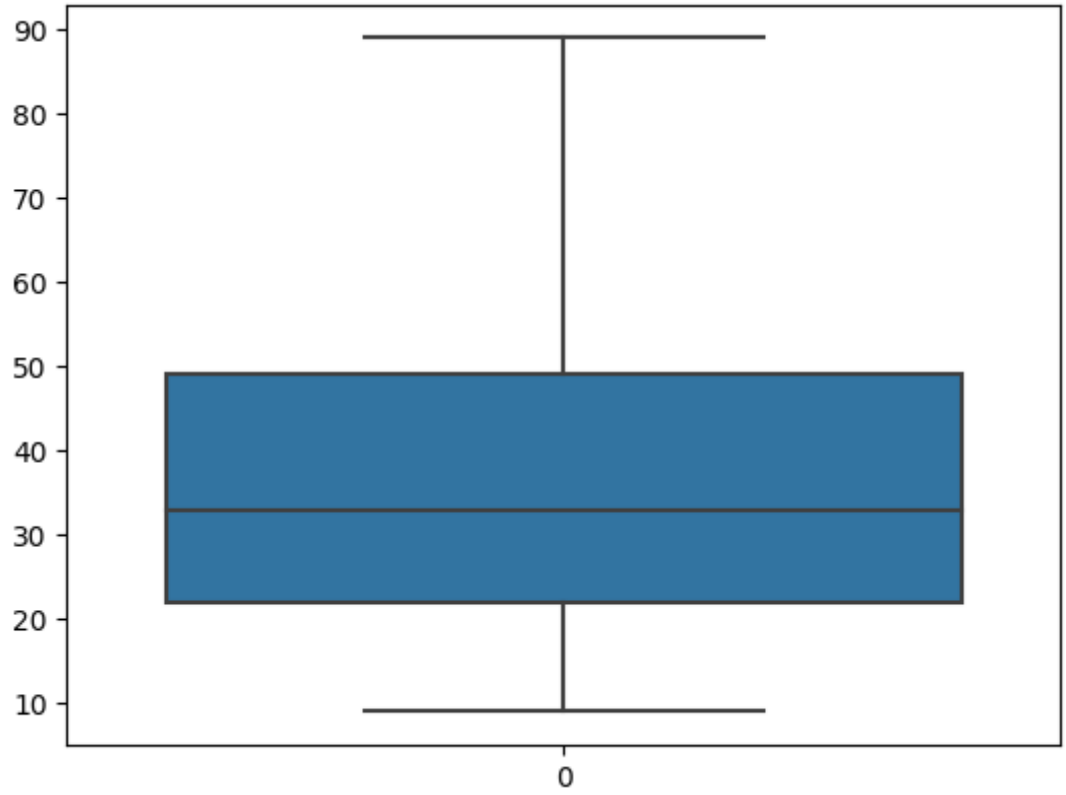
```
9.0
89.0
```

In [61]:

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

Out[61]:

```
<Axes: >
```



In [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)
```

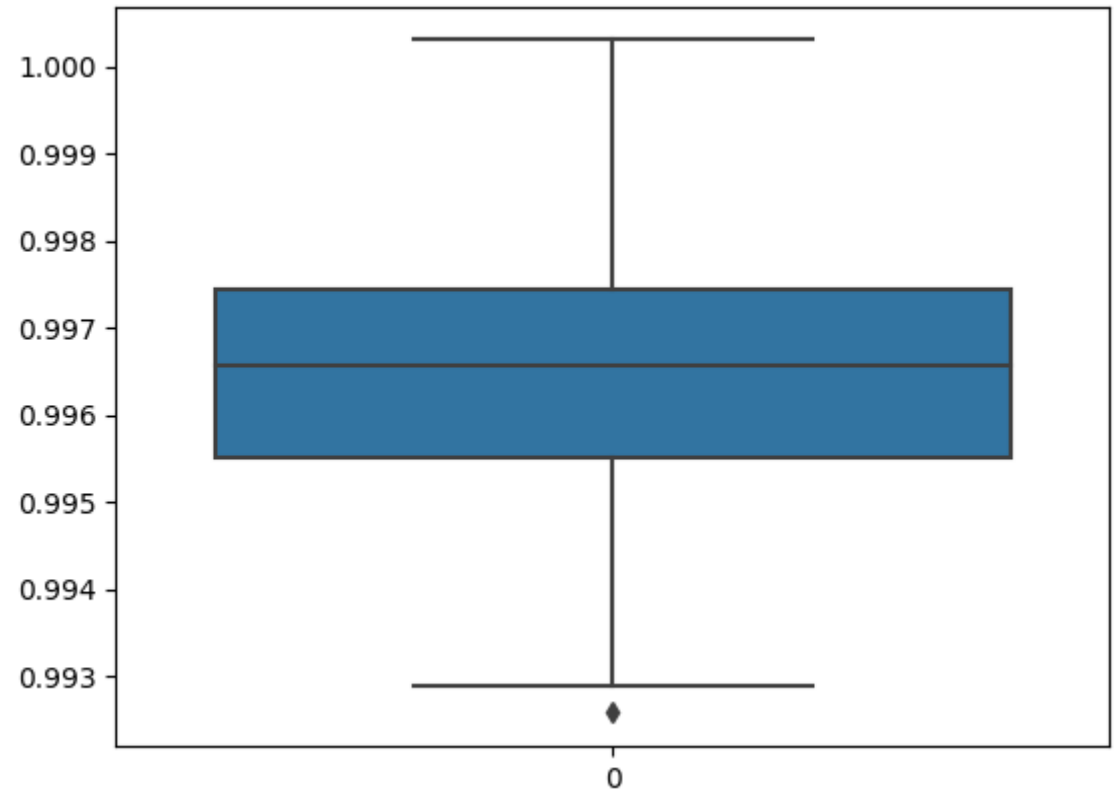
```
0.9955
0.99745
0.0019499999999998963
1.0003749999999998
0.9925750000000002
```

In [63]:

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

Out[63]:

```
<Axes: >
```



In [64]:

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

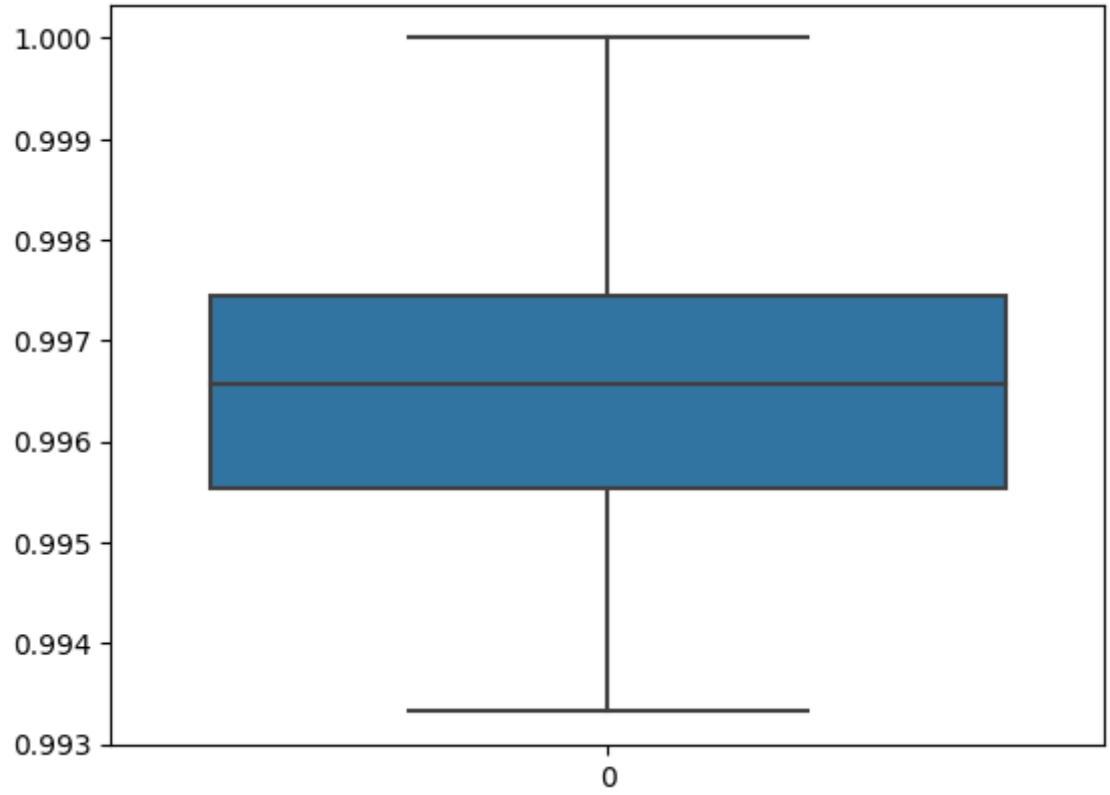
```
0.9933132
1.0
```

In [65]:

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

Out[65]:

```
<Axes: >
```



In [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)
```

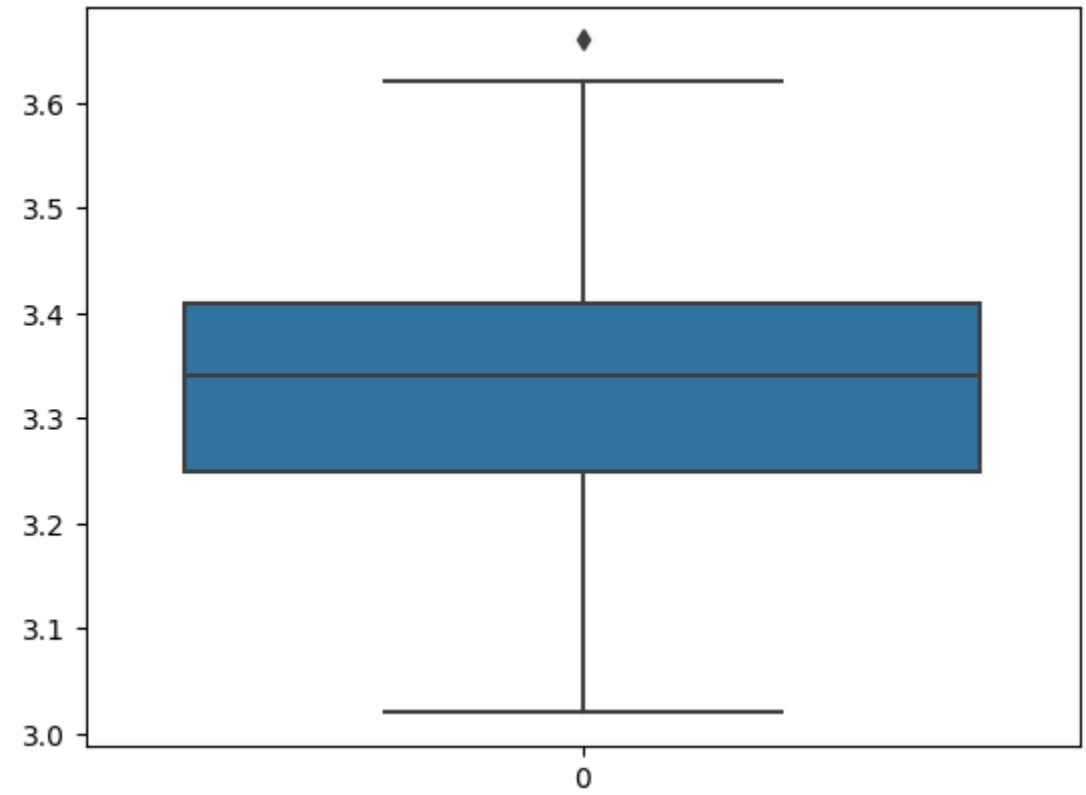
```
3.2425
3.41
0.16749999999999998
3.66125
2.99125
```

In [67]:

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

Out[67]:

```
<Axes: >
```



In [68]:

```
pH_01=df.pH.quantile(0.01)
pH_99=df.pH.quantile(0.99)
print(pH_01)
print(pH_99)
```

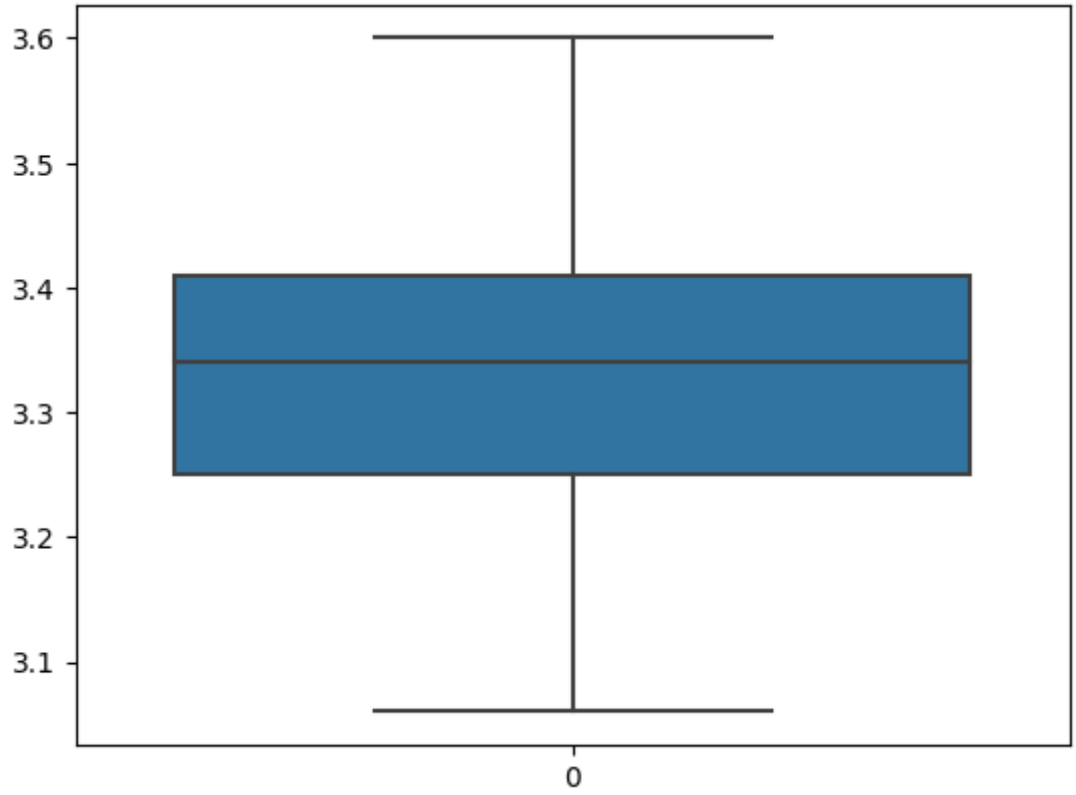
```
3.06
3.6066
```

In [69]:

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

Out[69]:

```
<Axes: >
```



In [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)
```

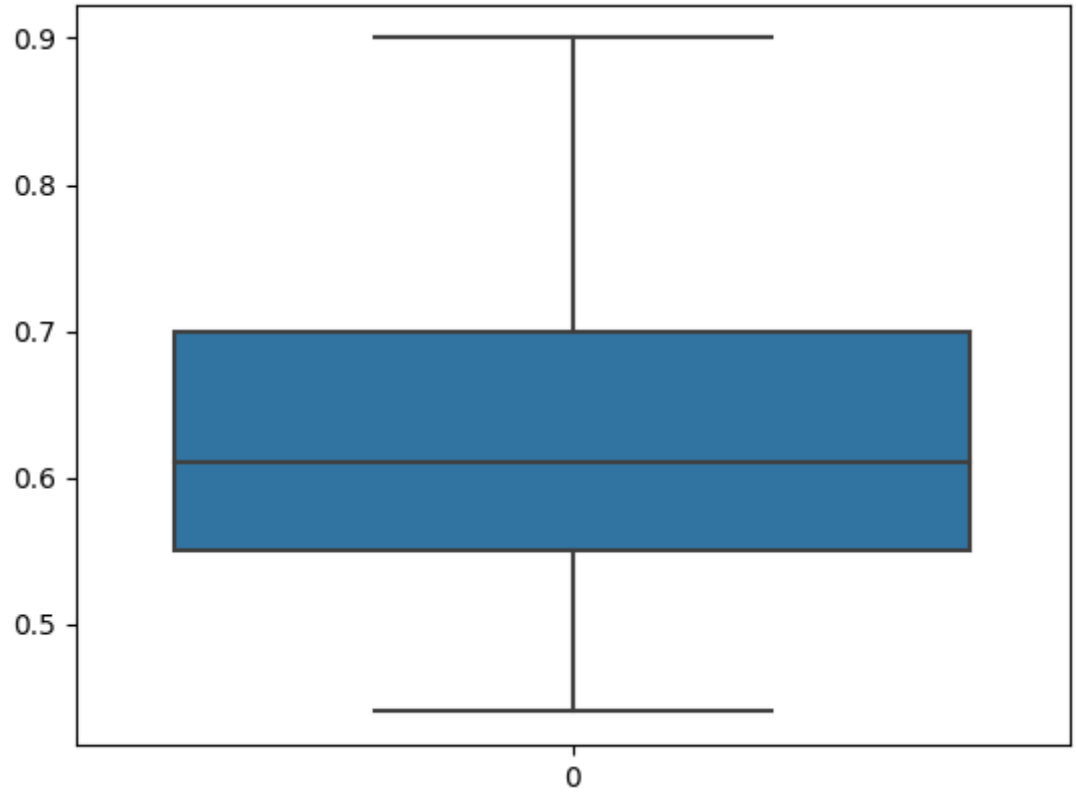
```
0.44
0.9
```

In [75]:

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

Out[75]:

```
<Axes: >
```



In [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)
```

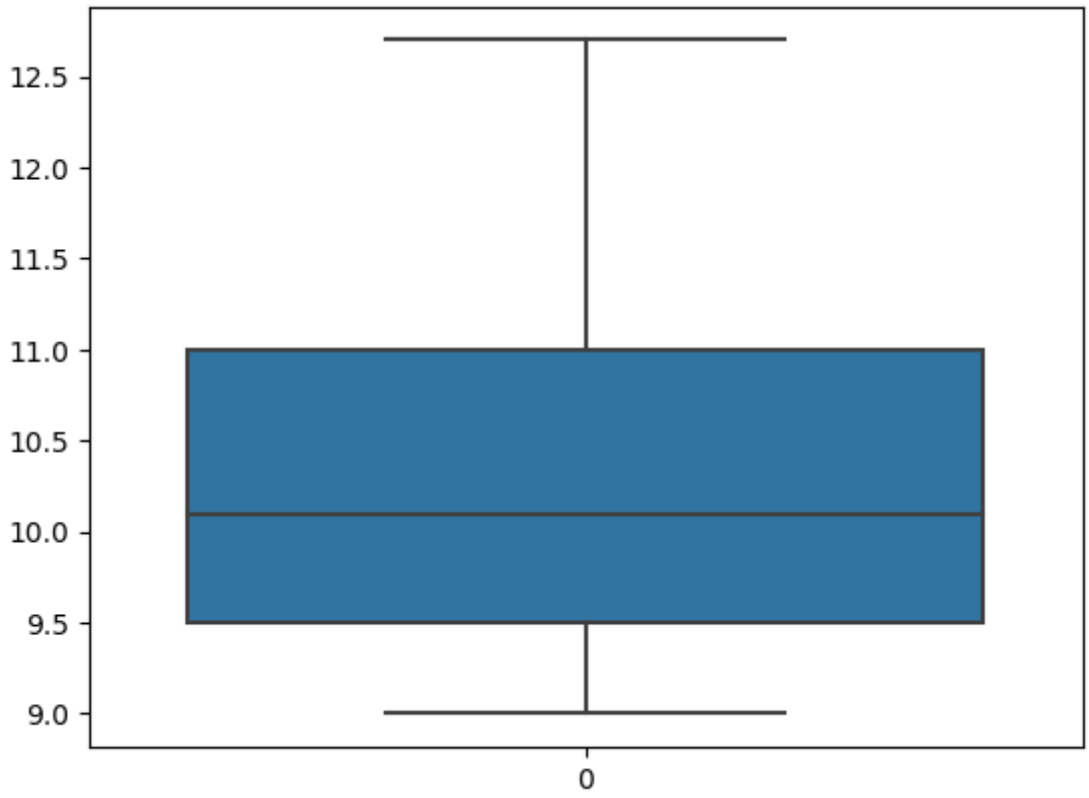
```
9.0
12.724
```

In [77]:

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

Out[77]:

```
<Axes: >
```



Therefore all the outliers are removed

Task - 3 : Machine Learning Model Building

In [233]:

```
# split into X and y

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

Out[233]:

	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_sulfur_dioxide	tot
0	7.4	0.70	0.00	1.9	0.076	11.0	
1	7.8	0.88	0.00	2.6	0.098	25.0	
2	7.8	0.76	0.04	2.3	0.092	15.0	
3	11.2	0.28	0.56	1.9	0.075	17.0	
4	7.4	0.70	0.00	1.9	0.076	11.0	

In [234]:

```
Y =df.quality
Y.head()
```

Out[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')

In [235]:

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

In [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
```

In [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)
```

In [238]:

```
X_train.shape
```

Out[238]:

```
(692, 11)
```

In [239]:

```
X_test.shape
```

Out[239]:

```
(174, 11)
```

In [240]:

```
print(Y.shape, Y_train.shape, Y_test.shape)
```

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

Decision Tree Classifier

In [242]:

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

Out[242]:

```
DecisionTreeClassifier(criterion='entropy', max_depth=2)
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [243]:

```
d_y_predict = model1.predict(X_test)
d_y_predict
```

Out[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])
```

In [245]:

```
d_y_predict_train = model1.predict(X_train)
```

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

In [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
```

Random Forest Classifier

In [247]:

```
from sklearn.ensemble import RandomForestClassifier
model2 =RandomForestClassifier(n_estimators=200,criterion='entropy')
model2.fit(X_train,Y_train)
```

Out[247]:

```
RandomForestClassifier(criterion='entropy', n_estimators=200)
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [248]:

```
r_y_predict = model2.predict(X_test)
r_y_predict_train = model2.predict(X_train)
```

Task - 4 : Evaluating Random Forest Model

In [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
```

Naive Bayesian Classification Model

In [251]:

```
from sklearn.naive_bayes import GaussianNB
gnb = GaussianNB()
gnb.fit(X_train,Y_train)
```

Out[251]:

```
GaussianNB()
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [252]:

```
y_pred2 = gnb.predict(X_test)
y_pred2
```

Out[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])
```

Task - 4 : Evaluating Naive Bayesian Classification Model

In [254]:

```
from sklearn.metrics import accuracy_score
gnb_acc=accuracy_score(Y_test,y_pred2)
gnb_acc
```

Out[254]:

```
0.8850574712643678
```

Accuracies of all the algorithms used in model nuilding phase :

Decision Tree Classification : 87.93 %

Random Forset Classification : 94.25 %

Naive Bayesian Classification : 88.50 %

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

Task - 5 : Test with random observation

In [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(
```

Out[262]:

```
array([0])
```

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

In [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(
```

Out[263]:

```
array([0])
```

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

In [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 featur
e names
  warnings.warn(
```

Out[264]:

```
array([0])
```

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

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

The End !!!!