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```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score
```

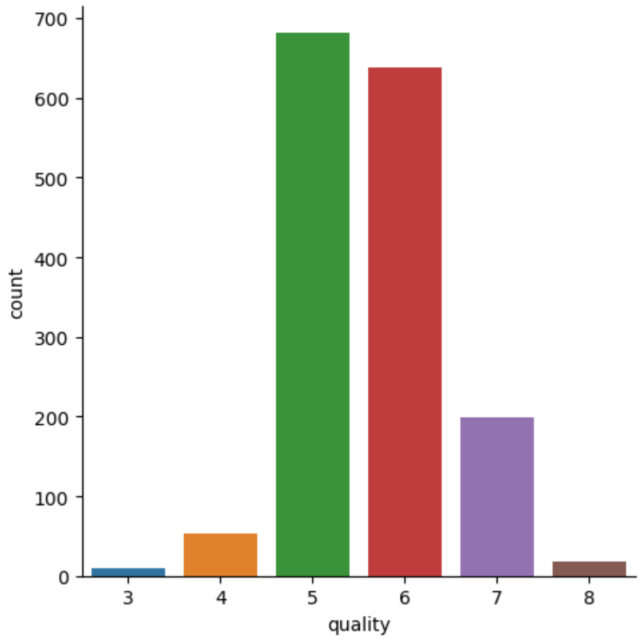
```
df=pd.read_csv('/content/winequality-red.csv')
df.head()
```

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

VISUALIZATION

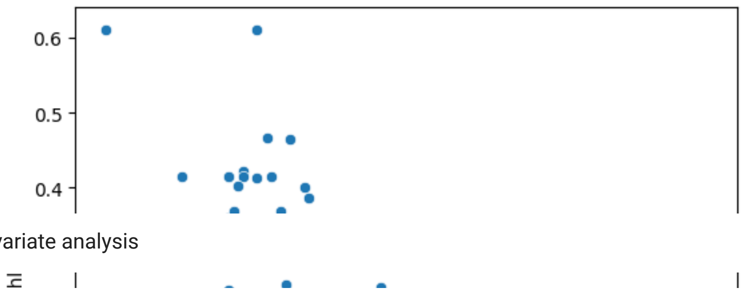
```
#UNIVARIATE ANALYSIS
sns.catplot(x='quality',data=df,kind='count')
```

```
    <seaborn.axisgrid.FacetGrid at 0x78d0b0117b20>
```



```
#BIVARIATE ANALYSIS
sns.scatterplot(x=df.pH,y=df.chlorides)
```

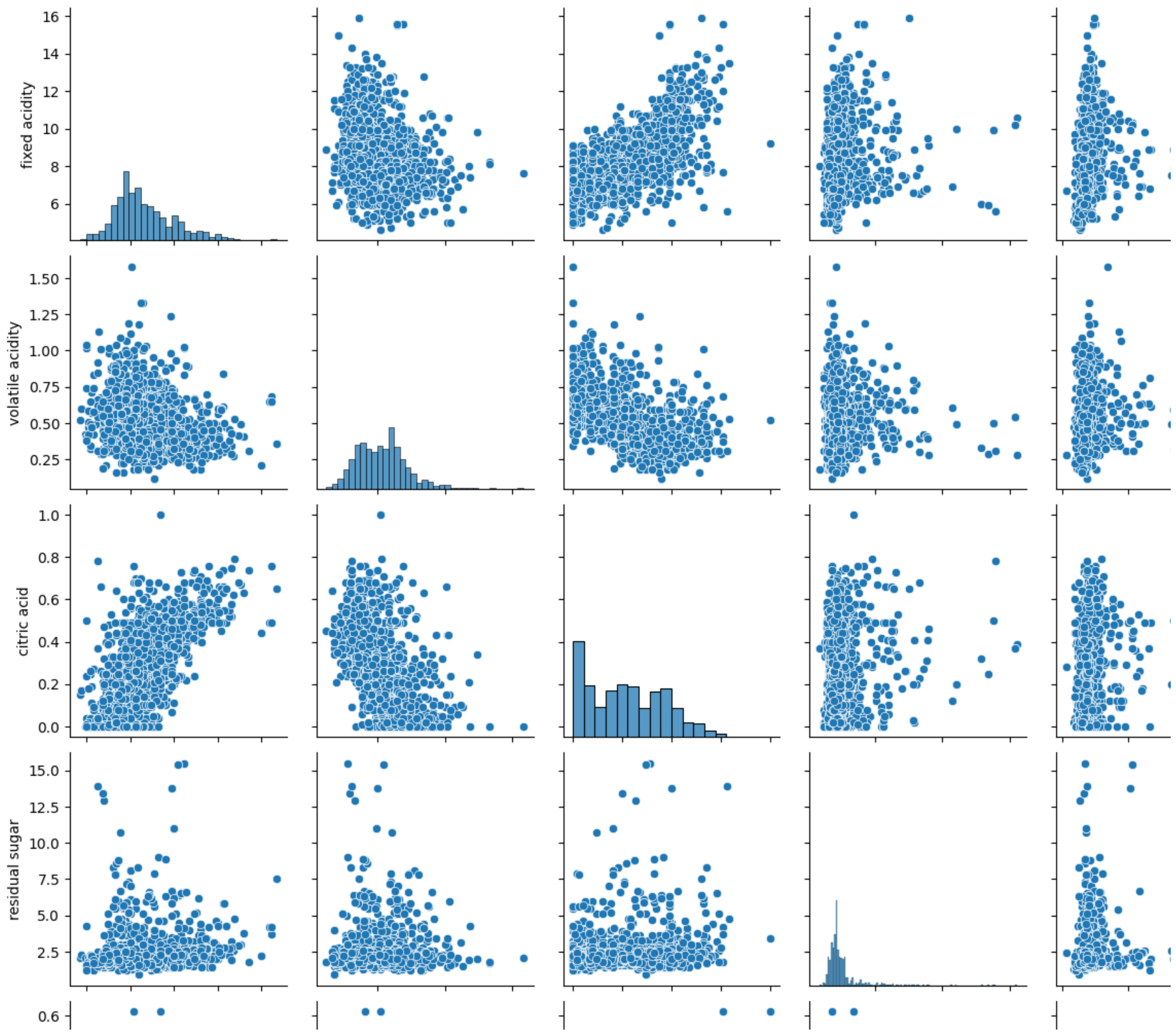
```
<Axes: xlabel='pH', ylabel='chlorides'>
```



Multivariate analysis

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

```
<seaborn.axisgrid.PairGrid at 0x78d0b103f310>
```



```
#Checking missing values
df.isnull().any()
```

```
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
```

```
df.describe()
```

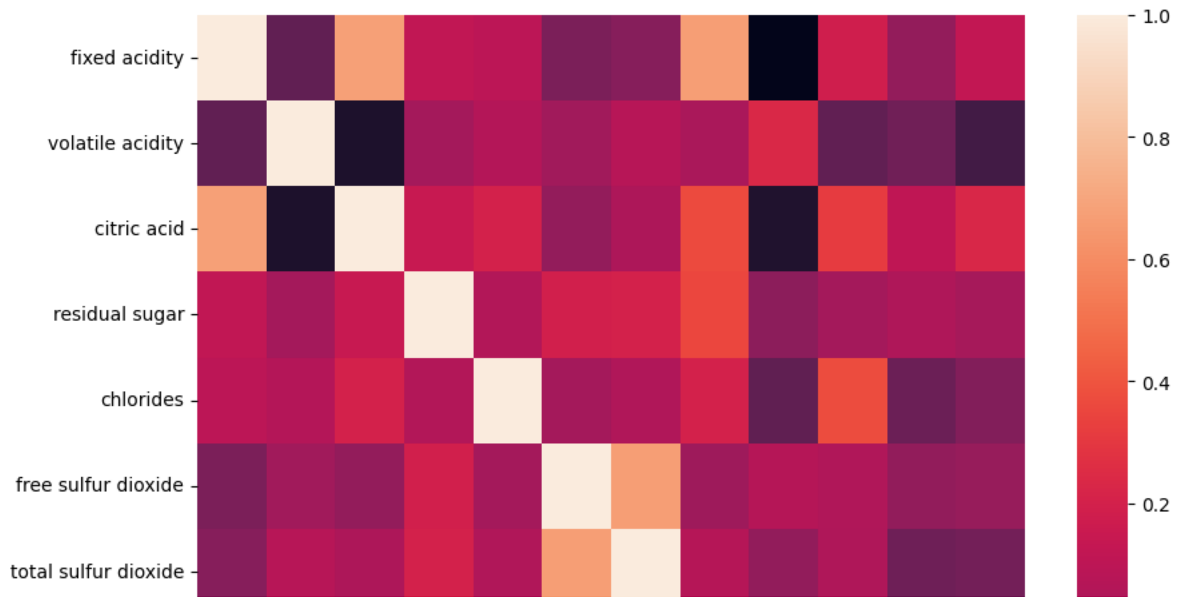
	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	dens
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.467792	0.996
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	0.001
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.990
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.995
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.996
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.997
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1.003

```
correlation=df.corr()
correlation
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxid
fixed acidity	1.000000	-0.256131	0.671703	0.114777	0.093705	-0.153794	-0.11318
volatile acidity	-0.256131	1.000000	-0.552496	0.001918	0.061298	-0.010504	0.07647
citric acid	0.671703	-0.552496	1.000000	0.143577	0.203823	-0.060978	0.03553
residual sugar	0.114777	0.001918	0.143577	1.000000	0.055610	0.187049	0.20302
chlorides	0.093705	0.061298	0.203823	0.055610	1.000000	0.005562	0.04740
free sulfur dioxide	-0.153794	-0.010504	-0.060978	0.187049	0.005562	1.000000	0.66766
total sulfur dioxide	-0.113181	0.076470	0.035533	0.203028	0.047400	0.667666	1.00000
density	0.668047	0.022026	0.364947	0.355283	0.200632	-0.021946	0.07126
pH	-0.682978	0.234937	-0.541904	-0.085652	-0.265026	0.070377	-0.06649
sulphates	0.183006	-0.260987	0.312770	0.005527	0.371260	0.051658	0.04294
alcohol	-0.061668	-0.202288	0.109903	0.042075	-0.221141	-0.069408	-0.20565
quality	0.124052	-0.390558	0.226373	0.013732	-0.128907	-0.050656	-0.18510

```
#Heatmap
plt.figure(figsize=(10,10))
sns.heatmap(correlation)
```

```
<Axes: >
```

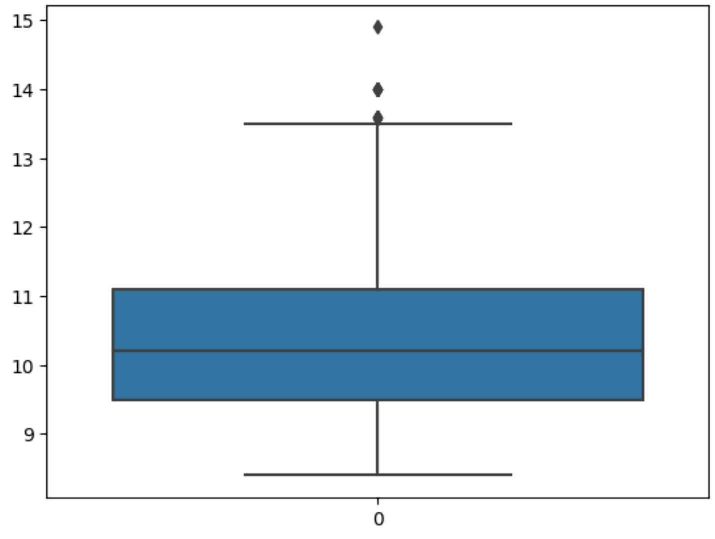


```
#Detecting outliers
df.columns = df.columns.str.replace(' ', '_')
df.head()
```

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

```
sns.boxplot(df.alcohol)
```

```
<Axes: >
```

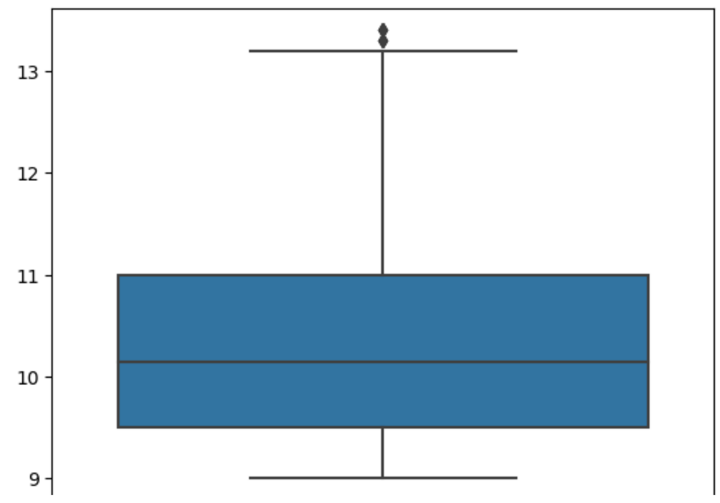


```
a_01=df.alcohol.quantile(0.01)
a_99=df.alcohol.quantile(0.99)
print(a_01)
print(a_99)
```

```
9.0
13.4
```

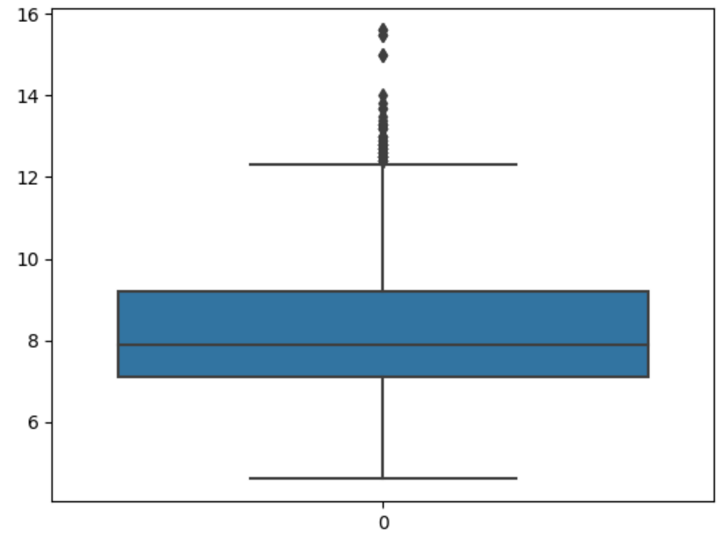
```
df=df[(df.alcohol>=a_01) & (df.alcohol<=a_99)]
sns.boxplot(df.alcohol)
```

```
<Axes: >
```



```
sns.boxplot(df.fixed_acidity)
```

```
<Axes: >
```

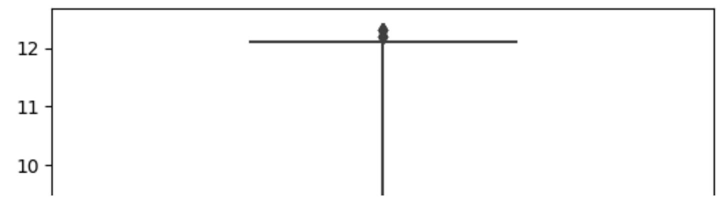


```
f1 = df.fixed_acidity.quantile(0.25) #Q1
f3 = df.fixed_acidity.quantile(0.75) #Q3
IQR_f = f3 - f1
upper_limit_f = f3+(1.5)*(IQR_f)
lower_limit_f = f1-(1.5)*(IQR_f)
print(f1)
print(f3)
print(IQR_f)
print(upper_limit_f)
print(lower_limit_f)
```

```
7.1
9.2
2.0999999999999996
12.349999999999998
3.95
```

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

```
<Axes: >
```

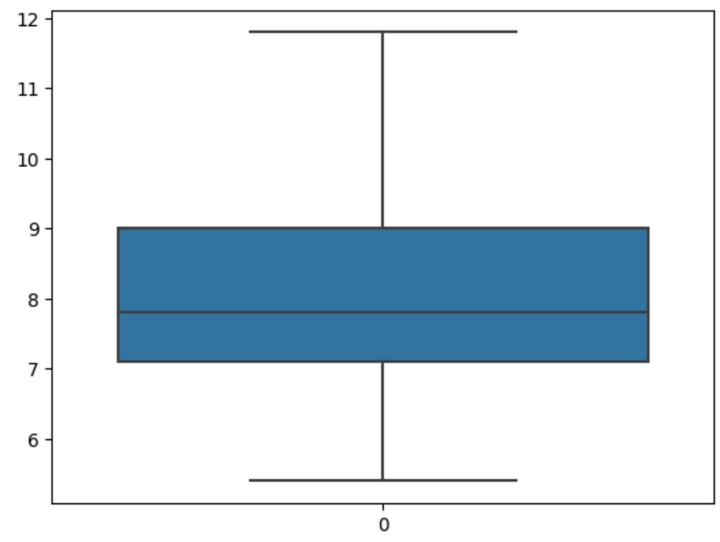


```
fa_01=df.fixed_acidity.quantile(0.01)
fa_98=df.fixed_acidity.quantile(0.98)
print(fa_01)
print(fa_98)
```

```
5.4
11.8
```

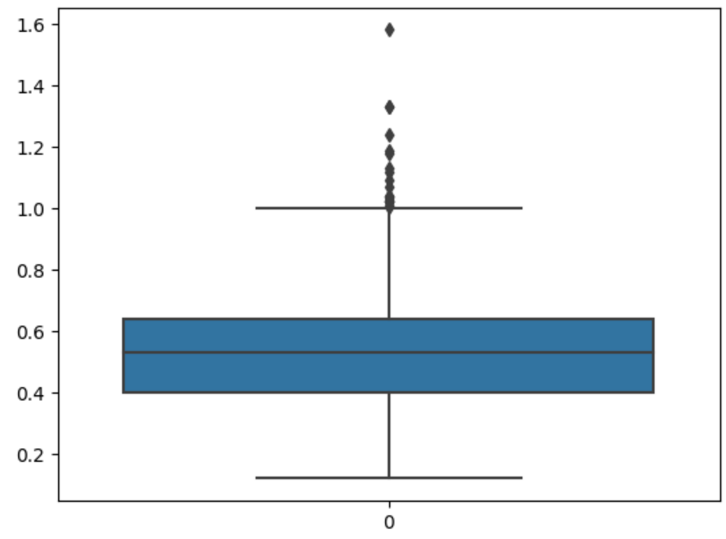
```
df=df[(df.fixed_acidity>=fa_01) & (df.fixed_acidity<=fa_98)]
sns.boxplot(df.fixed_acidity)
```

```
<Axes: >
```



```
sns.boxplot(df.volatile_acidity)
```

```
<Axes: >
```

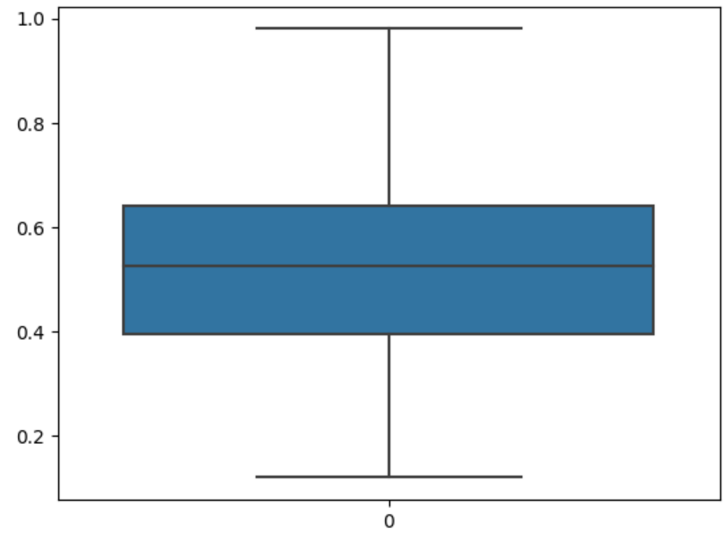


```
v1 = df.volatile_acidity.quantile(0.25) #Q1
v3 = df.volatile_acidity.quantile(0.75) #Q3
IQR_v = v3 - v1
upper_limit_v = v3+(1.5)*(IQR_v)
lower_limit_v = v1-(1.5)*(IQR_v)
print(v1)
print(v3)
print(IQR_v)
print(upper_limit_v)
print(lower_limit_v)
```

```
0.4
0.64
0.24
1.0
0.04000000000000036
```

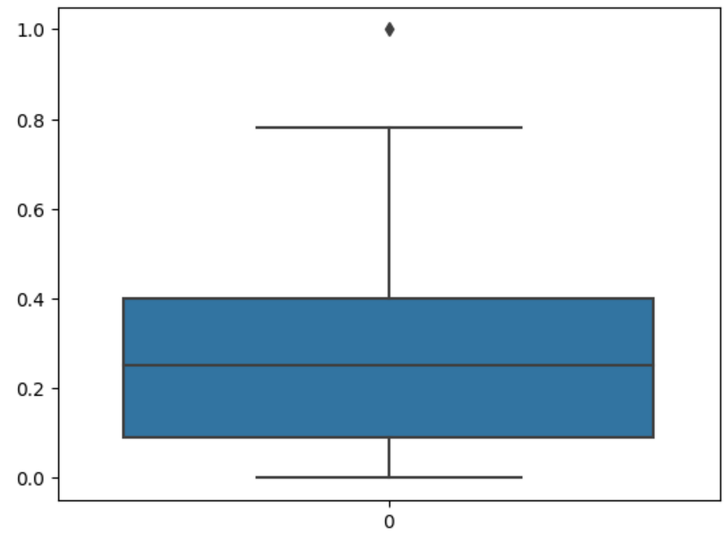
```
df=df[(df.volatile_acidity<upper_limit_v) & (df.volatile_acidity>lower_limit_v)]
sns.boxplot(df.volatile_acidity)
```

```
<Axes: >
```



```
sns.boxplot(df.citric_acid)
```

```
<Axes: >
```

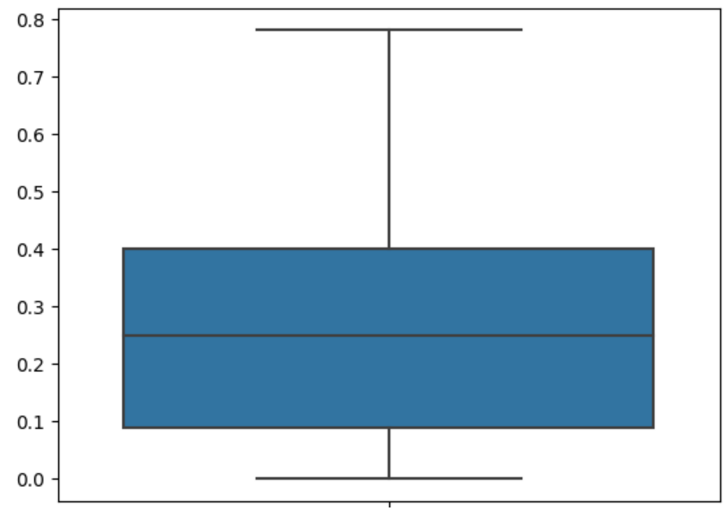


```
c1 = df.citric_acid.quantile(0.25) #Q1
c3 = df.citric_acid.quantile(0.75) #Q3
IQR_c = c3 - c1
upper_limit_c = c3+(1.5)*(IQR_c)
lower_limit_c = c1-(1.5)*(IQR_c)
print(c1)
print(c3)
print(IQR_c)
print(upper_limit_c)
print(lower_limit_c)
```

```
0.09
0.4
0.31000000000000005
0.8650000000000001
-0.3750000000000001
```

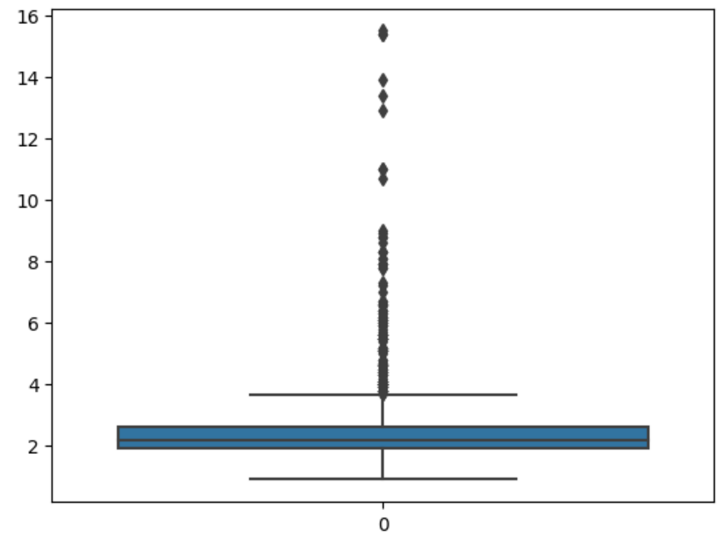
```
df=df[(df.citric_acid<upper_limit_c) & (df.citric_acid>lower_limit_c)]
sns.boxplot(df.citric_acid)
```

```
<Axes: >
```



```
sns.boxplot(df.residual_sugar)
```

```
<Axes: >
```

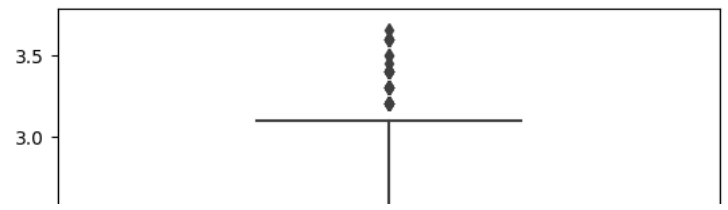


```
r1 = df.residual_sugar.quantile(0.25) #Q1
r3 = df.residual_sugar.quantile(0.75) #Q3
IQR_r = r3 - r1
upper_limit_r = r3+(1.5)*(IQR_r)
lower_limit_r = r1-(1.5)*(IQR_r)
print(r1)
print(r3)
print(IQR_r)
print(upper_limit_r)
print(lower_limit_r)
```

```
1.9
2.6
0.7000000000000002
3.6500000000000004
0.8499999999999996
```

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

```
<Axes: >
```

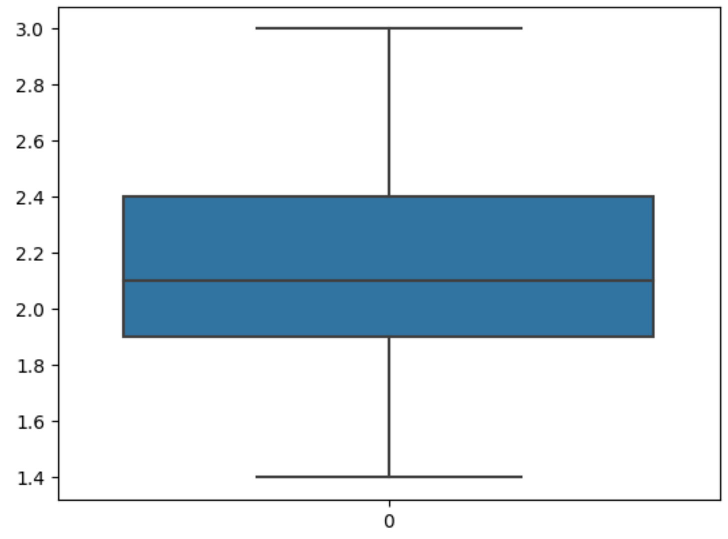


```
rs_02=df.residual_sugar.quantile(0.02)
rs_96=df.residual_sugar.quantile(0.96)
print(rs_02)
print(rs_96)
```

```
1.4
3.0
```

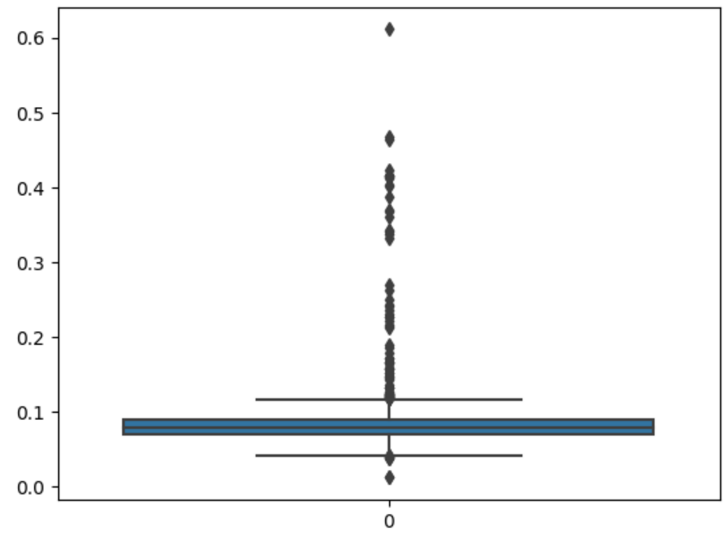
```
df=df[(df.residual_sugar>=rs_02) & (df.residual_sugar<=rs_96)]
sns.boxplot(df.residual_sugar)
```

```
<Axes: >
```



```
sns.boxplot(df.chlorides)
```

```
<Axes: >
```

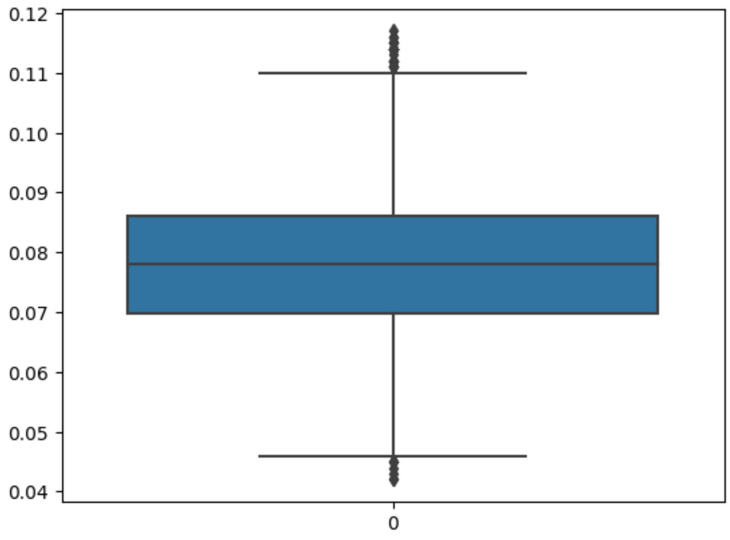


```
ch1 = df.chlorides.quantile(0.25) #Q1
ch3 = df.chlorides.quantile(0.75) #Q3
IQR_ch = ch3 - ch1
upper_limit_ch = ch3+(1.5)*(IQR_ch)
lower_limit_ch = ch1-(1.5)*(IQR_ch)
print(ch1)
print(ch3)
print(IQR_ch)
print(upper_limit_ch)
print(lower_limit_ch)
```

```
0.07
0.089
0.018999999999999999
0.11749999999999998
0.04150000000000002
```

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

```
<Axes: >
```

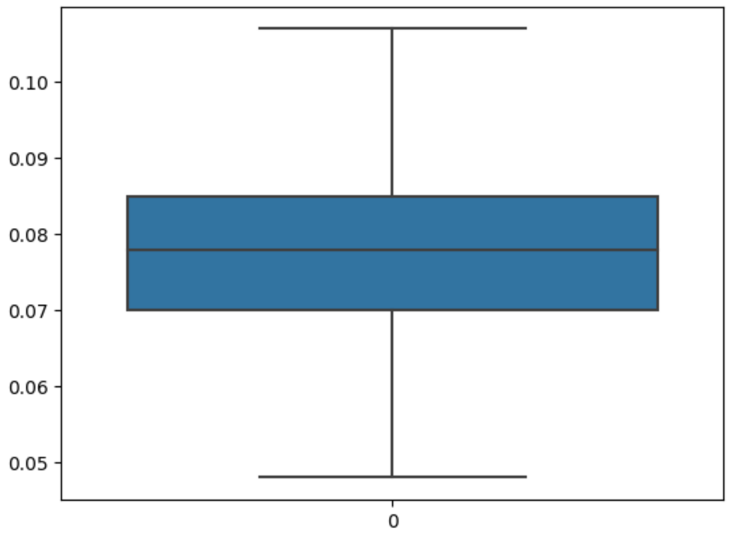


```
ch_01=df.chlorides.quantile(0.01)
ch_97=df.chlorides.quantile(0.97)
print(ch_01)
print(ch_97)
```

```
0.04775
0.107
```

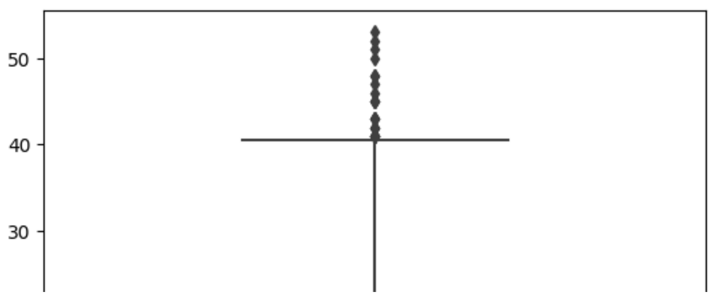
```
df=df[(df.chlorides>=ch_01) & (df.chlorides<=ch_97)]
sns.boxplot(df.chlorides)
```

```
<Axes: >
```



```
sns.boxplot(df.free_sulfur_dioxide)
```

```
<Axes: >
```

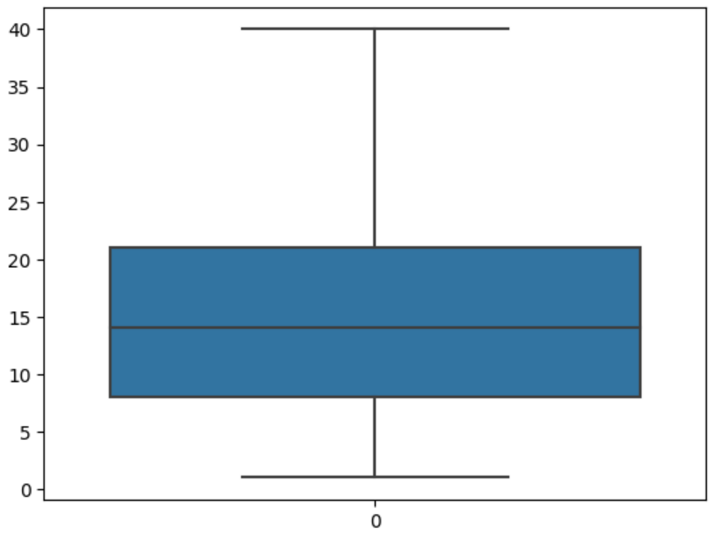


```
fs1 = df.free_sulfur_dioxide.quantile(0.25) #Q1
fs3 = df.free_sulfur_dioxide.quantile(0.75) #Q3
IQR_fs = fs3 - fs1
upper_limit_fs = fs3+(1.5)*(IQR_fs)
lower_limit_fs = fs1-(1.5)*(IQR_fs)
print(fs1)
print(fs3)
print(IQR_fs)
print(upper_limit_fs)
print(lower_limit_fs)
```

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

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

```
<Axes: >
```



```
sns.boxplot(df.total_sulfur_dioxide)
```

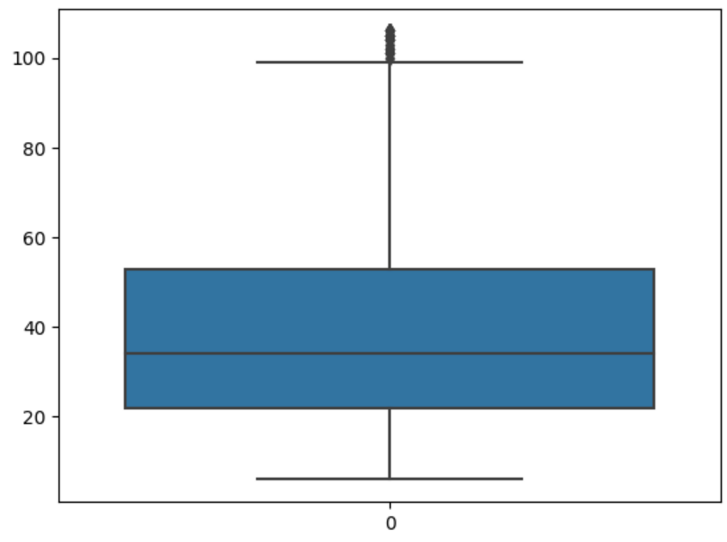
```
<Axes: >
```

```
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
```

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

```
<Axes: >
```

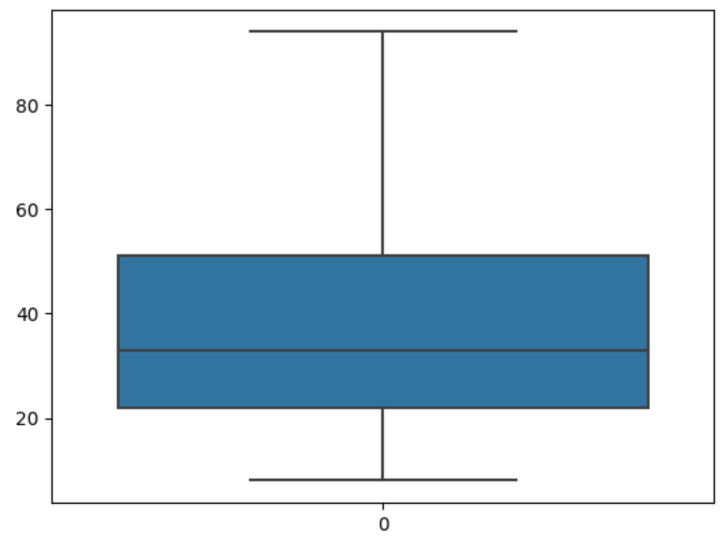


```
ts_01=df.total_sulfur_dioxide.quantile(0.01)
ts_97=df.total_sulfur_dioxide.quantile(0.97)
print(ts_01)
print(ts_97)
```

```
8.0
94.43999999999994
```

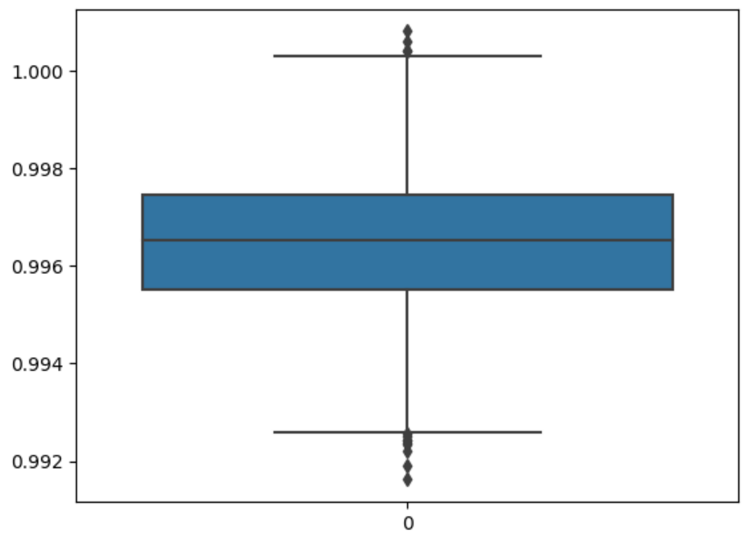
```
df=df[(df.total_sulfur_dioxide>=ts_01) & (df.total_sulfur_dioxide<=ts_97)]
sns.boxplot(df.total_sulfur_dioxide)
```

```
<Axes: >
```



```
sns.boxplot(df.density)
```

```
<Axes: >
```

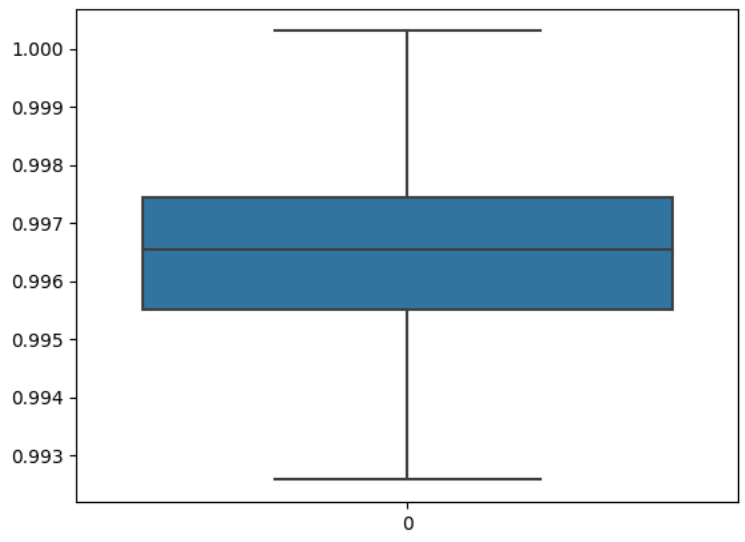


```
d1 = df.density.quantile(0.25) #Q1
d3 = df.density.quantile(0.75) #Q3
IQR_d = d3 - d1
upper_limit_d = d3+(1.5)*(IQR_d)
lower_limit_d = d1-(1.5)*(IQR_d)
print(d1)
print(d3)
print(IQR_d)
print(upper_limit_d)
print(lower_limit_d)
```

```
0.9955
0.99745
0.0019499999999998963
1.0003749999999998
0.9925750000000002
```

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

```
<Axes: >
```

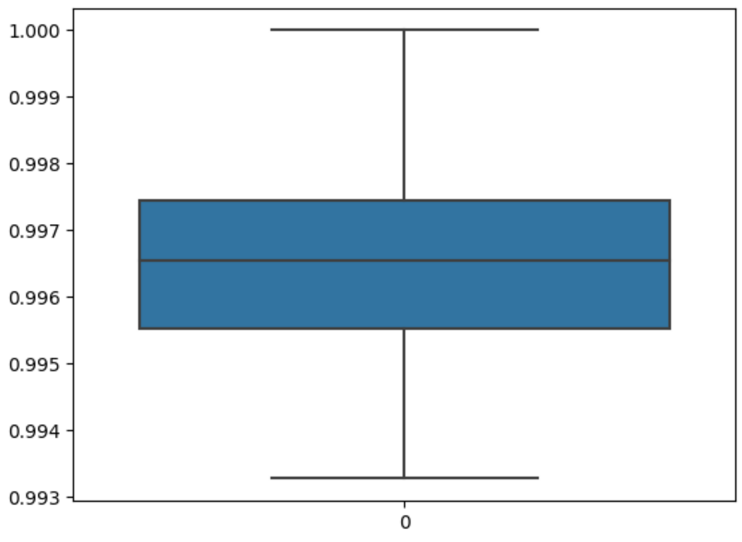


```
d_01=df.density.quantile(0.01)
d_99=df.density.quantile(0.99)
print(d_01)
print(d_99)
```

```
0.9932314999999999
1.0
```

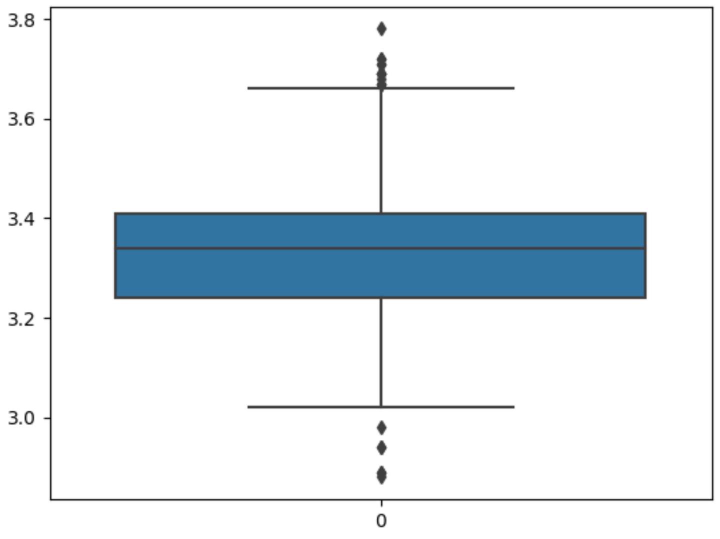
```
df=df[(df.density>=d_01) & (df.density<=d_99)]
sns.boxplot(df.density)
```

```
<Axes: >
```



```
sns.boxplot(df.pH)
```

```
<Axes: >
```

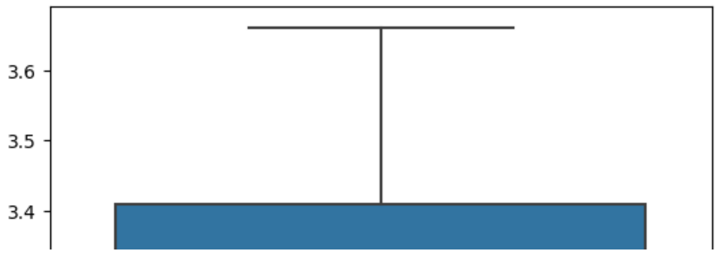


```
pH1 = df.pH.quantile(0.25) #Q1
pH3 = df.pH.quantile(0.75) #Q3
IQR_pH = pH3 - pH1
upper_limit_pH = pH3+(1.5)*(IQR_pH)
lower_limit_pH = pH1-(1.5)*(IQR_pH)
print(pH1)
print(pH3)
print(IQR_pH)
print(upper_limit_pH)
print(lower_limit_pH)
```

```
3.24
3.41
0.16999999999999993
3.665
2.9850000000000003
```

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

```
<Axes: >
```

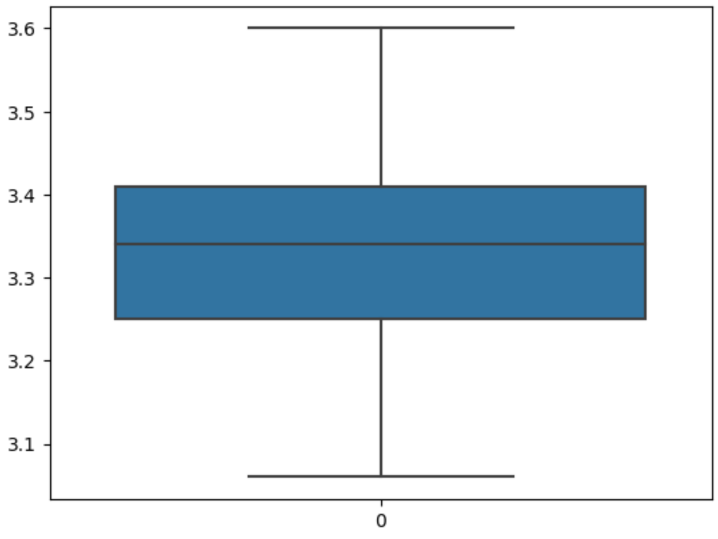


```
pH_01=df.pH.quantile(0.01)
pH_99=df.pH.quantile(0.99)
print(pH_01)
print(pH_99)
```

```
3.06
3.6034
```

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

```
<Axes: >
```



OUTLIERS REMOVED

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

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

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

```
0    5
1    5
2    5
3    6
4    5
Name: quality, dtype: int64
```

```
Y = df['quality'].apply(lambda y_value: 1 if y_value>=7 else 0)
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: 948, dtype: int64
```

```
#Train & Test split
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)
```

```
X_train.shape
```

```
(758, 11)
```

```
X_test.shape
```

```
(190, 11)
```

```
Y_train.shape
```

```
(758,)
```

```
Y_test.shape
```

```
(190,)
```

MODEL BUILDING

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

```
model.fit(X_train,Y_train)
```

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

MODEL EVALUATION

```
X_test_prediction = model.predict(X_test)
X_train_prediction=model.predict(X_train)
```

```
print('Testing Accuracy = ', accuracy_score(Y_test,X_test_prediction))
print('Training Accuracy = ', accuracy_score(Y_train,X_train_prediction))
```

```
Testing Accuracy =  0.9315789473684211
Training Accuracy =  1.0
```

```
input_data = [7.6, 1.0, 0, 3.0, 0.07, 30, 100, 0.9542, 3.1, 0.66, 9.6]
prediction = model.predict([input_data])
prediction
```

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