Importing the needed packages

In [1]:
```
import numpy as np
import pandas as pd
```

In [2]:
```
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import StandardScaler,LabelEncoder
from sklearn.model_selection import train_test_split,GridSearchCV
from sklearn.linear_model import LinearRegression
from sklearn.metrics import r2_score,mean_squared_error,roc_auc_score
from sklearn.linear_model import LogisticRegression
from sklearn import metrics
from sklearn.metrics import accuracy_score,recall_score,precision_score,auc
from sklearn.metrics import  classification_report,confusion_matrix,precision_recall_c
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import cross_val_score
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
import warnings
warnings.filterwarnings('ignore')
```

Loading the dataset

In [3]:
```
ds=pd.read_csv('QualityPrediction.csv')
ds
```

Out[3]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	9.4
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	9.8
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	9.8
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	9.8
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	9.4
...	...	...	...	...	...	...	...	...	...	...	...
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	10.5
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	11.2
1596	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	11.0
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	10.2
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	11.0

1599 rows × 12 columns

In [4]:
```
ds.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
```

Understanding the distribution of target variable

In [5]:
```
ds['quality'].value_counts()
```

Out[5]:
```
5    681
6    638
7    199
4     53
8     18
3     10
Name: quality, dtype: int64
```

In [6]:
```
ds['quality'].value_counts(normalize=True)
```

Out[6]:
```
5    0.425891
6    0.398999
7    0.124453
4    0.033146
8    0.011257
3    0.006254
Name: quality, dtype: float64
```

- There are two wine qualities majorly- 5 and 6. Others are 3,4,7 and 8.

- Understanding the distribution of all values

In [7]:
```
ds.describe()
```

Out[7]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	15
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.467792	
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	

- For a normal distribution, mean, median, mode are same

In [8]:
```
sk_data=pd.DataFrame()
sk_data['Features']=ds.columns
sk_data['Mean']=[ds[i].mean() for i in ds]
sk_data['Median']=[ds[i].median() for i in ds]
sk_data['mode']=[ds[i].mode()[0] for i in ds]
sk_data['Mean_median_diff_%']=[(abs(ds[i].median()-ds[i].mean()))*100)/ds[i].mean() for
sk_data
```

Out[8]:

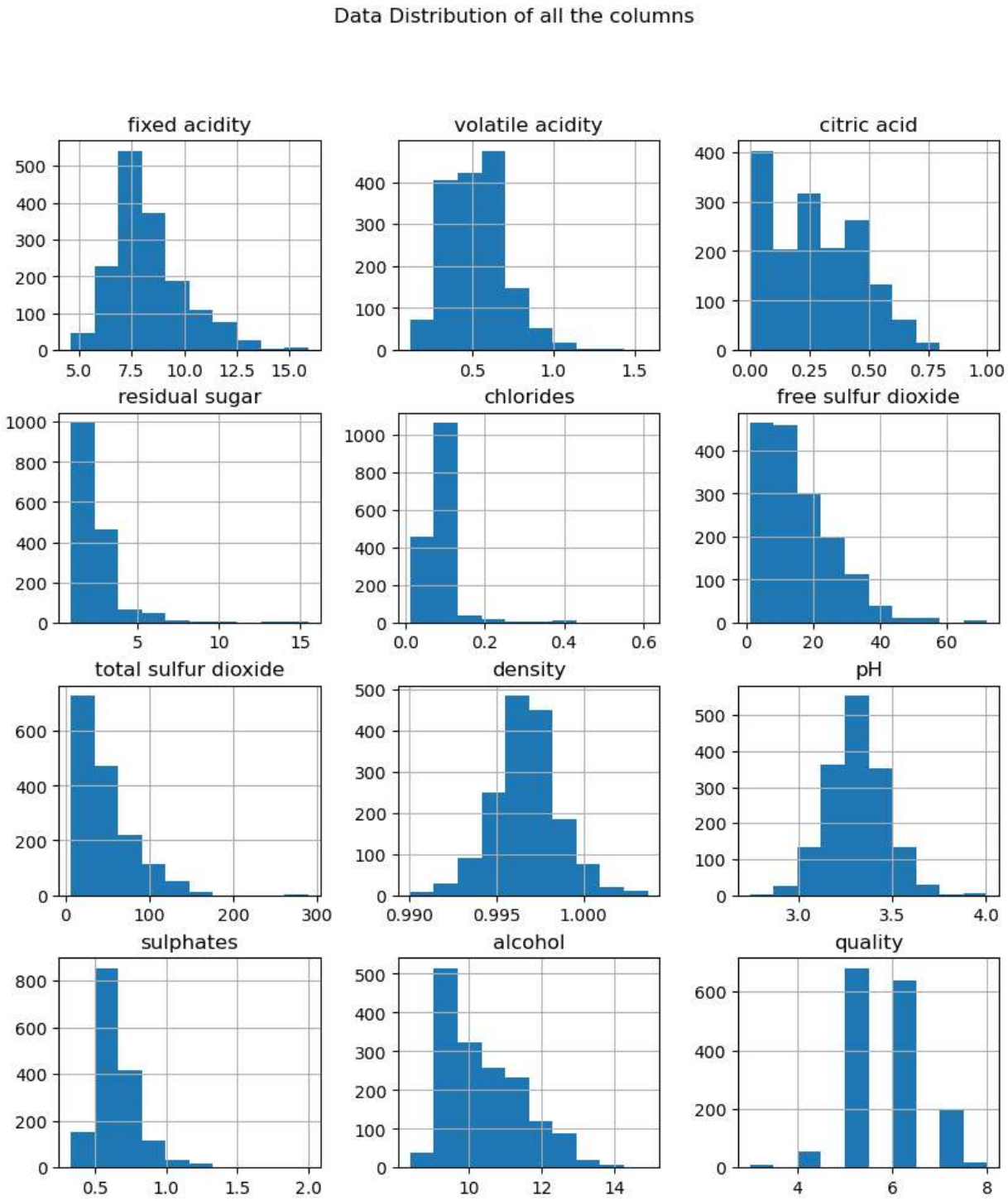
	Features	Mean	Median	mode	Mean_median_diff_%
0	fixed acidity	8.319637	7.90000	7.2000	5.043937
1	volatile acidity	0.527821	0.52000	0.6000	1.481661
2	citric acid	0.270976	0.26000	0.0000	4.050405
3	residual sugar	2.538806	2.20000	2.0000	13.345075
4	chlorides	0.087467	0.07900	0.0800	9.679749
5	free sulfur dioxide	15.874922	14.00000	6.0000	11.810589
6	total sulfur dioxide	46.467792	38.00000	28.0000	18.222928
7	density	0.996747	0.99675	0.9972	0.000333
8	pH	3.311113	3.31000	3.3000	0.033620
9	sulphates	0.658149	0.62000	0.6000	5.796385
10	alcohol	10.422983	10.20000	9.5000	2.139341
11	quality	5.636023	6.00000	5.0000	6.458056

Visualization

In [ ]:

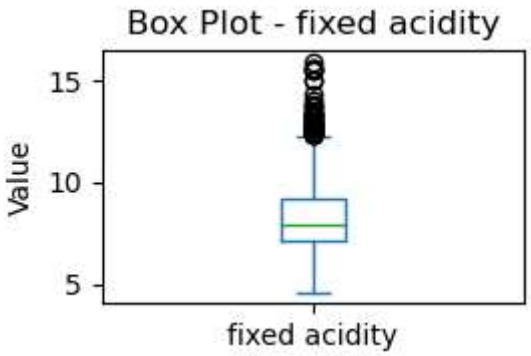
In [9]:
```
#sns.pairplot(ds, height = 4, aspect = 1, kind='reg',diag_kind = 'kde')
#plt.show()
```

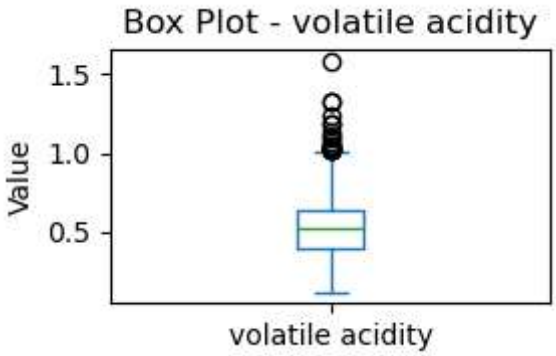
In [10]:
```
ds.hist(bins=10, figsize=(10,11))
plt.suptitle("Data Distribution of all the columns")
plt.show()
```

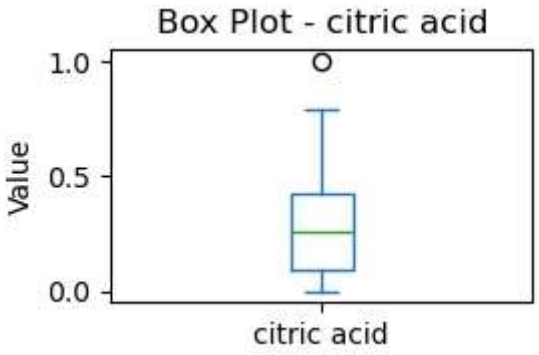


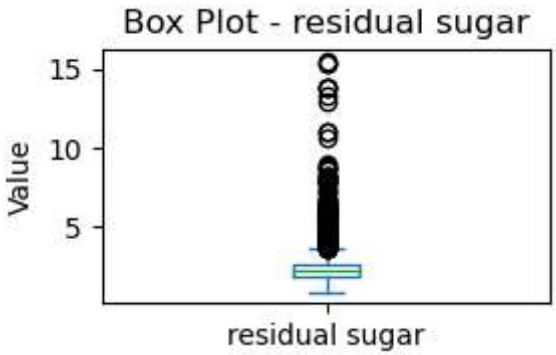
- Most columns are following normal distribution.
- The columns that are skewed are 'residual sugar','chlorides','free sulfur dioxide','total sulfur dioxide' as per the histogram

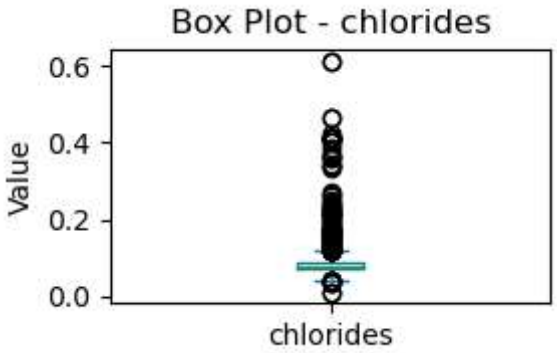
In [11]:
```
# Plot individual box plots for each column
for col in ds.columns:
    plt.figure(figsize=(3, 2))
    ds[col].plot(kind='box')
    plt.title(f"Box Plot - {col}")
    plt.ylabel("Value")
    plt.tight_layout()
    plt.show()
```

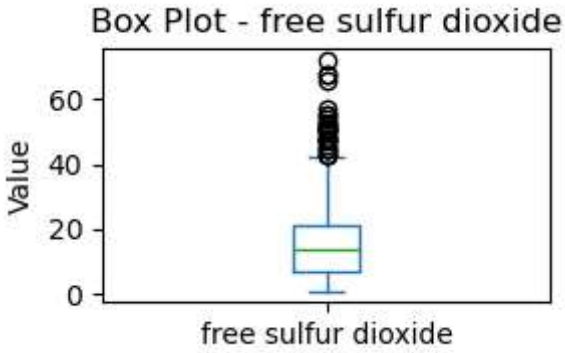

Box Plot - fixed acidity
Value
15
10
5
fixed acidity

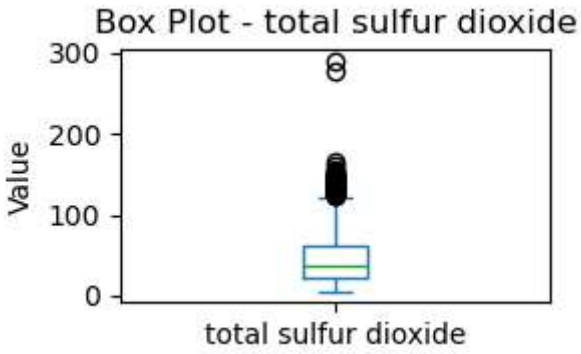

Box Plot - volatile acidity
Value
1.5
1.0
0.5
volatile acidity

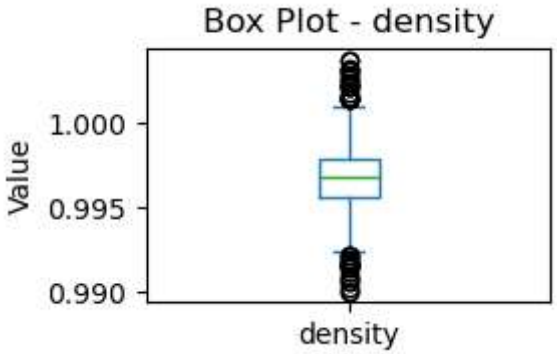

Box Plot - citric acid
Value
1.0
0.5
0.0
citric acid

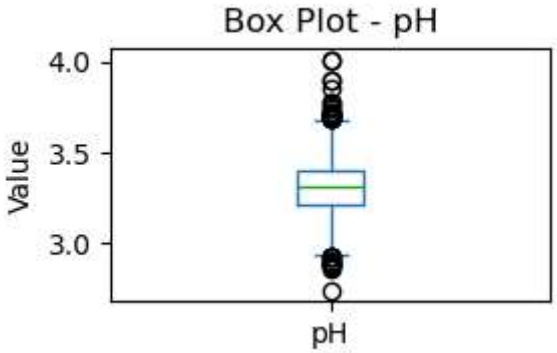

Box Plot - residual sugar
Value
15
10
5
residual sugar

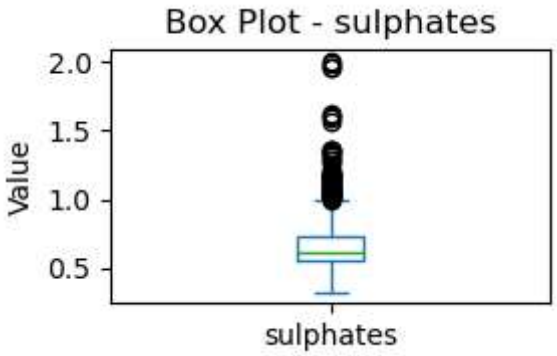

Box Plot - chlorides
Value
0.6
0.4
0.2
0.0
chlorides

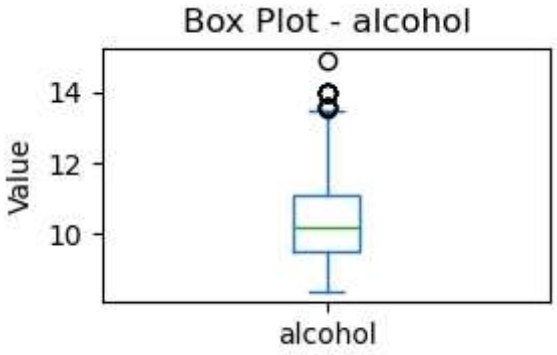

Box Plot - free sulfur dioxide
Value
60
40
20
0
free sulfur dioxide

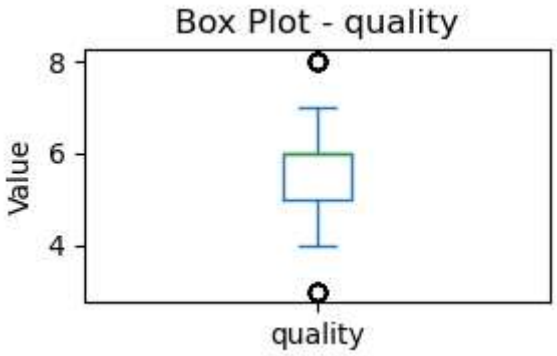

Box Plot - total sulfur dioxide
Value
300
200
100
0
total sulfur dioxide


Box Plot - density
Value
1.000
0.995
0.990
density


Box Plot - pH
Value
4.0
3.5
3.0
pH

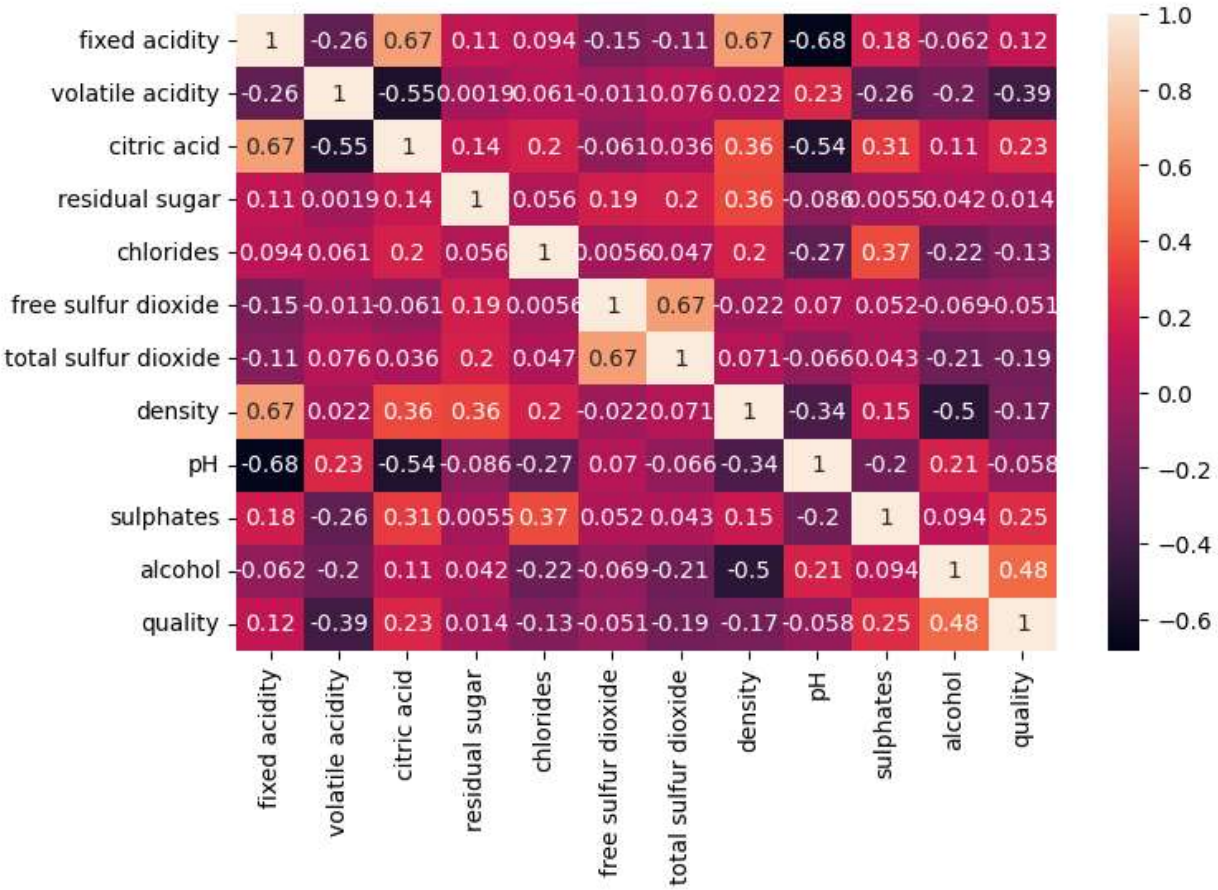






- The box plot shows outliers are present in the data

In [12]:
```
plt.figure(figsize = (8, 5))
sns.heatmap(ds.corr(), annot = True)
plt.show()
```



- The heat map shows that Free Sulphur Dioxide and Total Sulphur Dioxide have a positive correlation. Also Fixed Acidity with Citric acid and density. Quality shows the best correlation with Alcohol

Preprocessing

- The data does not have null values.
- We further check for outliers. Analysis can be done about the cause for these outliers. For our course of study, we maintain the outliers.

In [13]:
```
import statistics

def cal_outlier_zscore(col):
    l1=[]
    avg=col.mean()
    sd = statistics.stdev(col)
    for x in col:
        zsc=(x-avg)/sd
        if (zsc>3 or zsc<-3):
            l1.append(x)
    return(l1)

sk_data=pd.DataFrame(columns=['Features','No. of outliers','Outliers'])
sk_data['Features']=ds.columns
idx=0
```

```
for i in ds:

    s=cal_outlier_zscore(ds[i])
    sk_data. loc[idx, 'No. of outliers']= len(s)
    sk_data. loc[idx, 'Outliers']= str(s)
    idx=idx+1
sk_data
```

Out[13]:

	Features	No. of outliers	Outliers
0	fixed acidity	12	[15.0, 15.0, 13.8, 14.0, 13.7, 13.7, 15.6, 14....
1	volatile acidity	10	[1.13, 1.07, 1.33, 1.33, 1.09, 1.24, 1.185, 1....
2	citric acid	1	[1.0]
3	residual sugar	30	[10.7, 7.3, 7.2, 7.0, 11.0, 11.0, 7.9, 7.9, 15...
4	chlorides	31	[0.368, 0.341, 0.332, 0.464, 0.401, 0.467, 0.2...
5	free sulfur dioxide	22	[52.0, 51.0, 50.0, 68.0, 68.0, 54.0, 53.0, 52....
6	total sulfur dioxide	15	[148.0, 153.0, 165.0, 151.0, 149.0, 147.0, 148...
7	density	18	[1.0032, 1.0026, 1.00315, 1.00315, 1.00315, 1....
8	pH	8	[3.9, 3.85, 2.74, 3.9, 3.78, 3.78, 4.01, 4.01]
9	sulphates	27	[1.56, 1.28, 1.2, 1.28, 1.95, 1.22, 1.95, 1.98...
10	alcohol	8	[14.0, 14.0, 14.0, 14.0, 14.9, 14.0, 14.0, 14.0]
11	quality	10	[3, 3, 3, 3, 3, 3, 3, 3, 3, 3]

- Residual sugar, chlorides , sulphates and free sulphur dioxide have more than 20 outliers

- We drop duplicate records

In [14]:
```
print(ds.duplicated().sum())
ds.drop_duplicates(inplace=True)
```

```
240
```

- We further calculate skewness to understand the distribution.

In [15]:
```
#calculate skewness for each variable
sk_data=pd.DataFrame()
sk_data['Features']=ds.columns
from scipy.stats import skew
sk_data['Skewness']=[skew(ds[i]) for i in ds]
sk_data
```

Out[15]:

	Features	Skewness
0	fixed acidity	0.940002
1	volatile acidity	0.728474
2	citric acid	0.312380
3	residual sugar	4.543132
4	chlorides	5.496412
5	free sulfur dioxide	1.225225
6	total sulfur dioxide	1.538667
7	density	0.044728
8	pH	0.231776
9	sulphates	2.403848
10	alcohol	0.858892
11	quality	0.192194

- Residual sugar, chlorides and sulphates are highly skewed.

Train Test Split

In [16]:
```
x_col=ds.drop('quality',axis=1)
x=ds.drop('quality',axis=1).values
y=ds['quality'].values
```

- We perform oversampling here with the sampling strategy as 'all' indicating equal number of samples for each class.

In [17]:
```
"""from imblearn.over_sampling import SMOTE
from collections import Counter
from sklearn.datasets import make_classification
from imblearn.over_sampling import RandomOverSampler

# summarize class distribution
print(Counter(y))
# define oversampling strategy
oversample = RandomOverSampler(sampling_strategy='all')
# fit and apply the transform
x, y = oversample.fit_resample(x, y)
# summarize class distribution
print(Counter(y))"""
#should be used in cases where the dataset is not representative of true population
```

Out[17]:
```
"from imblearn.over_sampling import SMOTE\nfrom collections import Counter\nfrom skle
arn.datasets import make_classification\nfrom imblearn.over_sampling import RandomOve
rSampler\n\n# summarize class distribution\nprint(Counter(y))\n# define oversampling
strategy\noversample = RandomOverSampler(sampling_strategy='all')\n# fit and apply th
e transform\nx, y = oversample.fit_resample(x, y)\n# summarize class distribution\npr
int(Counter(y))"
```

In [18]:
```
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=5)
```

In [ ]:
```

```

In [19]:
```
ds.columns
```

Out[19]:
```
Index(['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar',
       'chlorides', 'free sulfur dioxide', 'total sulfur dioxide', 'density',
       'pH', 'sulphates', 'alcohol', 'quality'],
      dtype='object')
```

Feature Scaling to apply KNN and SVM since the two models are distance based

- Since many columns follow normal distribution, we follow StandardScaler

- Splitting for Standard Scaler

In [20]:
```
from sklearn.preprocessing import StandardScaler
ss=StandardScaler()

x_train=ss.fit_transform(x_train)
x_test=ss.transform(x_test)
```

- Multicollinearity will help to check if any two variables are highly correlated.

In [21]:
```
#multicllinearity-check
from statsmodels.stats.outliers_influence import variance_inflation_factor
vif_data=pd.DataFrame()
vif_data['Features']=x_col.columns
vif_data['VIF']=[variance_inflation_factor(x_train,i) for i in range(x_train.shape[1])
vif_data['multicollinear']=[True if vif_data['VIF'][i]>5 else False for i in range(x_t
vif_data
```

Out[21]:

	Features	VIF	multicollinear
0	fixed acidity	8.190673	True
1	volatile acidity	1.750200	False
2	citric acid	3.136416	False
3	residual sugar	1.676717	False
4	chlorides	1.527067	False
5	free sulfur dioxide	1.979689	False
6	total sulfur dioxide	2.260255	False
7	density	6.490853	True
8	pH	3.376254	False
9	sulphates	1.485474	False
10	alcohol	3.159173	False

- Since multi collinearity exists and we cannot remove the columns Logistic Regression and Naive Bayes cannot be applied

Model Building

Decision tree model with max_depth=3

In [22]:
```
mod_4=DecisionTreeClassifier(random_state=1,max_depth=3)
mod_4.fit(x_train,y_train)
y_pred=mod_4.predict(x_test)
acc=accuracy_score(y_test,y_pred)
print("Accuracy:",acc)
```

```
Accuracy: 0.5661764705882353
```

Decision tree model with max_depth=4

In [23]:
```
mod_4=DecisionTreeClassifier(random_state=1,max_depth=4)
mod_4.fit(x_train,y_train)
y_pred=mod_4.predict(x_test)
acc=accuracy_score(y_test,y_pred)
print(acc)
```

```
0.5625
```

In [24]:
```
mod_4=DecisionTreeClassifier(random_state=1,max_depth=6)
mod_4.fit(x_train,y_train)
y_pred=mod_4.predict(x_test)
accdt=accuracy_score(y_test,y_pred)
print("Accuracy:",acc)
```

```
Accuracy: 0.5625
```

In [25]:
```
mod_4=DecisionTreeClassifier(random_state=1,max_depth=5)
mod_4.fit(x_train,y_train)
y_pred=mod_4.predict(x_test)
acc=accuracy_score(y_test,y_pred)
print("Accuracy:",acc)
```

```
Accuracy: 0.5882352941176471
```

- max_depth= 5 showed the best possible results

Random Forest Classifier

In [26]:
```
rf=RandomForestClassifier(random_state=1,class_weight='balanced')
rf.fit(x_train,y_train)
y_pred=rf.predict(x_test)
accrf=accuracy_score(y_test,y_pred)
print("Accuracy:",accrf)
score=cross_val_score(rf,x_train,y_train,cv=10)
print("Accuracy after k-fold validation:",score.mean())
print(classification_report(y_test,y_pred))
```

```
Accuracy: 0.6507352941176471
Accuracy after k-fold validation: 0.6079595650696568
              precision    recall  f1-score   support

           3       0.00      0.00      0.00         1
           4       0.00      0.00      0.00         7
           5       0.66      0.82      0.73       105
           6       0.66      0.64      0.65       119
           7       0.62      0.42      0.50        36
           8       0.00      0.00      0.00         4

    accuracy                           0.65       272
   macro avg       0.32      0.31      0.31       272
weighted avg       0.62      0.65      0.63       272
```

KNN

In [27]:
```
knn=KNeighborsClassifier(n_neighbors=15)
knn.fit(x_train,y_train)
y_pred=knn.predict(x_test)
accknn=accuracy_score(y_test,y_pred)
print(accknn)
```

```
0.5661764705882353
```

- We use SVM further

In [28]:
```
svc=SVC(kernel='rbf',C=1,gamma=0.1)
svc.fit(x_train,y_train)
ypred=svc.predict(x_test)
print(metrics.accuracy_score(y_test,ypred))
```

```
0.6213235294117647
```

- Highest acuracy is obtained for Randome Forest. Hence we will tune and check the model further.

In [29]:
```
imp=rf.feature_importances_
fi=pd.DataFrame()
fi['Feature']=x_col.columns
fi['Score']=imp
fi.sort_values('Score',ascending=False)
```

Out[29]:

	Feature	Score
10	alcohol	0.129426
1	volatile acidity	0.128414
9	sulphates	0.117479
7	density	0.093324
6	total sulfur dioxide	0.091488
4	chlorides	0.091088
2	citric acid	0.076745
8	pH	0.075121
5	free sulfur dioxide	0.067579
0	fixed acidity	0.066734
3	residual sugar	0.062604

- All features are contributing to prediction.

Hyperparameter tuning for Random Forest with 5 features

In [30]:
```
param_dist={'max_depth':[4,5,6],

            'criterion':['gini','entropy'],
            'oob_score':[True,False],
             'max_features':['auto','sqrt','log2'],
            'bootstrap':[True,False]}
cv_rf=GridSearchCV(rf,cv=10,param_grid=param_dist,verbose=2,n_jobs=1)
cv_rf.fit(x_train,y_train)
rf.set_params(**cv_rf.best_params_)
rf.fit(x_train,y_train)
y_pred=rf.predict(x_test)
```

```
Fitting 10 folds for each of 72 candidates, totalling 720 fits
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ue; total time=   0.2s
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```

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```

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```

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```

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[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=True; total time=   0.0s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=True; total time=   0.0s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=True; total time=   0.0s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=True; total time=   0.0s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=True; total time=   0.0s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=True; total time=   0.0s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
```

```
[CV] END bootstrap=False, criterion=entropy, max_depth=6, max_features=log2, oob_scor
e=False; total time=   0.3s
```

In [31]:
```
acc=accuracy_score(y_test,y_pred)
print(acc)
```

```
0.5220588235294118
```

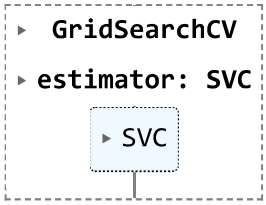
- Hyperparameter tuning showed reduced accuracy #### Hyperparameter tuning for SVM

In [32]:
```
paramm={'C':[0.1,1,10],
       'gamma':[1,0.1,0.01],
       'kernel': ['linear','rbf','poly']}
ms=GridSearchCV(svc,paramm,cv=5,scoring='accuracy',verbose=1)
```

In [33]:
```
ms.fit(x_train,y_train)
```

```
Fitting 5 folds for each of 27 candidates, totalling 135 fits
```

Out[33]:



In [34]:
```
print(ms.best_params_)
```

```
{'C': 1, 'gamma': 0.1, 'kernel': 'rbf'}
```

In [35]:
```
svcm=SVC(kernel='rbf',C=1,gamma=1)
svcm.fit(x_train,y_train)
ypred=svcm.predict(x_test)
accsvm=metrics.accuracy_score(y_test,ypred)
print(accsvm)
```

```
0.5845588235294118
```

RandomForestClassifier without hyperparameter tuning and SVM after tuning showed the best accuracy

In [36]:
```
print(classification_report(y_test,ypred))
```

```
              precision    recall  f1-score   support

           3       0.00      0.00      0.00         1
           4       0.00      0.00      0.00         7
           5       0.57      0.79      0.66       105
           6       0.60      0.56      0.58       119
           7       0.60      0.25      0.35        36
           8       0.00      0.00      0.00         4

    accuracy                           0.58       272
   macro avg       0.30      0.27      0.27       272
weighted avg       0.56      0.58      0.56       272
```

In [37]:
```
cm=confusion_matrix(y_test,ypred)
cm
```

Out[37]:
```
array([[ 0,  0,  1,  0,  0,  0],
       [ 0,  0,  7,  0,  0,  0],
       [ 0,  0, 83, 22,  0,  0],
       [ 0,  0, 48, 67,  4,  0],
       [ 0,  0,  7, 20,  9,  0],
       [ 0,  0,  0,  2,  2,  0]], dtype=int64)
```

Accuracy comparison

In [38]:
```
accpd=pd.DataFrame()
accpd['Model']=['Decision Tree','Random Forest','KNN','SVM after hyperparameter tuning
accpd['Accuracy']=[accdt,accrf,accknn,accsvm]
accpd
```

Out[38]:

	Model	Accuracy
0	Decision Tree	0.529412
1	Random Forest	0.650735
2	KNN	0.566176
3	SVM after hyperparameter tuning	0.584559

The accuracy achieved was 89% with Random Forest

In [ ]:
```
```