```
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
```

```
# loading the dataset to a Pandas DataFrame
wine_dataset = pd.read_csv('redwine.csv')
```

```
# number of rows & columns in the dataset
wine_dataset.shape
```

```
(1599, 12)
```

```
# first 5 rows of the dataset
wine_dataset.head()
```

```
   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      5.0
1      9.8      5.0
2      9.8      5.0
3      9.8      6.0
4      9.4      5.0
```

```
# checking for missing values
wine_dataset.fillna(wine_dataset.mean(),inplace=True)
```

```
# statistical measures of the dataset
wine_dataset.describe()
```

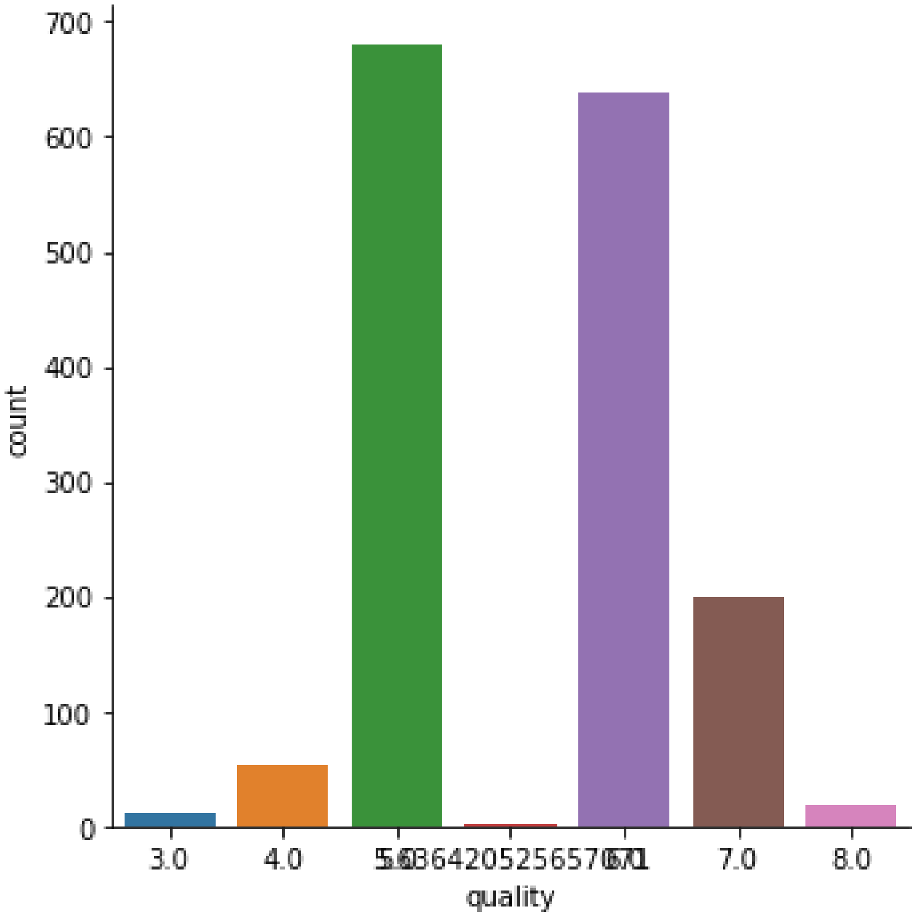
```
       fixed acidity  volatile acidity  citric acid  residual sugar  \
count    1599.000000       1599.000000  1599.000000     1599.000000   
mean        8.319637          0.527821     0.270976        2.538806   
std         1.741096          0.179060     0.194801        1.409928   
min         4.600000          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             46.433041
0.996747   
std       0.047065            10.460157             32.865961
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      3.498586     0.658149    10.422983     5.636421  
std       0.080321     0.169507     1.065668     0.807413  
min       2.740000     0.330000     8.400000     3.000000  
25%       3.520000     0.550000     9.500000     5.000000  
50%       3.520000     0.620000    10.200000     6.000000  
75%       3.520000     0.730000    11.100000     6.000000  
max       3.900000     2.000000    14.900000     8.000000  
```

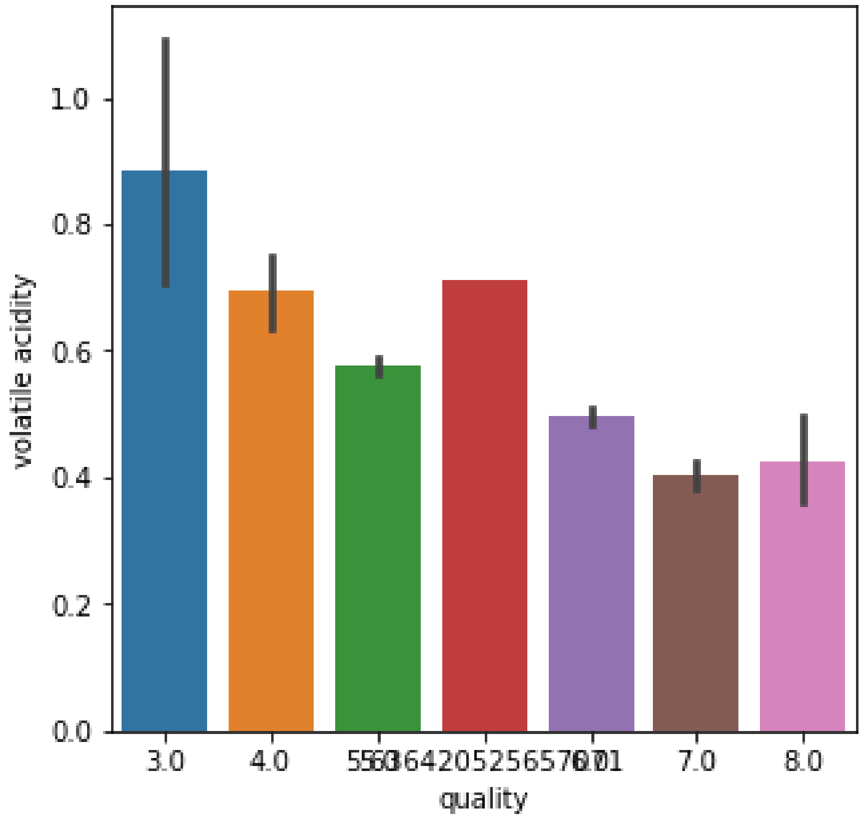
```
# number of values for each quality
sns.catplot(x='quality', data = wine_dataset, kind = 'count')
```

```
<seaborn.axisgrid.FacetGrid at 0x7faca42065e0>
```



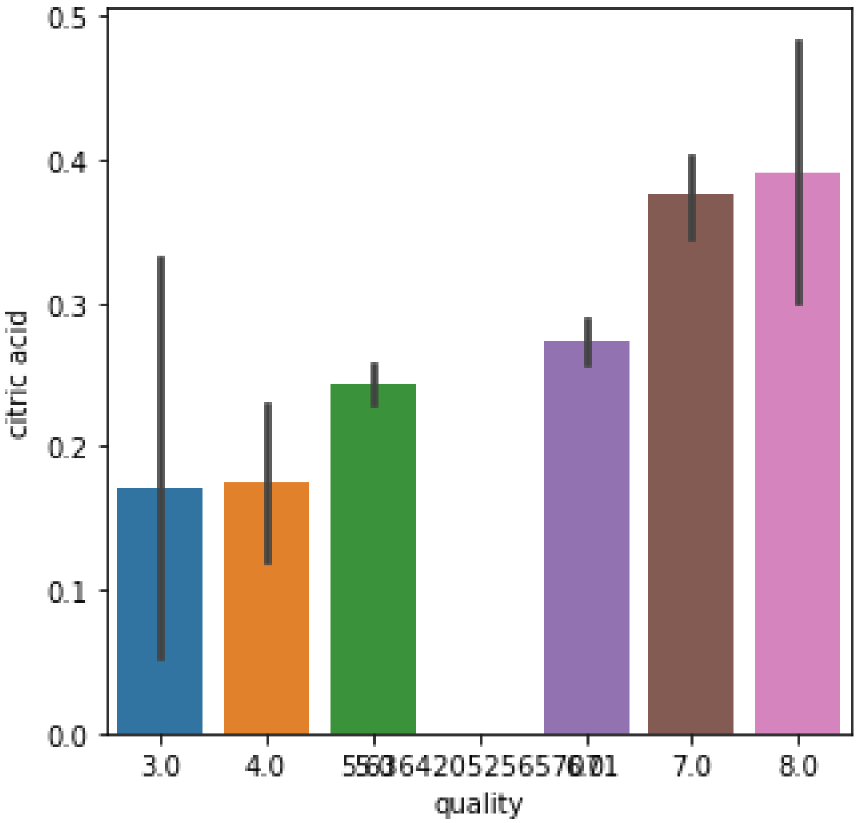
```
# volatile acidity vs Quality
plot = plt.figure(figsize=(5,5))
sns.barplot(x='quality', y = 'volatile acidity', data = wine_dataset)
```

```
<AxesSubplot:xlabel='quality', ylabel='volatile acidity'>
```



```
# citric acid vs Quality
plot = plt.figure(figsize=(5,5))
sns.barplot(x='quality', y = 'citric acid', data = wine_dataset)
```

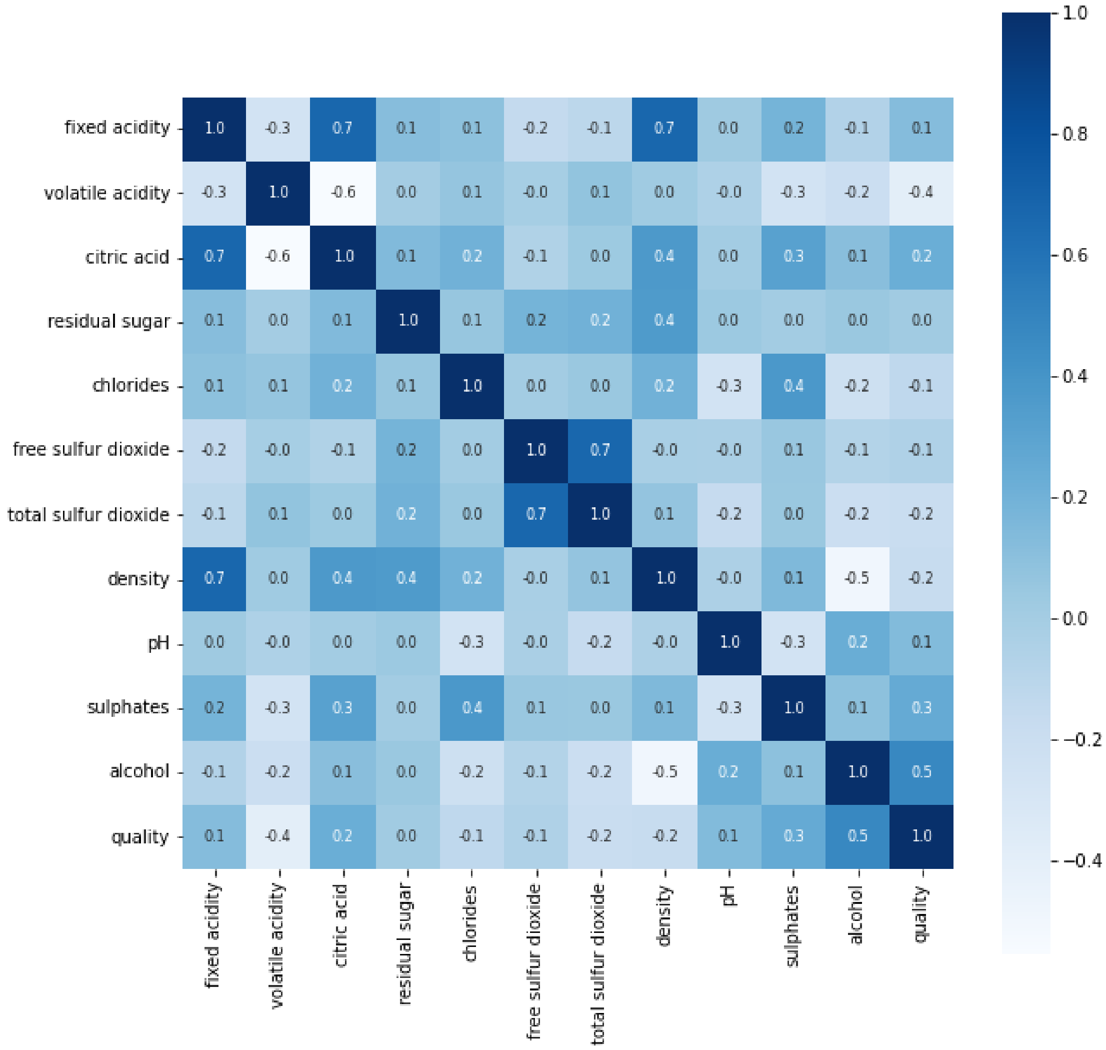
```
<AxesSubplot:xlabel='quality', ylabel='citric acid'>
```



```
correlation = wine_dataset.corr()

# constructing a heatmap to understand the correlation between the
columns
plt.figure(figsize=(10,10))
sns.heatmap(correlation, cbar=True, square=True, fmt = '.1f', annot =
True, annot_kws={'size':8}, cmap = 'Blues')
```

```
<AxesSubplot:>
```



```
# separate the data and Label
X = wine_dataset.drop('quality',axis=1)

print(X)
```

```
      fixed acidity  volatile acidity  citric acid  residual sugar
chlorides  \
0               7.4             0.700         0.00             1.9
0.076
1               7.8             0.880         0.00             2.6
0.098
2               7.8             0.760         0.04             2.3
0.092
3              11.2             0.280         0.56             1.9
0.075
4               7.4             0.700         0.00             1.9
0.076
...             ...               ...          ...             ...
...
```

```
1594            6.2             0.600         0.08             2.0
0.090
1595            5.9             0.550         0.10             2.2
0.062
1596            6.3             0.510         0.13             2.3
0.076
1597            5.9             0.645         0.12             2.0
0.075
1598            6.0             0.310         0.47             3.6
0.067

      free sulfur dioxide  total sulfur dioxide  density    pH
sulphates  \
0                    11.0                  34.0  0.99780  3.51
0.56
1                    25.0                  67.0  0.99680  3.20
0.68
2                    15.0                  54.0  0.99700  3.26
0.65
3                    17.0                  60.0  0.99800  3.16
0.58
4                    11.0                  34.0  0.99780  3.51
0.56
...                   ...                   ...      ...   ...
...
1594                 32.0                  44.0  0.99490  3.52
0.58
1595                 39.0                  51.0  0.99512  3.52
0.76
1596                 29.0                  40.0  0.99574  3.52
0.75
1597                 32.0                  44.0  0.99547  3.52
0.71
1598                 18.0                  42.0  0.99549  3.52
0.66

      alcohol
0         9.4
1         9.8
2         9.8
3         9.8
4         9.4
...       ...
1594     10.5
1595     11.2
1596     11.0
1597     10.2
1598     11.0

[1599 rows x 11 columns]
```

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

```
print(Y)
```

```
0       0
1       0
2       0
3       0
4       0
       ..
1594    0
1595    0
1596    0
1597    0
1598    0
Name: quality, Length: 1599, dtype: int64
```

```
X_train, X_test, Y_train, Y_test = train_test_split(X, Y,
test_size=0.2, random_state=0)
```

```
model = RandomForestClassifier()
```

```
wine_dataset.columns
```

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

```
wine_dataset['fixed acidity'] = wine_dataset['fixed
acidity'].astype("float32")
wine_dataset['volatile acidity'] = wine_dataset['volatile
acidity'].astype("float32")
wine_dataset['citric acid'] = wine_dataset['citric
acid'].astype("float32")
wine_dataset['residual sugar'] = wine_dataset['residual
sugar'].astype("float32")
wine_dataset['chlorides'] =
wine_dataset['chlorides'].astype("float32")
wine_dataset['free sulfur dioxide'] = wine_dataset['free sulfur
dioxide'].astype("float32")
wine_dataset['total sulfur dioxide'] = wine_dataset['total sulfur
dioxide'].astype("float32")
wine_dataset['density'] = wine_dataset['density'].astype("float32")
```

```
X_test_prediction = model.fit(X,Y)
```

```
input_data = (7.5,0.5,0.36,6.1,0.071,17.0,102.0,0.9978,3.35,0.8,10.5)
```

```
input_data_as_numpy_array = np.asarray(input_data)


input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

prediction = model.predict(input_data_reshaped)
print(prediction)

if (prediction[0]==1):
  print('Good Quality Wine')
else:
  print('Bad Quality Wine')
```

```
[0]
Bad Quality Wine
```

```
/Users/ronyzachariageorge/opt/anaconda3/lib/python3.9/site-packages/
sklearn/base.py:450: UserWarning: X does not have valid feature names,
but RandomForestClassifier was fitted with feature names
  warnings.warn(
```