Predicting wine quality using Random forest model

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

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

```
data.head(3)
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5

```
data.info()
# (shape = (1599,12))
# no null value
```

```
<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
```

```
data.describe()
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.00
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.467792	0.996747	3.31
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	0.001887	0.15
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.990070	2.74
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.995600	3.21
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.996750	3.31
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.997835	3.40
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1.003690	4.01

Number of values for each quality of wine

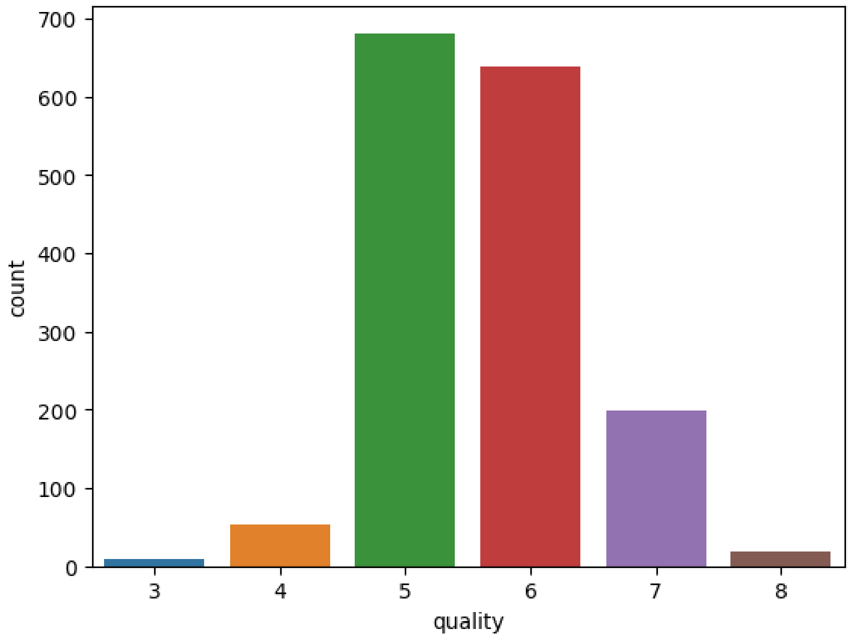
```
data['quality'].value_counts()
```

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

Data Visualisation

```
sns.countplot(x='quality', data=data,)
```

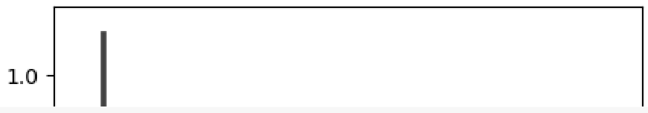
```
<Axes: xlabel='quality', ylabel='count'>
```



Plotting multiple graphs to check the correlation struture

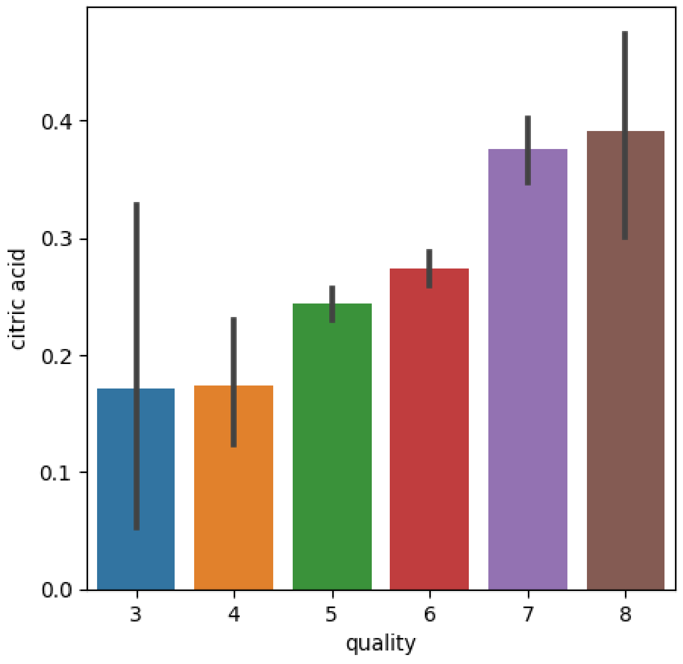
```
plot = plt.figure(figsize=(5,5))
sns.barplot(x='quality', y='volatile acidity', data=data)
```

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



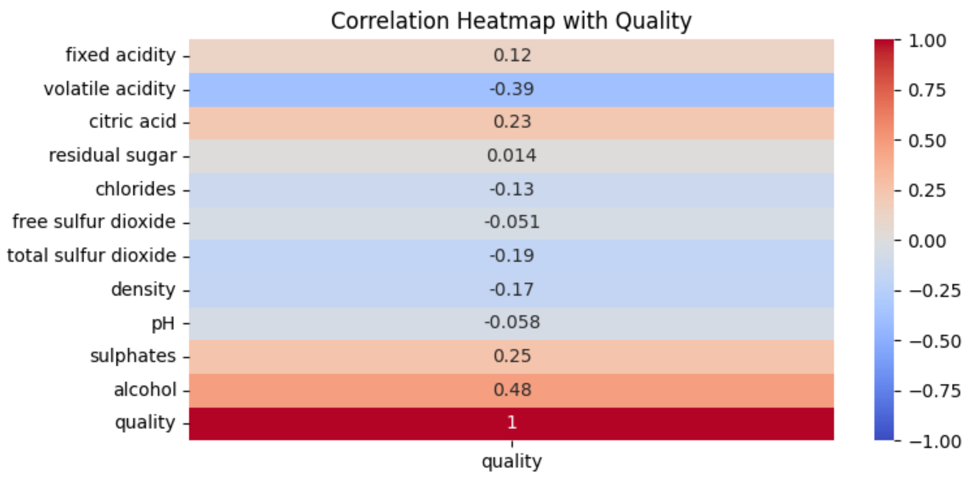
```
plot = plt.figure(figsize=(5,5))
sns.barplot(x='quality', y='citric acid', data=data)
```

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



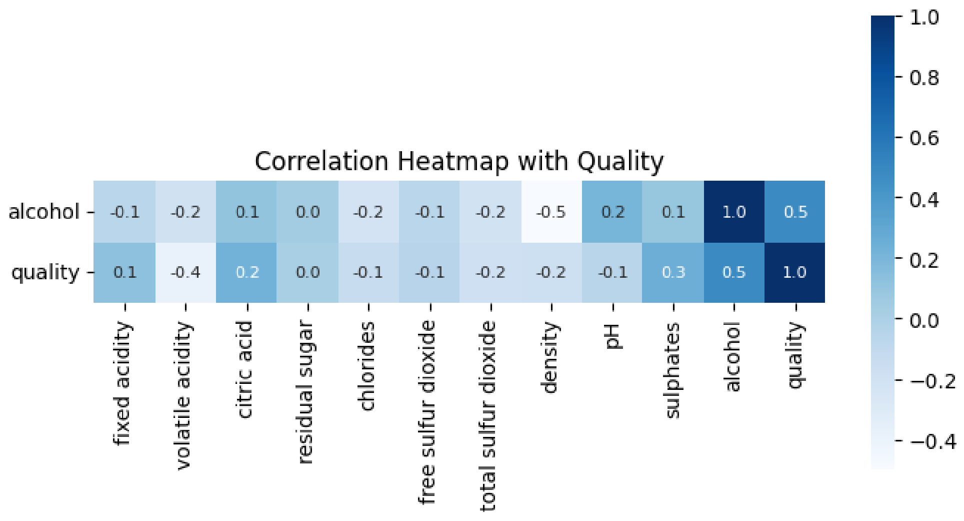
```
corr_matrix = data.corr()
plt.figure(figsize=(8, 4))
sns.heatmap(corr_matrix[['quality']], annot=True, cmap='coolwarm', vmin=-1, vmax=1)
plt.title('Correlation Heatmap with Quality')
plt.show()

# data.corr(): This calculates the correlation matrix for all numeric columns in your DataFrame.
# corr_matrix[['quality']]: This selects the correlation values between all columns and the 'quality' column.
# sns.heatmap(): This creates a heatmap using Seaborn to visualize the correlation matrix.
# annot=True: This adds the numerical values in each cell of the heatmap.
# cmap='coolwarm': This sets the color map for the heatmap.
# vmin and vmax: These set the minimum and maximum values for the color scale. Setting them to -1 and 1 ensures tha
```



	quality
fixed acidity	0.12
volatile acidity	-0.39
citric acid	0.23
residual sugar	0.014
chlorides	-0.13
free sulfur dioxide	-0.051
total sulfur dioxide	-0.19
density	-0.17
pH	-0.058
sulphates	0.25
alcohol	0.48
quality	1

```
plt.figure(figsize=(8, 4))
filtered_corr = corr_matrix[(corr_matrix['quality'] > 0.4) | (corr_matrix['quality'] < -0.4)]
sns.heatmap(filtered_corr, annot=True, cmap='Blues', annot_kws={'size':8}, fmt='.1f', square=True, cbar=True)
plt.title('Correlation Heatmap with Quality')
plt.show()
```



```
# Filter correlations greater than 0.40 or lesser than -0.40
filtered_corr = corr_matrix[(corr_matrix['quality'] > 0.25) | (corr_matrix['quality'] < -0.25)]

print("Filtered Correlation Matrix:")
print(filtered_corr[['quality']])
```

```
Filtered Correlation Matrix:
                   quality
volatile acidity -0.390558
sulphates         0.251397
alcohol           0.476166
quality           1.000000
```

Data Preprocesing

Label Binarisation

```
y = data['quality'].apply(lambda y_val: 1 if y_val >= 6 else 0)
# data['quality']: This extracts the 'quality' column from DataFrame data.
# .apply(lambda y_val: 1 if y_val >= 6 else 0): This applies a lambda function to each element in the 'quality' col
```

```
x = data.drop("quality", axis=1)
```

```
y.head()
x.head()
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sı
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	

Splitting train and test data

```
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2, random_state=42, stratify=y)
```

```
print(len(x_train)/(len(x_train)+len(x_test)))
```

```
0.7998749218261413
```

Model training

```
model = RandomForestClassifier()
```

```
model.fit(x_train, y_train)
```

```
▾ RandomForestClassifier
RandomForestClassifier()
```

Model Evaluation

```
# accuracy on test_data
x_test_pred = model.predict(x_test)
test_data_acc = accuracy_score(x_test_pred, y_test)
print('Accuracy on test data is:', test_data_acc)
```

```
Accuracy on test data is: 0.8125
```

Building a predictioin system

```
input_data = (7.3,0.65,0.0,1.2,0.065,15.0,21.0,0.9946,3.39,0.47,10.0) #label was 7 so output should be 1

# changing input data to a numpy array
input_data_as_np_arr = np.asarray(input_data)

# reshaping the data as we are only predicting only 1 instance.
input_data_rshp = input_data_as_np_arr.reshape(1, -1)

prediction = model.predict(input_data_rshp)

if (prediction[0] == 1):
  print('Quality of wine is good')
else:
  print('Quality is bad')
```

```
Quality of wine is good
/usr/local/lib/python3.10/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but
  warnings.warn(
```

```
1
```