In [1]:
```
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.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score, f1_score, precision_score
```

DATASET UPLOADING AND ANALYSIS

In [2]:
```
data = pd.read_csv("Wine quality dataset.csv")
```

In [3]:
```
data.head()
```

Out[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	5.0
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5.0
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5.0
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6.0
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5.0

In [4]:
```
data.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  1598 non-null   float64
 7   density               1599 non-null   float64
 8   pH                    1598 non-null   float64
 9   sulphates             1599 non-null   float64
 10  alcohol               1599 non-null   float64
 11  quality               1598 non-null   float64
dtypes: float64(12)
memory usage: 150.0 KB
```

In [5]:
```
data.shape
```

Out[5]:
```
(1599, 12)
```

In [6]:

```
data.isna().sum()
```

Out[6]:

```
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    1
density                 0
pH                      1
sulphates               0
alcohol                 0
quality                 1
dtype: int64
```

In [7]:

```
data[data['total sulfur dioxide'].isna() | data['pH'].isna() | data['quality'].isna()]
```

Out[7]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
9	7.5	0.50	0.36	6.1	0.071	17.0	NaN	0.9978	3.35	0.80	10.5	5.0
123	8.0	0.71	0.00	2.6	0.080	11.0	34.0	0.9976	3.44	0.53	9.5	NaN
184	6.7	0.62	0.21	1.9	0.079	8.0	62.0	0.9970	NaN	0.58	9.3	6.0

Handling missing values

In [8]:

```
data.dropna(inplace = True)
data.isna().sum()
```

Out[8]:

```
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
```

Data analysis and visualisation

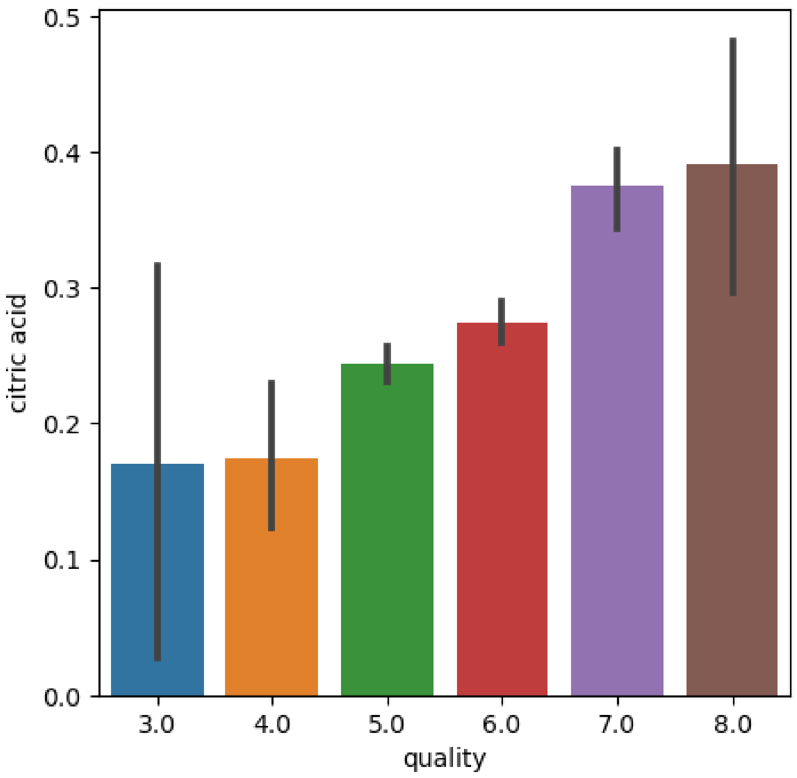
In [9]:
```
data.describe()
```

Out[9]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	densit
count	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000	1596.00000
mean	8.321366	0.527666	0.271128	2.536936	0.087487	15.882206	46.431078	0.99674
std	1.742121	0.179154	0.194847	1.408341	0.047107	10.467380	32.893072	0.00188
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.99007
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.99560
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.99674
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.99784
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1.00369

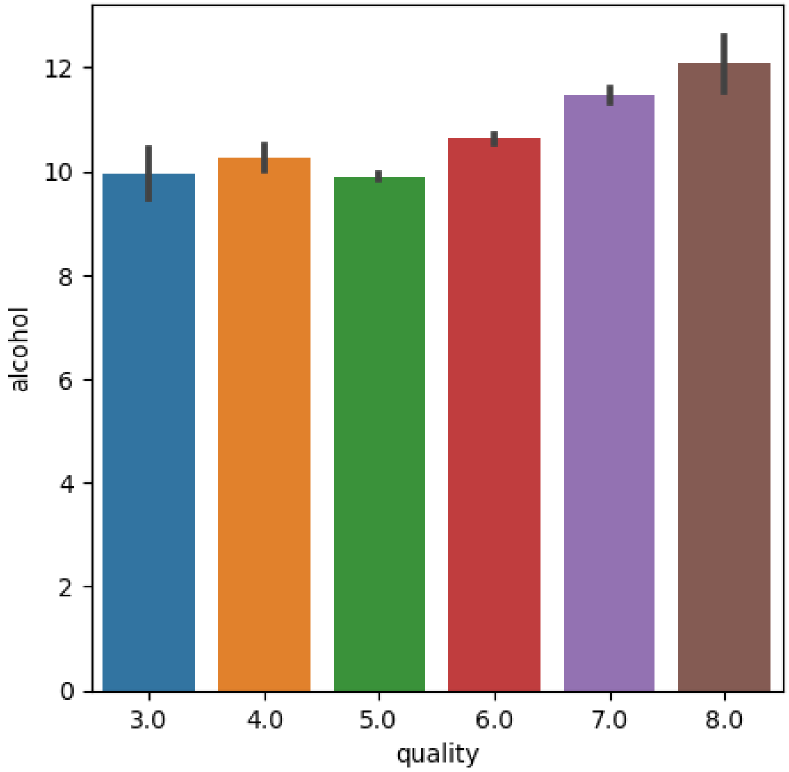
In [10]:
```
plot = plt.figure(figsize=(5, 5))
sns.barplot(x='quality', y = 'citric acid', data = data)
```

Out[10]:
```
<Axes: xlabel='quality', ylabel='citric acid'>
```



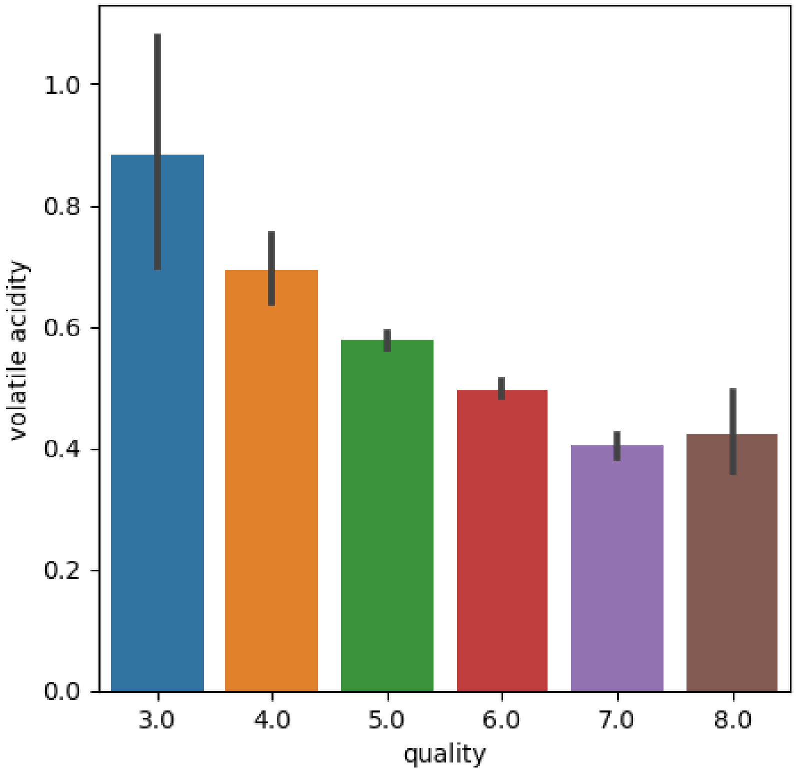
```
In [11]: plot = plt.figure(figsize=(5, 5))
         sns.barplot(x='quality', y = 'alcohol', data = data)
```

```
Out[11]: <Axes: xlabel='quality', ylabel='alcohol'>
```



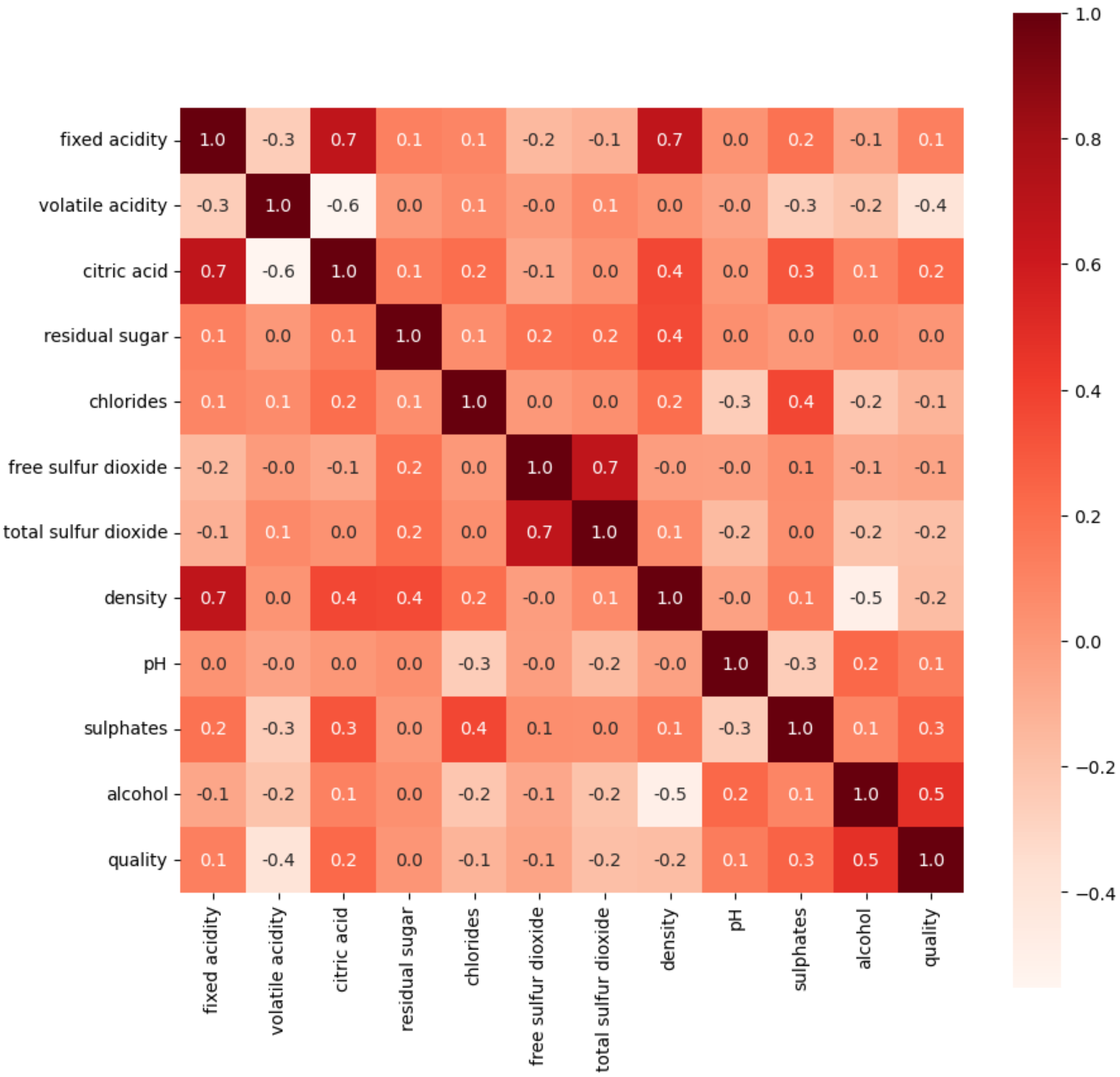
```
In [12]: plot = plt.figure(figsize=(5, 5))
         sns.barplot(x='quality', y = 'volatile acidity', data = data)
```

```
Out[12]: <Axes: xlabel='quality', ylabel='volatile acidity'>
```



In [13]:
```
plt.figure(figsize=(10, 10))
sns.heatmap(data.corr(), cbar=True, square=True, fmt= '.1f', annot=True, cmap = 'Reds')
```

Out[13]:
```
<Axes: >
```



machine learning model

In [14]:
```
x = data.drop('quality', axis=1)
y = data['quality'].apply(lambda y_value: 1 if y_value>=7 else 0)
```

In [15]:
```
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size = 0.2, random_state=1
```

In [16]:
```
model_rf = RandomForestClassifier(n_estimators = 500, min_samples_split = 3)
model_rf.fit(x_train, y_train)
```

Out[16]:
```
▾                        RandomForestClassifier
RandomForestClassifier(min_samples_split=3, n_estimators=500)
```

```
In [17]: def metrics(y_true, y_pred):
          print(f'RMSE: ', mean_squared_error(y_true, y_pred) ** 0.5)
          print(f'R_square value: ', r2_score(y_true, y_pred))
```

```
In [18]: y_pred = model_rf.predict(x_test)
         f1_score(y_test, y_pred, average = 'weighted')

Out[18]: 0.9414063848889809
```

```
In [19]: precision_score(y_test, y_pred, average = 'weighted')

Out[19]: 0.9430462056303549
```

```
In [20]: accuracy_rf = accuracy_score(y_test, y_pred) * 100
         print('The accuracy is:', accuracy_rf,'%')

         The accuracy is: 94.6875 %
```