

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

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

```
wine_data.describe()
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	quality
count	1599.000000	1599.000000	1599.000000	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	0.996747	3.311113	6.411554
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	0.001887	0.154386	1.011609
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.990070	2.740000	4.000000
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.995600	3.210000	5.000000
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.996750	3.310000	6.000000
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.997835	3.400000	7.000000
max	15.000000	1.550000	1.000000	15.500000	0.201000	52.000000	220.000000	1.000000	4.010000	9.000000

```
wine_data.shape
```

(1599, 12)

```
wine_data.head
```

```
pandas.core.generic.NDFrame.head
def head(n: int=5) -> Self

/usr/local/lib/python3.12/dist-packages/pandas/core/generic.py
Return the first `n` rows.

This function returns the first `n` rows for the object based
on position. It is useful for quickly testing if your object
has the right type of data in it.
```

```
wine_data.head()
```

	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
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6

Next steps: [Generate code with wine\\_data](#) [New interactive sheet](#)

```
wine_data.isnull().sum()
```

	0
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

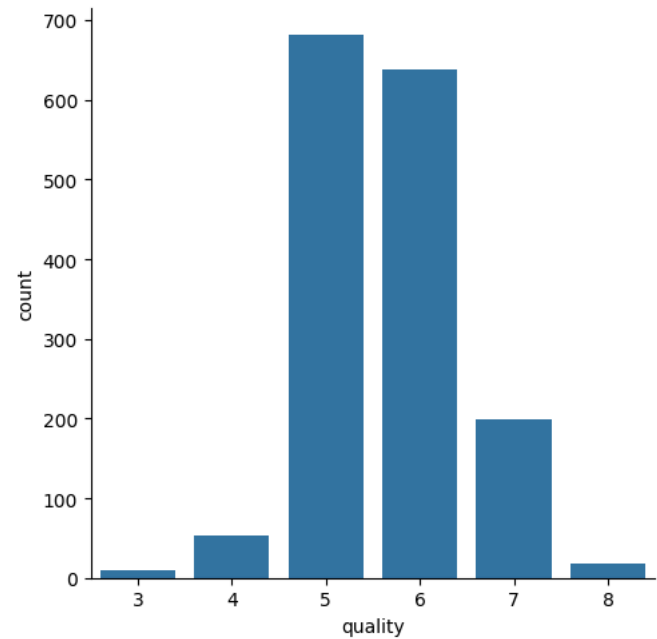
dtype: int64

wine\_data.describe()

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	su
count	1599.000000	1599.000000	1599.000000	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	0.996747	3.311113	0.499878
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	0.001887	0.154386	0.006763
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.990070	2.740000	0.450000
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.995600	3.210000	0.470000
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.996750	3.310000	0.490000
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.997835	3.400000	0.510000
max	15.000000	1.550000	1.000000	15.500000	0.201000	52.000000	200.000000	1.000000	4.000000	0.550000

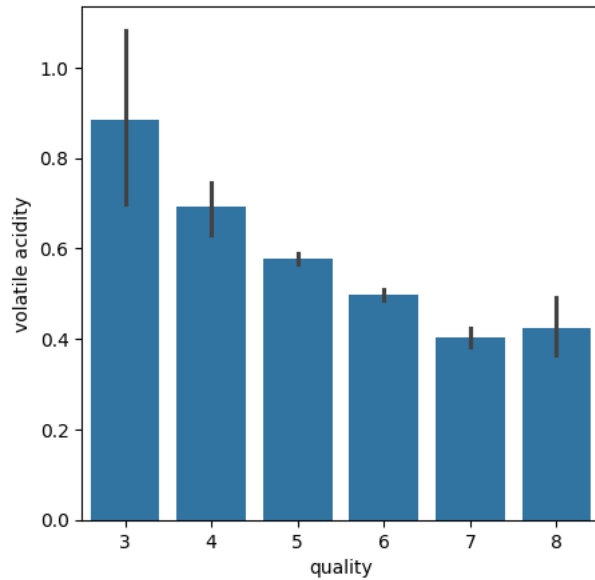
sns.catplot(x='quality',data=wine\_data,kind='count')

<seaborn.axisgrid.FacetGrid at 0x7aad933b0590>



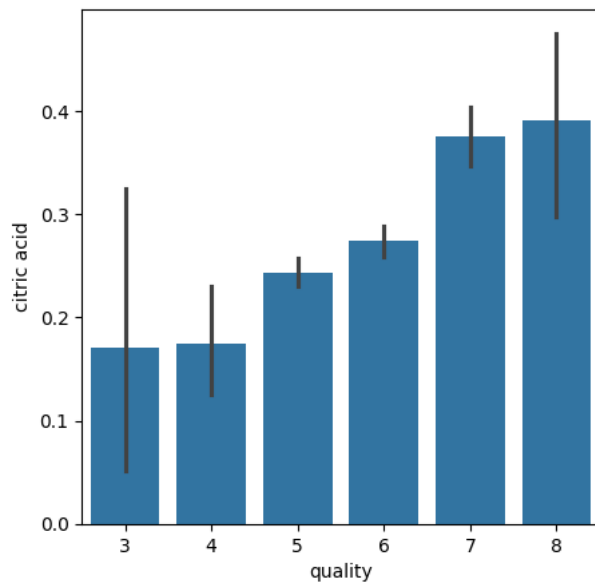
```
plot=plt.figure(figsize=(5,5))
sns.barplot(x='quality',y='volatile acidity',data=wine_data)
```

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



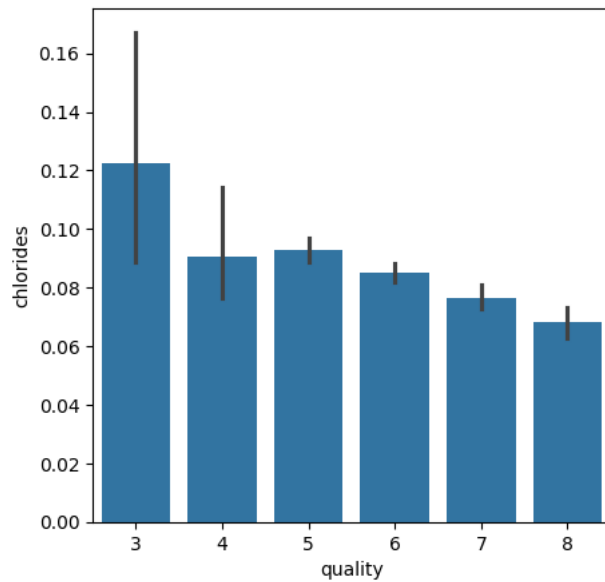
```
plot=plt.figure(figsize=(5,5))  
sns.barplot(x='quality',y='citric acid',data=wine_data)
```

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



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

<Axes: xlabel='quality', ylabel='chlorides'>



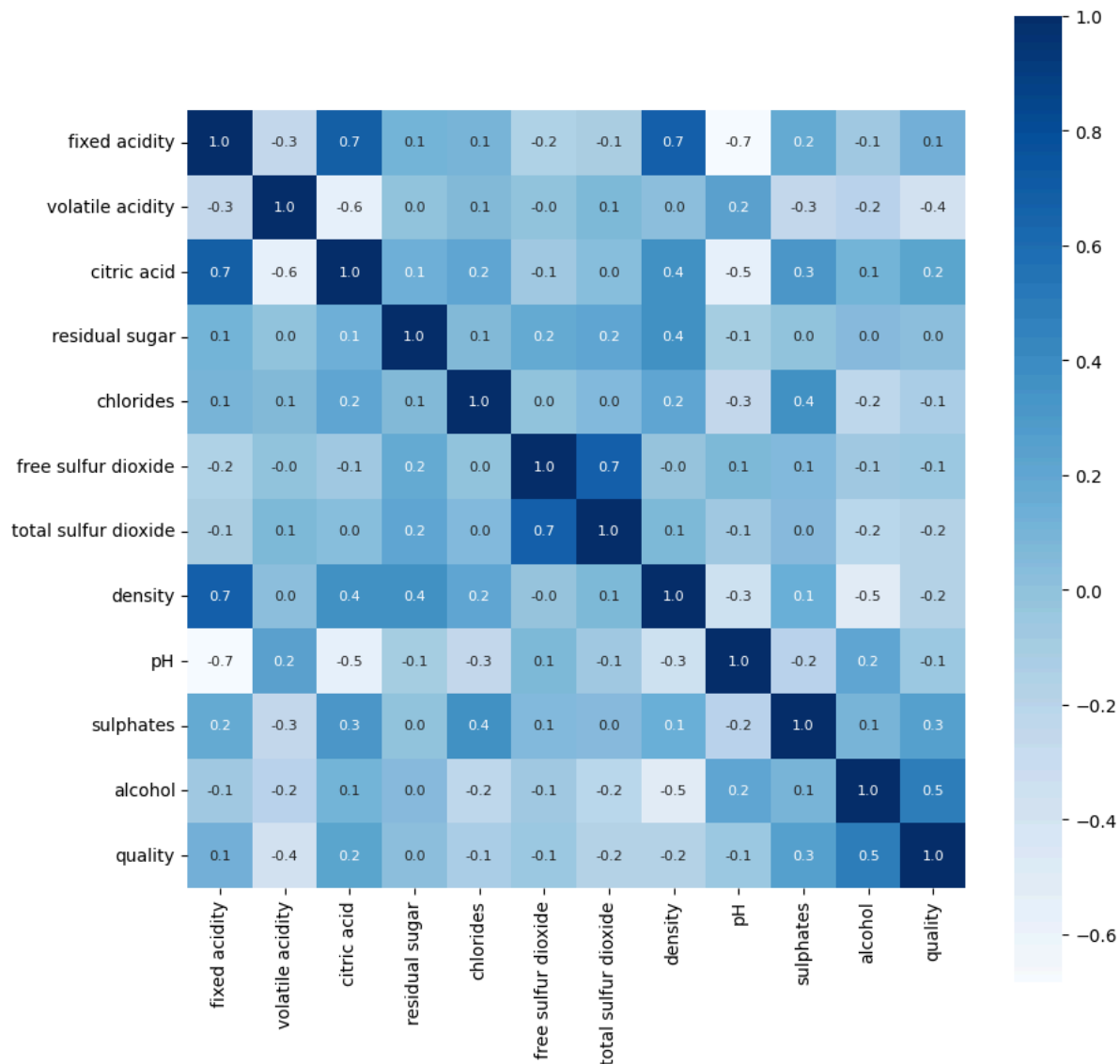
correlation

```
correlation=wine_data.corr()
```

constructing the heat map to understand the correlations

```
plt.figure(figsize=(10,10))  
sns.heatmap(correlation,cbar=True,square=True,fmt='.1f',annot=True,annot_kws={'size':8},cmap='Blues')
```

&lt;Axes: &gt;



## Data Preprocessing

```
X=wine_data.drop('quality',axis=1)
print(X)
```

```

    fixed acidity  volatile acidity  citric acid  ...  pH  sulphates  alcohol
0             7.4             0.700         0.00  ...  3.51         0.56         9.4
1             7.8             0.880         0.00  ...  3.20         0.68         9.8
2             7.8             0.760         0.04  ...  3.26         0.65         9.8
3            11.2             0.280         0.56  ...  3.16         0.58         9.8
4             7.4             0.700         0.00  ...  3.51         0.56         9.4
...           ...             ...         ...  ...  ...         ...         ...
1594           6.2             0.600         0.08  ...  3.45         0.58        10.5
1595           5.9             0.550         0.10  ...  3.52         0.76        11.2
1596           6.3             0.510         0.13  ...  3.42         0.75        11.0
1597           5.9             0.645         0.12  ...  3.57         0.71        10.2
1598           6.0             0.310         0.47  ...  3.39         0.66        11.0
```

[1599 rows x 11 columns]

## label binarisation

```
Y=wine_data['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=.2,random_state=2,stratify=Y)
```

```
print(X.shape,Y.shape,Y_train.shape,Y_test.shape)
```

```
(1599, 11) (1599, 1) (1279, 1) (320, 1)
```