Data Set Information:

The two datasets are related to red and white variants of the Portuguese "Vinho Verde" wine.

Due to privacy and logistic issues, only physicochemical (inputs) and sensory (the output) variables are available (e.g. there is no data about grape types, wine brand, wine selling price, etc.).

These datasets can be viewed as classification or regression tasks. The classes are ordered and not balanced (e.g. there are many more normal wines than excellent or poor ones).

Outlier detection algorithms could be used to detect the few excellent or poor wines. Also, we are not sure if all input variables are relevant. So it could be interesting to test feature selection methods.

Attribute Information:

Input variables (based on physicochemical tests):

1 - fixed acidity

2 - volatile acidity

3 - citric acid

4 - residual sugar

5 - chlorides

6 - free sulfur dioxide

7 - total sulfur dioxide

8 - density

9 - pH

10 - sulphates

11 - alcohol

Output variable (based on sensory data):

12 - quality (score between 0 and 10)

In [ ]:
```
#EDA with Red Wine Data
```

In [ ]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
```

In [ ]:
```
df=pd.read_csv("/content/sample_data/winequality-red.csv")
df.head(5)
```

Out[ ]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4

In [ ]:
```
#summary of DataSet

df.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
```

In [ ]:
```
#descriptive summary of the dataset

df.describe()
```

Out[ ]:

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

In [ ]:
```
## shape of the data

df.shape
```

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

In [ ]:
```
## List down all the columns names

df.columns
```

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

In [ ]:
```
df['quality'].unique()  #unique values within a particular columns
```

Out[ ]:
```
array([5, 6, 7, 4, 8, 3])
```

In [ ]:
```
df.nunique() # unique values of all values from the dataset
```

Out[ ]:
```
fixed acidity            96
volatile acidity        143
citric acid              80
residual sugar           91
chlorides               153
free sulfur dioxide      60
total sulfur dioxide    144
density                 436
pH                       89
sulphates                96
alcohol                  65
quality                   6
dtype: int64
```

In [ ]:
```
# missing values within the values

df.isnull().sum()
```

Out[ ]:
```
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
```

In [ ]:
```
# checking the Duplicate records

df.duplicated()
```

Out[ ]:
```
0       False
1       False
2       False
3       False
4        True
        ...
1594    False
1595    False
1596     True
1597    False
1598    False
Length: 1599, dtype: bool
```

In [ ]:
```
# checking the Duplicate records within the dataframe

df[df.duplicated()]
```

Out[ ]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcoh
4	7.4	0.700	0.00	1.90	0.076	11.0	34.0	0.99780	3.51	0.56	9
11	7.5	0.500	0.36	6.10	0.071	17.0	102.0	0.99780	3.35	0.80	10
27	7.9	0.430	0.21	1.60	0.106	10.0	37.0	0.99660	3.17	0.91	9
40	7.3	0.450	0.36	5.90	0.074	12.0	87.0	0.99780	3.33	0.83	10
65	7.2	0.725	0.05	4.65	0.086	4.0	11.0	0.99620	3.41	0.39	10
...	...	...	...	...	...	...	...	...	...	...	
1563	7.2	0.695	0.13	2.00	0.076	12.0	20.0	0.99546	3.29	0.54	10
1564	7.2	0.695	0.13	2.00	0.076	12.0	20.0	0.99546	3.29	0.54	10
1567	7.2	0.695	0.13	2.00	0.076	12.0	20.0	0.99546	3.29	0.54	10
1581	6.2	0.560	0.09	1.70	0.053	24.0	32.0	0.99402	3.54	0.60	11
1596	6.3	0.510	0.13	2.30	0.076	29.0	40.0	0.99574	3.42	0.75	11

240 rows × 12 columns

In [ ]:
```
#remove the duplicate data if any


df.drop_duplicates(inplace=True)
```

In [ ]:
```
df.shape
```

Out[ ]:
```
(1359, 12)
```

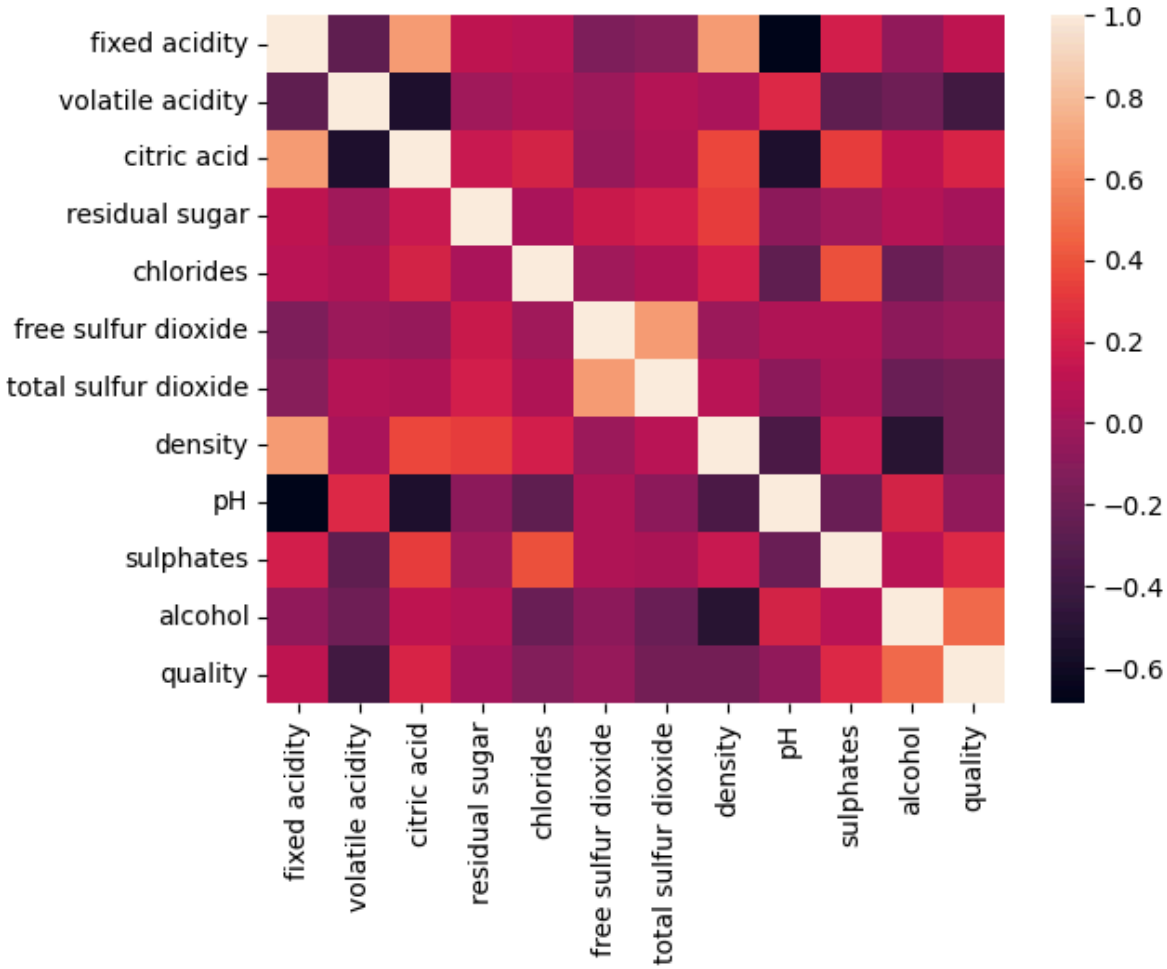
In [ ]:
```
## Correlation

df.corr()
```

Out[ ]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	
fixed acidity	1.000000	-0.255124	0.667437	0.111025	0.085886	-0.140580	-0.103777	0.670195	-0
volatile acidity	-0.255124	1.000000	-0.551248	-0.002449	0.055154	-0.020945	0.071701	0.023943	0
citric acid	0.667437	-0.551248	1.000000	0.143892	0.210195	-0.048004	0.047358	0.357962	-0
residual sugar	0.111025	-0.002449	0.143892	1.000000	0.026656	0.160527	0.201038	0.324522	-0
chlorides	0.085886	0.055154	0.210195	0.026656	1.000000	0.000749	0.045773	0.193592	-0
free sulfur dioxide	-0.140580	-0.020945	-0.048004	0.160527	0.000749	1.000000	0.667246	-0.018071	0
total sulfur dioxide	-0.103777	0.071701	0.047358	0.201038	0.045773	0.667246	1.000000	0.078141	-0
density	0.670195	0.023943	0.357962	0.324522	0.193592	-0.018071	0.078141	1.000000	-0
pH	-0.686685	0.247111	-0.550310	-0.083143	-0.270893	0.056631	-0.079257	-0.355617	1
sulphates	0.190269	-0.256948	0.326062	-0.011837	0.394557	0.054126	0.035291	0.146036	-0
alcohol	-0.061596	-0.197812	0.105108	0.063281	-0.223824	-0.080125	-0.217829	-0.504995	0
quality	0.119024	-0.395214	0.228057	0.013640	-0.130988	-0.050463	-0.177855	-0.184252	-0

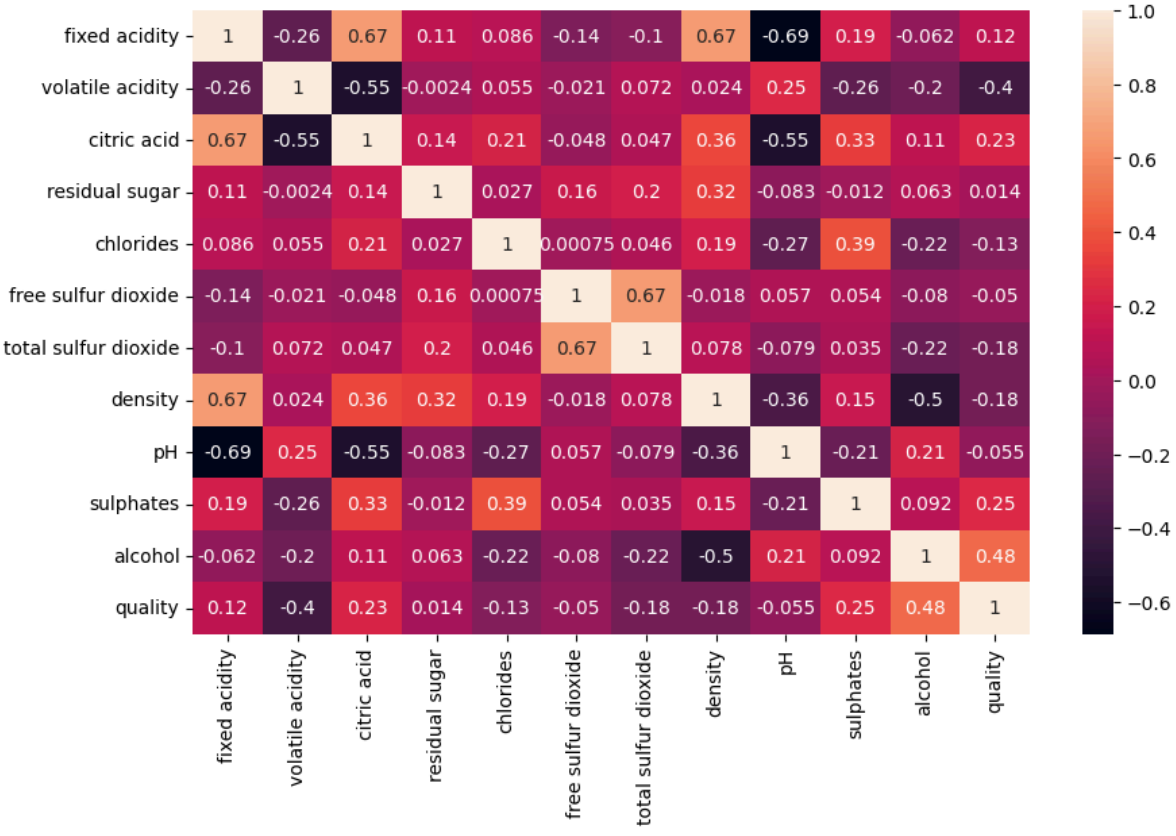
In [ ]:
```
#correlation in the form of graph

sns.heatmap(df.corr())
```

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



In [ ]:
```
plt.figure(figsize=(10,6))
sns.heatmap(df.corr(),annot=True)
```

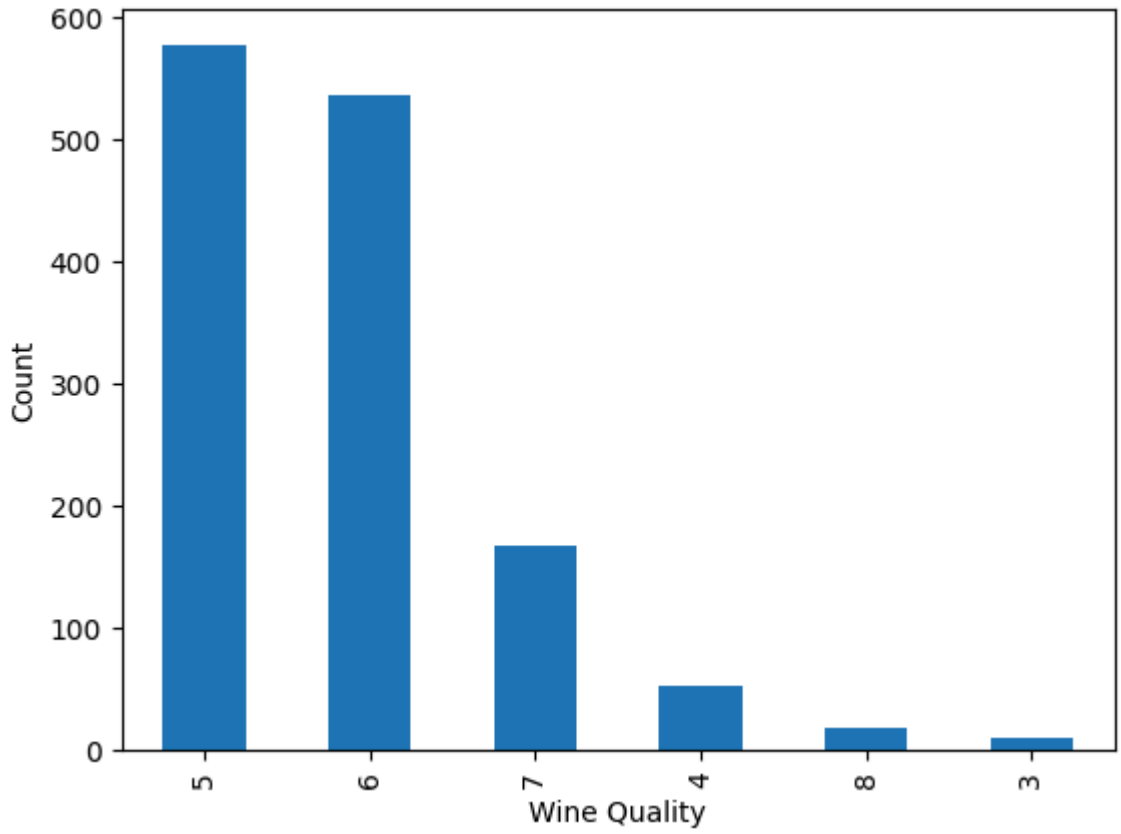
Out[ ]:
```
<Axes: >
```



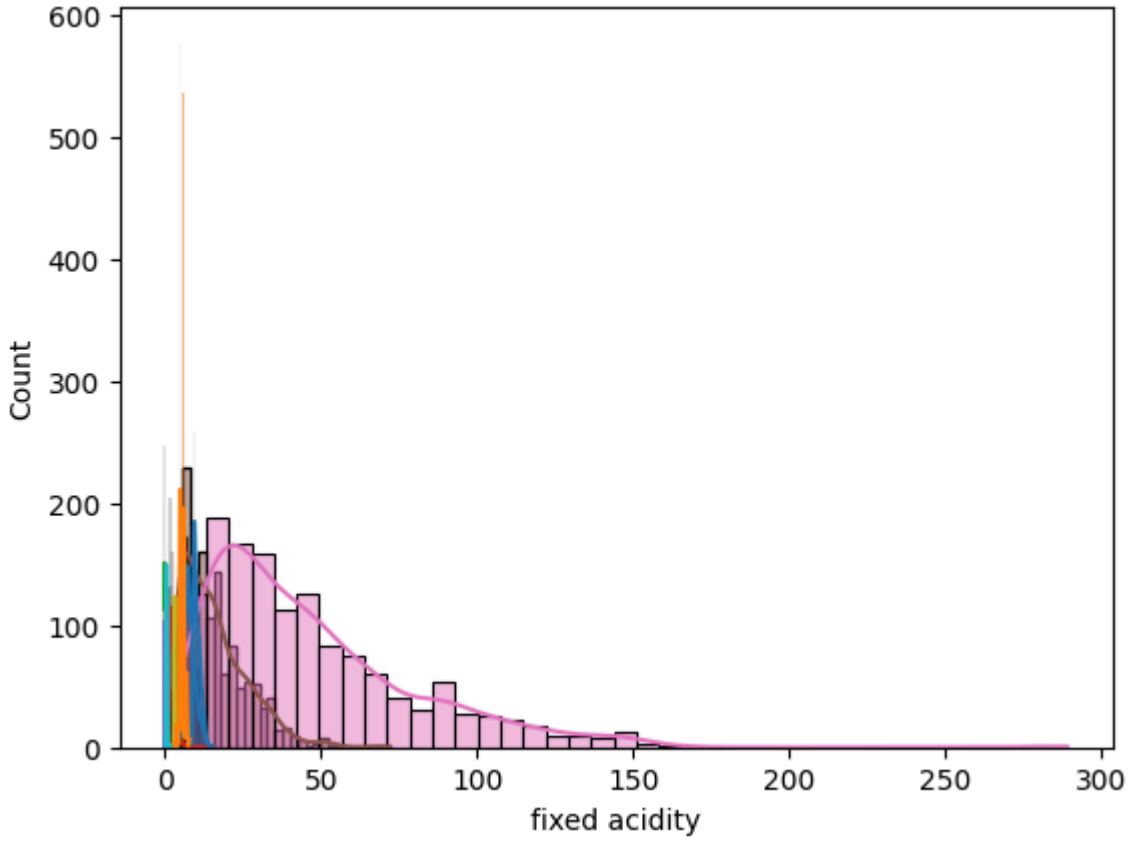
In [ ]:
```
## Visualization
#conclusion - It is a imbalance dataset

df.quality.value_counts()
```

Out[ ]:
```
quality
5    577
6    535
7    167
4     53
8     17
3     10
Name: count, dtype: int64
```

In [ ]:
```
df.quality.value_counts().plot(kind="bar")
plt.xlabel("Wine Quality")
plt.ylabel("Count")
plt.show()
```

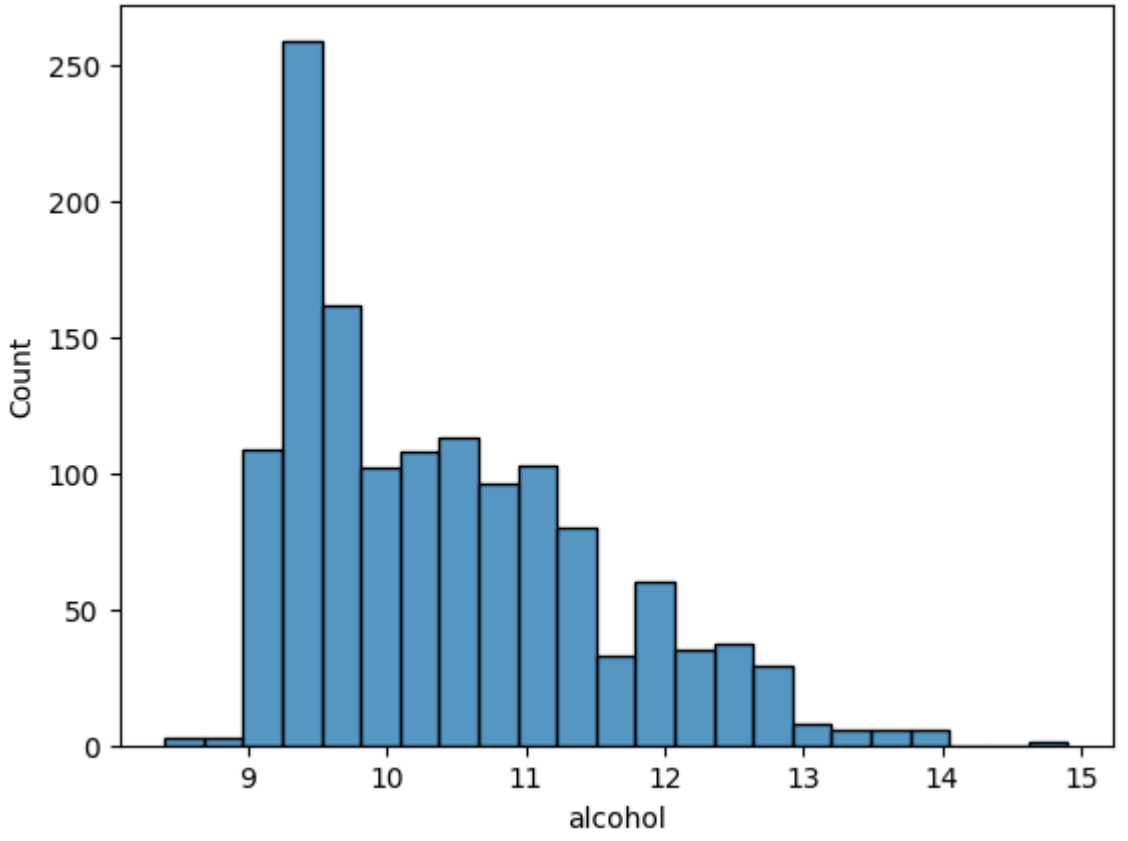


In [ ]:
```
for column in df.columns:                    #distribution for each and every dataset
  sns.histplot(df[column],kde=True)
```



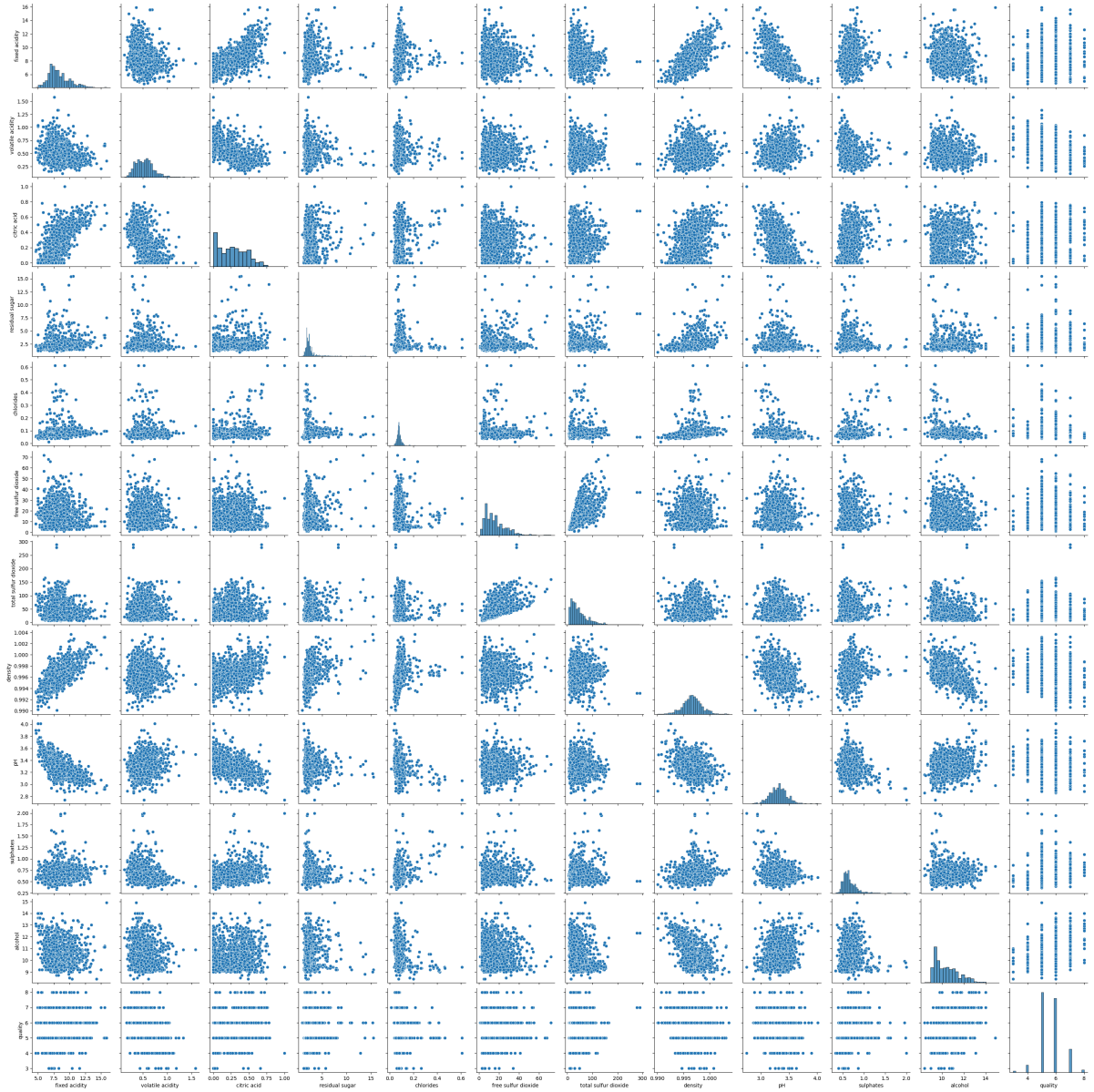
In [ ]:
```
sns.histplot(df["alcohol"])
```

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



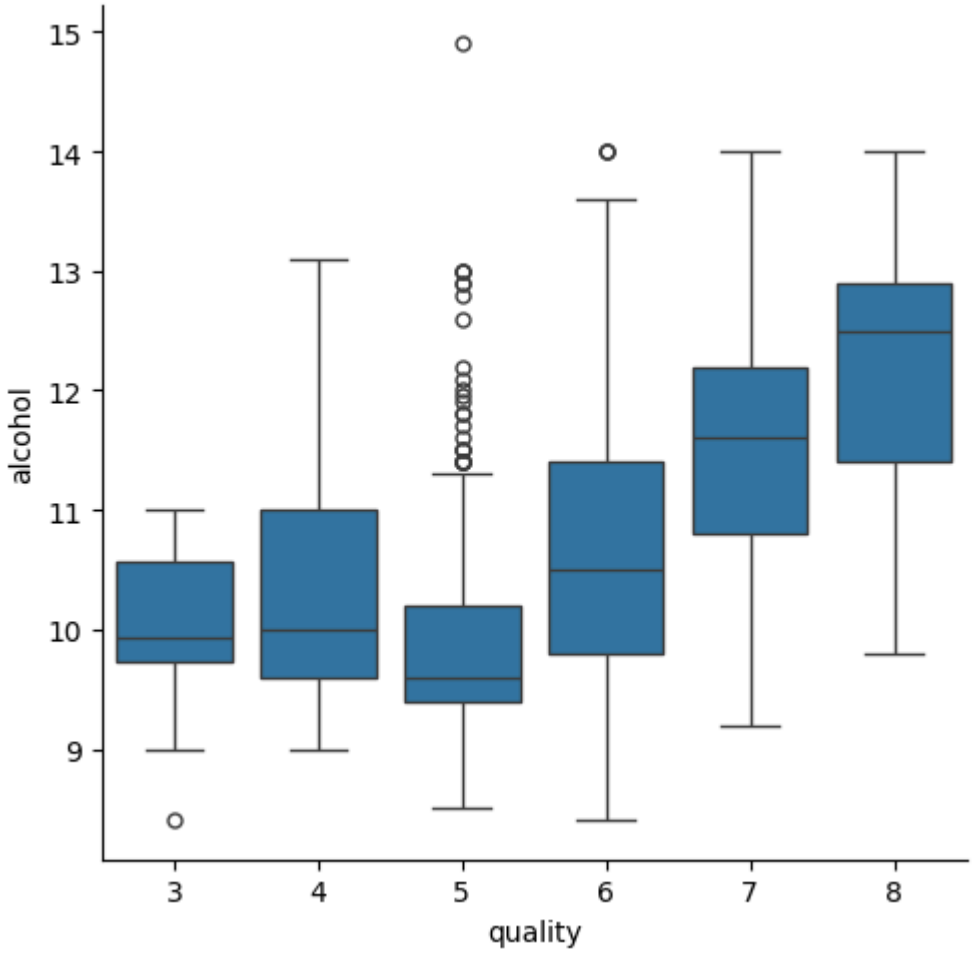
In [ ]:
```
#univariate,bivariate,multivariate analysis
sns.pairplot(df) #comparing one feature with other feature
```

Out[ ]:
```
<seaborn.axisgrid.PairGrid at 0x7d11b6420e50>
```



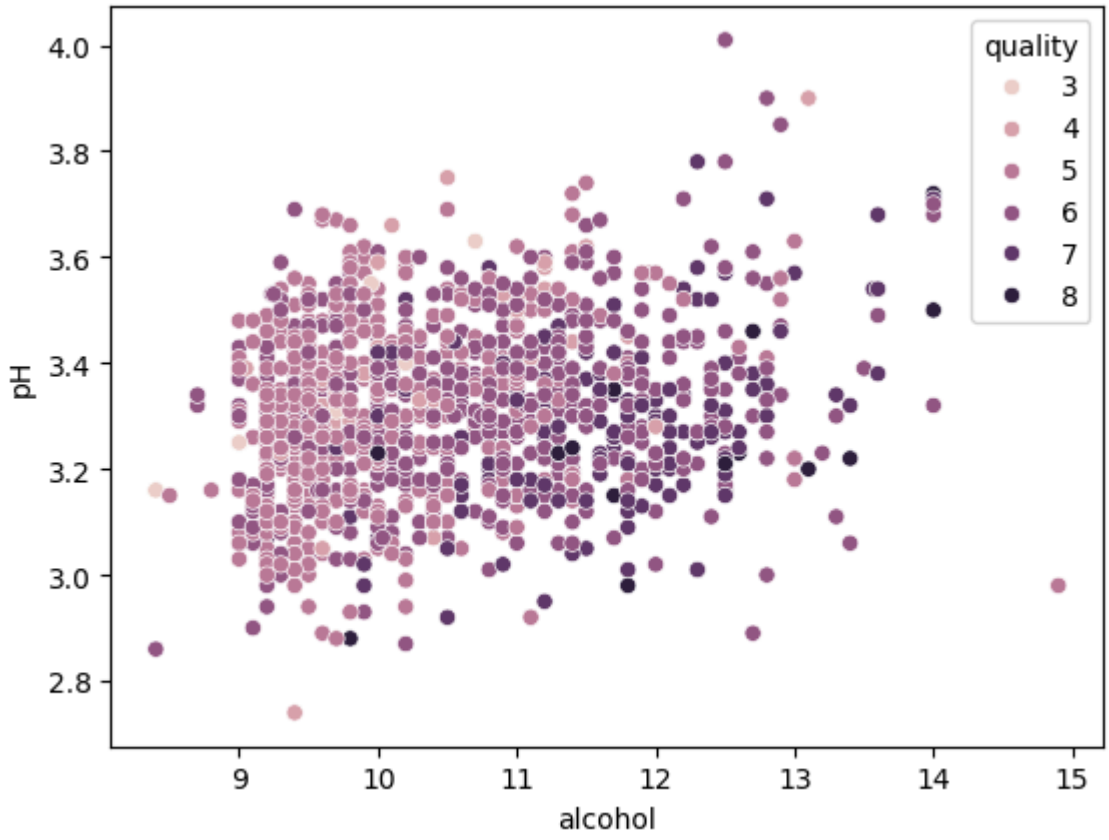
In [ ]:
```
#Categorical Plot

sns.catplot(x="quality",y="alcohol",data=df,kind="box")
```

Out[ ]:
```
<seaborn.axisgrid.FacetGrid at 0x7d11aed468c0>
```



In [ ]:
```
#ScatterPlot - numerical features

sns.scatterplot(x="alcohol",y="pH",hue="quality",data=df)
```

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



In [ ]: