21bce5304-lab3

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Objective: Implementation of Decision Tree

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[ ]:
```
Dataset Description:
This dataset is related to red variants of the Portuguese "Vinho Verde" wine.␣
 ↪The dataset provides information about the amount of various chemicals␣
 ↪present in wine and their effect on its quality. The datasets can be viewed␣
 ↪as either classification or regression tasks. It's important to note that␣
 ↪the classes are ordered and not balanced, meaning there are more normal␣
 ↪wines than excellent or poor ones. The task is to predict the quality of␣
 ↪wine using the given data.

This project is both simple and challenging, requiring the anticipation of wine␣
 ↪quality. The complexity arises from the dataset having fewer samples and␣
 ↪being highly imbalanced. The goal is to overcome these obstacles and build a␣
 ↪good predictive model for wine quality classification.

Data Frame Columns:
Input variables (based on physicochemical tests):

fixed acidity
volatile acidity
citric acid
residual sugar
chlorides
free sulfur dioxide
total sulfur dioxide
density
pH
sulphates
alcohol
Output variable (based on sensory data):
12. quality (score between 0 and 10)
```

[ ]:
```
import numpy as np
import pandas as pd
```

```
import matplotlib.pyplot as plt
import seaborn as sns
```

[ ]:
```
data=pd.read_csv("winequality-red.csv")
data.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
1      9.8        5
2      9.8        5
3      9.8        6
4      9.4        5
```

1 Exploratory Data Analysis

[ ]:
```
data.columns
```

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

[ ]:
```
data.describe().transpose()
```

[ ]:
```
                      count       mean        std      min      25%  \
fixed acidity        1599.0   8.319637   1.741096  4.60000   7.1000
volatile acidity     1599.0   0.527821   0.179060  0.12000   0.3900
citric acid          1599.0   0.270976   0.194801  0.00000   0.0900
residual sugar       1599.0   2.538806   1.409928  0.90000   1.9000
chlorides            1599.0   0.087467   0.047065  0.01200   0.0700
free sulfur dioxide  1599.0  15.874922  10.460157  1.00000   7.0000
total sulfur dioxide 1599.0  46.467792  32.895324  6.00000  22.0000
```

```
density               1599.0   0.996747   0.001887  0.99007   0.9956
pH                    1599.0   3.311113   0.154386  2.74000   3.2100
sulphates             1599.0   0.658149   0.169507  0.33000   0.5500
alcohol               1599.0  10.422983   1.065668  8.40000   9.5000
quality               1599.0   5.636023   0.807569  3.00000   5.0000

                          50%        75%        max
fixed acidity         7.90000   9.200000   15.90000
volatile acidity      0.52000   0.640000    1.58000
citric acid           0.26000   0.420000    1.00000
residual sugar        2.20000   2.600000   15.50000
chlorides             0.07900   0.090000    0.61100
free sulfur dioxide  14.00000  21.000000   72.00000
total sulfur dioxide 38.00000  62.000000  289.00000
density               0.99675   0.997835    1.00369
pH                    3.31000   3.400000    4.01000
sulphates             0.62000   0.730000    2.00000
alcohol              10.20000  11.100000   14.90000
quality               6.00000   6.000000    8.00000
```

[ ]:
```
data.duplicated().sum()
```

[ ]:
```
240
```

[ ]:
```
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  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.isnull().sum()
```

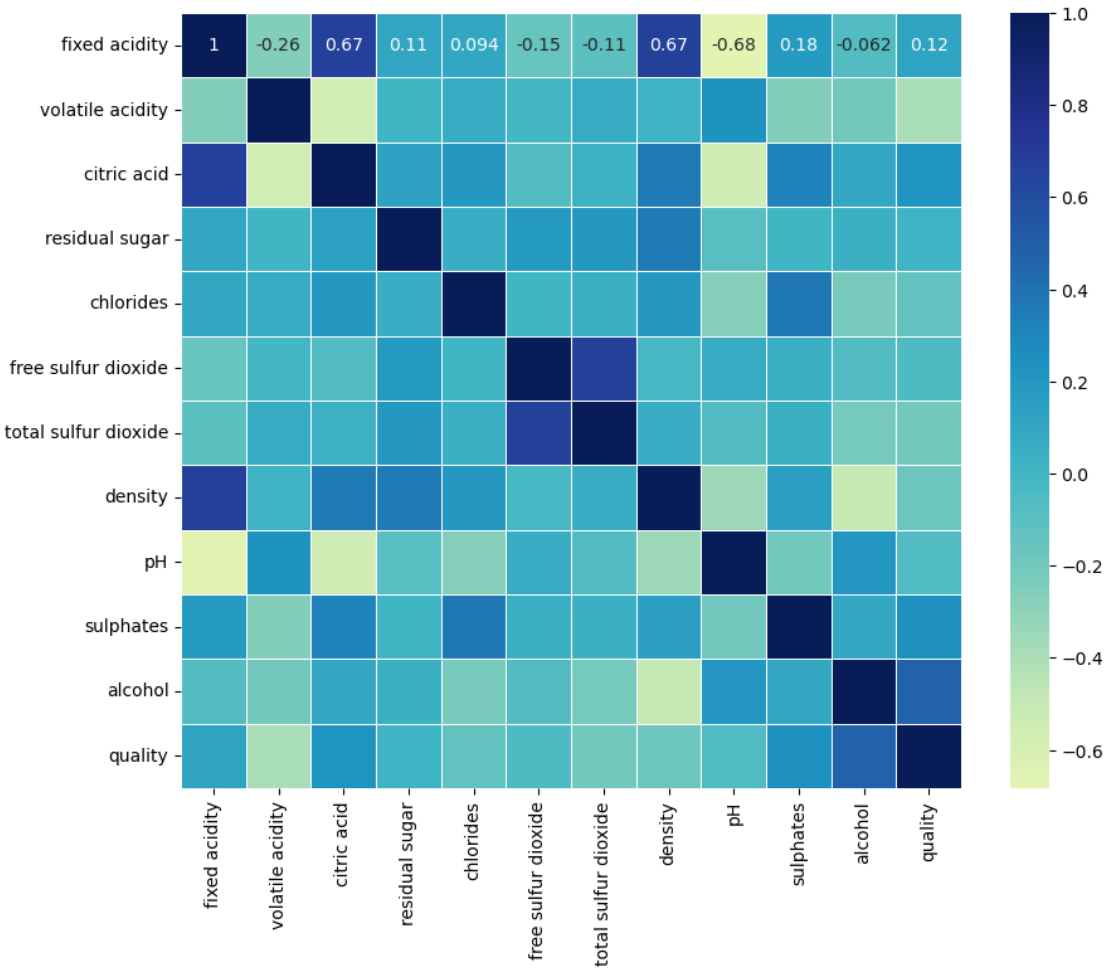
[ ]:
```
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    0
density                 0
pH                      0
sulphates               0
alcohol                 0
quality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

[ ]:
```
data.quality.value_counts().head()
```

[ ]:
```
quality
5    681
6    638
7    199
4     53
8     18
Name: count, dtype: int64
```

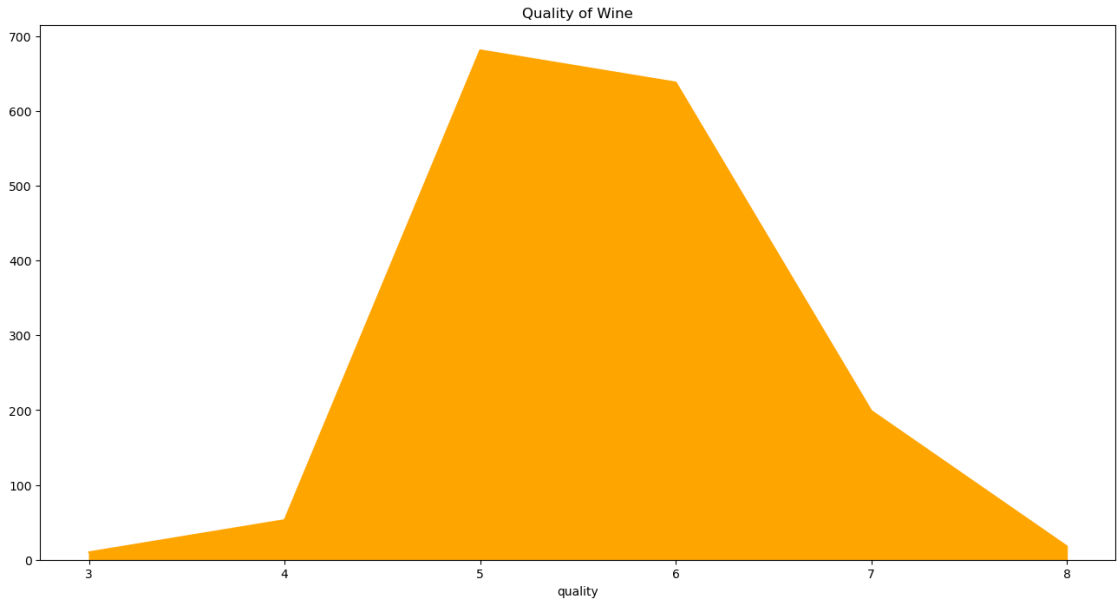
[ ]:
```
plt.figure(figsize=(10,8))
sns.heatmap(data.corr(),annot=True,lw=.5,center=0,cmap="YlGnBu")
```

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



[ ]:
```
data['quality'].value_counts().sort_index().plot.
  ↪area(figsize=(16,8),title='Quality of Wine',color='orange')
```

[ ]:
```
<Axes: title={'center': 'Quality of Wine'}, xlabel='quality'>
```



[ ]:
```
plt.figure(figsize=(16,8))
sns.lineplot(x='residual sugar',y='quality',data=data,color='cyan')
```

```
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[ ]:
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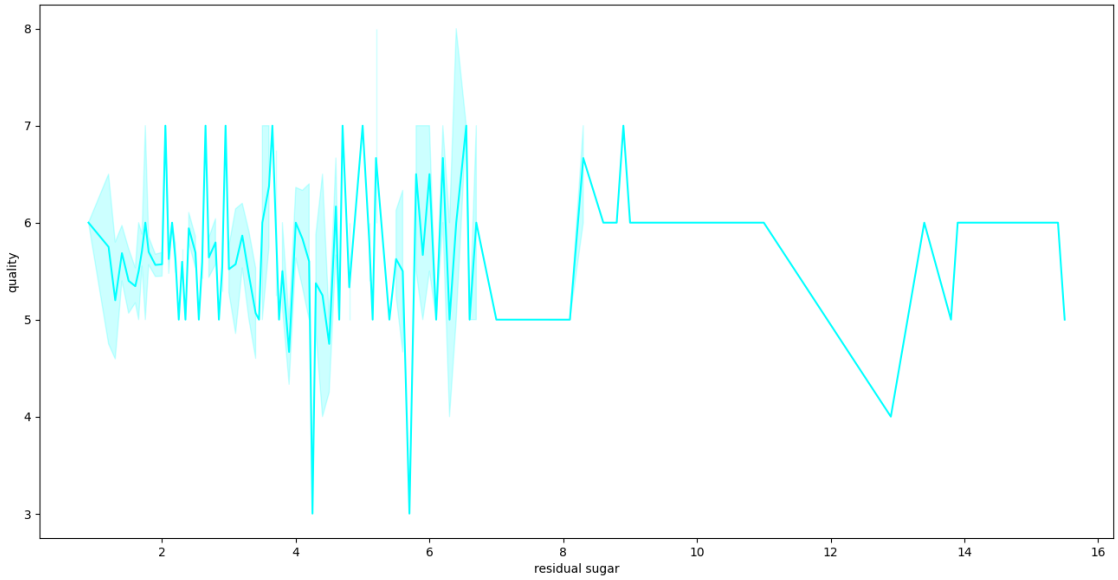
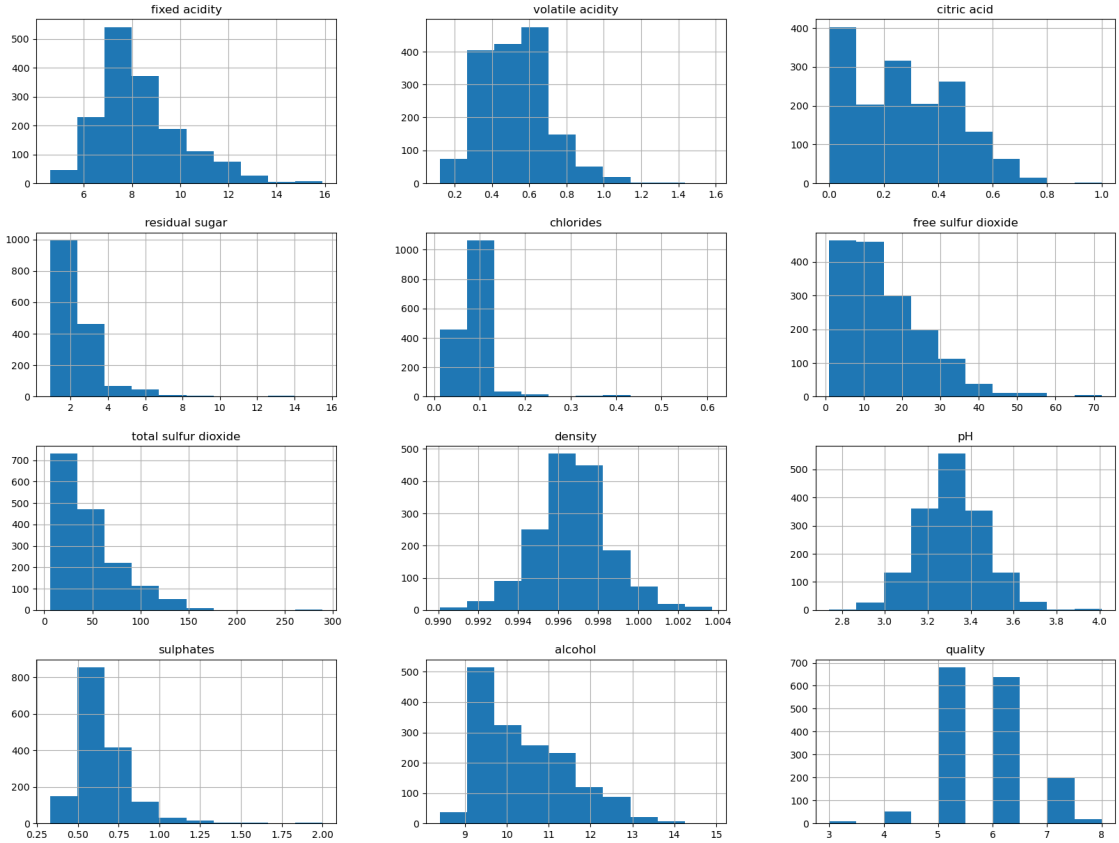
<Axes: xlabel='residual sugar', ylabel='quality'>
```



[ ]:
```
data.hist(figsize=(20,15))
plt.show()
```



```
[ ]: cols_to_draw = ['fixed acidity', 'volatile acidity', 'citric acid', 'residual␣
      ↪sugar',
                     'chlorides', 'free sulfur dioxide', 'total sulfur dioxide',␣
      ↪'density',
                     'pH', 'sulphates', 'alcohol']
     cols = 3
     rows = int(np.ceil(len(cols_to_draw) / cols))
     fig, ax = plt.subplots(rows, cols, figsize=(16, rows * 5))
     ax = ax.flatten()

     quality_colors = ['tab:blue', 'tab:orange', 'tab:green', 'tab:red', 'tab:
      ↪purple', 'tab:brown', 'tab:pink']

     for x, col in enumerate(cols_to_draw):
         for quality in range(1, 8):
             sns.kdeplot(data=data[data['quality'] == quality][col], ax=ax[x],␣
      ↪color=quality_colors[quality - 1],
                         common_norm=False, label=f'Quality {quality}')
         ax[x].set_title(f'{col} distribution')
         ax[x].set_xlabel(None)
         ax[x].legend()

     plt.tight_layout()
     plt.show()
```

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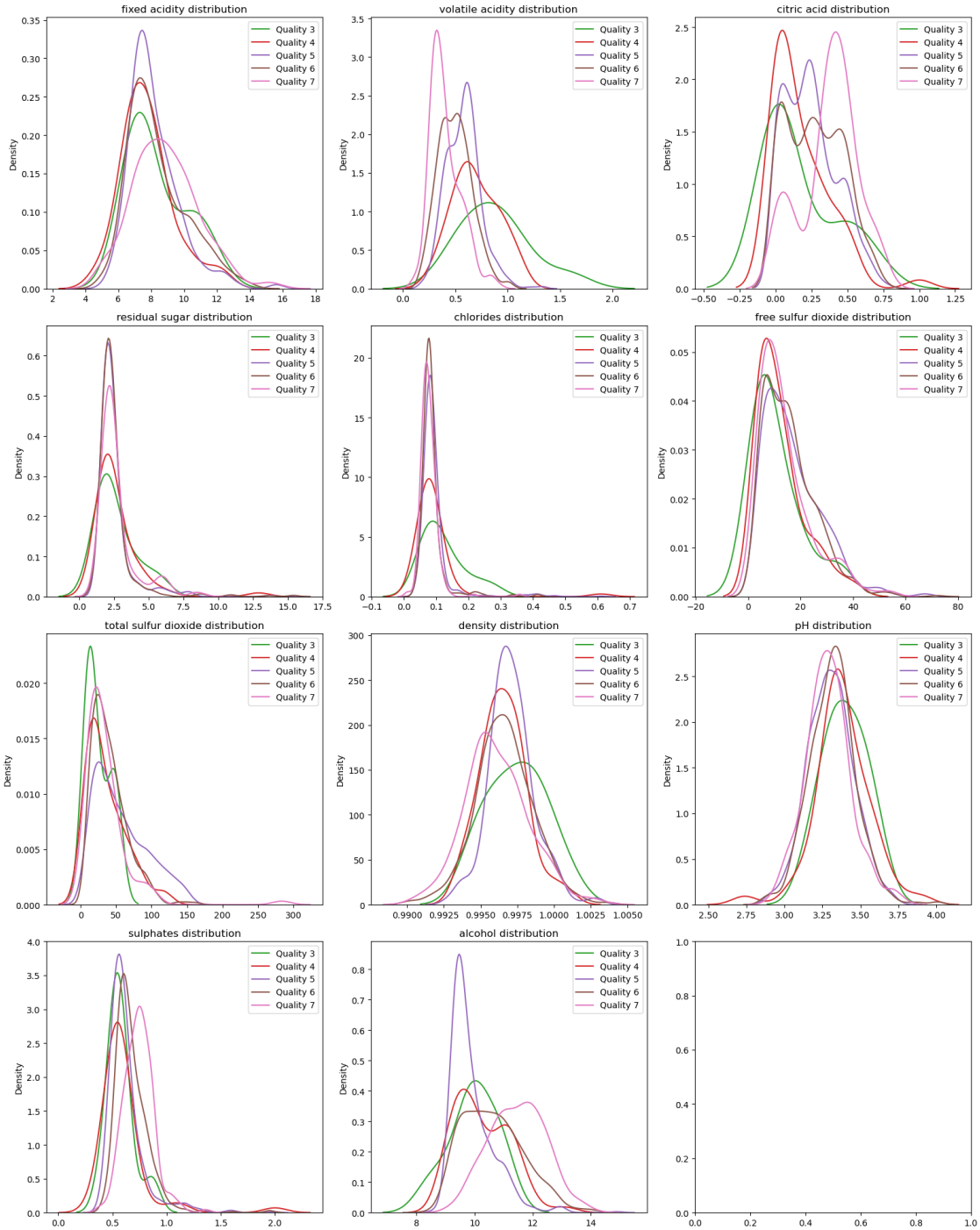
future version. Convert inf values to NaN before operating instead.
  with pd.option_context('mode.use_inf_as_na', True):
C:\Users\gauth\anaconda3\Lib\site-packages\seaborn\_oldcore.py:1119:
FutureWarning: use_inf_as_na option is deprecated and will be removed in a
future version. Convert inf values to NaN before operating instead.
  with pd.option_context('mode.use_inf_as_na', True):
```



[ ]:
```
plt.figure(figsize=(16,7))
sns.distplot(data['volatile acidity'],color='red')
```

```
C:\Users\gauth\AppData\Local\Temp\ipykernel_4592\4045769402.py:2: UserWarning:

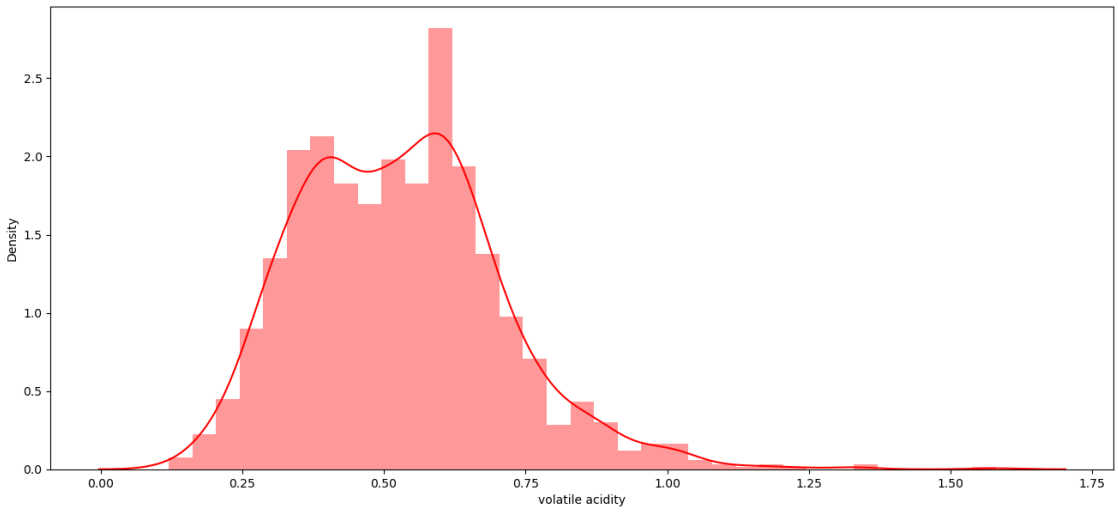
`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  sns.distplot(data['volatile acidity'],color='red')
C:\Users\gauth\anaconda3\Lib\site-packages\seaborn\_oldcore.py:1119:
FutureWarning: use_inf_as_na option is deprecated and will be removed in a
future version. Convert inf values to NaN before operating instead.
  with pd.option_context('mode.use_inf_as_na', True):
```

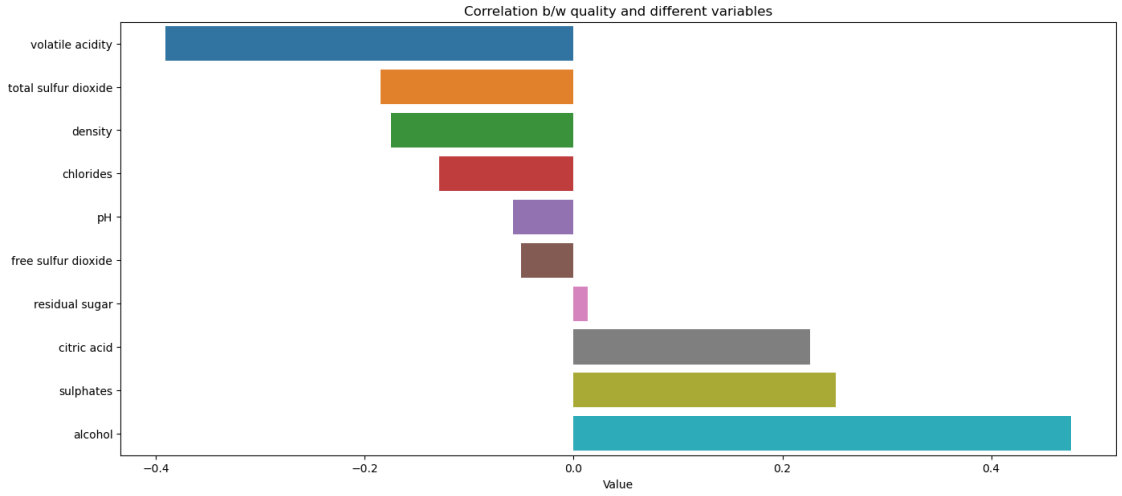
[ ]:
```
<Axes: xlabel='volatile acidity', ylabel='Density'>
```



[ ]:
```
d_corr=data.corr()['quality'][1:].drop('quality',axis=0)

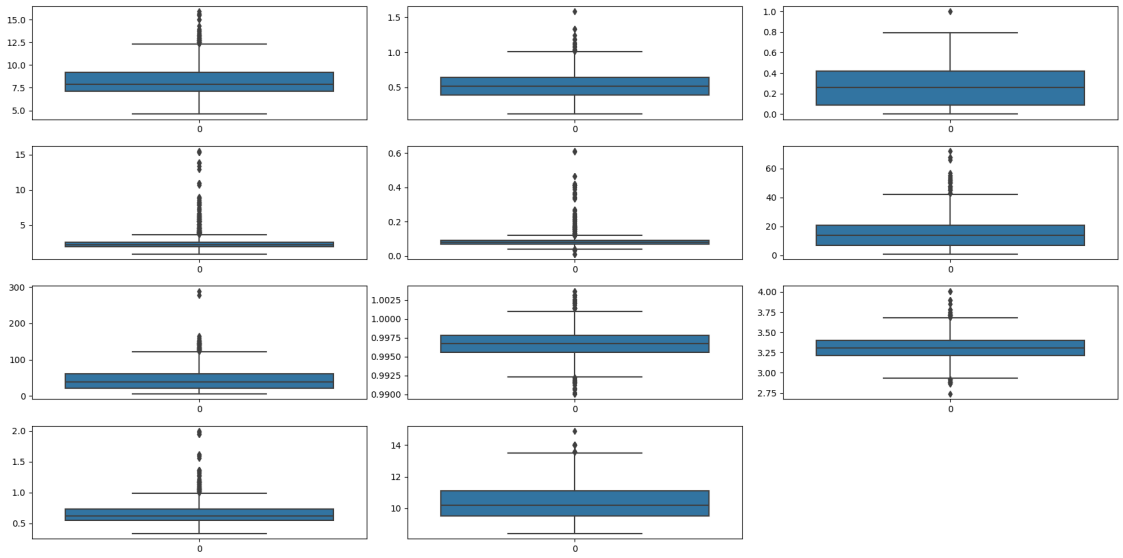
plt.figure(figsize=(16,7))
plt.title('Correlation b/w quality and different variables')
sns.barplot(y=d_corr.sort_values().index,x=d_corr.sort_values().values)
plt.xlabel('Value')
```

[ ]: Text(0.5, 0, 'Value')



2 Outliers

[ ]:
```
plt.figure(figsize=(18,9))
o_count=1
for i in cols_to_draw:
    plt.subplot(4,3,o_count)
    sns.boxplot(data[i])
    o_count=o_count+1
plt.tight_layout()
```



[ ]:
```
df=data.copy()
df.quality.value_counts()
```

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

[ ]:
```
df['quality']=df['quality'].map({3:'Bad',4:'Bad',5:'Bad',6:'Good',7:'Good',8:
  ↪'Good'})
df['quality'].value_counts()
```

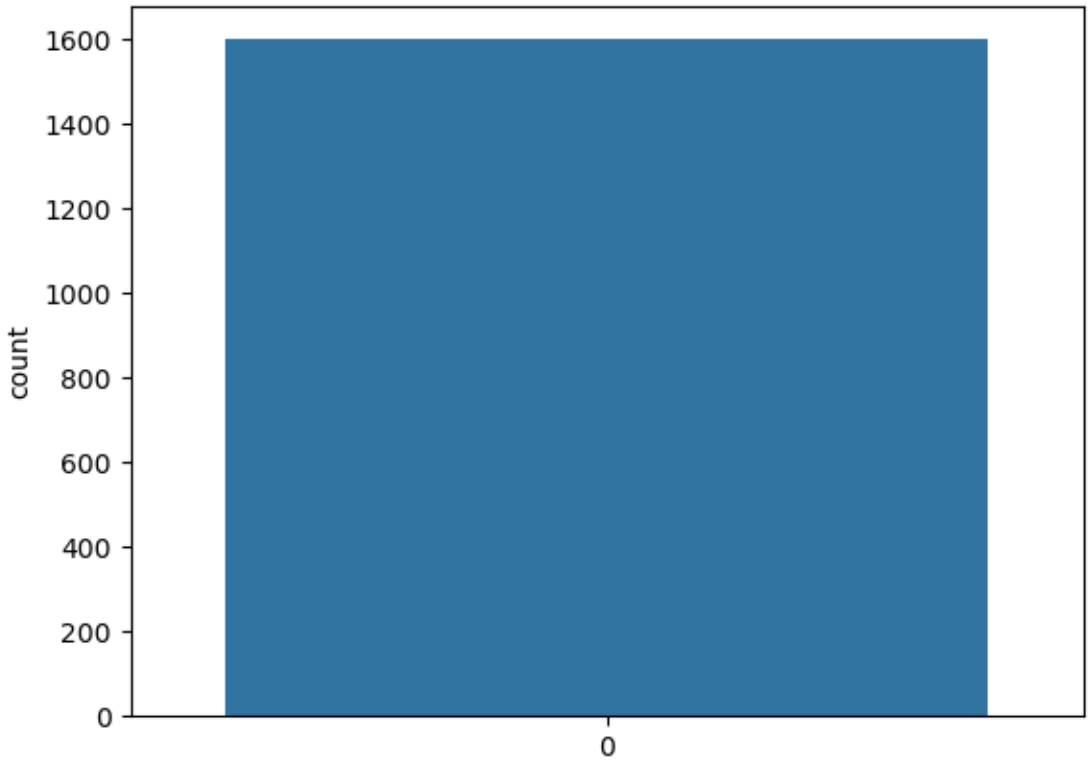
[ ]:
```
quality
Good    855
Bad     744
Name: count, dtype: int64
```

[ ]:
```
from sklearn.preprocessing import LabelEncoder
le=LabelEncoder()
df['quality']=le.fit_transform(df['quality'])
df['quality'].value_counts()
```

[ ]:
```
quality
1    855
0    744
Name: count, dtype: int64
```

[ ]:
```
sns.countplot(df.quality)
```

[ ]:
```
<Axes: ylabel='count'>
```



[ ]:
```
x=df.drop(['quality'],axis=1)
y=df.quality
```

[ ]:
```
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  3.45       0.58
1595                 39.0                 51.0  0.99512  3.52       0.76
1596                 29.0                 40.0  0.99574  3.42       0.75
1597                 32.0                 44.0  0.99547  3.57       0.71
1598                 18.0                 42.0  0.99549  3.39       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
```

[ ]:
```
0       0
1       0
2       0
3       1
4       0
       ..
1594    0
1595    1
1596    1
1597    0
1598    1
Name: quality, Length: 1599, dtype: int32
```

[ ]:
```
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.
  ↪25,random_state=30)
print(x_train.shape)
print(y_train.shape)
print(x_test.shape)
print(y_test.shape)
```

```
(1199, 11)
(1199,)
(400, 11)
(400,)
```

[ ]:
```
from sklearn.preprocessing import StandardScaler
sc=StandardScaler()
x_train=sc.fit_transform(x_train)
x_test=sc.fit_transform(x_test)
```

Methodology AND Multiple Model Analysis

[ ]:
```
import pandas as pd
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score
from sklearn.model_selection import train_test_split

# Assuming you have your data loaded and split into x_train, x_test, y_train,␣
 ↪y_test

# Create a list to store results
results_list = []

# Train five different decision tree models
for i in range(1, 11, 2):
    max_depth = i
    model = DecisionTreeClassifier(criterion='entropy', max_depth=max_depth,␣
 ↪random_state=42)
    model.fit(x_train, y_train)

    # Predictions
    y_train_preds = model.predict(x_train)
    y_test_preds = model.predict(x_test)

    # Calculate accuracies
    train_accuracy = accuracy_score(y_train, y_train_preds)
    test_accuracy = accuracy_score(y_test, y_test_preds)

    # Append results to the list
    results_list.append({'Model': f'Decision Tree {i}', 'Max Depth': max_depth,
                         'Training Accuracy': train_accuracy, 'Testing␣
 ↪Accuracy': test_accuracy})

# Create a DataFrame from the list
results_df = pd.DataFrame(results_list)

# Display the results as a table
```

[ ]:
```
print(results_df)
```

```
             Model  Max Depth  Training Accuracy  Testing Accuracy
0  Decision Tree 1          1           0.704754            0.6900
1  Decision Tree 3          3           0.711426            0.7100
2  Decision Tree 5          5           0.774812            0.7375
3  Decision Tree 7          7           0.844871            0.7050
4  Decision Tree 9          9           0.913261            0.7200
```

Conclusion: Decision Tree models with varying Max Depth values demonstrate a trade-off between training accuracy and testing accuracy. A Max Depth of 5 appears to strike a balance, achieving a relatively high testing accuracy of 0.7375.