Assignment 4

Grapes to Greatness: Machine Learning in Wine Quality Prediction

21BCE0516

ANUSHKA

anushka.2021a@vitstudent.ac.in (mailto:anushka.2021a@vitstudent.ac.in)

In [1]:
```
import pandas as pd
```

1. load the dataset

In [4]:
```
df = pd.read_csv('winequality-red.csv')
```

In [5]:
```
df
```

Out[5]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alc
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
...	...	...	...	...	...	...	...	...	...	...	
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	
1596	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	

1599 rows × 12 columns

2. Data preprocessing including visualization

2. Data preprocessing including visualization

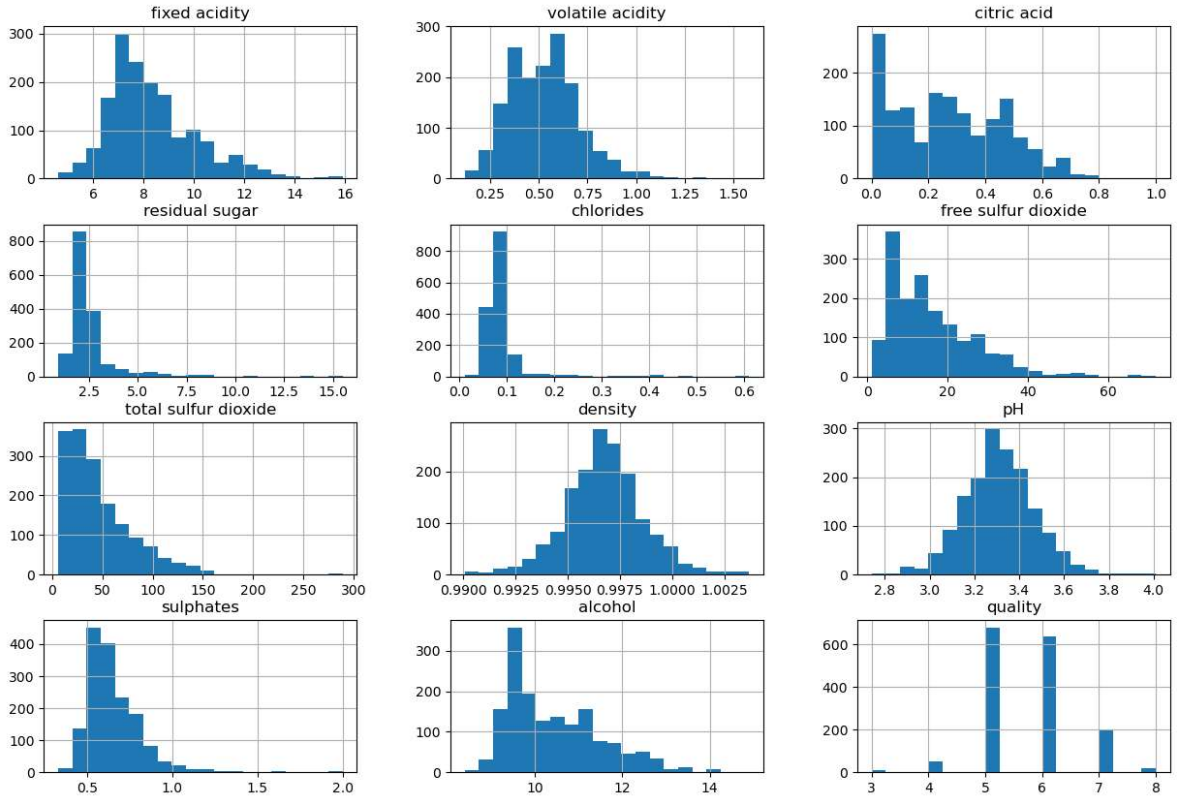
In [8]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [7]:
```
df.describe()
```

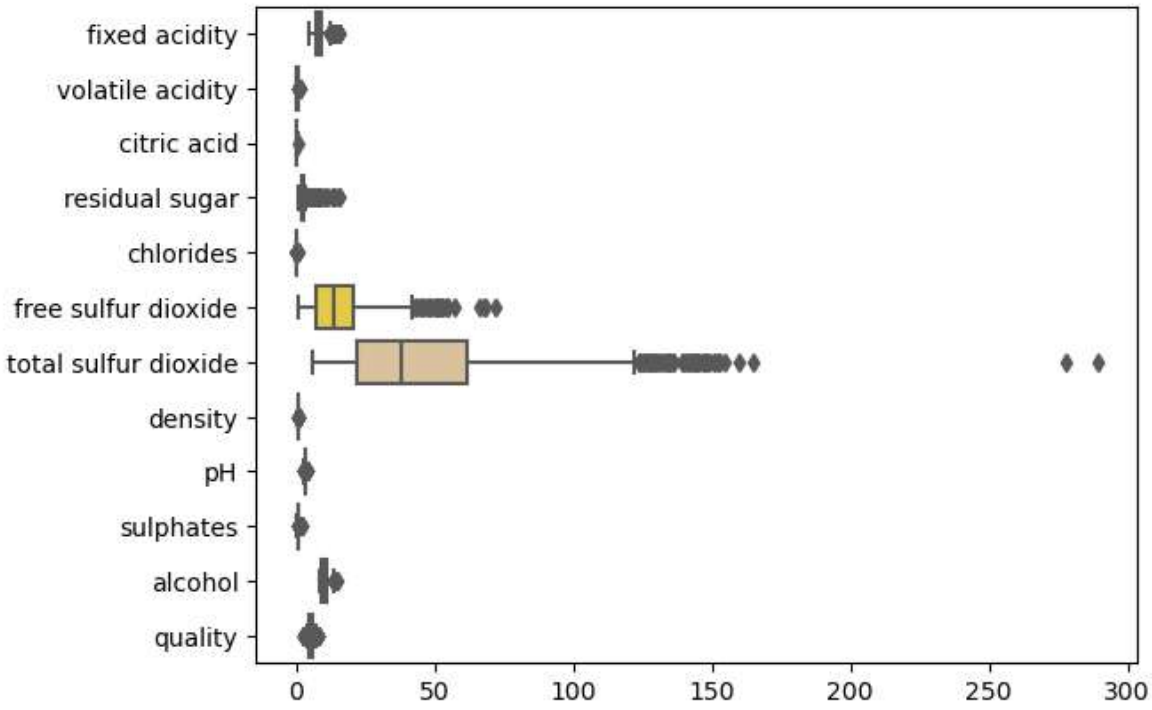
Out[7]:

ılorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	qua
.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000(
.087467	15.874922	46.467792	0.996747	3.311113	0.658149	10.422983	5.636(
.047065	10.460157	32.895324	0.001887	0.154386	0.169507	1.065668	0.807[
.012000	1.000000	6.000000	0.990070	2.740000	0.330000	8.400000	3.000(
.070000	7.000000	22.000000	0.995600	3.210000	0.550000	9.500000	5.000(
.079000	14.000000	38.000000	0.996750	3.310000	0.620000	10.200000	6.000(
.090000	21.000000	62.000000	0.997835	3.400000	0.730000	11.100000	6.000(
.611000	72.000000	289.000000	1.003690	4.010000	2.000000	14.900000	8.000(

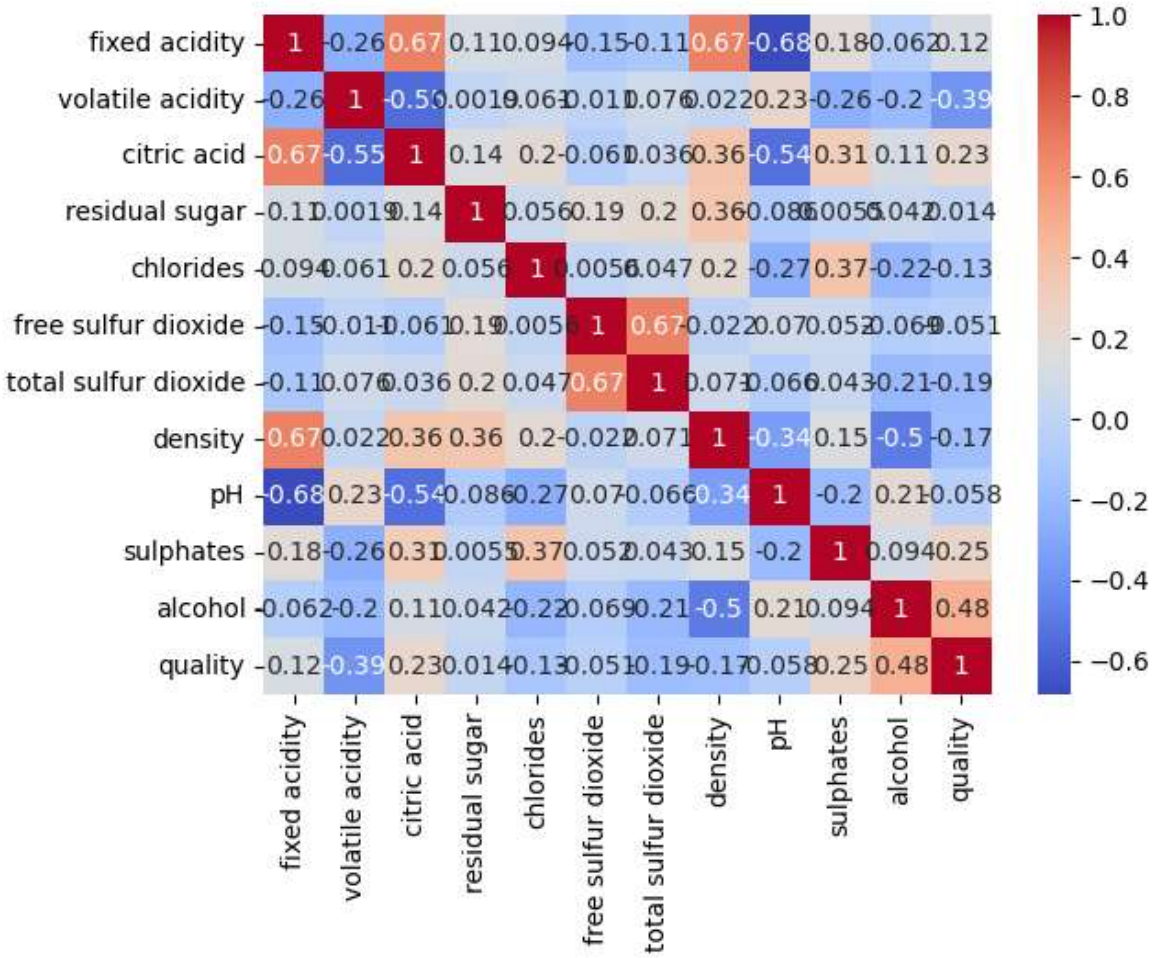
In [9]:
```
df.hist(bins=20, figsize=(15, 10))
plt.show()
```



In [10]:
```
sns.boxplot(data=df, orient="h", palette="Set2")
plt.show()
```



In [11]:
```
corr_matrix = df.corr()
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm')
plt.show()
```



In [13]:
```
# Check for missing values
df.isnull().sum()
#since no missing values, dont have to deal with it
```

Out[13]:
```
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 [17]:
```
from sklearn.preprocessing import StandardScaler


# Define the columns for feature scaling (exclude the target variable)
columns_to_scale = ['fixed acidity', 'volatile acidity', 'citric acid', 'resi
                    'chlorides', 'free sulfur dioxide', 'total sulfur dioxide
                    'pH', 'sulphates', 'alcohol']

# Feature Scaling (Standardization)
scaler = StandardScaler()
df[columns_to_scale] = scaler.fit_transform(df[columns_to_scale])

# Verify the transformed DataFrame
print(df.head())
```

```
   fixed acidity  volatile acidity  citric acid  residual sugar  chlorides
\
0      -0.528360          0.961877    -1.391472       -0.453218  -0.243707
1      -0.298547          1.967442    -1.391472        0.043416   0.223875
2      -0.298547          1.297065    -1.186070       -0.169427   0.096353
3       1.654856         -1.384443     1.484154       -0.453218  -0.264960
4      -0.528360          0.961877    -1.391472       -0.453218  -0.243707

   free sulfur dioxide  total sulfur dioxide   density        pH  sulphates
\
0            -0.466193             -0.379133  0.558274  1.288643  -0.579207
1             0.872638              0.624363  0.028261 -0.719933   0.128950
2            -0.083669              0.229047  0.134264 -0.331177  -0.048089
3             0.107592              0.411500  0.664277 -0.979104  -0.461180
4            -0.466193             -0.379133  0.558274  1.288643  -0.579207

    alcohol  quality
0 -0.960246        5
1 -0.584777        5
2 -0.584777        5
3 -0.584777        6
4 -0.960246        5
```

In [18]:
```
X = df.drop(columns=['quality'])
y = df['quality']
```

In [19]:
```
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, rand
```

In [20]:
```
from sklearn.linear_model import LinearRegression

# Create the model
model = LinearRegression()

# Train the model on the training data
model.fit(X_train, y_train)
```

Out[20]:
```
LinearRegression
LinearRegression()
```

In [21]:
```
from sklearn.metrics import mean_absolute_error, mean_squared_error, r2_score

# Make predictions on the test set
y_pred = model.predict(X_test)

# Calculate evaluation metrics
mae = mean_absolute_error(y_test, y_pred)
mse = mean_squared_error(y_test, y_pred)
r2 = r2_score(y_test, y_pred)

print(f"Mean Absolute Error (MAE): {mae}")
print(f"Mean Squared Error (MSE): {mse}")
print(f"R-squared (R2) Score: {r2}")
```

```
Mean Absolute Error (MAE): 0.5035304415524375
Mean Squared Error (MSE): 0.39002514396395493
R-squared (R2) Score: 0.4031803412796219
```

4.Evaluate the model

In [23]:
```
import numpy as np
from sklearn.metrics import mean_squared_error

rmse = np.sqrt(mean_squared_error(y_test, y_pred))
print(f"Root Mean Squared Error (RMSE): {rmse}")
```

```
Root Mean Squared Error (RMSE): 0.624519930798013
```

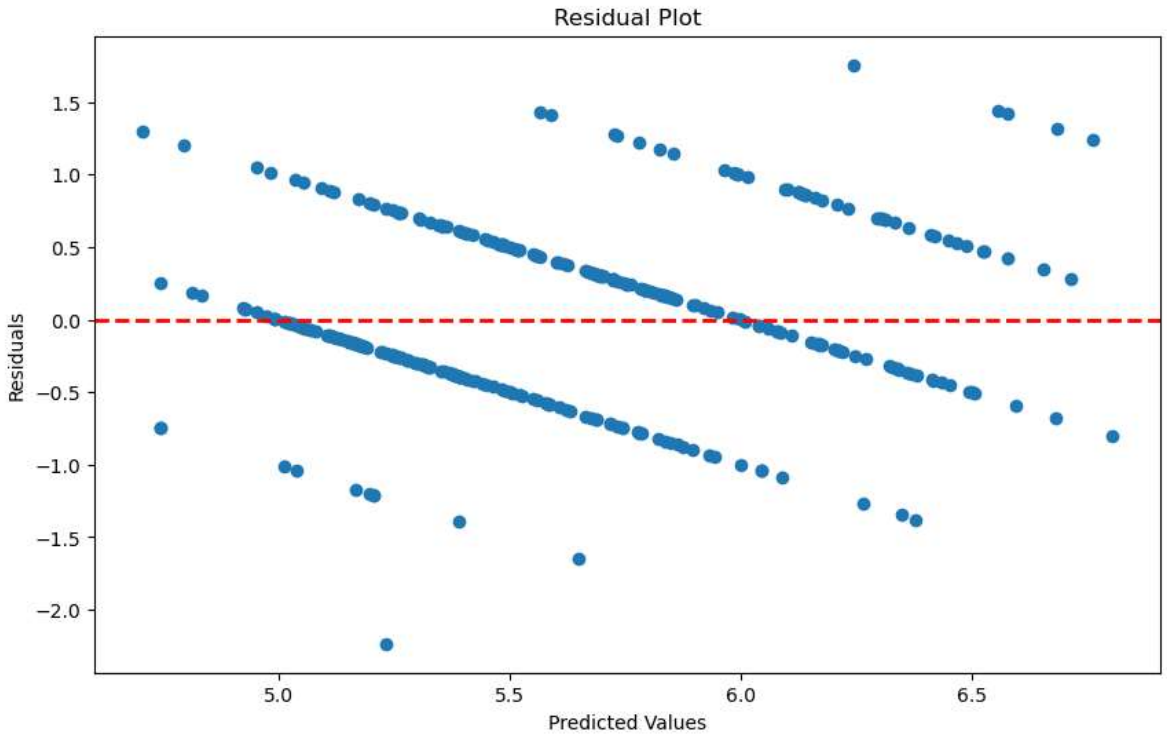
In [24]:
```
n = len(X_test)  # Number of samples
k = len(X_test.columns)  # Number of features

adjusted_r2 = 1 - ((1 - r2) * (n - 1) / (n - k - 1))
print(f"Adjusted R-squared (Adjusted R2): {adjusted_r2}")
```

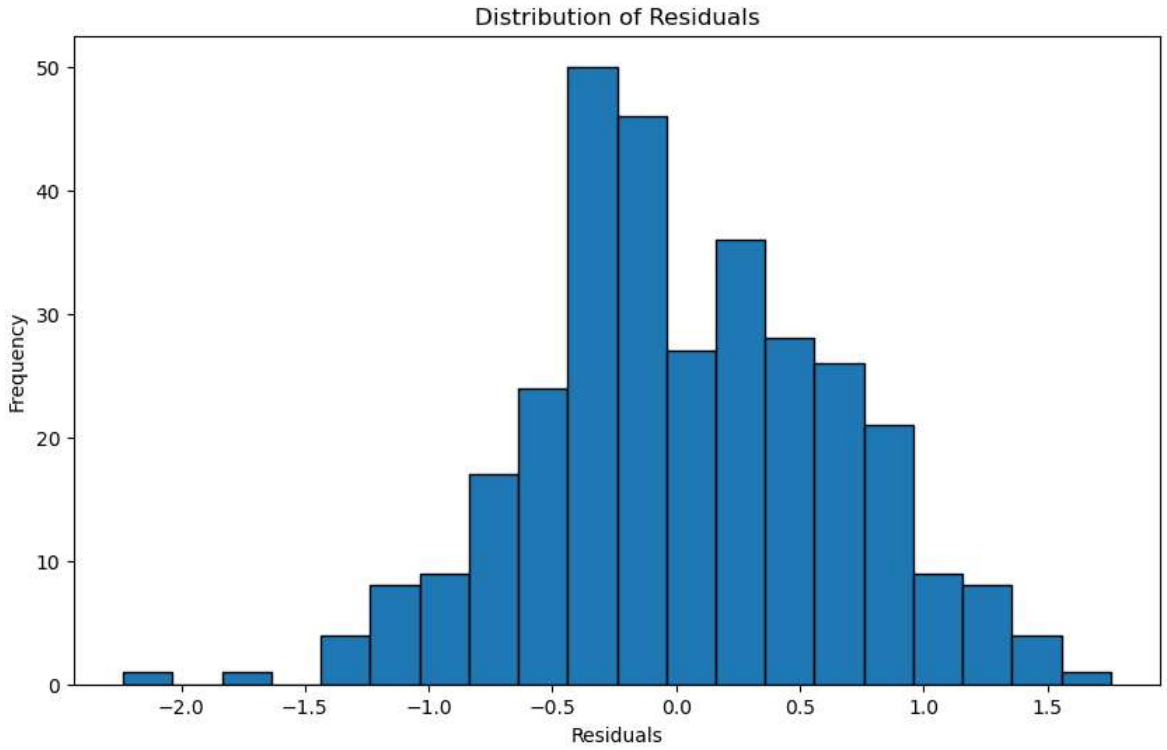
```
Adjusted R-squared (Adjusted R2): 0.38186535346817985
```

In [25]:
```
residuals = y_test - y_pred

# Create residual plots
plt.figure(figsize=(10, 6))
plt.scatter(y_pred, residuals)
plt.xlabel("Predicted Values")
plt.ylabel("Residuals")
plt.axhline(0, color='red', linestyle='--', lw=2)
plt.title("Residual Plot")
plt.show()
```



In [26]:
```
# Histogram of residuals
plt.figure(figsize=(10, 6))
plt.hist(residuals, bins=20, edgecolor='k')
plt.xlabel("Residuals")
plt.ylabel("Frequency")
plt.title("Distribution of Residuals")
plt.show()
```



In [27]:
```
from sklearn.model_selection import cross_val_score

cross_val_scores = cross_val_score(model, X, y, cv=5, scoring='neg_mean_squar
rmse_scores = np.sqrt(-cross_val_scores)

print(f"Cross-Validation RMSE scores: {rmse_scores}")
```

```
Cross-Validation RMSE scores: [0.66737398 0.6724422  0.66661889 0.63973512
0.65722039]
```

5.Test with random observation

In [39]:
```
import pandas as pd
import numpy as np

# Define hypothetical values for the features
random_observation = {
    'fixed acidity': np.random.uniform(4.6, 15.9),
    'volatile acidity': np.random.uniform(0.12, 1.58),
    'citric acid': np.random.uniform(0.0, 1.0),
    'residual sugar': np.random.uniform(0.9, 15.5),
    'chlorides': np.random.uniform(0.012, 0.611),
    'free sulfur dioxide': np.random.uniform(1, 72),
    'total sulfur dioxide': np.random.uniform(6, 289),
    'density': np.random.uniform(0.99007, 1.00369),
    'pH': np.random.uniform(2.74, 4.01),
    'sulphates': np.random.uniform(0.33, 2.0),
    'alcohol': np.random.uniform(8.4, 14.9)
}

# Create a DataFrame for the random observation
random_observation_df = pd.DataFrame([random_observation])
```

In [40]:
```
# Make predictions using the trained model
predicted_quality = model.predict(random_observation_df)

print(f"Predicted Wine Quality: {predicted_quality[0]}")
```

```
Predicted Wine Quality: 4.15743449496132
```

In [ ]:
```

```