**Program:**

import pandas as pd import seaborn as sns

import matplotlib.pyplot as plt data = {

'fixed acidity': [7.4, 7.8, 7.8, 11.2, 7.4, 7.4, 7.9, 7.3, 7.8, 7.5],

'volatile acidity': [0.70, 0.88, 0.76, 0.28, 0.70, 0.66, 0.60, 0.65, 0.58, 0.50],

'citric acid': [0.00, 0.00, 0.04, 0.56, 0.00, 0.00, 0.06, 0.00, 0.02, 0.36],

'residual sugar': [1.9, 2.6, 2.3, 1.9, 1.9, 1.8, 1.6, 1.2, 2.0, 6.1],

'chlorides': [0.076, 0.098, 0.092, 0.075, 0.076, 0.075, 0.069, 0.065, 0.073, 0.071],

'free sulfur dioxide': [11, 25, 15, 17, 11, 13, 15, 15, 9, 17],

'total sulfur dioxide': [34, 67, 54, 60, 34, 40, 59, 21, 18, 102],

'density': [0.9978, 0.9968, 0.9970, 0.9980, 0.9978, 0.9978, 0.9964, 0.9956, 0.9968,

0.9940],

'pH': [3.51, 3.20, 3.26, 3.16, 3.51, 3.51, 3.30, 3.39, 3.36, 3.22],

'sulphates': [0.56, 0.68, 0.65, 0.58, 0.56, 0.56, 0.46, 0.54, 0.57, 0.60],

'alcohol': [9.4, 9.8, 10.0, 9.8, 9.4, 9.4, 10.1, 9.5, 9.5, 10.5],

'quality': [5, 5, 5, 6, 5, 5, 5, 7, 7, 6]

}

df = pd.DataFrame(data) print("Shape:", df.shape) print(df.head())

print(df.info()) print(df.describe()) print(df.isnull().sum())

print("Duplicates:", df.duplicated().sum()) sns.countplot(x='quality', data=df, palette='Set2') plt.title("Quality Distribution") plt.xlabel("Quality")

plt.ylabel("Count")

plt.show()

df.hist(bins=10, figsize=(15, 10), color='skyblue', edgecolor='black') plt.suptitle("Feature Distributions", fontsize=16)

plt.show() plt.figure(figsize=(12, 8))

sns.heatmap(df.corr(), annot=True, cmap="YlGnBu", fmt=".2f", linewidths=0.5) plt.title("Correlation Matrix")

plt.show()

features = df.columns[:-1] plt.figure(figsize=(18, 18))

for i, col in enumerate(features, 1):

plt.subplot(4, 3, i)

sns.boxplot(data=df, x='quality', y=col, palette='Pastel1') plt.title(f"{col} vs Quality")

plt.tight\_layout()

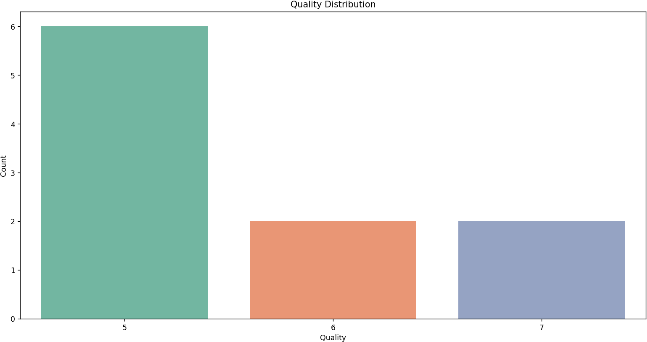
plt.suptitle("Boxplots of Features vs Quality", y=1.02) plt.show()

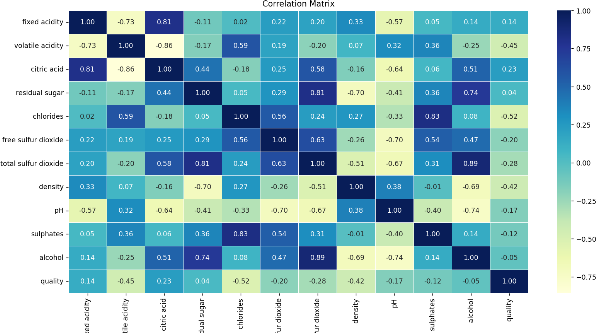
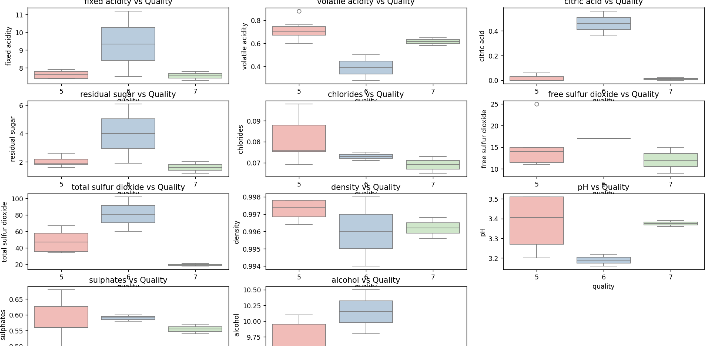
corr\_quality = df.corr()['quality'].sort\_values(ascending=False) print(corr\_quality)

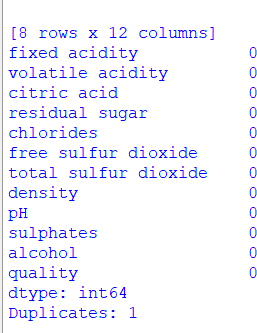
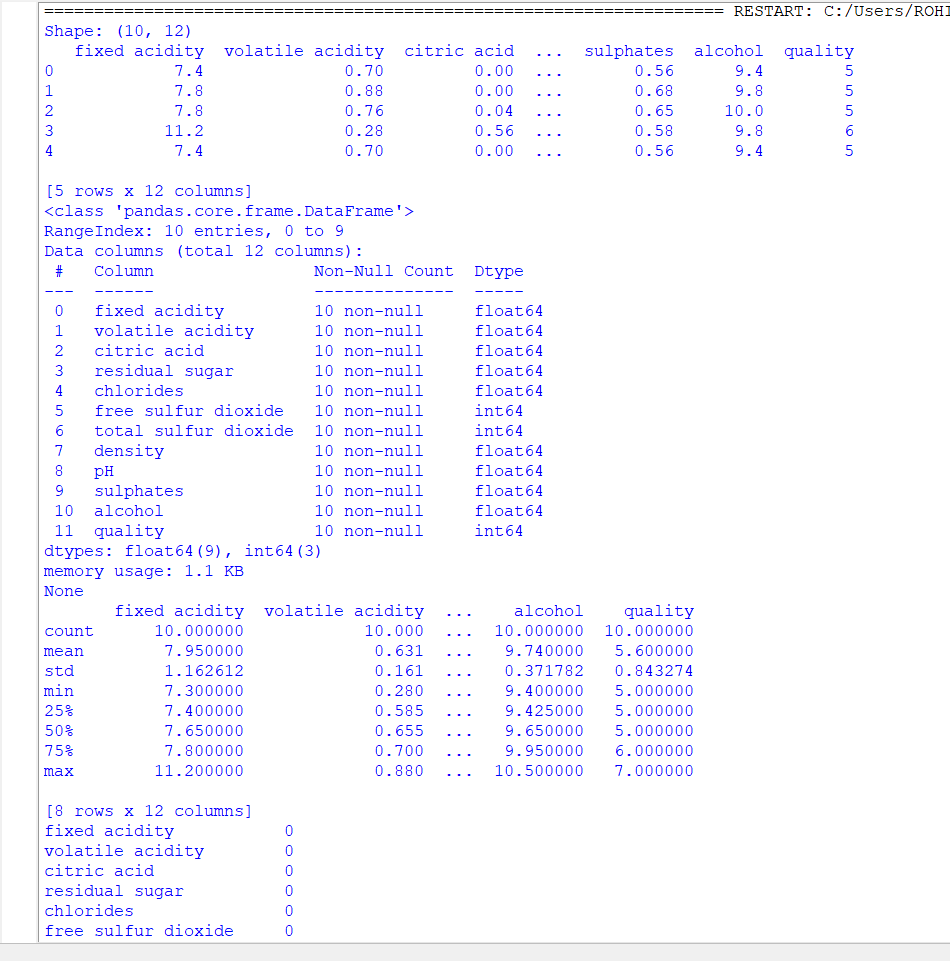
print(corr\_quality[corr\_quality > 0.1])

print(corr\_quality[corr\_quality < -0.1])

# Output:

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