analysis

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1 Tugas Besar Probabilitas dan Statistika

1.0.1 Analisis Data dan Tes Hipotesis

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2 Import Necessary Libraries

[92]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
import scipy
from math import sqrt
from scipy.stats import t, f
from IPython.display import Markdown, display
```

3 Import Dataset

[93]:
```
df = pd.read_csv("../data/anggur.csv")
df
```

[93]:
```
     fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0             5.90            0.4451       0.1813        2.049401   0.070574
1             8.40            0.5768       0.2099        3.109590   0.101681
2             7.54            0.5918       0.3248        3.673744   0.072416
3             5.39            0.4201       0.3131        3.371815   0.072755
4             6.51            0.5675       0.1940        4.404723   0.066379
..             …                 …           …              …          …
995           7.96            0.6046       0.2662        1.592048   0.057555
996           8.48            0.4080       0.2227        0.681955   0.051627
997           6.11            0.4841       0.3720        2.377267   0.042806
998           7.76            0.3590       0.3208        4.294486   0.098276
999           5.87            0.5214       0.1883        2.179490   0.052923
```

```
     free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0              16.593818                 42.27   0.9982  3.27       0.71
1              22.555519                 16.01   0.9960  3.35       0.57
2               9.316866                 35.52   0.9990  3.31       0.64
3              18.212300                 41.97   0.9945  3.34       0.55
4               9.360591                 46.27   0.9925  3.27       0.45
..                   …                     …       …     …          …
995            14.892445                 44.61   0.9975  3.35       0.54
996            23.548965                 25.83   0.9972  3.41       0.46
997            21.624585                 48.75   0.9928  3.23       0.55
998            12.746186                 44.53   0.9952  3.30       0.66
999            16.203864                 24.37   0.9983  3.29       0.70

     alcohol  quality
0       8.64        7
1      10.03        8
2       9.23        8
3      14.07        9
4      11.49        8
..       …        …
995    10.41        8
996     9.91        8
997     9.94        7
998     9.76        8
999    10.17        7

[1000 rows x 12 columns]
```

4 Exploratory Data Analysis

For a full and thorough overview of the dataset, you can open the `EDA.html` file in the `public` folder.

4.1 Descriptive Statistics

In this section, we will examine a brief overview of the dataset.

4.1.1 Missing Values

[94]:
```
missing_values = df.isnull().sum(axis=0)
nan_cols = missing_values[missing_values > 0]
display(Markdown(f"Missing Data: {len(nan_cols)}"))
```

Missing Data: 0

The dataset contains no missing data.

4.1.2 Feature Information

```
[95]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1000 entries, 0 to 999
Data columns (total 12 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   fixed acidity         1000 non-null   float64
 1   volatile acidity      1000 non-null   float64
 2   citric acid           1000 non-null   float64
 3   residual sugar        1000 non-null   float64
 4   chlorides             1000 non-null   float64
 5   free sulfur dioxide   1000 non-null   float64
 6   total sulfur dioxide  1000 non-null   float64
 7   density               1000 non-null   float64
 8   pH                    1000 non-null   float64
 9   sulphates             1000 non-null   float64
 10  alcohol               1000 non-null   float64
 11  quality               1000 non-null   int64
dtypes: float64(11), int64(1)
memory usage: 93.9 KB
```

Based on the information above, all features are of numeric type

4.1.3 Statistical Summary

```
[96]: df.describe()
```

```
[96]:        fixed acidity  volatile acidity  citric acid  residual sugar  \
       count    1000.000000       1000.000000  1000.000000     1000.000000
       mean        7.152530          0.520838     0.270517        2.567104
       std         1.201598          0.095848     0.049098        0.987915
       min         3.320000          0.139900     0.116700        0.032555
       25%         6.377500          0.456100     0.237800        1.896330
       50%         7.150000          0.524850     0.272200        2.519430
       75%         8.000000          0.585375     0.302325        3.220873
       max        11.490000          0.805100     0.409600        5.550755

                chlorides  free sulfur dioxide  total sulfur dioxide      density  \
       count  1000.000000          1000.000000           1000.000000  1000.000000
       mean      0.081195            14.907679             40.290150     0.995925
       std       0.020111             4.888100              9.965767     0.002020
       min       0.015122             0.194679              3.150000     0.988800
       25%       0.066574            11.426717             33.785000     0.994600
       50%       0.082167            14.860346             40.190000     0.996000
       75%       0.095312            18.313098             47.022500     0.997200
```

```
max       0.140758            27.462525            69.960000     1.002600

                 pH    sulphates      alcohol      quality
count  1000.000000  1000.000000  1000.000000  1000.000000
mean      3.303610     0.598390    10.592280     7.958000
std       0.104875     0.100819     1.510706     0.902802
min       2.970000     0.290000     6.030000     5.000000
25%       3.230000     0.530000     9.560000     7.000000
50%       3.300000     0.595000    10.610000     8.000000
75%       3.370000     0.670000    11.622500     9.000000
max       3.710000     0.960000    15.020000    10.000000
```

4.1.4 Mode

[97]:
```
def show_feature_modes(df):
    for col in df.columns:
        if df[col].nunique() == df[col].count():
            display(Markdown(f"{col}: Contains all unique values"))
        else:
            modes = df[col].mode().to_list()
            mode_str = ", ".join(str(mode) for mode in modes)
            display(Markdown(f"{col}: {mode_str}"))
```

[98]:
```
show_feature_modes(df)
```

fixed acidity: 6.54

volatile acidity: 0.5546

citric acid: 0.3019

residual sugar: Contains all unique values

chlorides: Contains all unique values

free sulfur dioxide: Contains all unique values

total sulfur dioxide: 35.2, 37.25, 39.64, 40.61, 41.05, 41.59, 44.51

density: 0.9959, 0.9961, 0.9965, 0.997

pH: 3.34

sulphates: 0.59

alcohol: 9.86, 10.31

quality: 8

4.1.5 Median

```
[99]: df.median()
```

```
[99]: fixed acidity            7.150000
      volatile acidity         0.524850
      citric acid              0.272200
      residual sugar           2.519430
      chlorides                0.082167
      free sulfur dioxide     14.860346
      total sulfur dioxide    40.190000
      density                  0.996000
      pH                       3.300000
      sulphates                0.595000
      alcohol                 10.610000
      quality                  8.000000
      dtype: float64
```

4.1.6 Variance

```
[100]: df.var()
```

```
[100]: fixed acidity            1.443837
       volatile acidity         0.009187
       citric acid              0.002411
       residual sugar           0.975977
       chlorides                0.000404
       free sulfur dioxide     23.893519
       total sulfur dioxide    99.316519
       density                  0.000004
       pH                       0.010999
       sulphates                0.010164
       alcohol                  2.282233
       quality                  0.815051
       dtype: float64
```

4.1.7 Range

```
[101]: range_df = df.max() - df.min()

       print(range_df)
```

```
fixed acidity            8.170000
volatile acidity         0.665200
citric acid              0.292900
residual sugar           5.518200
chlorides                0.125635
```

```
free sulfur dioxide     27.267847
total sulfur dioxide    66.810000
density                  0.013800
pH                       0.740000
sulphates                0.670000
alcohol                  8.990000
quality                  5.000000
dtype: float64
```

4.1.8 Unique Values

[102]:
```
df.nunique()
```

[102]:
```
fixed acidity            417
volatile acidity         879
citric acid              769
residual sugar          1000
chlorides               1000
free sulfur dioxide     1000
total sulfur dioxide     881
density                  107
pH                        61
sulphates                 60
alcohol                  490
quality                    6
dtype: int64
```

From the output above, we can see that most of the features on the data contain a high number of unique values. The reason for this could be that the features are all of numerical type. On the other side, the target variable `quality` is a categorical column of numeric type, containing six different levels of quality.

4.1.9 Skewness

[103]:
```
df.skew()
```

[103]:
```
fixed acidity          -0.028879
volatile acidity       -0.197699
citric acid            -0.045576
residual sugar          0.132638
chlorides              -0.051319
free sulfur dioxide     0.007130
total sulfur dioxide   -0.024060
density                -0.076883
pH                      0.147673
sulphates               0.149199
alcohol                -0.018991
quality                -0.089054
```

```
dtype: float64
```

Skewness is a statistical measure that indicates the symmetry of the distribution of a variable. A skewness value of 0 indicates a perfectly symmetrical distribution, while a positive or negative value indicates that the distribution is skewed to the right or left, respectively.

In the provided output, the skewness values for the columns implies the following:

Columns	Skewness	Interpretation
`fixed acidity`	-0.028879	Almost symmetrical distribution
`volatile acidity`	-0.197699	Moderately skewed to the left
`citric acid`	-0.045576	Almost symmetrical distribution
`residual sugar`	0.132638	Moderately skewed to the right
`chlorides`	-0.051319	Almost symmetrical distribution
`free sulfur dioxide`	0.007130	Almost symmetrical distribution
`total sulfur dioxide`	-0.024060	Almost symmetrical distribution
`density`	-0.076883	Almost symmetrical distribution
`pH`	0.147673	Moderately skewed to the right
`sulphates`	0.149199	Moderately skewed to the right
`alcohol`	-0.018991	Almost symmetrical distribution
`quality`	-0.089054	Almost symmetrical distribution

4.1.10 Kurtosis

```
[104]: df.kurtosis()
```

```
[104]: fixed acidity          -0.019292
       volatile acidity        0.161853
       citric acid            -0.104679
       residual sugar         -0.042980
       chlorides              -0.246508
       free sulfur dioxide    -0.364964
       total sulfur dioxide    0.063950
       density                 0.016366
       pH                      0.080910
       sulphates               0.064819
       alcohol                -0.131732
       quality                 0.108291
       dtype: float64
```

Kurtosis is a statistical measure that describes the shape of the distribution of a variable, specifically the degree of peakedness and thickness of the tails compared to a normal distribution. A kurtosis value of 0 indicates a normal distribution, while a positive value indicates a more peaked and thicker-tailed distribution (leptokurtic), and a negative value indicates a flatter and thinner-tailed distribution (platykurtic).

In the provided output, the kurtosis values for the columns are as follows:

Columns	Kurtosis	Interpretation
`fixed acidity`	-0.019292	Slightly platykurtic
`volatile acidity`	0.161853	Slightly leptokurtic
`citric acid`	-0.104679	Slightly platykurtic
`residual sugar`	-0.042980	Slightly platykurtic
`chlorides`	-0.246508	Moderately platykurtic
`free sulfur dioxide`	-0.364964	Moderately platykurtic
`total sulfur dioxide`	0.063950	Slightly leptokurtic
`density`	0.016366	Slightly leptokurtic
`pH`	0.080910	Slightly leptokurtic
`sulphates`	0.064819	Slightly leptokurtic
`alcohol`	-0.131732	Slightly platykurtic
`quality`	0.108291	Slightly leptokurtic

4.1.11 Quartiles and Interquartile Range

[105]:
```
# Examine interquartile range
def iqr(data, col):
    # Determine IQR for column
    col_values = data[col].values
    q25, q75 = np.percentile(col_values, 25), np.percentile(col_values, 75)
    iqr = q75 - q25
    cut_off = iqr * 1.5
    lower, upper = q25 - cut_off, q75 + cut_off
    return ("| `{}` | {} | {} | {} | {} | {} | {} |\n".format(col,␣
  ↪str(round(q25,4)), str(round(q75,4)), str(round(iqr,4)),␣
  ↪str(round(cut_off,4)), str(round(lower,4)), str(round(upper,4))))
```

[106]:
```
iqr_table = "| Columns | Q25 | Q75 | IQR | Cut Off | Lower Bound | Upper Bound␣
  ↪|\n"
iqr_table += "| ------ | --- | --- | --- | ------- | ----------- | -----------␣
  ↪|\n"
for col in df.columns:
    iqr_table += iqr(df, col)

display(Markdown(iqr_table))
```

Columns	Q25	Q75	IQR	Cut Off	Lower Bound	Upper Bound
`fixed acidity`	6.3775	8.0	1.6225	2.4338	3.9437	10.4338
`volatile acidity`	0.4561	0.5854	0.1293	0.1939	0.2622	0.7793
`citric acid`	0.2378	0.3023	0.0645	0.0968	0.141	0.3991
`residual sugar`	1.8963	3.2209	1.3245	1.9868	-0.0905	5.2077
`chlorides`	0.0666	0.0953	0.0287	0.0431	0.0235	0.1384
`free sulfur dioxide`	11.4267	18.3131	6.8864	10.3296	1.0971	28.6427
`total sulfur dioxide`	33.785	47.0225	13.2375	19.8563	13.9287	66.8788
`density`	0.9946	0.9972	0.0026	0.0039	0.9907	1.0011

Columns	Q25	Q75	IQR	Cut Off	Lower Bound	Upper Bound
`pH`	3.23	3.37	0.14	0.21	3.02	3.58
`sulphates`	0.53	0.67	0.14	0.21	0.32	0.88
`alcohol`	9.56	11.6225	2.0625	3.0937	6.4663	14.7162
`quality`	7.0	9.0	2.0	3.0	4.0	12.0

Quartiles divides a dataset into four equal parts. Q1 or the first quartile is the value that separates the lowest 25% of the data. Q2 or the second quartile is the value that separates the data into two equal parts. Q3 or the third quartile is the value that separates the highest 25% of the data.

The interquartile range (IQR) is a measure of the spread of a dataset with quartiles. The formula for IQR:

$$IQR = Q_3 - Q_1$$

While the upper and lower bound cutoff for outlier detection by IQR method is defined by the following formula:

$$\mathit{Bound} = \pm\, 1.5 \times IQR$$

In the provided output, the IQR values for the columns are as follows:

Columns	IQR	Interpretation
`fixed acidity`	1.6225	Moderately variable
`volatile acidity`	0.1293	Relatively less variable
`citric acid`	0.0645	Relatively less variable
`residual sugar`	1.3245	Moderately variable
`chlorides`	0.0287	Relatively less variable
`free sulfur dioxide`	6.8864	Moderately variable
`total sulfur dioxide`	13.2375	Highly variable
`density`	0.0026	Relatively less variable
`pH`	0.14	Moderately variable
`sulphates`	0.14	Moderately variable
`alcohol`	2.0625	Moderately variable
`quality`	2.0	Moderately variable

4.2 Univariate Analysis

In this section, we will analyze each feature of the dataset in isolation. We will also conduct normality testing to check whether a feature is normally distributed.

4.2.1 Brief Introduction

4.2.2 Histograms

Histograms shows the frequency distribution of the data in a column. The x-axis represents the values of the column, while the y-axis shows the frequency of those values.

4.2.3 Boxplots

Boxplots displays the distribution of the data in a compact manner. It shows the quartiles of the distribution, with the horizontal line in the box representing the median, the top and bottom of the box representing the first and third quartiles, and the whiskers representing the range of the data.

4.2.4 Normal test

A normal test is a statistical method used to determine whether a set of data is normally distributed, which means that it follows a normal or Gaussian distribution. In this section, we will use D'Agostino-Pearson test provided by the scipy library. the D'Agostino-Pearson test is based on the following null hypothesis: the data comes from a normal distribution. The test statistic is a combination of the measures of skewness and kurtosis, and the p-value is computed based on the null distribution of this test statistic under the assumption that the data are normally distributed.

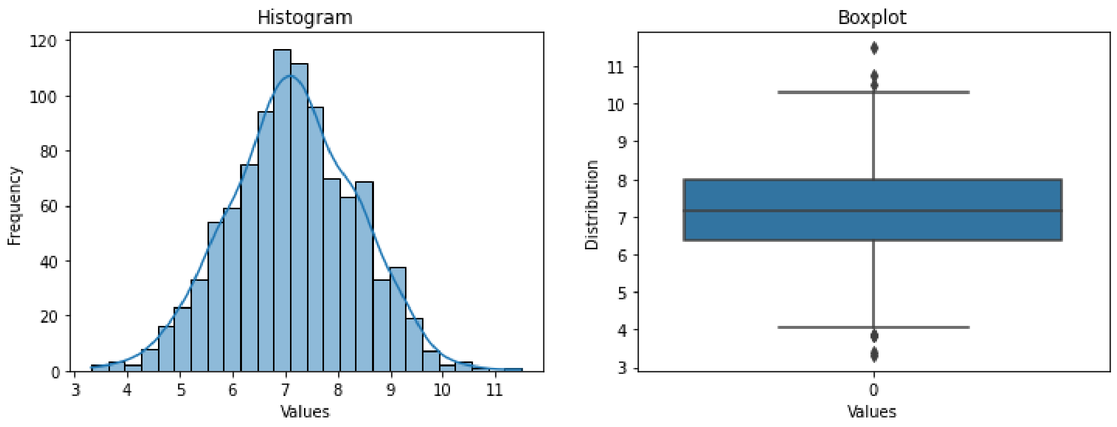
[107]:
```python
def hist_box_plot(data):
    # Create a figure with two subplots
    fig, ax = plt.subplots(ncols=2, figsize=(12, 4))

    # Create a histogram subplot
    sns.histplot(data=data, ax=ax[0], kde=True)
    ax[0].set_xlabel('Values')
    ax[0].set_ylabel('Frequency')
    ax[0].set_title('Histogram')

    # Create a boxplot subplot
    sns.boxplot(data=data, ax=ax[1])
    ax[1].set_xlabel('Values')
    ax[1].set_ylabel('Distribution')
    ax[1].set_title('Boxplot')

    # Display the plot
    plt.show()
```

[108]:
```python
def describe_feature(data, feature):
    hist_box_plot(data[feature])

    # Calculate statistics
    median = data[feature].median()
    q1 = data[feature].quantile(0.25)
    q3 = data[feature].quantile(0.75)
    iqr = q3 - q1
    lower = q1 - 1.5 * iqr
    upper = q3 + 1.5 * iqr

    # Create description
    if (feature != 'pH'):
        description = f"### {feature.capitalize()}\n"
    else:
        description = "### pH\n"
    description += f"The distribution of `{feature}` is:\n"

    # Shape
    if data[feature].skew() < -1 or data[feature].skew() > 1:
        description += "- Highly skewed\n"
    elif data[feature].skew() < -0.5 or data[feature].skew() > 0.5:
        description += "- Moderately skewed\n"
    else:
        description += "- Approximately symmetric\n"

    # Central tendency
    description += f"- The median is {median:.2f}\n"

    # Spread
    if data[feature].kurtosis() > 3:
        description += "- Heavy-tailed\n"
    elif data[feature].kurtosis() < 3:
        description += "- Light-tailed\n"
    else:
        description += "- Mesokurtic\n"

    # Boxplot
    description += f"\nThe boxplot of `{feature}` shows:\n"
    description += f"- The median is {median:.2f}\n"
    description += f"- The first quartile is {q1:.2f}\n"
    description += f"- The third quartile is {q3:.2f}\n"
    description += f"- The interquartile range is {iqr:.2f}\n"
    description += f"- Values below {lower:.2f} or above {upper:.2f} are␣
↪considered outliers\n"

    # Display description
    display(Markdown(description))
```

[109]:
```
def normality_test(df, col, alpha):
    statistic_value, p_value = scipy.stats.normaltest(df[col])
    message = "After conducting the normality test, we get:\n\n"
    message += f"Statistic Value: {statistic_value}\n\n"
    message += f"P-Value: {p_value}\n\n"
    if(p_value < alpha):
        message += f"With {(1.0 - alpha) * 100}% confidence, we can conclude␣
↪that the {col} feature is not normally distributed"
    else:
        message += f"With {(1.0 - alpha) * 100}% confidence, we can conclude␣
↪that the {col} feature is normally distributed"
    display(Markdown(message))
```

Fixed Acidity

[110]:
```
describe_feature(df, 'fixed acidity')
```



4.2.5 Fixed acidity

The distribution of `fixed acidity` is: - Approximately symmetric - The median is 7.15 - Light-tailed

The boxplot of `fixed acidity` shows: - The median is 7.15 - The first quartile is 6.38 - The third quartile is 8.00 - The interquartile range is 1.62 - Values below 3.94 or above 10.43 are considered outliers

The `fixed acidity` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 7, spreading across ranges of 3 to 11.

From the boxplot, we can see that this feature have most of the values ranging from 6 to 8, with 7 being the median. It also has minimal datapoints on the whiskers indicating that it does not have many outliers.

[111]:
```
normality_test(df, 'fixed acidity', 0.05)
```

After conducting the normality test, we get:

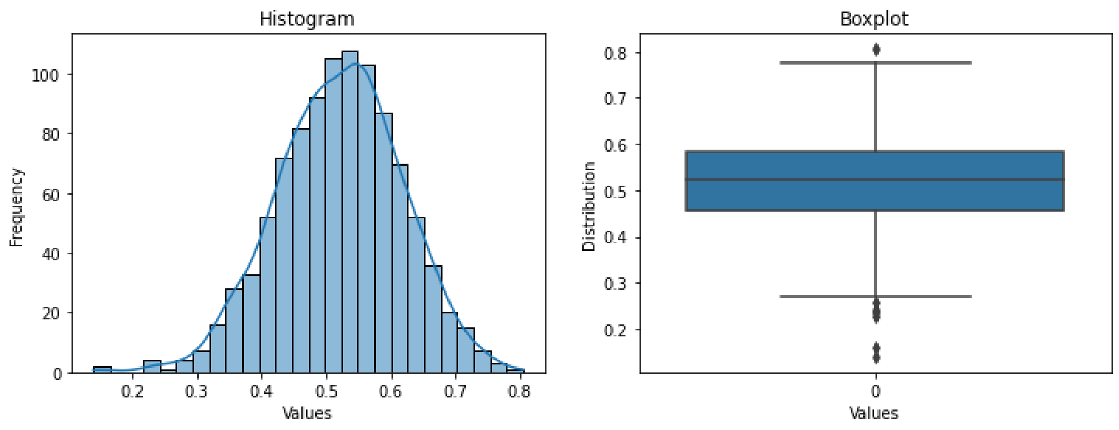
Statistic Value: 0.14329615661430725

P-Value: 0.9308584274486692

With 95.0% confidence, we can conclude that the fixed acidity feature is normally distributed

Volatile Acidity

```
[112]: describe_feature(df, 'volatile acidity')
```



4.2.6 Volatile acidity

The distribution of `volatile acidity` is: - Approximately symmetric - The median is 0.52 - Light-tailed

The boxplot of `volatile acidity` shows: - The median is 0.52 - The first quartile is 0.46 - The third quartile is 0.59 - The interquartile range is 0.13 - Values below 0.26 or above 0.78 are considered outliers

The `volatile acidity` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 0.5, with values a little bit shifted to the right.

From the boxplot, we can see that this feature have most of the values ranging from 0.45 to 0.6, with 0.5 being the median. It also has moderate amount of datapoints on the whiskers indicating outliers.

```
[113]: normality_test(df, 'volatile acidity', 0.05)
```

After conducting the normality test, we get:

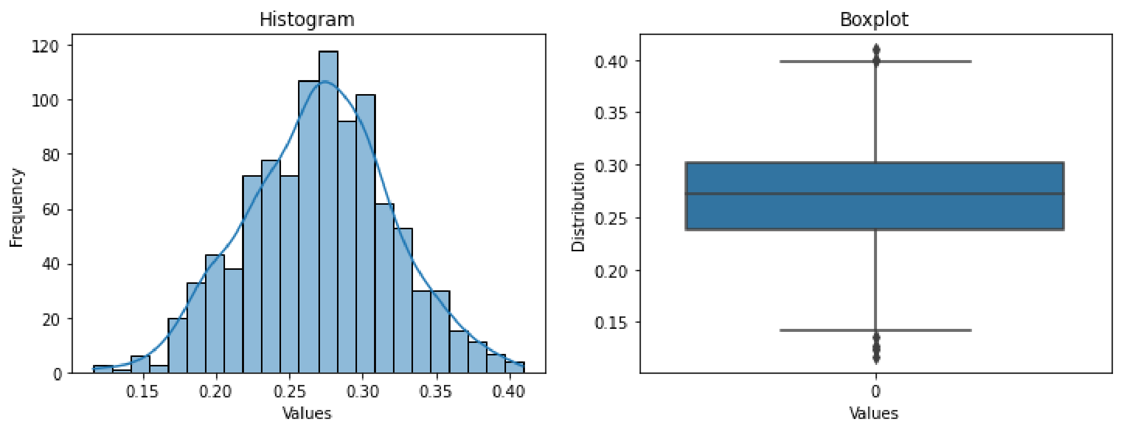
Statistic Value: 7.5812519855533493

P-Value: 0.0225814615941138835

With 95.0% confidence, we can conclude that the volatile acidity feature is not normally distributed

Citric Acid

```
[114]: describe_feature(df, 'citric acid')
```



4.2.7 Citric acid

The distribution of `citric acid` is: - Approximately symmetric - The median is 0.27 - Light-tailed

The boxplot of `citric acid` shows: - The median is 0.27 - The first quartile is 0.24 - The third quartile is 0.30 - The interquartile range is 0.06 - Values below 0.14 or above 0.40 are considered outliers

The `citric acid` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 0.25, with values that has minimal spread.

From the boxplot, we can see that this feature have most of the values ranging from 0.25 to 0.3, with 0.25 being the median. It also has moderate amount of datapoints on the whiskers indicating outliers.

[115]:
```
normality_test(df, 'citric acid', 0.05)
```

After conducting the normality test, we get:

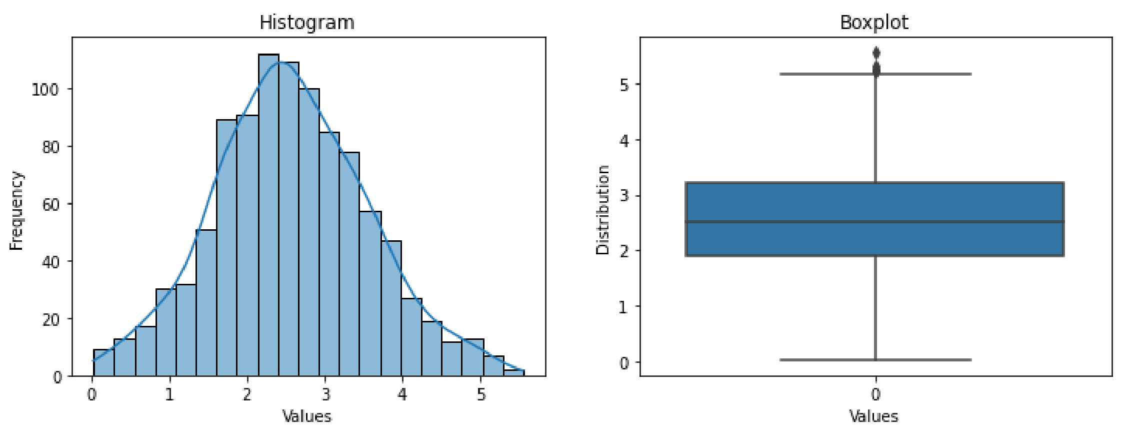
Statistic Value: 0.7663607229418252

P-Value: 0.6816899375976969

With 95.0% confidence, we can conclude that the citric acid feature is normally distributed

`Residual Sugar`

[116]:
```
describe_feature(df, 'residual sugar')
```



4.2.8 Residual sugar

The distribution of `residual sugar` is: - Approximately symmetric - The median is 2.52 - Light-tailed

The boxplot of `residual sugar` shows: - The median is 2.52 - The first quartile is 1.90 - The third quartile is 3.22 - The interquartile range is 1.32 - Values below -0.09 or above 5.21 are considered outliers

The `residual sugar` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 2.5, with a little bit of skewness to the left.

From the boxplot, we can see that this feature have most of the values ranging from 2 to 3, with 2.5 being the median. It also has minimal amount of datapoints on the whiskers indicating that most of the values lie between Q1 and Q3.

[117]:
```
normality_test(df, 'residual sugar', 0.05)
```

After conducting the normality test, we get:

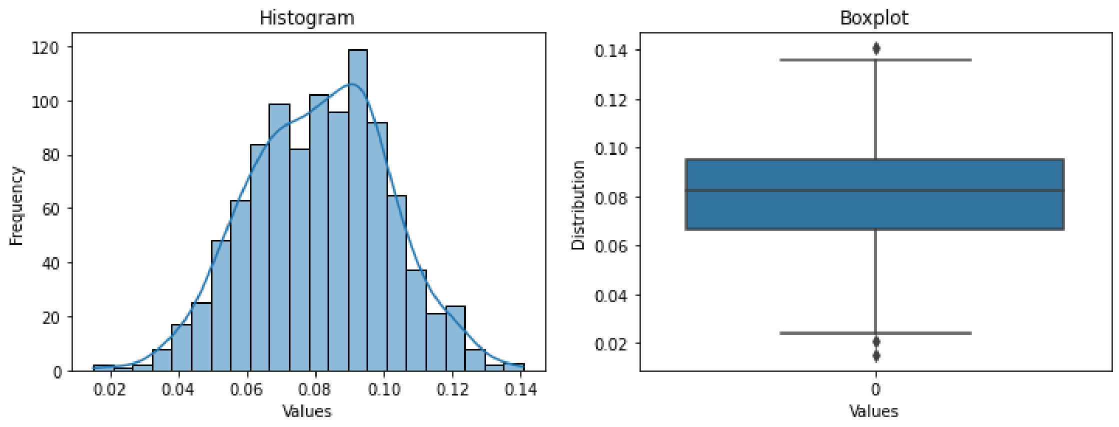
Statistic Value: 2.9862716504538622

P-Value: 0.22466703321310558

With 95.0% confidence, we can conclude that the residual sugar feature is normally distributed

Chlorides

[118]:
```
describe_feature(df, 'chlorides')
```



4.2.9 Chlorides

The distribution of `chlorides` is: - Approximately symmetric - The median is 0.08 - Light-tailed

The boxplot of `chlorides` shows: - The median is 0.08 - The first quartile is 0.07 - The third quartile is 0.10 - The interquartile range is 0.03 - Values below 0.02 or above 0.14 are considered outliers

The `chlorides` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 0.08, with jagged frequencies having the most at around 0.09.

From the boxplot, we can see that this feature has most of the values ranging from 0.06 to 0.09, with 0.08 being the median. It also has minimal amount of datapoints on the whiskers indicating it does not have many outliers.

[119]:
```
normality_test(df, 'chlorides', 0.05)
```

After conducting the normality test, we get:

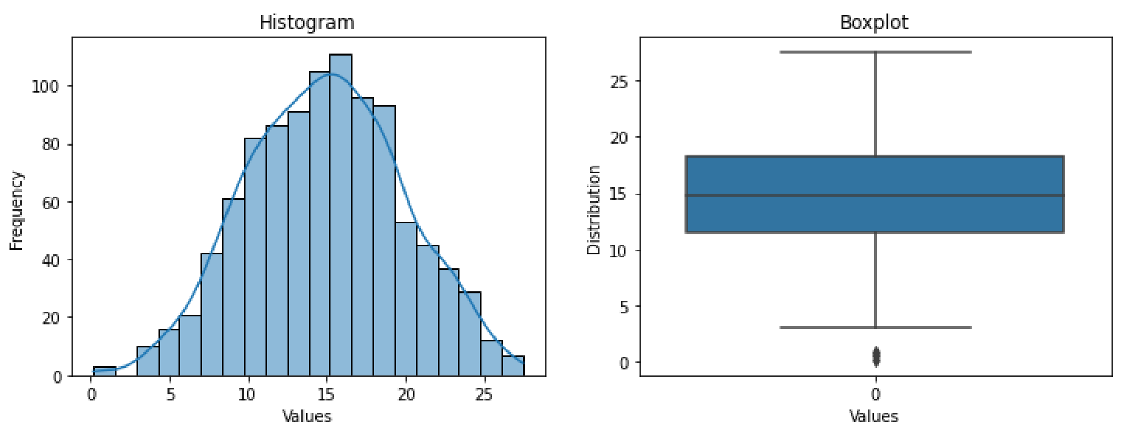
Statistic Value: 3.538242355484952

P-Value: 0.17048274704296862

With 95.0% confidence, we can conclude that the chlorides feature is normally distributed

`Free Sulfur Dioxide`

[120]:
```
describe_feature(df, 'free sulfur dioxide')
```



4.2.10 Free sulfur dioxide

The distribution of `free sulfur dioxide` is: - Approximately symmetric - The median is 14.86 - Light-tailed

The boxplot of `free sulfur dioxide` shows: - The median is 14.86 - The first quartile is 11.43 - The third quartile is 18.31 - The interquartile range is 6.89 - Values below 1.10 or above 28.64 are considered outliers

The `free sulfur dioxide` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 15, having a wide spread of values around 0 to 25.

From the boxplot, we can see that this feature has most of the values ranging from 12 to 18, with 15 being the median. It also has little to no amount of datapoints on the whiskers indicating outliers.

[121]:
```
normality_test(df, 'free sulfur dioxide', 0.05)
```

After conducting the normality test, we get:

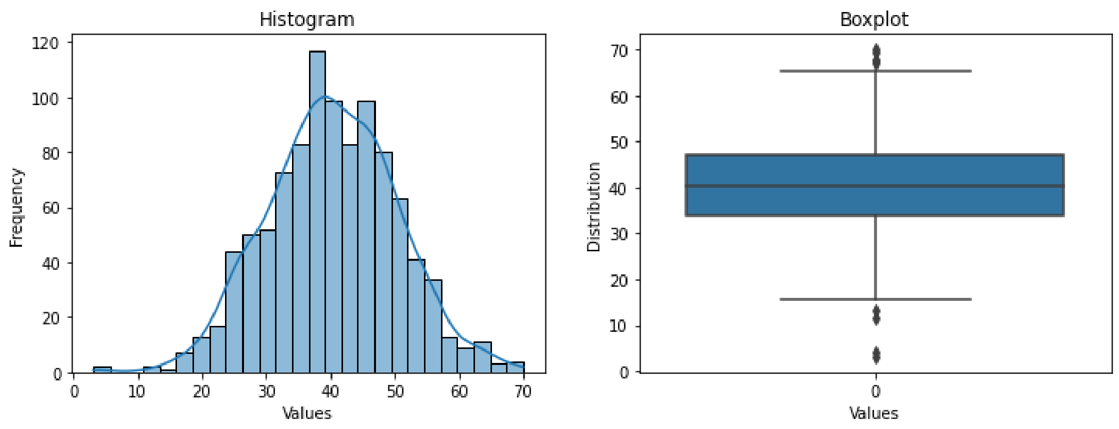
Statistic Value: 8.099074980855514

P-Value: 0.017430434518277735

With 95.0% confidence, we can conclude that the free sulfur dioxide feature is not normally distributed

`Total Sulfur Dioxide`

[122]:
```
describe_feature(df, 'total sulfur dioxide')
```



4.2.11 Total sulfur dioxide

The distribution of `total sulfur dioxide` is: - Approximately symmetric - The median is 40.19 - Light-tailed

The boxplot of `total sulfur dioxide` shows: - The median is 40.19 - The first quartile is 33.78 - The third quartile is 47.02 - The interquartile range is 13.24 - Values below 13.93 or above 66.88 are considered outliers

The `total sulfur dioxide` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 40, with high frequency around the median.

From the boxplot, we can see that this feature has most of the values ranging from 35 to 45, with 40 being the median. It also has moderate amount of datapoints on the whiskers indicating outliers.

[123]:
```
normality_test(df, 'total sulfur dioxide', 0.05)
```

After conducting the normality test, we get:

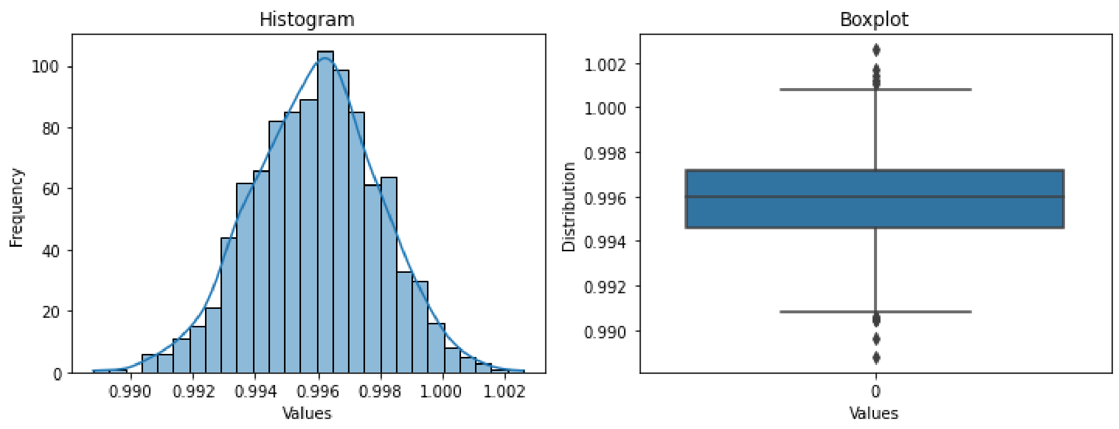
Statistic Value: 0.3276640291639825

P-Value: 0.8488846101395726

With 95.0% confidence, we can conclude that the total sulfur dioxide feature is normally distributed

Density

[124]:
```
describe_feature(df, 'density')
```



4.2.12 Density

The distribution of `density` is: - Approximately symmetric - The median is 1.00 - Light-tailed

The boxplot of `density` shows: - The median is 1.00 - The first quartile is 0.99 - The third quartile is 1.00 - The interquartile range is 0.00 - Values below 0.99 or above 1.00 are considered outliers

The `density` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 0.996, with minimal spread ranging around 0.990 to 1.002.

From the boxplot, we can see that this feature has most of the values ranging from 0.995 to 0.997, with 0.996 being the median. It also has a moderately high amount of datapoints on the whiskers indicating outliers.

[125]:
```
normality_test(df, 'density', 0.05)
```

After conducting the normality test, we get:

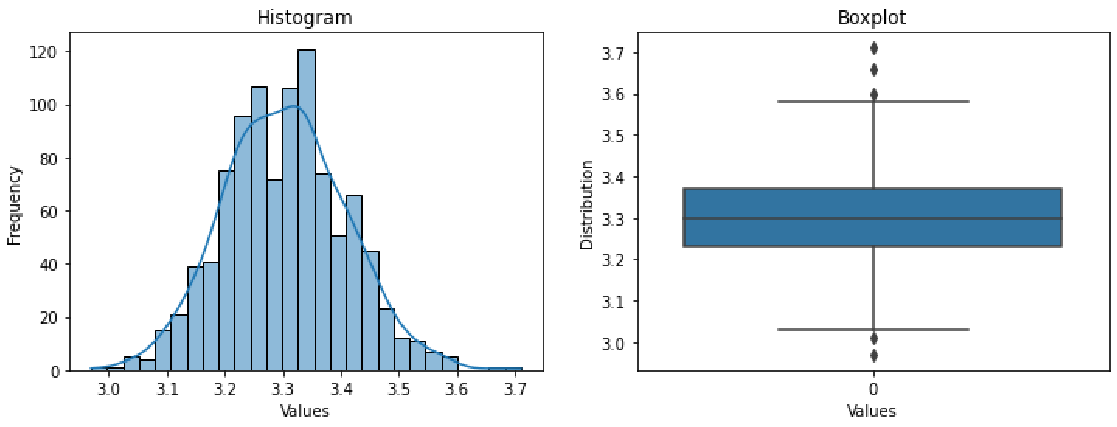
Statistic Value: 1.026581544320803

P-Value: 0.5985227325531981

With 95.0% confidence, we can conclude that the density feature is normally distributed

pH

[126]:
```
describe_feature(df, 'pH')
```



4.2.13 pH

The distribution of `pH` is: - Approximately symmetric - The median is 3.30 - Light-tailed

The boxplot of `pH` shows: - The median is 3.30 - The first quartile is 3.23 - The third quartile is 3.37 - The interquartile range is 0.14 - Values below 3.02 or above 3.58 are considered outliers

The `pH` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 3.3, with values a little bit skewed to the left.

From the boxplot, we can see that this feature has most of the values ranging from 3.23 to 3.38, with 3.3 being the median. It also has moderate amount of datapoints on the whiskers indicating outliers.

[127]:
```
normality_test(df, 'pH', 0.05)
```

After conducting the normality test, we get:

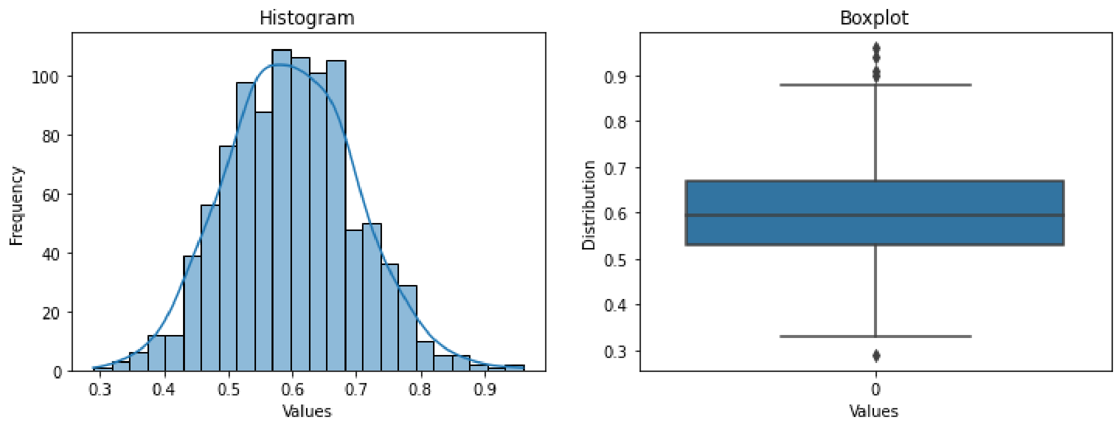
Statistic Value: 3.9786546459928545

P-Value: 0.13678740824860436

With 95.0% confidence, we can conclude that the pH feature is normally distributed

`Sulphates`

[128]:
```
describe_feature(df, 'sulphates')
```



4.2.14 Sulphates

The distribution of `sulphates` is: - Approximately symmetric - The median is 0.59 - Light-tailed

The boxplot of `sulphates` shows: - The median is 0.59 - The first quartile is 0.53 - The third quartile is 0.67 - The interquartile range is 0.14 - Values below 0.32 or above 0.88 are considered outliers

The `sulphates` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 0.6, with values spreading around 0.3 to 0.9.

From the boxplot, we can see that this feature has most of the values ranging from 0.52 to 0.68, with 0.6 being the median. It also has moderate amount of datapoints on the whiskers indicating outliers.

[129]:
```
normality_test(df, 'sulphates', 0.05)
```

After conducting the normality test, we get:

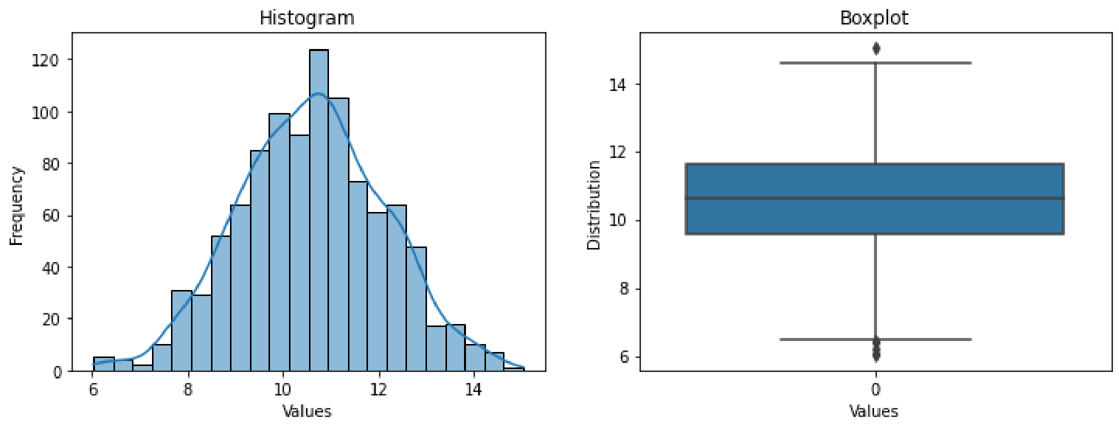
Statistic Value: 3.948820277859041

P-Value: 0.13884318628391681

With 95.0% confidence, we can conclude that the sulphates feature is normally distributed

Alcohol

[130]:
```
describe_feature(df, 'alcohol')
```



4.2.15 Alcohol

The distribution of `alcohol` is: - Approximately symmetric - The median is 10.61 - Light-tailed

The boxplot of `alcohol` shows: - The median is 10.61 - The first quartile is 9.56 - The third quartile is 11.62 - The interquartile range is 2.06 - Values below 6.47 or above 14.72 are considered outliers

The `alcohol` feature has a bell-shaped distribution resembling a normal distribution. It has a tendency to be centrally clustered around the value 11, with values spread around 6 to 14.

From the boxplot, we can see that this feature has most of the values ranging from 9 to 11.5, with 10.5 being the median. It also has moderate amount of datapoints on the whiskers indicating outliers.

[131]:
```
normality_test(df, 'alcohol', 0.05)
```

After conducting the normality test, we get:

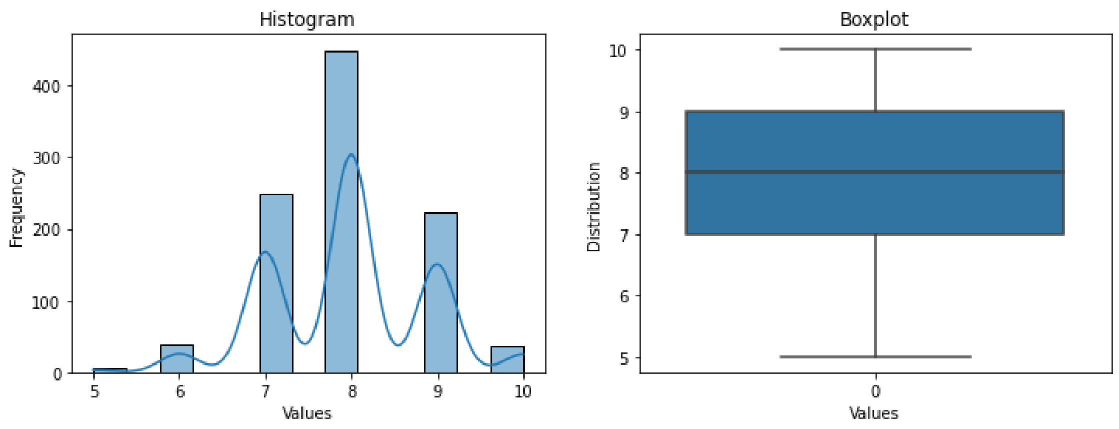
Statistic Value: 0.7740076714171271

P-Value: 0.6790884901361043

With 95.0% confidence, we can conclude that the alcohol feature is normally distributed

`Quality`

[132]:
```
describe_feature(df, 'quality')
```



4.2.16 Quality

The distribution of `quality` is: - Approximately symmetric - The median is 8.00 - Light-tailed

The boxplot of `quality` shows: - The median is 8.00 - The first quartile is 7.00 - The third quartile is 9.00 - The interquartile range is 2.00 - Values below 4.00 or above 12.00 are considered outliers

The `quality` feature is the target variable with values ranging from 5 to 10. The dataset contains the highest frequency of quality level with the value of 8, followed by 7 and 9.

From the boxplot, we can see that this feature does not have any outliers, as the feature is of categoric type containing numerical values, having integer classes from 5 to 10.

[133]:
```
normality_test(df, 'quality', 0.05)
```

After conducting the normality test, we get:

Statistic Value: 1.8893087092494893

P-Value: 0.3888139394184818

With 95.0% confidence, we can conclude that the quality feature is normally distributed

4.2.17 Proportion of the Target Variable

[134]:
```
def plot_classes(y):
    counts = y.value_counts().sort_index()
    counts = counts.rename_axis("Quality").reset_index(name="Count")
    fig = px.pie(counts, values="Count", names="Quality", title="Quality␣
 ↪Proportion Percentage", template="seaborn")
    fig.update_traces(textposition="inside", textinfo="percent+label")
    fig.show()
    print(counts)
    print()
```

[135]:
```
plot_classes(df['quality'])
```

```
   Quality  Count
0        5      5
1        6     38
2        7    248
3        8    449
4        9    223
5       10     37
```

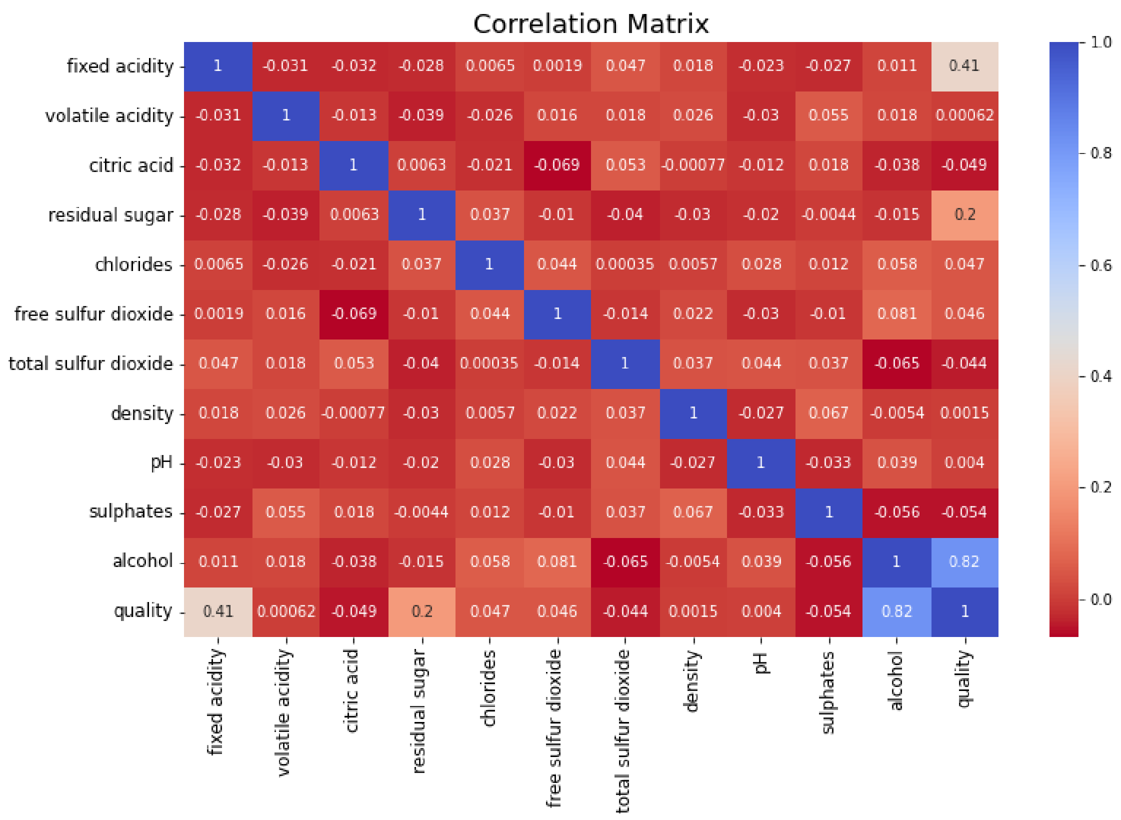
From the pie chart, we can infer that the quality classes are highly imbalanced, with class 8 having the highest proportion.

4.3 Multivariate Analysis

In this section, we will analyze the underlying relationships and interactions between the variables in the dataset.

4.3.1 Feature Correlation

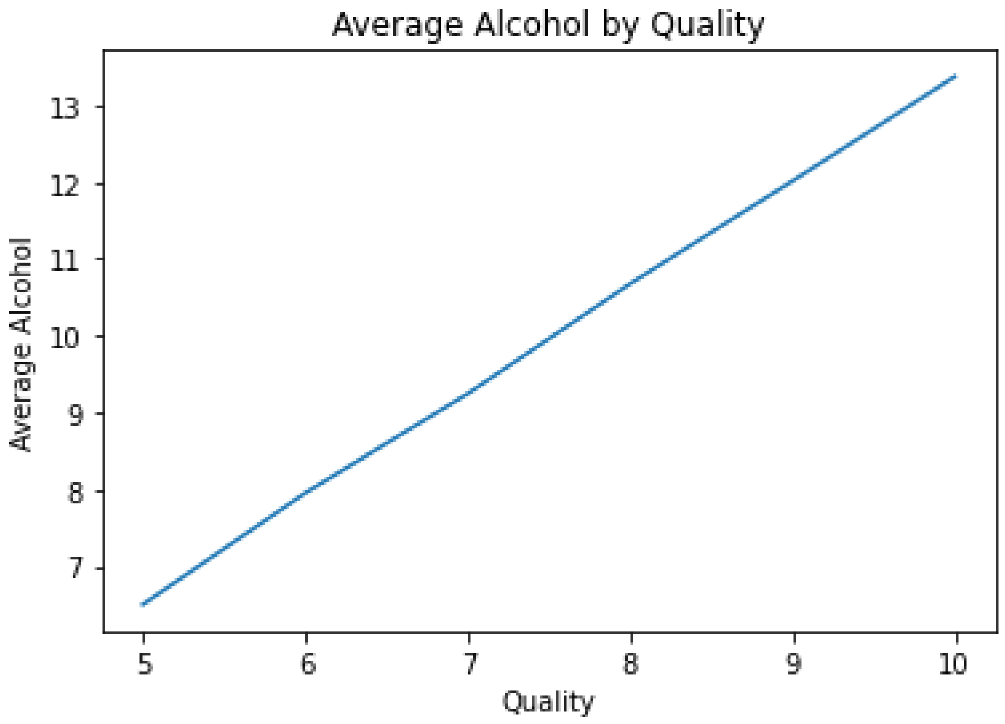
[136]:
```
plt.figure(figsize = (12.5,7.5))
plt.title("Correlation Matrix", fontsize = 18)
sns.heatmap(df.corr(), cmap = 'coolwarm_r', annot = True)
plt.xticks(fontsize=12, rotation = 90)
plt.yticks(fontsize=12, rotation = 0)
plt.show()
```



The correlation matrix reveals that the `alcohol` feature has a strong positive correlation with the target variable, followed by `fixed acidity` and `residual sugar`. This suggests that higher quality wines generally have high alcohol contents. Furthermore, we can also see that the correlation between the predictor variables are minimal, indicating that there is little multicollinearity among the non-target variables.

4.3.2 Alcohol vs Quality

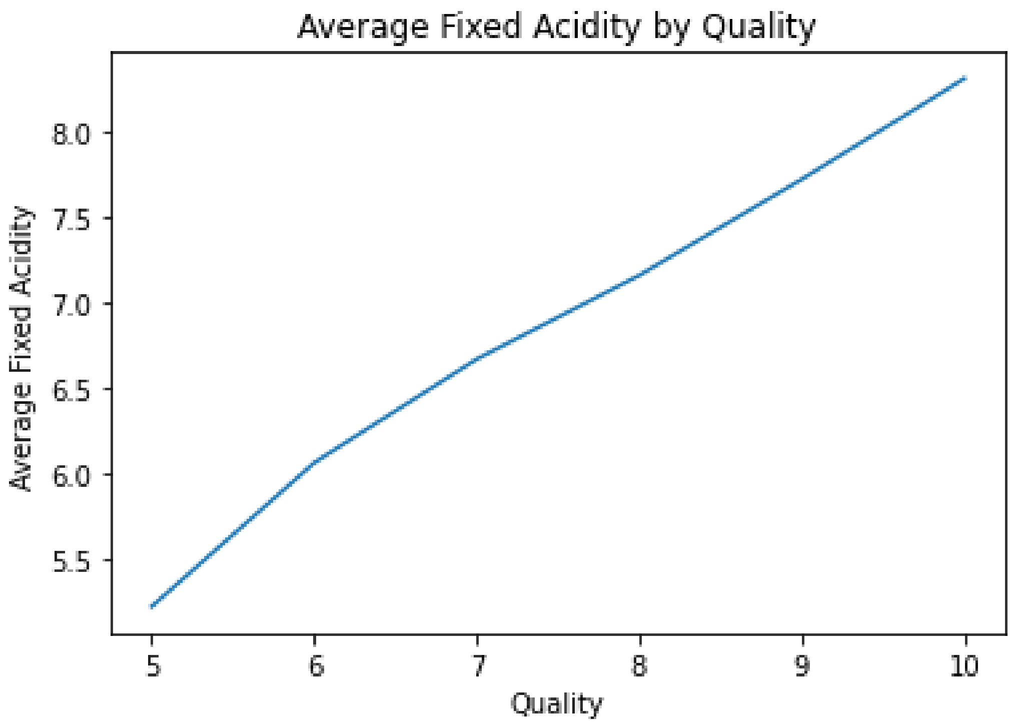
[137]:
```python
# Group the data by the 'quality' column and calculate the mean of 'alcohol'
alcohol_by_quality = df.groupby('quality')['alcohol'].mean()

# Plot a line chart of the average 'alcohol' value for each 'quality' level
alcohol_by_quality.plot(kind='line', x='quality', y='alcohol')
plt.xlabel('Quality')
plt.ylabel('Average Alcohol')
plt.title('Average Alcohol by Quality')
plt.show()
```



From the line plot above, we can conclude that the `alcohol` feature has a linear relationship towards the `quality` of wine.

4.3.3 Fixed Acidity vs Quality

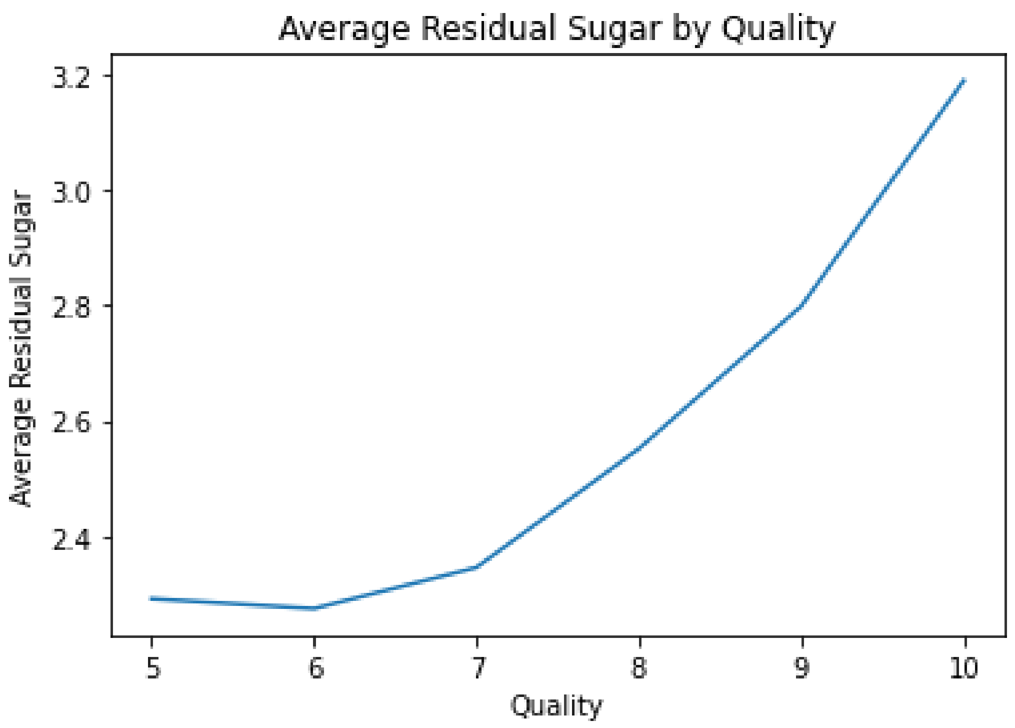
[138]:
```
# Group the data by the 'quality' column and calculate the mean of 'fixed␣
↪acidity'
fixed_acidity_by_quality = df.groupby('quality')['fixed acidity'].mean()

# Plot a line chart of the average 'fixed acidity' value for each 'quality'␣
↪level
fixed_acidity_by_quality.plot(kind='line', x='quality', y='fixed acidity')
plt.xlabel('Quality')
plt.ylabel('Average Fixed Acidity')
plt.title('Average Fixed Acidity by Quality')
plt.show()
```



Similar to `alcohol`, the `fixed acidity` feature also have an approximately linear relationship with the `quality` variable.

4.3.4 Residual Sugar vs Alcohol

[139]:
```
# Group the data by the 'quality' column and calculate the mean of 'residual␣
↪sugar'
residual_sugar_by_quality = df.groupby('quality')['residual sugar'].mean()

# Plot a line chart of the average 'residual sugar' value for each 'quality'␣
↪level
residual_sugar_by_quality.plot(kind='line', x='quality', y='residual sugar')
plt.xlabel('Quality')
plt.ylabel('Average Residual Sugar')
plt.title('Average Residual Sugar by Quality')
plt.show()
```



From this insight, we can say that the `quality` of wine improves exponentially towards the `residual sugar` feature.

5 Hypothesis Testing

In this section, we will conduct single-sample and multisample hypothesis testing on the dataset.

5.1 Single-sample Hypothesis

[140]:
```
def t_test_mean(sample, attribute, mean, tail):
    computed_average = sample[attribute].mean()
    computed_std = sample[attribute].std()

    t_value = (computed_average - mean) / (computed_std / sqrt(len(sample)))
    degree = len(sample) - 1

    if (tail == 2):
        p_value = 2 * (1 - scipy.stats.t.cdf(abs(t_value), degree))
    else:
        p_value = scipy.stats.t.cdf(t_value, degree)

    display(Markdown(f"Computed Average : {computed_average}"))
    display(Markdown(f"Computed Standard Derivation : {computed_std}"))
    display(Markdown(f"T-Value : {t_value}"))
    display(Markdown(f"P-Value : {p_value}"))

    return t_value, p_value
```

[141]:
```
def z_test_proportion(sample, qualified_sample, proportion):
    n = len(sample)
    x = len(qualified_sample)

    p = x / n
    z_value = (p - proportion) / sqrt((proportion * (1 - proportion) / n))
    p_value = scipy.stats.norm.sf(abs(z_value)) * 2

    display(Markdown(f"n       : {n}"))
    display(Markdown(f"x       : {x}"))
    display(Markdown(f"Z-Value : {z_value}"))
    display(Markdown(f"P-Value : {p_value}"))
```

[142]:
```
def calculate_t_critical_value(LOS, degree):
    critical_value = scipy.stats.t.ppf(LOS, degree)

    return critical_value
```

5.1.1 1. Is the mean pH value greater than 3.29?

Step 1 : Specifying the null hypothesis (H0)

H0 : The mean pH value equals to 3.29 ($= 3.29$)

Step 2 : Specifying the alternative hypothesis (H1)

H1 : The mean pH value is greater than 3.29 (> 3.29) (one-tailed test)

Step 3 : Decide the level of significance ( )

$= 0.05$

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = T-Test → Variance of population is unknown Critical area = t > t0.95, 999

[143]:
```
t_critical_value = calculate_t_critical_value(0.95, len(df) - 1)

display(Markdown(f"Critical Value = {t_critical_value}"))
display(Markdown(f"So, the t-value must be greater than {t_critical_value} to␣
↪reject the null hypothesis"))
```

Critical Value = 1.646380345427535

So, the t-value must be greater than 1.646380345427535 to reject the null hypothesis

Step 5 : Calculate T-Test and P-Value from Data Sample

The formula of t-value:

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

[144]:
```
t_value, p_value = t_test_mean(df, "pH", 3.29, 1)
```

Computed Average : 3.303610000000003

Computed Standard Derivation : 0.10487548220040155

T-Value : 4.103780793366056

P-Value : 0.9999780204169363

Step 6 : Make a decision and conclusion

Reject H0 and conclude that the mean pH value is greater than 3.29 because the T-Value is greater than the critical value (t > 1.646) and the P-Value is also far greater than 0.95 (1 - level of significance)

5.1.2 2. Is the mean of `Residual Sugar` not equal to 2.5?

Step 1 : Specifying the null hypothesis (H0)

H0 : the mean of Residual Sugar equals to 2.5 (= 2.5)

Step 2 : Specifying the alternative hypothesis (H1)

H1 : the mean of Residual Sugar is not equal to 2.5 (2.5) (two-tailed test)

Step 3 : Decide the level of significance ( )

 = 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = T-Test → Variance of population is unknown Critical area = t < t0.025, 999 and t > t0.975, 999

[145]:
```
t_critical_value = abs(calculate_t_critical_value(0.025, 999))

display(Markdown(f"Critical Value = \xB1 {t_critical_value}"))
display(Markdown(f"So, the t-value must be greater than {t_critical_value} or␣
↪less than - {t_critical_value} to reject the null hypothesis"))
```

Critical Value = ± 1.962341461133449

So, the t-value must be greater than 1.962341461133449 or less than - 1.962341461133449 to reject the null hypothesis

Step 5 : Calculate T-Test and P-Value from Data Sample

The formula of t-value:

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

```
[146]: t_value, p_value = t_test_mean(df, "residual sugar", 2.5, 2)
```

Computed Average : 2.5671036825067572

Computed Standard Derivation : 0.9879154365046932

T-Value : 2.147961943553881

P-Value : 0.031956726708622485

Step 6 : Make a decision and conclusion

Reject H0 and conclude that the mean Residual Sugar value is not equal to 2.5 but greater than 2.5 because the T-Value is greater than the critical value (t > 1.962) and the P-Value is also less than 0.05 (level of significance)

5.1.3 3. Is the mean value of the first 150 rows of the sulphates column not equal to 0.65?

Step 1 : Specifying the null hypothesis (H0)

H0 : = 0.65

Step 2 : Specifying the alternative hypothesis (H1)

H1 : 0.65 (two-tailed test)

Step 3 : Decide the level of significance ( )

 = 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = T-Test → Variance of population is unknown Critical area = t < t0.025, 149 and t > t0.975, 149

```
[147]: t_critical_value = abs(calculate_t_critical_value(0.025, 149))

       display(Markdown(f"Critical Value = \xB1 {t_critical_value}"))
       display(Markdown(f"So, the t-value must be greater than {t_critical_value} or␣
        ↪less than - {t_critical_value} to reject the null hypothesis"))
```

Critical Value = ± 1.9760131776791554

So, the t-value must be greater than 1.9760131776791554 or less than - 1.9760131776791554 to reject the null hypothesis

Step 5 : Calculate T-Test and P-Value from Data Sample

The formula of t-value:

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

[148]:
```
sample_first_150_anggur = df[:150]
sample_first_150_anggur
```

[148]:
```
     fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0             5.90            0.4451       0.1813        2.049401   0.070574
1             8.40            0.5768       0.2099        3.109590   0.101681
2             7.54            0.5918       0.3248        3.673744   0.072416
3             5.39            0.4201       0.3131        3.371815   0.072755
4             6.51            0.5675       0.1940        4.404723   0.066379
..             …                 …          …              …         …
145           6.95            0.6208       0.2290        2.754654   0.112577
146           7.75            0.4674       0.3274        3.217126   0.108268
147           9.05            0.4682       0.2965        3.764248   0.079567
148           6.91            0.6403       0.1973        0.978649   0.050830
149           7.37            0.3637       0.3091        2.073881   0.058615

     free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0              16.593818                 42.27   0.9982  3.27       0.71
1              22.555519                 16.01   0.9960  3.35       0.57
2               9.316866                 35.52   0.9990  3.31       0.64
3              18.212300                 41.97   0.9945  3.34       0.55
4               9.360591                 46.27   0.9925  3.27       0.45
..                   …                     …       …     …         …
145            17.574028                 49.56   0.9955  3.35       0.73
146            11.898973                 35.76   0.9996  3.34       0.79
147            15.533967                 27.50   0.9934  3.26       0.73
148            20.351469                 38.92   0.9962  3.10       0.63
149            22.407884                 64.03   0.9924  3.39       0.60

     alcohol  quality
0       8.64        7
1      10.03        8
2       9.23        8
3      14.07        9
4      11.49        8
..       …        …
145    10.18        8
146    11.11        8
147    10.95        9
148    11.67        8
149    12.04        9

[150 rows x 12 columns]
```

[149]:
```
t_value, p_value = t_test_mean(sample_first_150_anggur, "sulphates", 0.65, 2)
```

Computed Average : 0.6058666666666668

Computed Standard Derivation : 0.10886964477104122

T-Value : -4.964843393315906

P-Value : 1.8590151213970785e-06

Step 6 : Make a decision and conclusion

Reject H0 and conclude that the mean Sulphates value is not equal to 0.65 but less than 0.65 because the T-Value is far less than the critical value (t < -1.976) and the P-Value is also far less than 0.05 (level of significance)

5.1.4 4. Is the mean value of `total sulfur dioxide` below 35?

Step 1 : Specifying the null hypothesis (**H0**)

H0 : = 35

Step 2 : Specifying the alternative hypothesis (**H1**)

H1 : < 35 (one-tailed test)

Step 3 : Decide the level of significance ( )

= 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = T-Test → Variance of population is unknown Critical area = t < t0.05, 999

[150]:
```
t_critical_value = calculate_t_critical_value(0.05, 999)

display(Markdown(f"Critical Value = {t_critical_value}"))
display(Markdown(f"So, the t-value must be less than {t_critical_value} to␣
 ↪reject the null hypothesis"))
```

Critical Value = -1.6463803454275356

So, the t-value must be less than -1.6463803454275356 to reject the null hypothesis

Step 5 : Calculate T-Test and P-Value from Data Sample

The formula of t-value:

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

[151]:
```
t_value, p_value = t_test_mean(df, "total sulfur dioxide", 35, 1)
```

Computed Average : 40.290150000000075

Computed Standard Derivation : 9.965767376218295

T-Value : 16.786387372296968

P-Value : 1.0

Step 6 : Make a decision and conclusion

Do not reject H0 and cannot conclude that the mean total sulfur dioxide is less than 35 because the T-Value is not less than the critical value (t > -1.6464) and the P-Value is also not less than 0.05 (level of significance)

5.1.5 5. Is the proportion of the total sulfur dioxide that is more than 40, not the same as 50%?

Step 1 : Specifying the null hypothesis (**H0**)

H0 : p = 0.5

Step 2 : Specifying the alternative hypothesis (**H1**)

H1 : p 0.5

Step 3 : Decide the level of significance ( )

 = 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = Z-Test → Proportion, not mean Critical area = Z < Z0.025 and Z > Z0.975

```
[152]: z_critical_value = abs(scipy.stats.norm.ppf(0.05 / 2))

       display(Markdown(f"Critical Value = \xB1 {z_critical_value}"))
       display(Markdown(f"So, the t-value must be greater than {z_critical_value} or␣
        ↪less than - {z_critical_value} to reject the null hypothesis"))
```

Critical Value = ± 1.9599639845400545

So, the t-value must be greater than 1.9599639845400545 or less than - 1.9599639845400545 to reject the null hypothesis

Step 5 : Calculate Z-Test and P-Value from Data Sample

The formula of z-value:

$$Z = \frac{\hat{p} - p_0}{\sqrt{\frac{p_0(1-p_0)}{n}}}$$

```
[153]: tsd_more_than_40 = df[df["total sulfur dioxide"] > 40]
       tsd_more_than_40
```

```
[153]:     fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
       0            5.90            0.4451       0.1813        2.049401   0.070574
       3            5.39            0.4201       0.3131        3.371815   0.072755
       4            6.51            0.5675       0.1940        4.404723   0.066379
```

```
5             9.18            0.3332       0.2476        2.633491   0.082304
6             4.29            0.4997       0.2932        3.781844   0.079649
..             …               …           …              …        …
992           5.62            0.4597       0.2868        2.314833   0.041796
993           4.88            0.5899       0.2721        3.004077   0.095569
995           7.96            0.6046       0.2662        1.592048   0.057555
997           6.11            0.4841       0.3720        2.377267   0.042806
998           7.76            0.3590       0.3208        4.294486   0.098276

     free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0              16.593818                 42.27   0.9982  3.27       0.71
3              18.212300                 41.97   0.9945  3.34       0.55
4               9.360591                 46.27   0.9925  3.27       0.45
5              12.232170                 51.05   0.9965  3.40       0.63
6              10.152389                 44.26   0.9969  3.47       0.44
..                   …                     …      …    …         …
992            21.445849                 41.54   0.9980  3.27       0.71
993            22.288864                 45.74   0.9947  3.23       0.79
995            14.892445                 44.61   0.9975  3.35       0.54
997            21.624585                 48.75   0.9928  3.23       0.55
998            12.746186                 44.53   0.9952  3.30       0.66

     alcohol  quality
0       8.64        7
3      14.07        9
4      11.49        8
5      10.82        8
6       9.76        7
..       …       …
992    11.23        8
993     8.57        6
995    10.41        8
997     9.94        7
998     9.76        8

[512 rows x 12 columns]
```

[154]:
```
z_test_proportion(df, tsd_more_than_40, 0.5)
```

n : 1000

x : 512

Z-Value : 0.7589466384404118

P-Value : 0.4478844782641115

Step 6 : Make a decision and conclusion

Don't reject H0 and cannot conclude that the proportion of total sulfur dioxide is not equal to 50 because the Z-Value is not less than the critical value (Z > -1.96) and not greater than the critical value (Z < 1.96)

5.2 Multi-sample Hypothesis Testing

[155]:
```
def compare_two_variance(sample1, sample2, LOS):
    F = sample1.var() / sample2.var()
    p = scipy.stats.f.cdf(F, len(sample1) - 1, len(sample2) - 1)

    if p < LOS:
        return False
    else:
        return True
```

[156]:
```
def two_sample_hypothesis_test(data1, data2, alpha, d0, tail, equal_var=False,␣
↪operator="Not Equal"):
    """
    Perform a hypothesis test using the t-test.

    Parameters:
    data1 (series): The first data to be tested.
    data2 (series): The second data to be tested.
    alpha (float): The level of significance for the test.
    d0 (float): The difference between mean.
    tail (int): The type of test to be performed (1 or 2) tailed.
    operator (string) : Less, Greater, or Not Equal

    Returns:
    results (Series): A Pandas Series containing the test statistic, p-value,␣
↪and conclusion.
    """

    # Calculate the sample variance
    s1 = data1.std()
    s2 = data2.std()
    n1, n2 = len(data1), len(data2)

    # Perform the t-test
    if equal_var:
        # Calculate the degrees of freedom
        dof = n1 + n2 - 2

        # Calculate t-statistic
        sp = sqrt(((n1-1) * (s1**2) + (n2-1) * (s2**2)) / (n1+n2-2))
        t_stat = ((data1.mean() - data2.mean()) - d0)/(sp * sqrt(1/n1 + 1/n2))
    else:
        # Calculate the degrees of freedom
        dof = (s1**2 / n1 + s2**2 / n2)**2 / (((s1**2/n1)**2/(n1-1)) + ((s2**2/
↪n2)**2/(n2-1)))
        t_stat = ((data1.mean() - data2.mean()) - d0)/(sqrt(s1**2/n1 + s2**2/
↪n2))

    if tail == 2:
        p_val = 2 * (1 - scipy.stats.t.cdf(abs(t_stat), dof))
    else:
        p_val = scipy.stats.t.cdf(t_stat, dof)

    # Determine the critical value and the rejection region
    if tail == 2:
        cv = t.ppf(1 - alpha / 2, dof)
        not_crit_region = (-cv, cv)
    else:
        cv = t.ppf(1 - alpha, dof)
        if t_stat < 0:
            not_crit_region = (-float("inf"), -cv)
        else:
            not_crit_region = (cv, float("inf"))

    # Determine the conclusion
    if tail == 2:
        if p_val / 2 < alpha and t_stat not in not_crit_region:
            conclusion = 'Reject the null hypothesis'
        else:
            conclusion = 'Fail to reject the null hypothesis'
    else:
        if operator == "Less":
            if p_val < alpha and t_stat not in not_crit_region:
                conclusion = 'Reject the null hypothesis'
            else:
                conclusion = 'Fail to reject the null hypothesis'
        else: # Greater
            if p_val > alpha and t_stat not in not_crit_region:
                conclusion = 'Reject the null hypothesis'
            else:
                conclusion = 'Fail to reject the null hypothesis'

    # Create a Pandas Series with the results
    results = pd.Series({
        'test statistic': t_stat,
        'p-value': p_val,
        'conclusion': conclusion
    })

    return results
```

[157]:
```
def calculate_f_critical_value(dfnum, dfden, alpha):
    """
    Calculates the F critical value for a given alpha level and degrees of␣
 ↪freedom
    for the numerator and denominator.

    Parameters:
    dfnum (int): Degrees of freedom for the numerator.
    dfden (int): Degrees of freedom for the denominator.
    alpha (float): Alpha level for the test.

    Returns:
    f_crit (float): F critical value.
    """

    f_crit = f.ppf(1 - alpha, dfnum, dfden)
    return f_crit
```

5.2.1 1. Can the mean of `fixed acidity` for the first and second half of the data be considered the same?

Step 1 : Specifying the null hypothesis (**H0**)

H0 : mean of fixed acidity first half = mean of fixed acidity second half

Step 2 : Specifying the alternative hypothesis (**H1**)

H1 : mean of fixed acidity first half   mean of fixed acidity second half

Step 3 : Decide the level of significance ( )

= 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = T-Test → Variance of population is unknown but proofed that both variances are equal with F-Test Critical area = t < t0.025, 998 and t > t0.975, 998

The formula of F-Test:

$$F = \frac{s_1^2}{s_2^2}$$

[158]:
```
eq_var = compare_two_variance(df['fixed acidity'][:len(df)//2], df['fixed␣
 ↪acidity'][len(df)//2:], 0.05)

if (eq_var):
    display(Markdown("Variances are equal."))
else:
    display(Markdown("Variances are not equal."))
```

Variances are equal.

[159]:
```
t_critical_value = abs(calculate_t_critical_value(0.025, 998))

display(Markdown(f"Critical Value = \xB1 {t_critical_value}"))
display(Markdown(f"So, the t-value must be greater than {t_critical_value} or␣
↪less than - {t_critical_value} to reject the null hypothesis"))
```

Critical Value = ± 1.962343846216334

So, the t-value must be greater than 1.962343846216334 or less than - 1.962343846216334 to reject the null hypothesis

Step 5 : Calculate T-Test and P-Value from Data Sample

The formula of t-test two sample with equal variances but unknown:

$$t = \frac{(\bar{x_1} - \bar{x_2}) - d_0}{s_p\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

The formula of s_p :

$$s_p = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}}$$

[160]:
```
two_sample_hypothesis_test(df['fixed acidity'][:len(df)//2], df['fixed␣
↪acidity'][len(df)//2:], 0.05, 0, 2, eq_var)
```

[160]:
```
test statistic                                   0.026041
p-value                                           0.97923
conclusion        Fail to reject the null hypothesis
dtype: object
```

Step 6 : Make a decision and conclusion

Don't reject H0 and cannot conclude that the mean of fixed acidity first half is not equal to the mean of fixed acidity second half because the T-Value is not less than the critical value (T > -1.96) and not greater than the critical value (T < 1.96)

5.2.2 2. Is the difference between the mean of `chlorides` for the first and second half of the data equals to 0.001?

Step 1 : Specifying the null hypothesis (**H0**)

H0 : mean of chlorides first half - mean of chlorides second half = 0.001

Step 2 : Specifying the alternative hypothesis (**H1**)

H1 : mean of chlorides first half - mean of chlorides second half   0.001

Step 3 : Decide the level of significance ( )

= 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = T-Test → Variance of population is unknown but proofed that both variances are equal with F-Test Critical area = t < t0.025, 998 and t > t0.975, 998

The formula of F-Test:

$$F = \frac{s_1^2}{s_2^2}$$

```
[161]: eq_var = compare_two_variance(df['chlorides'][:len(df)//2],␣
        ↪df['chlorides'][len(df)//2:], 0.05)

       if (eq_var):
           display(Markdown("Variances are equal."))
       else:
           display(Markdown("Variances are not equal."))
```

Variances are equal.

```
[162]: t_critical_value = abs(calculate_t_critical_value(0.025, 998))

       display(Markdown(f"Critical Value = \xB1 {t_critical_value}"))
       display(Markdown(f"So, the t-value must be greater than {t_critical_value} or␣
        ↪less than - {t_critical_value} to reject the null hypothesis"))
```

Critical Value = ± 1.962343846216334

So, the t-value must be greater than 1.962343846216334 or less than - 1.962343846216334 to reject the null hypothesis

Step 5 : Calculate T-Test and P-Value from Data Sample

The formula of t-test two sample with equal variances but unknown:

$$t = \frac{(\bar{x_1} - \bar{x_2}) - d_0}{s_p\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

The formula of s_p :

$$s_p = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}}$$

```
[163]: two_sample_hypothesis_test(df['chlorides'][:len(df)//2],␣
        ↪df['chlorides'][len(df)//2:], 0.05, 0.001, 2, eq_var)
```

```
[163]: test statistic                              -0.467317
       p-value                                      0.640375
       conclusion        Fail to reject the null hypothesis
       dtype: object
```

Step 6 : Make a decision and conclusion

Don't reject H0 and cannot conclude that the mean of fixed acidity first half is not equal to the mean of fixed acidity second half because the T-Value is not less than the critical value (T > -1.96) and not greater than the critical value (T < 1.96)

5.2.3 3. Can the mean of volatile acidity and sulphates for the first 25 rows of the data be considered the same?

Step 1 : Specifying the null hypothesis (**H0**)

H0 : mean of volatile acidity first 25 rows = mean of sulphates first 25 rows

Step 2 : Specifying the alternative hypothesis (**H1**)

H1 : mean of volatile acidity first 25 rows   mean of sulphates first 25 rows

Step 3 : Decide the level of significance ( )

  = 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = T-Test → Variance of population is unknown and proofed that both variances are equal with F-Test Critical area = t < t0.025, 48 and t > t0.975, 48

The formula of F-Test:

$$F = \frac{s_1^2}{s_2^2}$$

```
[164]: eq_var = compare_two_variance(df['volatile acidity'][:25], df['sulphates'][:
        ↪25], 0.05)

       if (eq_var):
           display(Markdown("Variances are equal."))
       else:
           display(Markdown("Variances are not equal."))
```

Variances are equal.

```
[165]: s1 = df['volatile acidity'][:25].std()
       s2 = df['sulphates'][:25].std()
       n1, n2 = 25, 25
       dof = n1 + n2 - 2
       print("Degree of freedom =", dof)
```

```
t_critical_value = abs(calculate_t_critical_value(0.025, dof))

display(Markdown(f"Critical Value = \xB1 {t_critical_value}"))
display(Markdown(f"So, the t-value must be greater than {t_critical_value} or␣
↪less than - {t_critical_value} to reject the null hypothesis"))
```

```
Degree of freedom = 48
```

Critical Value = ± 2.010634754696446

So, the t-value must be greater than 2.010634754696446 or less than - 2.010634754696446 to reject the null hypothesis

Step 5 : Calculate T-Test and P-Value from Data Sample

The formula of t-test two sample with equal variances but unknown:

$$t = \frac{(\bar{x_1} - \bar{x_2}) - d_0}{s_p\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

The formula of s_p :

$$s_p = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}}$$

[166]:
```
two_sample_hypothesis_test(df['volatile acidity'][:25], df['sulphates'][:25], 0.
↪05, 0, 2, eq_var)
```

[166]:
```
test statistic                      -2.637482
p-value                              0.011223
conclusion        Reject the null hypothesis
dtype: object
```

Step 6 : Make a decision and conclusion

Reject H0 and conclude that the mean of volatile acidity first 25 rows is not equal to the mean of sulphates first 25 rows because the T-Value is less than the critical value (T < -2.016) and the P-Value is also less than the level of significance.

5.2.4 4. Can the variance of residual sugar for the first and second half of the data be considered the same?

Step 1 : Specifying the null hypothesis (**H0**)

H0 : ² First half = ² Second half

Step 2 : Specifying the alternative hypothesis (**H1**)

H1 : ² First half ² Second half

Step 3 : Decide the level of significance ( )

= 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = F-Test → Compare the ratio of the variances of the two samples to a critical value that depends on the degrees of freedom of the two samples.

Critical area = F < F0.05(499, 499) and F > F0.95(499, 499)

[167]:
```
f_upper_critical_value = abs(calculate_f_critical_value(500, 500, 0.025))
f_lower_critical_value = abs(calculate_f_critical_value(500, 500, 0.975))

display(Markdown(f"Critical Value Upper = \xB1 {f_upper_critical_value}"))
display(Markdown(f"Critical Value Lower = \xB1 {f_lower_critical_value}"))
display(Markdown(f"So, the t-value must be greater than␣
↪{f_upper_critical_value} or less than - {f_lower_critical_value} to reject␣
↪the null hypothesis"))
```

Critical Value Upper = ± 1.1918474156364356

Critical Value Lower = ± 0.8390335766814657

So, the t-value must be greater than 1.1918474156364356 or less than - 0.8390335766814657 to reject the null hypothesis

Step 5 : Calculate F-Test from Sample Data

The formula of F-Test:

$$F = \frac{s_1^2}{s_2^2}$$

[168]:
```
F = df['residual sugar'][:len(df)//2].var() / df['residual sugar'][len(df)//2:].
↪var()
p = scipy.stats.f.sf(F, len(df['residual sugar'][:len(df)//2]) - 1,␣
↪len(df['residual sugar'][len(df)//2:]) - 1)
display(Markdown(f"F-value = {F}"))
display(Markdown(f"P-value = {p}"))
```

F-value = 0.9420041066941619

P-value = 0.7475898202376903

[169]:
```
eq_var = compare_two_variance(df['residual sugar'][:len(df)//2], df['residual␣
↪sugar'][len(df)//2:], 0.05)

if (eq_var):
    display(Markdown("Variances are equal."))
else:
    display(Markdown("Variances are not equal."))
```

Variances are equal.

Step 6 : Make a decision and conclusion

Do not reject H0 and cannot conclude that the variance of the first half of residual sugar is not equal to the variance of the second half of residual sugar, as the F-Value is not less than the critical value (F > -1.16) and not greater than the critical value (F < 1.16)

5.2.5 5. Can the proportion of `alcohol` having a value greater than 7 on the first and second half be considered the same?

Step 1 : Specifying the null hypothesis (**H0**)

H0 : p1 = p2

Step 2 : Specifying the alternative hypothesis (**H1**)

H1 : p1 > p2

Step 3 : Decide the level of significance ( )

= 0.05

Step 4 : Choosing the appropriate statistical test and determine the critical area

Statistical test = Z-Test → Proportion, not mean

Critical area = Z > Z0.95

```
[170]: z_critical_value = scipy.stats.norm.ppf(0.95)

display(Markdown(f"Critical Value = {z_critical_value}"))
display(Markdown(f"So, the Z-Value must be greater than {z_critical_value} to␣
 ↪reject the null hypothesis"))
```

Critical Value = 1.6448536269514722

So, the Z-Value must be greater than 1.6448536269514722 to reject the null hypothesis

Step 5 : Calculate Z-Test and P-Value from Data Sample

The formula of z-test two sample for proportion :

$$z = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\hat{p}(1-\hat{p})\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$$

The formula of $\hat{p}$

$$\hat{p} = \frac{x_1 + x_2}{n_1 + n_2}$$

```
[171]: first_half_alcohol = df[:len(df)//2].loc[df['alcohol'] > 7]
second_half_alcohol = df[len(df)//2:].loc[df['alcohol'] > 7]
```

```
[172]: first_half_alcohol
```

[172]:
```
     fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0             5.90            0.4451       0.1813        2.049401   0.070574
1             8.40            0.5768       0.2099        3.109590   0.101681
2             7.54            0.5918       0.3248        3.673744   0.072416
3             5.39            0.4201       0.3131        3.371815   0.072755
4             6.51            0.5675       0.1940        4.404723   0.066379
..             …                 …            …              …         …
494           5.94            0.4406       0.3149        3.329801   0.097498
496           7.82            0.3760       0.2012        3.743606   0.056809
497           7.17            0.5158       0.1855        2.803720   0.092192
498           7.57            0.5686       0.2382        3.365912   0.041608
499           7.03            0.6953       0.3534        2.328736   0.071467

     free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0              16.593818                 42.27   0.9982  3.27       0.71
1              22.555519                 16.01   0.9960  3.35       0.57
2               9.316866                 35.52   0.9990  3.31       0.64
3              18.212300                 41.97   0.9945  3.34       0.55
4               9.360591                 46.27   0.9925  3.27       0.45
..                   …                    …        …     …          …
494            14.527711                 37.93   0.9933  3.36       0.46
496            18.885695                 47.21   0.9969  3.31       0.55
497            17.949297                 66.99   0.9963  3.08       0.72
498             5.066432                 48.37   0.9979  3.38       0.59
499            13.300705                 49.99   0.9956  3.48       0.52

     alcohol  quality
0       8.64        7
1      10.03        8
2       9.23        8
3      14.07        9
4      11.49        8
..        …       …
494     8.60        7
496    14.56       10
497     9.95        8
498     9.73        8
499     8.37        7

[495 rows x 12 columns]
```

[173]:
```
second_half_alcohol
```

[173]:
```
     fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
500           8.10            0.6758       0.1956        2.684752   0.079678
501           7.28            0.6842       0.3041        3.834531   0.094940
502           6.88            0.4673       0.2766        3.513471   0.074843
```

```
503           8.32            0.4955        0.2549         1.572885   0.091232
504           8.71            0.3536        0.2398         1.705161   0.085907
..             …               …             …               …          …
995           7.96            0.6046        0.2662         1.592048   0.057555
996           8.48            0.4080        0.2227         0.681955   0.051627
997           6.11            0.4841        0.3720         2.377267   0.042806
998           7.76            0.3590        0.3208         4.294486   0.098276
999           5.87            0.5214        0.1883         2.179490   0.052923

     free sulfur dioxide  total sulfur dioxide  density   pH  sulphates  \
500            16.506123                 53.75   0.9972  3.24       0.72
501            14.675257                 45.25   0.9945  3.27       0.60
502            11.967985                 42.31   0.9947  3.35       0.49
503            13.856693                 41.27   0.9971  3.46       0.43
504            23.880561                 25.59   0.9960  3.38       0.59
..                   …                     …       …     …         …
995            14.892445                 44.61   0.9975  3.35       0.54
996            23.548965                 25.83   0.9972  3.41       0.46
997            21.624585                 48.75   0.9928  3.23       0.55
998            12.746186                 44.53   0.9952  3.30       0.66
999            16.203864                 24.37   0.9983  3.29       0.70

     alcohol  quality
500    12.75        9
501    10.24        8
502    11.34        8
503    10.72        8
504    11.09        8
..       …       …
995    10.41        8
996     9.91        8
997     9.94        7
998     9.76        8
999    10.17        7

[495 rows x 12 columns]
```

[174]:
```python
x1 = len(first_half_alcohol)
x2 = len(second_half_alcohol)
n1, n2 = len(df) // 2, len(df) // 2
p1 = x1 / n1
p2 = x2 / n2
p = (x1 + x2) / (n1 + n2)

display(Markdown(f"p1-hat = {p1}"))
display(Markdown(f"p2-hat = {p2}"))
display(Markdown(f"p-hat = {p}"))
```

p1-hat = 0.99

p2-hat = 0.99

p-hat = 0.99

```
[175]: z_value = (p1-p2) / sqrt(p * (1-p) * (1/n1 + 1/n2))
       p_value = scipy.stats.norm.sf(z_value)

       display(Markdown(f"Z-Value = {z_value}"))
       display(Markdown(f"P-Value = {p_value}"))
```

Z-Value = 0.0

P-Value = 0.5

Step 6 : Make a decision and conclusion

Do not reject H0 as the proportion in the first and second half is exactly the same concluded by normal inspection and backed by the Z-test, having the Z-value less than the critical value ($Z < 1.96$) and the P-value less than 0.95 (1 - level of significance).