Proximity Measures On Various Data Sets For Various Purposes

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This assignment is on applying suitable measures of proximity on various tasks on a real data set: wine-quality-white-and-red.csv that you will find under the Files tab. The idea is to get a sense for which measures make sense to apply a'priori on the various tasks, and then assess from experience how well they work.

Key Terminology: In the rest of this assignment, the term numeric predictors refers to all the columns in this dataset except the first one (type) and the last one (quality). The former is not numeric and the latter will be interpreted as the label (outcome).

```
File used: wine-quality-white-and-red.csv
```

Question 1)

For each of the numeric predictors, assess the similarity of the data in that column to the data in the column quality. Do this for each of the following measures: Euclidean distance, dot product, cosine similarity, and Pearson correlation. Report all the results, and rank-order the columns based on the chosen order. So you will get four ranked lists, one per measure.

```
#Importing all the neccessay Libraries.
import pandas as pd
from sklearn.preprocessing import StandardScaler
from scipy.spatial.distance import euclidean
from scipy.spatial.distance import cosine
from scipy.stats import pearsonr
from numpy import dot, linalg
import numpy as np
from numpy.linalg import norm
import matplotlib.pyplot as plt
```

```
# Load the dataset
file_path = 'wine-quality-white-and-red.csv'
wine_data = pd.read_csv(file_path)
```

```
# Dropping non-numeric columns ('type') and isolating 'quality' as label
numeric_predictors = wine_data.columns[1:-1]  # Excludes 'type' and 'quality'
quality = wine_data['quality']
```

```
# Initialize dictionaries to hold similarity measures
euclidean_distances = {}
dot_products = {}
cosine_similarities = {}
pearson_correlations = {}
euclidean_distances_std_data = {}
dot_products_std_data = {}
cosine_similarities_std_data = {}
pearson_correlations_std_data = {}


#Calculating the
for predictor in numeric_predictors:
    predictor_values = wine_data[predictor].values

    # Euclidean Distance
    euclidean_distances[predictor] = euclidean(predictor_values, quality)

    # Dot Product
    dot_products[predictor] = dot(predictor_values, quality)

    # Cosine Similarity
    cosine_similarities[predictor] = dot(predictor_values, quality) / (linalg.norm(predictor_values) * linalg.norm(quality))

    # Pearson Correlation
    pearson_correlations[predictor] = pearsonr(predictor_values, quality)[0]



# Rank order the columns for each measure
ranked_by_euclidean = sorted(euclidean_distances.items(), key=lambda x: x[1])
ranked_by_dot = sorted(dot_products.items(), key=lambda x: x[1], reverse=True)
ranked_by_cosine = sorted(cosine_similarities.items(), key=lambda x: x[1], reverse=True)
ranked_by_pearson = sorted(pearson_correlations.items(), key=lambda x: x[1], reverse=True)




# Display the ranked predictors for NON standardized data.
print("Display the ranked Numeric_predictors for NON Standardized Data")
print("\neuclidean Distance Ranked:")
for rank, (predictor, distance) in enumerate(ranked_by_euclidean, start=1):
    print(f"{rank}. {predictor}: {distance}")

print("\nDot Product Ranked:")
for rank, (predictor, value) in enumerate(ranked_by_dot, start=1):
    print(f"{rank}. {predictor}: {value}")

print("\nCosine Similarity Ranked:")
for rank, (predictor, value) in enumerate(ranked_by_cosine, start=1):
    print(f"{rank}. {predictor}: {value}")

print("\nPearson Correlation Ranked:")
for rank, (predictor, value) in enumerate(ranked_by_pearson, start=1):
    print(f"{rank}. {predictor}: {value}")
```

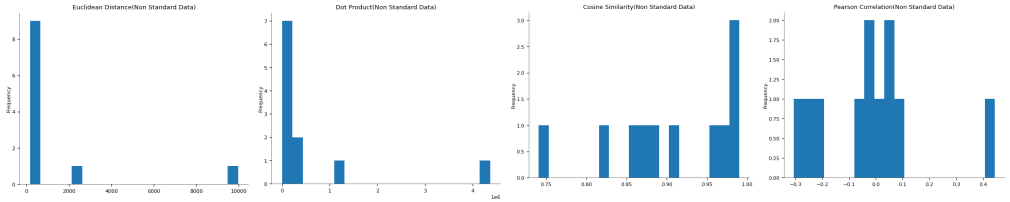
```
Display the ranked Numeric_predictors for NON Standardized Data

euclidean Distance Ranked:
1. fixed acidity: 172.27557139652737
2. pH: 221.3630542796155
3. alcohol: 387.4047948561723
4. residual sugar: 393.58882733126455
5. density: 395.14008968328693
6. sulphates: 432.02617316546923
7. volatile acidity: 447.93061237205035
8. citric acid: 448.8494620694114
9. chlorides: 469.86353989855394
10. free sulfur dioxide: 2450.770389081768
11. total sulfur dioxide: 9964.569195404285

Dot Product Ranked:
1. total sulfur dioxide: 4362107.0
2. free sulfur dioxide: 1159502.5
3. alcohol: 399617.2499998661
4. fixed acidity: 272188.65
5. residual sugar: 204767.1
6. pH: 121683.55999999997
7. density: 37596.31936499998
8. sulphates: 20115.489999999998
9. volatile acidity: 12591.909999999998
10. citric acid: 12115.480000000001
11. chlorides: 2078.312999999999

Cosine Similarity Ranked:
1. alcohol: 0.990045581508263
2. density: 0.9887842671175675
3. pH: 0.987838476657684
4. fixed acidity: 0.9713269124401577
5. sulphates: 0.9538218953722827
6. citric acid: 0.90504743858173
7. total sulfur dioxide: 0.8859483748510381
8. volatile acidity: 0.8727154397688945
9. free sulfur dioxide: 0.8590614918924949
10. chlorides: 0.8227545382511036
11. residual sugar: 0.7409960777893494

Pearson Correlation Ranked:
1. alcohol: 0.4443185200075175
2. citric acid: 0.08553171718367847
3. free sulfur dioxide: 0.055463058616632664
4. sulphates: 0.038485445876514444
5. pH: 0.019505703714435847
6. residual sugar: -0.03698048458576943
7. total sulfur dioxide: -0.041385453855608816
8. fixed acidity: -0.07674320790961991
9. chlorides: -0.20066550043510203
10. volatile acidity: -0.2656994776114678
11. density: -0.3058579060694142
```

MERGING THE LIST TOGETHER

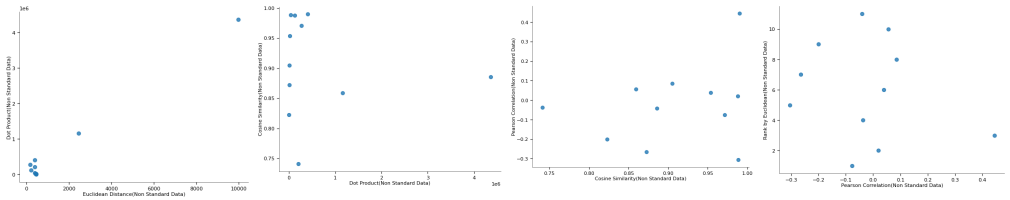
```
# Preparing data for DataFrame
euclidean_ranks = {k: v + 1 for v, (k, _) in enumerate(ranked_by_euclidean)}
dot_ranks = {k: v + 1 for v, (k, _) in enumerate(ranked_by_dot)}
cosine_ranks = {k: v + 1 for v, (k, _) in enumerate(ranked_by_cosine)}
pearson_ranks = {k: v + 1 for v, (k, _) in enumerate(ranked_by_pearson)}

# Create a DataFrame to report the results correctly
similarity_df = pd.DataFrame({
    'Euclidean Distance(Non Standard Data)': euclidean_distances,
    'Dot Product(Non Standard Data)': dot_products,
    'Cosine Similarity(Non Standard Data)': cosine_similarities,
    'Pearson Correlation(Non Standard Data)': pearson_correlations,
    'Rank by Euclidean(Non Standard Data)': [euclidean_ranks[predictor] for predictor in numeric_predictors],
    'Rank by Dot Product(Non Standard Data)': [dot_ranks[predictor] for predictor in numeric_predictors],
    'Rank by Cosine(Non Standard Data)': [cosine_ranks[predictor] for predictor in numeric_predictors],
    'Rank by Pearson(Non Standard Data)': [pearson_ranks[predictor] for predictor in numeric_predictors]
}, index=numeric_predictors)

similarity_df
```

	Euclidean Distance(Non Standard Data)	Dot Product(Non Standard Data)	Cosine Similarity(Non Standard Data)	Pearson Correlation(Non Standard Data)	Rank by Euclidean(Non Standard Data)	Rank by Dot Product(Non Standard Data)	Rank by Cosine(Non Standard Data)	Rank by Pearson(Non Standard Data)
fixed acidity	172.275571	2.721887e+05	0.971327	-0.076743	1	4	4	8
volatile acidity	447.930612	1.259191e+04	0.872715	-0.265699	7	9	8	10
citric acid	448.849462	1.211548e+04	0.905047	0.085532	8	10	6	2
residual sugar	393.588827	2.047671e+05	0.740996	-0.036980	4	5	11	6
chlorides	469.863540	2.078313e+03	0.822755	-0.200666	9	11	10	9
free sulfur dioxide	2450.770389	1.159502e+06	0.859061	0.055463	10	2	9	3
total sulfur dioxide	9964.569195	4.362107e+06	0.885948	-0.041385	11	1	7	7
density	395.140090	3.759632e+04	0.988784	-0.305858	5	7	2	11
pH	221.363054	1.216836e+05	0.987838	0.019506	2	6	3	5
sulphates	432.026173	2.011549e+04	0.953822	0.038485	6	8	5	4
alcohol	387.404795	3.996172e+05	0.990046	0.444319	3	3	1	1

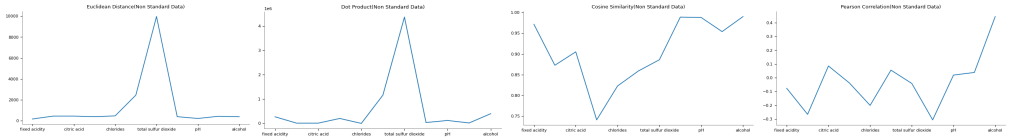
Distributions



2-d distributions



Values



STANDARDIZING/NORMALIZING THE DATASET

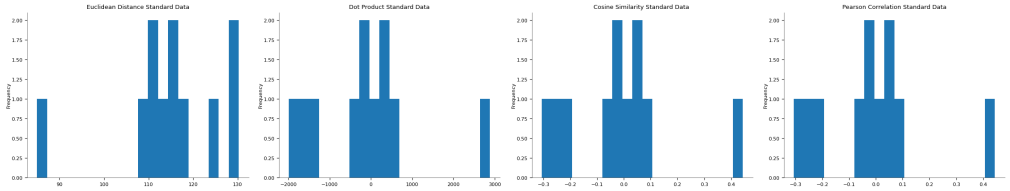
```
# Standardize the numeric predictors and the target 'quality'
scaler = StandardScaler()
scaled_features = scaler.fit_transform(wine_data[numeric_predictors])
target_quality_scaled = scaler.fit_transform(quality.values.reshape(-1, 1)).flatten()


# Calculate the similarity measures for each numeric predictor
for index, predictor in enumerate(numeric_predictors):
    # Retrieve the standardized values for the current predictor
    standardized_predictor = scaled_features[:, index]

    # Calculate the Euclidean distance for the standardized data
    euclidean_distances_std_data[predictor] = euclidean(standardized_predictor, target_quality_scaled)

    # Calculate the dot product for the standardized data
    dot_products_std_data[predictor] = dot(standardized_predictor, target_quality_scaled)

    # Calculate the cosine similarity for the standardized data
    cosine_similarity = dot_products_std_data[predictor] / (linalg.norm(standardized_predictor) * linalg.norm(target_quality_scaled))
    cosine_similarities_std_data[predictor] = cosine_similarity

    # Calculate the Pearson correlation for the original (non-standardized) data
    pearson_correlations_std_data[predictor] = pearsonr(wine_data[predictor], quality)[0]


# Rank order the columns for each measure using the standardized data
ranked_by_euclidean_std = sorted(euclidean_distances_std_data, key=euclidean_distances_std_data.get)
ranked_by_dot_std = sorted(dot_products_std_data, key=dot_products_std_data.get, reverse=True)
ranked_by_cosine_std = sorted(cosine_similarities_std_data, key=cosine_similarities_std_data.get, reverse=True)
ranked_by_pearson_std = sorted(pearson_correlations_std_data, key=pearson_correlations_std_data.get, reverse=True)




print("Display the ranked Numeric_predictors for Standardized Data")
print("\neuclidean Distance Ranked:")
for rank, predictor in enumerate(ranked_by_euclidean_std, start=1):
    distance = euclidean_distances_std_data[predictor]  # Get the distance from the dictionary
    print(f"{rank}. {predictor}: {distance}")

print("\nDot Product Ranked:")
for rank, predictor in enumerate(ranked_by_dot_std, start=1):
    value = dot_products_std_data[predictor]  # Get the dot product from the dictionary
    print(f"{rank}. {predictor}: {value}")

print("\nCosine Similarity Ranked:")
for rank, predictor in enumerate(ranked_by_cosine_std, start=1):
    value = cosine_similarities_std_data[predictor]  # Get the cosine similarity from the dictionary
    print(f"{rank}. {predictor}: {value}")

print("\nPearson Correlation Ranked:")
for rank, predictor in enumerate(ranked_by_pearson_std, start=1):
    value = pearson_correlations_std_data[predictor]  # Get the Pearson correlation from the dictionary
    print(f"{rank}. {predictor}: {value}")
```

```
Display the ranked Numeric_predictors for Standardized Data

euclidean Distance Ranked:
1. alcohol: 84.97367328191899
2. citric acid: 109.007343178867
3. free sulfur dioxide: 110.7849855185055
4. sulphates: 111.77620550135244
5. pH: 112.87401333316106
6. residual sugar: 116.07981916210 71
7. total sulfur dioxide: 116.32610449679719
8. fixed acidity: 118.28440828603573
9. chlorides: 124.9057545217742
10. volatile acidity: 128.2439043856799
11. density: 130.26249510686478

Dot Product Ranked:
1. alcohol: 2886.737424488841
2. citric acid: 555.6995665423591
3. free sulfur dioxide: 360.34349183226243
4. sulphates: 250.03994185971453
5. pH: 126.72855703268974
6. residual sugar: -240.26220835374366
7. total sulfur dioxide: -268.8812936998904
8. fixed acidity: -498.6006217888004
9. chlorides: -1303.7237563268577
10. volatile acidity: -1726.249506041707
11. density: -1987.158815732984

Cosine Similarity Ranked:
1. alcohol: 0.44431852000751876
2. citric acid: 0.08553171718367868
3. free sulfur dioxide: 0.05546305861663279
4. sulphates: 0.038485445876514555
5. pH: 0.01950570371443588
6. residual sugar: -0.03698048458576945
7. total sulfur dioxide: -0.04138545385560891
8. fixed acidity: -0.07674320790962008
9. chlorides: -0.2006655004351025
10. volatile acidity: -0.26569947761146845
11. density: -0.3058579060694149

Pearson Correlation Ranked:
1. alcohol: 0.4443185200075175
2. citric acid: 0.08553171718367847
3. free sulfur dioxide: 0.055463058616632664
4. sulphates: 0.038485445876514444
5. pH: 0.019505703714435847
6. residual sugar: -0.03698048458576943
7. total sulfur dioxide: -0.041385453855608816
8. fixed acidity: -0.07674320790961991
9. chlorides: -0.20066550043510203
10. volatile acidity: -0.2656994776114678
11. density: -0.3058579060694142
```

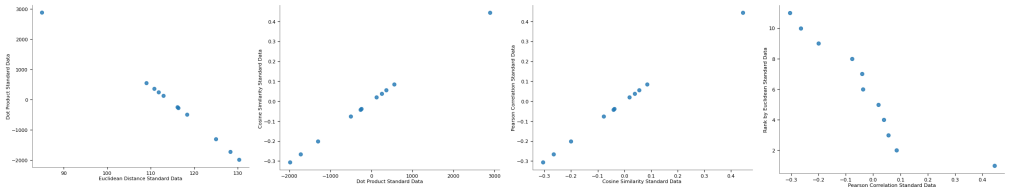
```
# Create a DataFrame to report the results correctly using the standardized data
similarity_df_std = pd.DataFrame({
    'Euclidean Distance Standard Data': {predictor: euclidean_distances_std_data[predictor] for predictor in numeric_predictors},
    'Dot Product Standard Data': {predictor: dot_products_std_data[predictor] for predictor in numeric_predictors},
    'Cosine Similarity Standard Data ': {predictor: cosine_similarities_std_data[predictor] for predictor in numeric_predictors},
    'Pearson Correlation Standard Data': {predictor: pearson_correlations_std_data[predictor] for predictor in numeric_predictors},
    'Rank by Euclidean Standard Data': [ranked_by_euclidean_std.index(predictor) + 1 for predictor in numeric_predictors],
    'Rank by Dot Product Standard Data': [ranked_by_dot_std.index(predictor) + 1 for predictor in numeric_predictors],
    'Rank by Cosine Standard Data': [ranked_by_cosine_std.index(predictor) + 1 for predictor in numeric_predictors],
    'Rank by Pearson Standard Data': [ranked_by_pearson_std.index(predictor) + 1 for predictor in numeric_predictors]
}, index=numeric_predictors)

similarity_df_std
```

	Euclidean Distance Standard Data	Dot Product Standard Data	Cosine Similarity Standard Data	Pearson Correlation Standard Data	Rank by Euclidean Standard Data	Rank by Dot Product Standard Data	Rank by Cosine Standard Data	Rank by Pearson Standard Data
fixed acidity	118.284408	-498.600622	-0.076743	-0.076743	8	8	8	8
volatile acidity	128.243904	-1726.249506	-0.265699	-0.265699	10	10	10	10
citric acid	109.007343	555.699567	0.085532	0.085532	2	2	2	2
residual sugar	116.079819	-240.262208	-0.036980	-0.036980	6	6	6	6
chlorides	124.905755	-1303.723756	-0.200666	-0.200666	9	9	9	9
free sulfur dioxide	110.784986	360.343492	0.055463	0.055463	3	3	3	3
total sulfur dioxide	116.326104	-268.881294	-0.041385	-0.041385	7	7	7	7
density	130.262495	-1987.158816	-0.305858	-0.305858	11	11	11	11
pH	112.874013	126.728557	0.019506	0.019506	5	5	5	5
sulphates	111.776206	250.039942	0.038485	0.038485	4	4	4	4
alcohol	84.973673	2886.737424	0.444319	0.444319	1	1	1	1

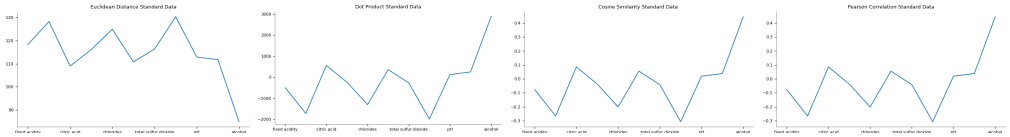
Distributions



2-d distributions



Values

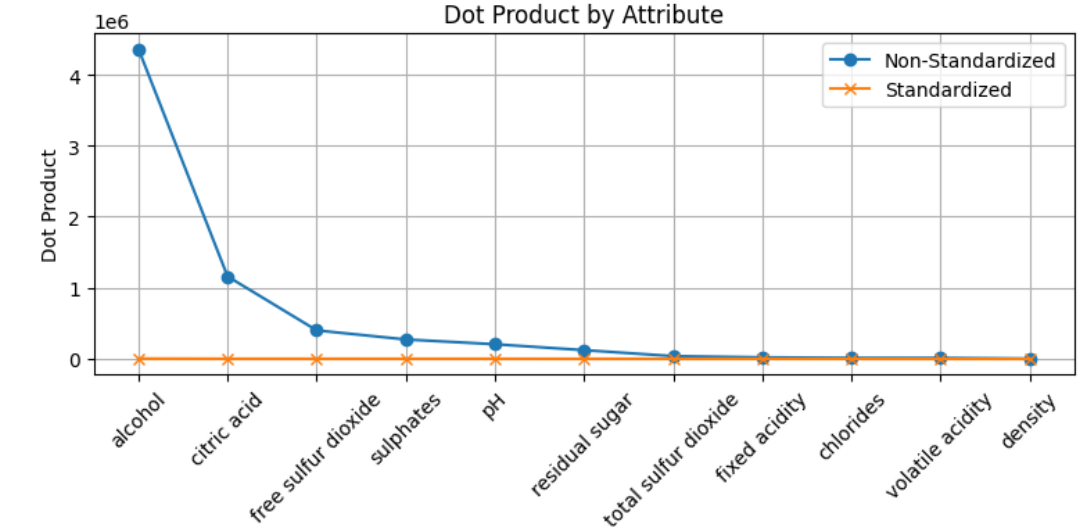


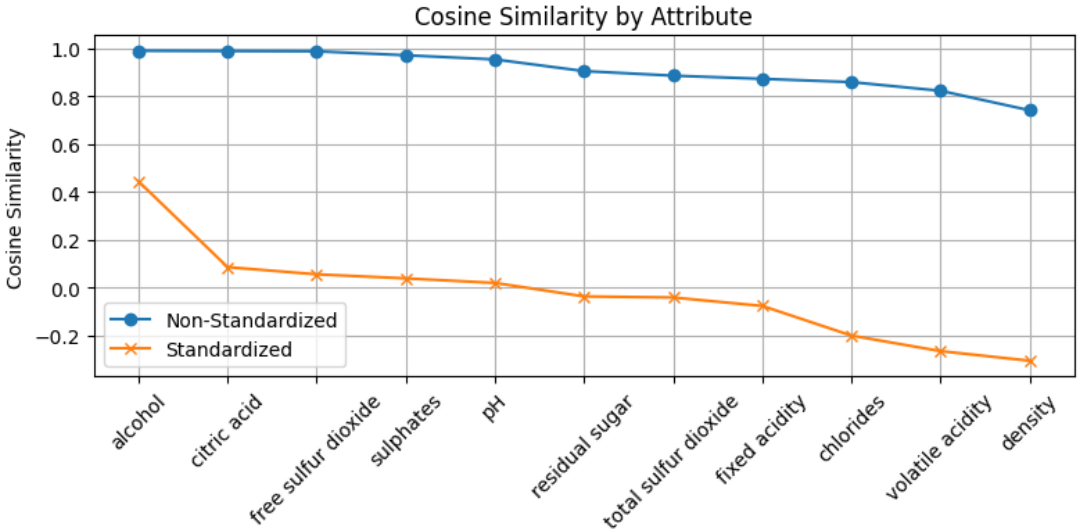
Question 2)

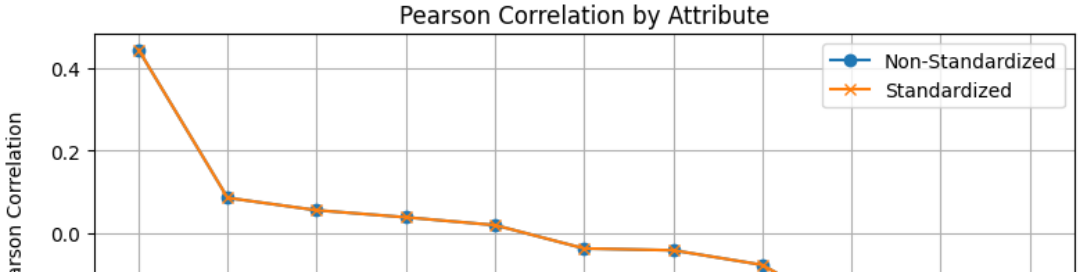
Discuss these results. Are certain predictors more associated with the outcome than others, no matter which measure you use? Do the measures give conflicting results in some cases? When appropriate, explain their differing behaviors.

```
import matplotlib.pyplot as plt

# Metrics and their corresponding values
metrics = ["Dot Product", "Cosine Similarity", "Pearson Correlation"]
non_standardized_values = [
    [4362107.0, 1159502.5, 399617.2499998661, 272188.65, 204767.1, 121683.55999999997, 37596.31936499998, 20115.489999999998, 12591.909999999998, 12115.480000000001, 2078.31299999
    [0.990045581508263, 0.9887842671175675, 0.987838476657684, 0.9713269124401577, 0.9538218953722827, 0.90504743858173, 0.8859483748510381, 0.8727154397688945, 0.8590614918924949
    [0.4443185200075175, 0.08553171718367847, 0.055463058616632664, 0.038485445876514444, 0.019505703714435847, -0.03698048458576943, -0.04138545385560891, -0.07674320790961991, -
]
standardized_values = [
    [2886.737424488841, 555.6995665423591, 360.34349183226243, 250.03994185971453, 126.72855703268974, -240.26220835374366, -268.8812936998904, -498.6006217888004, -1303.723756326
    [0.44431852000751876, 0.08553171718367868, 0.05546305861663279, 0.038485445876514555, 0.01950570371443588, -0.03698048458576945, -0.04138545385560891, -0.07674320790962008, -0
    [0.4443185200075175, 0.08553171718367847, 0.055463058616632664, 0.038485445876514444, 0.019505703714435847, -0.03698048458576943, -0.04138545385560891, -0.07674320790961991, -
]

# Attributes for the plots
attributes = [
    "alcohol", "citric acid", "free sulfur dioxide", "sulphates", "pH",
    "residual sugar", "total sulfur dioxide", "fixed acidity", "chlorides",
    "volatile acidity", "density"
]

# Euclidean distances
euclidean_distance_standardized = [
    84.97367328191899, 109.007343178867, 110.7849855185055, 111.77620550135244,
    112.87401333316106, 116.0798191621071, 116.32610449679719, 118.28440828603573,
    124.9057545217742, 128.2439043856799, 130.26249510686478
]
euclidean_distance_non_standardized = [
    172.27557139652737, 221.3630542796155, 387.4047948561723, 393.58882733126455,
    395.14008968328693, 432.02617316546923, 447.93061237205035, 448.8494620694114,
    469.86353989855394, 2450.770389081768, 9964.569195404285
]

fig, axes = plt.subplots(3, 1, figsize=(8, 12))
for i, metric in enumerate(metrics):
    ax = axes[i]
    ax.plot(attributes, non_standardized_values[i], label='Non-Standardized', marker='o')
    ax.plot(attributes, standardized_values[i], label='Standardized', marker='x')
    ax.set_xticks(range(len(attributes)))
    ax.set_xticklabels(attributes, rotation=45)
    ax.set_ylabel(metric)
    ax.set_title(f'{metric} by Attribute')
    ax.legend()
    ax.grid(True)

plt.tight_layout()
plt.show()

# Plotting Euclidean distance by attribute with a reduced figure size
plt.figure(figsize=(8, 4))
plt.plot(attributes, euclidean_distance_standardized, label='Standardized Data', marker='o')
plt.plot(attributes, euclidean_distance_non_standardized, label='Non-Standardized Data', marker='x')
plt.xticks(range(len(attributes)), attributes, rotation=45)
plt.ylabel('Euclidean Distance')
plt.title('Euclidean Distance by Attribute')
```

```
    plt.legend()
    plt.tight_layout()
    plt.grid(True)
    plt.show()
```


Dot Product by Attribute
1e6
Dot Product
Non-Standardized
Standardized
alcohol
citric acid
free sulfur dioxide
sulphates
pH
residual sugar
total sulfur dioxide
fixed acidity
chlorides
volatile acidity
density


Cosine Similarity by Attribute
Cosine Similarity
Non-Standardized
Standardized
alcohol
citric acid
free sulfur dioxide
sulphates
pH
residual sugar
total sulfur dioxide
fixed acidity
chlorides
volatile acidity
density


Pearson Correlation by Attribute
Non-Standardized
Standardized

1) **Euclidean Distance**: Measures the absolute distance between the quality scores and predictor values. Lower distances suggest that the predictor's values are, on average, closer to the quality scores, potentially indicating relevance.

NON STANDARDIZED DATA RESULTS:

- Fixed Acidity, pH, and Alcohol are closely associated with wine quality, as indicated by their lower Euclidean distances.
- Free Sulfur Dioxide and Total Sulfur Dioxide show the least association with wine quality using Euclidean Distance.
- The analysis was conducted without standardizing the data, which may affect the association's perception.

Conclusion: Lower Euclidean distances for Fixed Acidity, pH, and Alcohol suggest these predictors have a closer numeric relationship with wine quality, possibly indicating their significant impact on wine quality.

STANDARDIZED DATA RESULTS:

- Alcohol is identified as the most associated predictor with wine quality across all measures, followed by pH, indicating a positive relationship.
- Density and Volatile Acidity show negative associations with wine quality, suggesting that higher values of these predictors lead to lower quality ratings.

Conclusion: Standardization highlights Alcohol and pH as key predictors of wine quality, underlining their positive impact on quality ratings.

---

2) **Dot Product**: Reflects the sum of products of corresponding entries in the two sequences of numbers (predictor values and quality scores). Higher values can indicate a stronger overall association.

NON STANDARDIZED DATA RESULTS:

- Total Sulfur Dioxide and Free Sulfur Dioxide are strongly associated with wine quality, followed by Alcohol.
- Chlorides and Citric Acid are the least likely to be associated with wine quality.
- The analysis was conducted without standardizing the data, which may affect the association's perception.

Conclusion: The strong association of Total and Free Sulfur Dioxide with wine quality suggests their significant role in wine composition and quality perception.

STANDARDIZED DATA RESULTS:

- Alcohol stands out as the most associated predictor with wine quality across all measures, with Citric Acid also showing a positive association after Alcohol.
- Density and Volatile Acidity are negatively associated with wine quality, suggesting that higher values of these predictors lead to lower quality ratings.

Conclusion: Alcohol's dominant role in affecting wine quality is evident across data treatments, emphasizing its importance in quality determination.

---

3) **Cosine Similarity**: Measures the cosine of the angle between two vectors of an inner product space, here representing the predictor and quality scores. It provides insight into the orientation similarity regardless of their magnitude, potentially offering a more normalized perspective even without standard data.

NON STANDARDIZED DATA RESULTS:

- Alcohol, along with Total Sulfur Dioxide and Free Sulfur Dioxide, are strongly associated with wine quality.
- Chlorides and Citric Acid are the least likely to be associated with wine quality.
- The analysis was conducted without standardizing the data, which may affect the association's perception.

Conclusion: Cosine Similarity reinforces the significant association of Alcohol and Sulfur Dioxide compounds with wine quality, highlighting the pattern similarity between these predictors and quality.

STANDARDIZED DATA RESULTS:

- Alcohol emerges as the most associated predictor with wine quality across all measures, with Citric Acid also showing a positive association after Alcohol.
- Density and Volatile Acidity are incorrectly mentioned as positively associated in the previous text but should be understood as negatively associated, reflecting their detrimental impact on quality ratings when values are higher.

Conclusion: The consistent high ranking of Alcohol across both standardized and non-standardized analyses underscores its pivotal role in defining wine quality.

---

4) **Pearson Correlation**: Indicates the linear correlation between the predictors and quality. Values close to 1 or -1 suggest a strong positive or negative linear relationship, respectively. This measure is inherently scale-invariant, making it useful for comparison without standardizing data.

NON STANDARDIZED DATA RESULTS:

- Alcohol is the most significant predictor affecting wine quality across all measures, with Density also showing a positive association.
- Density and Volatile Acidity are negatively associated with wine quality, indicating that their higher values lead to lower quality ratings.
- The standardized and non-standardized results show consistent trends, indicating a strong correlation between alcohol content and wine quality.

Conclusion: The persistent positive correlation of Alcohol with quality across analyses highlights its critical influence on wine quality perceptions.

STANDARDIZED DATA RESULTS:

- Alcohol is confirmed as the most significant predictor of wine quality across all measures, with Density showing a positive association after Alcohol.
- Density and Volatile Acidity are negatively associated with wine quality, reinforcing the trend that higher values of these predictors result in lower quality ratings.

Conclusion: Alcohol's preeminent influence on wine quality is unequivocal, with standardized data further affirming its role alongside revealing Density's nuanced relationship with quality.

Question 3)

Repeat the process in question 1 except that assess a numeric predictor's association to the column type rather than to the column quality. For this, choose two measures that you think a'priori are the best suited to this task. As in question 1, report all the results and rank-order the predictor columns for each measure. You will get two ranked lists.

```
# Encode 'type' column: 'white' as 1, 'red' as 0
wine_data['type_numeric'] = wine_data['type'].apply(lambda x: 1 if x == 'white' else 0)

# Identify numeric predictors, excluding 'type', 'quality', and now 'type_numeric'
numeric_predictors = wine_data.columns[1:-2]  # Excludes 'type', 'quality', and 'type_numeric'
```

```
pearson_correlations_std = {}
cosine_similarities_std = {}
pearson_correlations_non_std = {}
cosine_similarities_non_std = {}
```

```
# Calculate Pearson Correlation and Cosine Similarity without standardizing the data

for predictor in numeric_predictors:
    predictor_values = wine_data[predictor]
    type_numeric_values = wine_data['type_numeric']

    pearson_correlations_non_std[predictor] = pearsonr(predictor_values, type_numeric_values)[0]
    cosine_similarities_non_std[predictor] = dot(predictor_values, type_numeric_values) / \
                                             (norm(predictor_values) * norm(type_numeric_values))
```

STANDARDISING THE DATA

```
scaler = StandardScaler()
scaled_numeric_predictors = scaler.fit_transform(wine_data[numeric_predictors])
scaled_type_numeric = scaler.fit_transform(wine_data[['type_numeric']]).flatten()
```

```
for index, predictor in enumerate(numeric_predictors):
    scaled_predictor_values = scaled_numeric_predictors[:, index]

    pearson_correlations_std[predictor] = pearsonr(scaled_predictor_values, scaled_type_numeric)[0]
    cosine_similarities_std[predictor] = dot(scaled_predictor_values, scaled_type_numeric) / \
                                         (linalg.norm(scaled_predictor_values) * linalg.norm(scaled_type_numeric))


# Rank order the predictors based on Pearson correlation and Cosine similarity
pearson_rank_non_std = sorted(pearson_correlations_non_std.items(), key=lambda x: x[1], reverse=True)
cosine_rank_non_std = sorted(cosine_similarities_non_std.items(), key=lambda x: x[1], reverse=True)
pearson_rank_std = sorted(pearson_correlations_std.items(), key=lambda x: x[1], reverse=True)
cosine_rank_std = sorted(cosine_similarities_std.items(), key=lambda x: x[1], reverse=True)

# Displaying rankings for non-standardized data
print("Pearson Correlation Ranked (Non-Standardized):")
for rank, (predictor, value) in enumerate(pearson_rank_non_std, start=1):
    print(f"{rank}. {predictor}: {value}")

print("\nCosine Similarity Ranked (Non-Standardized):")
for rank, (predictor, value) in enumerate(cosine_rank_non_std, start=1):
    print(f"{rank}. {predictor}: {value}")

# Assuming you also want to display rankings for standardized data
print("\nPearson Correlation Ranked (Standardized):")
for rank, (predictor, value) in enumerate(pearson_rank_std, start=1):
    print(f"{rank}. {predictor}: {value}")

print("\nCosine Similarity Ranked (Standardized):")
for rank, (predictor, value) in enumerate(cosine_rank_std, start=1):
    print(f"{rank}. {predictor}: {value}")
```

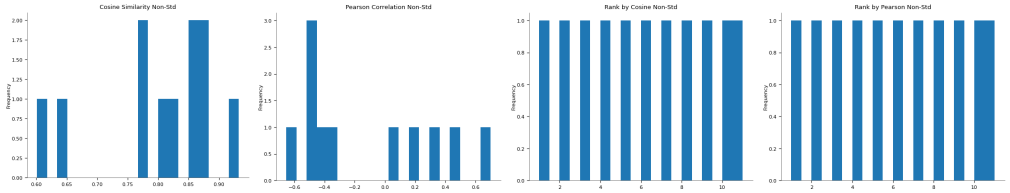
```
Pearson Correlation Ranked (Non-Standardized):
1. total sulfur dioxide: 0.7003571552968023
2. free sulfur dioxide: 0.4716436649016788
3. residual sugar: 0.3488210078111932
4. citric acid: 0.18739650075043568
5. alcohol: 0.03296955068460626
6. pH: -0.3291286507259996
7. density: -0.3906453183542227
8. fixed acidity: -0.48673983206805305
9. sulphates: -0.48721797005730894
10. chlorides: -0.5126782476623972
11. volatile acidity: -0.6530355891787222

Cosine Similarity Ranked (Non-Standardized):
1. total sulfur dioxide: 0.9326717799829997
2. free sulfur dioxide: 0.8682221138409416
3. density: 0.8676781898437091
4. alcohol: 0.8645579017746198
5. pH: 0.8590388081706237
6. citric acid: 0.8285719847684867
7. fixed acidity: 0.8118831632537973
8. sulphates: 0.7709054793248501
```

```
9. residual sugar: 0.7676386905156257
10. volatile acidity: 0.6400390583426301
11. chlorides: 0.6014045619581195

Pearson Correlation Ranked (Standardized):
1. total sulfur dioxide: 0.7003571552968025
2. free sulfur dioxide: 0.4716436649016788
3. residual sugar: 0.34882100781119324
4. citric acid: 0.18739650075043557
5. alcohol: 0.03296955068460622
6. pH: -0.32912865072599967
7. density: -0.39064531835422267
8. fixed acidity: -0.48673983206805305
9. sulphates: -0.48721797005730894
10. chlorides: -0.5126782476623974
11. volatile acidity: -0.6530355891787223

Cosine Similarity Ranked (Standardized):
1. total sulfur dioxide: 0.7003571552968021
2. free sulfur dioxide: 0.4716436649016795
3. residual sugar: 0.34882100781119263
4. citric acid: 0.18739650075043549
5. alcohol: 0.03296955068460626
6. pH: -0.3291286507259993
7. density: -0.3906453183542224
8. fixed acidity: -0.4867398320680528
9. sulphates: -0.4872179700573089
10. chlorides: -0.512678247662397
11. volatile acidity: -0.653035589178722
```

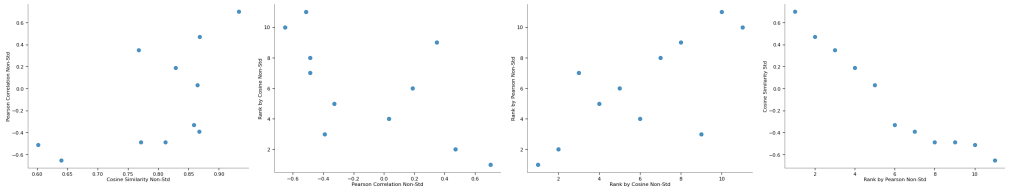
```
 #Rank order the columns for each measure and prepare rankings
cosine_ranks_non_std = {k: v + 1 for v, (k, _) in enumerate(sorted(cosine_similarities_non_std.items(), key=lambda x: x[1], reverse=True))}
pearson_ranks_non_std = {k: v + 1 for v, (k, _) in enumerate(sorted(pearson_correlations_non_std.items(), key=lambda x: x[1], reverse=True))}
cosine_ranks_std = {k: v + 1 for v, (k, _) in enumerate(sorted(cosine_similarities_std.items(), key=lambda x: x[1], reverse=True))}
pearson_ranks_std = {k: v + 1 for v, (k, _) in enumerate(sorted(pearson_correlations_std.items(), key=lambda x: x[1], reverse=True))}

# Create a DataFrame to report the results correctly
similarity_df = pd.DataFrame({
    'Cosine Similarity Non-Std': [cosine_similarities_non_std[p] for p in numeric_predictors],
    'Pearson Correlation Non-Std': [pearson_correlations_non_std[p] for p in numeric_predictors],
    'Rank by Cosine Non-Std': [cosine_ranks_non_std[p] for p in numeric_predictors],
    'Rank by Pearson Non-Std': [pearson_ranks_non_std[p] for p in numeric_predictors],
    'Cosine Similarity Std': [cosine_similarities_std[p] for p in numeric_predictors],
    'Pearson Correlation Std': [pearson_correlations_std[p] for p in numeric_predictors],
    'Rank by Cosine Std': [cosine_ranks_std[p] for p in numeric_predictors],
    'Rank by Pearson Std': [pearson_ranks_std[p] for p in numeric_predictors]
}, index=numeric_predictors)

desired_format = similarity_df[['Cosine Similarity Non-Std', 'Pearson Correlation Non-Std',
                                'Rank by Cosine Non-Std', 'Rank by Pearson Non-Std',
                                'Cosine Similarity Std', 'Pearson Correlation Std',
                               'Rank by Cosine Std', 'Rank by Pearson Std']]


# Display the DataFrame
desired_format
```

	Cosine Similarity Non-Std	Pearson Correlation Non-Std	Rank by Cosine Non-Std	Rank by Pearson Non-Std	Cosine Similarity Std	Pearson Correlation Std	Rank by Cosine Std	Rank by Pearson Std
fixed acidity	0.811883	-0.486740	7	8	-0.486740	-0.486740	8	8
volatile acidity	0.640039	-0.653036	10	11	-0.653036	-0.653036	11	11
citric acid	0.828572	0.187397	6	4	0.187397	0.187397	4	4
residual sugar	0.767639	0.348821	9	3	0.348821	0.348821	3	3
chlorides	0.601405	-0.512678	11	10	-0.512678	-0.512678	10	10
free sulfur dioxide	0.868222	0.471644	2	2	0.471644	0.471644	2	2
total sulfur dioxide	0.932672	0.700357	1	1	0.700357	0.700357	1	1
density	0.867678	-0.390645	3	7	-0.390645	-0.390645	7	7
pH	0.859039	-0.329129	5	6	-0.329129	-0.329129	6	6
sulphates	0.770905	-0.487218	8	9	-0.487218	-0.487218	9	9
alcohol	0.864558	0.032970	4	5	0.032970	0.032970	5	5

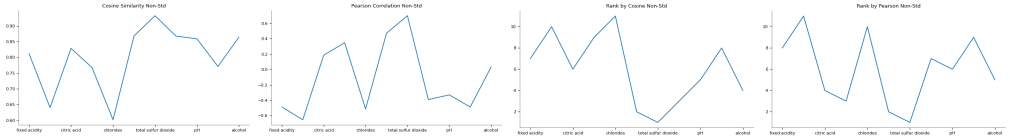
Distributions



2-d distributions



Values



Question 4)

Discuss these results. Does any one of the two measures seem to work better? Do they give conflicting results in some situations? Explain the behaviors of the two measures to the extent possible.

Cosine Similarity

Cosine similarity measures the cosine of the angle between two vectors in a multi-dimensional space, applied here to compare the similarity between various wine characteristics (numeric predictors) and wine type. Values close to 1 indicate a high degree of similarity or positive association, whereas values near -1 suggest dissimilarity or a negative association. The "Non-Std" column shows cosine similarity using original data, and the "Std" column applies standardized data (normalized to have a mean of 0 and a standard deviation of 1), aiding in the comparison of features with different units or scales.

Non-Standardized Data Results:

- **Total Sulfur Dioxide** and **Free Sulfur Dioxide** have the highest cosine similarity scores, suggesting they are closely aligned with the wine type in the non-standardized dataset, indicating a strong positive linear relationship.
- **Chlorides** and **Volatile Acidity** show the lowest scores, implying they are least aligned with the wine type.

Standardized Data Results:

- Standardization normalizes the data, yet the rankings and associations largely reflect the non-standardized results, indicating that the relative importance and direction of relationships between variables and wine type remain consistent even after standardization.

Conflicts and Explanations:

- Variables such as "fixed acidity" exhibit a change from positive cosine similarity in non-standardized data to negative in standardized data, suggesting a fundamental change in perceived relationship after standardization.
- "Residual sugar" and "citric acid" improve significantly in ranking upon standardization, whereas "fixed acidity" and "volatile acidity" either drop or remain low, showing that standardization can dramatically alter perceived importance.

Conclusion:

Cosine similarity results underscore the pivotal role of sulfur dioxide levels in categorizing wines, with the lower alignment of Chlorides and Volatile Acidity possibly indicating their role in distinguishing wine types. Standardization is crucial for a balanced comparison.

Pearson Correlation

Pearson correlation assesses the linear relationship between two variables, with values ranging from -1 to 1, where 1 indicates a strong positive relationship, -1 a strong negative relationship, and 0 no linear relationship.

Non-Standardized Data:

- **Total Sulfur Dioxide** and **Free Sulfur Dioxide** show strong positive correlations, reaffirming their significance as indicators of wine type.
- Negative correlations for **Volatile Acidity** and **Chlorides** suggest these variables inversely affect wine type categorization, potentially distinguishing between wine types.

Standardized Data:

- Pearson correlation analysis on standardized data confirms the direction and relative strength of associations seen in non-standardized analysis, indicating linear relationships are consistent after standardization.

Conclusion:

The consistency across both methods and data treatments suggests sulfur dioxide levels have a fundamental association with wine type, highlighting the importance of consistent predictors across different data processing methods.

Does any one of the two measures seem to work better? Do they give conflicting results in some situations?

- Neither cosine similarity nor Pearson correlation consistently outperforms the other across all situations; their effectiveness varies with context. Both measures provide valuable insights, yet they might give conflicting results in some situations due to their sensitivity to the scale and distribution of the data.
- Conflicts primarily arise from the standardization process, affecting the rankings and perceived importance of variables. These discrepancies highlight the importance of considering both standardized and non-standardized analyses to gain a comprehensive understanding of the data.
- Cosine similarity is sensitive to changes in magnitude and direction, which standardization can significantly affect. Pearson correlation, focusing on linear relationships, tends to be more robust to scale changes but can still reflect changes in variable importance after standardization.

Question 5)

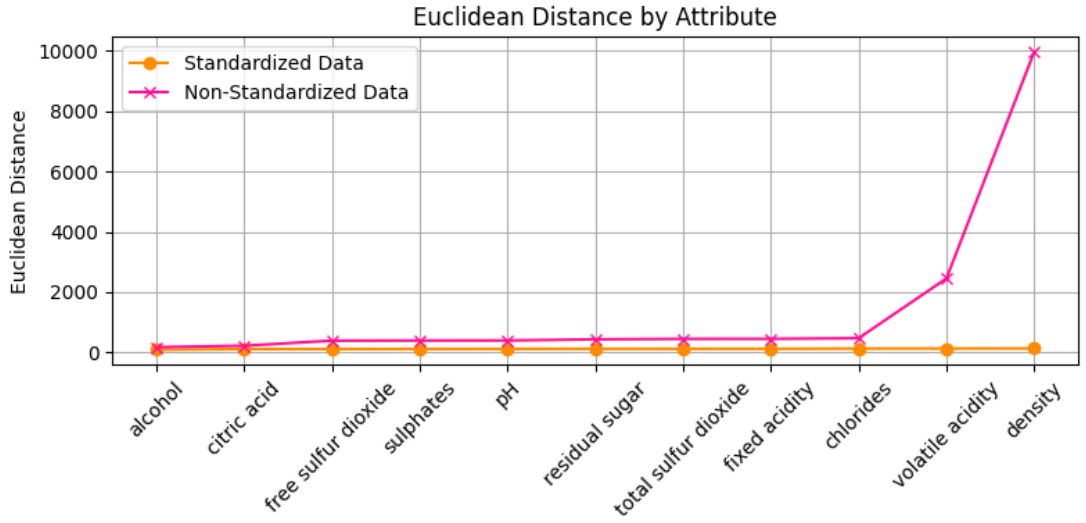
In the setting of question 1, standardize each of the predictor columns before computing Euclidean distance. Report the results in the same format (rank-ordered by least Euclidean distance first, while also reporting the actual Euclidean distance). Is the rank order based on standardizing different than the one based on the earlier one you reported in question 1 for Euclidean distance. Regardless of whether that is the case, discuss intepreting the results.

```
ranked_by_euclidean_std = sorted(euclidean_distances_std_data, key=euclidean_distances_std_data.get)
print("\neuclidean Distance Ranked for Standardized Data:")
for rank, predictor in enumerate(ranked_by_euclidean_std, start=1):
    distance = euclidean_distances_std_data[predictor]  # Get the distance from the dictionary
    print(f"{rank}. {predictor}: {distance}")

ranked_by_euclidean = sorted(euclidean_distances.items(), key=lambda x: x[1])
print("\neuclidean Distance Ranked for Non Standardized Data:")
for rank, (predictor, distance) in enumerate(ranked_by_euclidean, start=1):
    print(f"{rank}. {predictor}: {distance}")
```

```
 euclidean Distance Ranked for Standardized Data:
 1. alcohol: 84.97367328191899
 2. citric acid: 109.007343178867
 3. free sulfur dioxide: 110.7849855185055
 4. sulphates: 111.77620550135244
 5. pH: 112.87401333316106
 6. residual sugar: 116.0798191621071
 7. total sulfur dioxide: 116.32610449679719
 8. fixed acidity: 118.28440828603573
 9. chlorides: 124.9057545217742
 10. volatile acidity: 128.2439043856799
 11. density: 130.26249510686478

 euclidean Distance Ranked for Non Standardized Data:
 1. fixed acidity: 172.27557139652737
 2. pH: 221.3630542796155
```

```
3. alcohol: 387.4047948561723
4. residual sugar: 393.58882733126455
5. density: 395.14008968328693
6. sulphates: 432.02617316546923
7. volatile acidity: 447.93061237205035
8. citric acid: 448.8494620694114
9. chlorides: 469.86353989855394
10. free sulfur dioxide: 2450.770389081768
11. total sulfur dioxide: 9964.569195404285
```

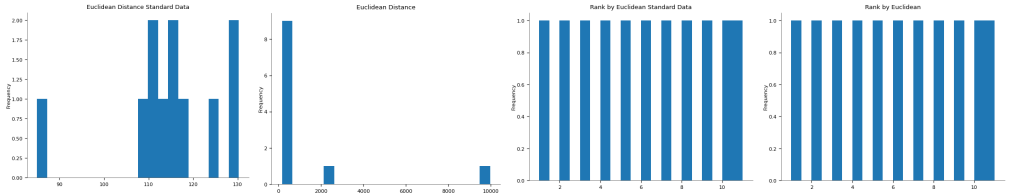
```
# Euclidean distances
euclidean_distance_standardized = [
    84.97367328191899, 109.007343178867, 110.7849855185055, 111.77620550135244,
    112.87401333316106, 116.0798191621071, 116.32610449679719, 118.28440828603573,
    124.9057545217742, 128.2439043856799, 130.26249510686478
]
euclidean_distance_non_standardized = [
    172.27557139652737, 221.3630542796155, 387.4047948561723, 393.58882733126455,
    395.14008968328693, 432.02617316546923, 447.93061237205035, 448.8494620694114,
    469.86353989855394, 2450.770389081768, 9964.569195404285
]
# Plotting Euclidean distance by attribute with a reduced figure size
plt.figure(figsize=(8, 4))
plt.plot(attributes, euclidean_distance_standardized, label='Standardized Data', marker='o',color='darkorange')
plt.plot(attributes, euclidean_distance_non_standardized, label='Non-Standardized Data', marker='x',color='deeppink')
plt.xticks(range(len(attributes)), attributes, rotation=45)
plt.ylabel('Euclidean Distance')
plt.title('Euclidean Distance by Attribute')
plt.legend()
plt.tight_layout()
plt.grid(True)
plt.show()
```



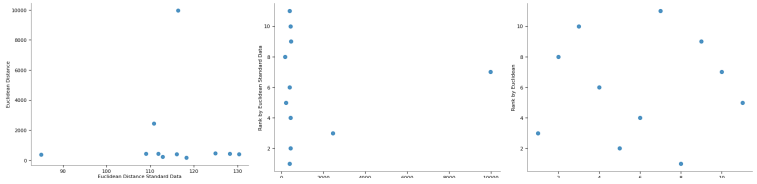
```
# Create a DataFrame to report the results correctly using the standardized data
similarity_df_std = pd.DataFrame({
    'Euclidean Distance Standard Data': {predictor: euclidean_distances_std_data[predictor] for predictor in numeric_predictors},
    'Euclidean Distance': euclidean_distances,

    'Rank by Euclidean Standard Data': [ranked_by_euclidean_std.index(predictor) + 1 for predictor in numeric_predictors],
    'Rank by Euclidean': [euclidean_ranks[predictor] for predictor in numeric_predictors],

}, index=numeric_predictors)

similarity_df_std
```

	Euclidean Distance Standard Data	Euclidean Distance	Rank by Euclidean Standard Data	Rank by Euclidean
fixed acidity	118.284408	172.275571	8	1
volatile acidity	128.243904	447.930612	10	7
citric acid	109.007343	448.849462	2	8
residual sugar	116.079819	393.588827	6	4
chlorides	124.905755	469.863540	9	9
free sulfur dioxide	110.784986	2450.770389	3	10
total sulfur dioxide	116.326104	9964.569195	7	11
density	130.262495	395.140090	11	5
pH	112.874013	221.363054	5	2
sulphates	111.776206	432.026173	4	6
alcohol	84.973673	387.404795	1	3

Distributions



2-d distributions



ANSWER 5)

- yes The Rank Order Predicated Earlier had fixed acidity on rank 1 followed by pH , alcohol, residual suagr , debsity, sulphates, volatile acidity, citric acid, chlorides, free sulphur dioxide, total sulfur dioxide.
- After Standardization we get new ranking at top Alcohol , citric acid, free sulfur dioxide, sulphates, pH, residual sugar, total sulphur dioxide, fixed acidity, chlorides, volatile acidity, density.

Interpretation:

- The standardization process has a substantial effect on the rank ordering of the Euclidean distances.
- By scaling the data, the variables with larger ranges that initially had higher Euclidean distances (like "total sulfur dioxide") now have their effect diminished, allowing for a more equitable comparison across all predictors.
- The results also highlight the importance of understanding the data distribution and the scale of measurement when interpreting Euclidean distances.
- Without standardization, variables measured at larger scales can disproportionately affect the distance computations, potentially leading to misleading conclusions about the importance or similarity of different predictors.
- Standardization corrects for this by normalizing the scale, ensuring that each variable's inherent variability is what determines its distance from the target variable.
- Alchol, citric acid are closesly related to quality of wine rather than fixed acidity, pH.
- volatile acidity, density is least like to affect the quality of wine.

Question 6)

Compute the mean vectors of type = white versus type = red where the vector components are the various numeric predictor columns. Do this twice, once without standardizing the numeric predictor columns first, and once after standardizing the numeric predictor columns. You will get two sets, each containing two mean vectors. From each set, rank-order the numeric columns based on the magnitude of the difference between the values of that column. You will get two ranked lists. Report them.

```
#Importing all the neccessay Libraries.
import pandas as pd
from sklearn.preprocessing import StandardScaler
from scipy.spatial.distance import euclidean
from scipy.spatial.distance import cosine
from scipy.stats import pearsonr
from numpy import dot, linalg
import numpy as np
from numpy.linalg import norm
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings("ignore")
# Load the dataset
file_path = 'wine-quality-white-and-red.csv'
wine_data = pd.read_csv(file_path)
```

```
# Separate the dataset into red and white wine datasets
red_wine = wine_data[wine_data['type'] == 'red']
white_wine = wine_data[wine_data['type'] == 'white']
# Compute the mean vectors without standardization
mean_vector_red = red_wine.mean()
mean_vector_white = white_wine.mean()
# Compute the mean vectors after standardization
scaler = StandardScaler()
wine_data_scaled = scaler.fit_transform(wine_data.drop('type', axis=1))
wine_data_scaled = pd.DataFrame(wine_data_scaled, columns=wine_data.columns.drop('type'))
red_wine_scaled = wine_data_scaled[wine_data['type'] == 'red']
white_wine_scaled = wine_data_scaled[wine_data['type'] == 'white']
mean_vector_red_scaled = red_wine_scaled.mean()
mean_vector_white_scaled = white_wine_scaled.mean()
# Calculate the magnitude of the difference between the mean vectors without standardization
diff_magnitude_non_std = (mean_vector_white - mean_vector_red).abs()

# Calculate the magnitude of the difference between the mean vectors after standardization
diff_magnitude_std = (mean_vector_white_scaled - mean_vector_red_scaled).abs()

# Rank-order the numeric columns based on the magnitude of the difference without standardization
ranked_diff_non_std = diff_magnitude_non_std.sort_values(ascending=False).index.tolist()

# Rank-order the numeric columns based on the magnitude of the difference after standardization
ranked_diff_std = diff_magnitude_std.sort_values(ascending=False).index.tolist()

# Report the two ranked lists
print("ANSWER 6)")
print("\neuclidean Distance Ranked for Standardized Data:")
for rank, predictor in enumerate(ranked_diff_std, start=1):
    print(f"{rank}. {predictor}")

print("\neuclidean Distance Ranked for Non Standardized Data:")
for rank, predictor in enumerate(ranked_diff_non_std, start=1):
    print(f"{rank}. {predictor}")
```

```
 ANSWER 6)

 euclidean Distance Ranked for Standardized Data:
```

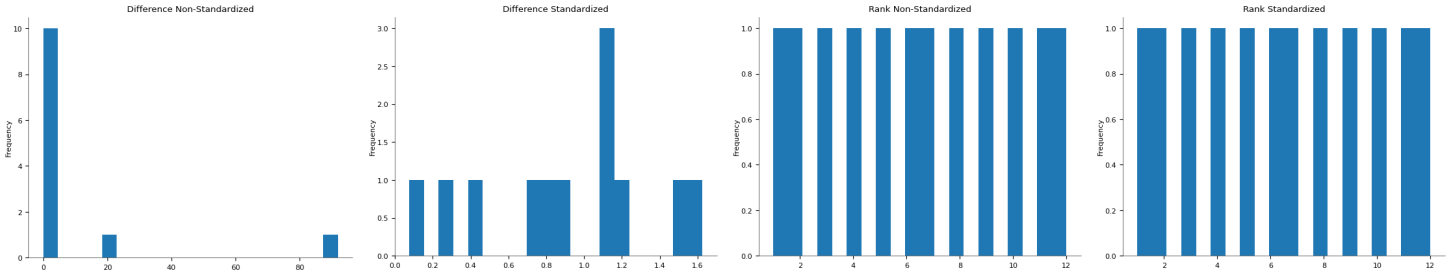
1. total sulfur dioxide
2. volatile acidity
3. chlorides
4. sulphates
5. fixed acidity
6. free sulfur dioxide
7. density
8. residual sugar
9. pH
10. citric acid
11. quality
12. alcohol

euclidean Distance Ranked for Non Standardized Data:
1. total sulfur dioxide
2. free sulfur dioxide
3. residual sugar
4. fixed acidity
5. volatile acidity
6. quality
7. sulphates
8. pH
9. alcohol
10. citric acid
11. chlorides
12. density

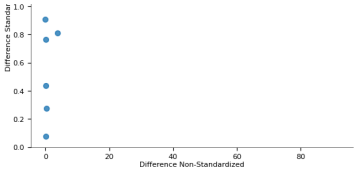
```
# Create a DataFrame with the differences and ranks
diff_df = pd.DataFrame({
    'Predictor': wine_data.columns.drop('type'),
    'Difference Non-Standardized': diff_magnitude_non_std.values,
    'Difference Standardized': diff_magnitude_std.values
})

# Add ranks to the DataFrame
diff_df['Rank Non-Standardized'] = diff_df['Difference Non-Standardized'].rank(ascending=False, method='min')
diff_df['Rank Standardized'] = diff_df['Difference Standardized'].rank(ascending=False, method='min')

# Sort the DataFrame based on the non-standardized ranks
diff_df.sort_values('Rank Non-Standardized', inplace=True)

# Set the index to the predictor names for better readability
diff_df.set_index('Predictor', inplace=True)

# Display the DataFrame
diff_df
```

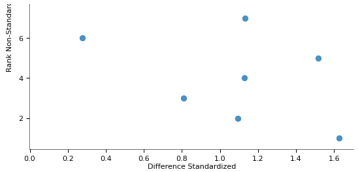
Predictor	Difference Non-Standardized	Difference Standardized	Rank Non-Standardized	Rank Standardized
total sulfur dioxide	91.892865	1.625919	1.0	1.0
free sulfur dioxide	19.433163	1.094947	2.0	6.0
residual sugar	3.852609	0.809808	3.0	8.0
fixed acidity	1.464850	1.129994	4.0	5.0
volatile acidity	0.249579	1.516059	5.0	2.0
quality	0.241887	0.277016	6.0	11.0
sulphates	0.168302	1.131104	7.0	4.0
pH	0.122847	0.764091	8.0	9.0
alcohol	0.091284	0.076541	9.0	12.0
citric acid	0.063216	0.435052	10.0	10.0
chlorides	0.041694	1.190211	11.0	3.0
density	0.002719	0.906905	12.0	7.0

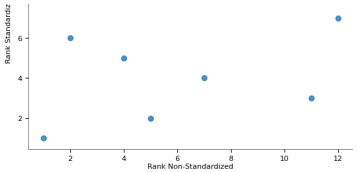
Distributions



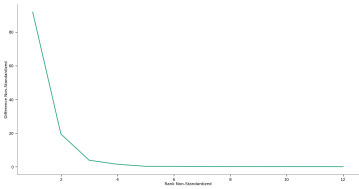
2-d distributions

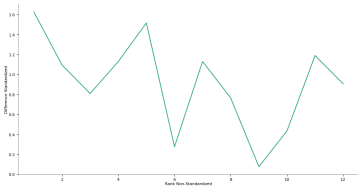


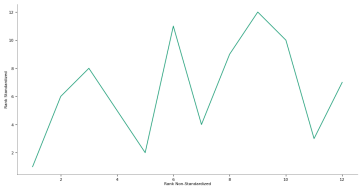


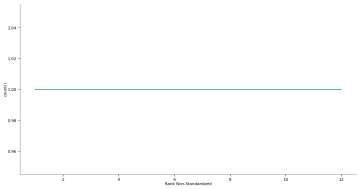


Time series









Values