DSC630-T301 Predictive Analytics (2243-1)_week4_Samanta_Rajib

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0.1 Class : DSC630-T301 Predictive Analytics (2243-1)

0.2 Name : Rajib Samanta

0.2.1 Assignment 4.2 : Week 4

You will be using the dataset als_data.csv to apply clustering methods for this assignment. This data gives anonymized data on ALS patients. With this data, complete the following steps: 1. Remove any data that is not relevant to the patient's ALS condition. 2. Apply a standard scalar to the data. 3. Create a plot of the cluster silhouette score versus the number of clusters in a K-means cluster. 4. Use the plot created in (3) to choose on optimal number of clusters for K-means. Justify your choice. 5. Fit a K-means model to the data with the optimal number of clusters chosen in part (4). 6. Fit a PCA transformation with two features to the scaled data. 7. Make a scatterplot the PCA transformed data coloring each point by its cluster value. 8. Summarize your results and make a conclusion. You can use R or Python to complete this assignment. Submit your code and output to the submission link. Make sure to add comments to all of your code and to document your steps, process, and analysis.

[36]:
```
# Load the Libraries
import os
import pandas as pd
import matplotlib.pyplot as plt
#%matplotlib inline
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score
from sklearn.decomposition import PCA
```

[37]:
```
# 1. Load the dataset as a Pandas data frame.
# 2. Display the first ten rows of data.
# Read  anonymized data on ALS patients  data file ('als_data.csv') from local:
directory = '/Users/rajibsamanta/Documents/Rajib/College/Sem 7 Winter 2023/
 ↪Week4'
# Set the working directory
```

```
os.chdir(directory)
print(os.getcwd())
dataset1_csv = pd.read_csv("als_data.csv")
dataset1_csv.head(5)
# Display the DataFrame 10 rows
```

```
/Users/rajibsamanta/Documents/Rajib/College/Sem 7 Winter 2023/Week4
```

[37]:

```
   ID  Age_mean  Albumin_max  Albumin_median  Albumin_min  Albumin_range  \
0   1        65         57.0            40.5         38.0       0.066202
1   2        48         45.0            41.0         39.0       0.010453
2   3        38         50.0            47.0         45.0       0.008929
3   4        63         47.0            44.0         41.0       0.012111
4   5        63         47.0            45.5         42.0       0.008292

   ALSFRS_slope  ALSFRS_Total_max  ALSFRS_Total_median  ALSFRS_Total_min  …  \
0     -0.965608                30                 28.0                22  …
1     -0.921717                37                 33.0                21  …
2     -0.914787                24                 14.0                10  …
3     -0.598361                30                 29.0                24  …
4     -0.444039                32                 27.5                20  …

   Sodium_min  Sodium_range  SubjectID  trunk_max  trunk_median  trunk_min  \
0       143.0      0.017422        533          8           7.0          7
1       136.0      0.010453        649          8           7.0          5
2       140.0      0.008929       1234          5           0.0          0
3       138.0      0.012469       2492          5           5.0          3
4       138.0      0.008292       2956          6           4.0          1

   trunk_range  Urine.Ph_max  Urine.Ph_median  Urine.Ph_min
0     0.002646           6.0              6.0           6.0
1     0.005386           7.0              5.0           5.0
2     0.008929           6.0              5.0           5.0
3     0.004988           7.0              6.0           5.0
4     0.008489           6.0              5.0           5.0

[5 rows x 101 columns]
```

1. Remove any data that is not relevant to the patient's ALS condition.

[38]:

```
# 1. Remove any data that is not relevant to the patient's ALS condition.
# Identify and remove irrelevant columns
columns_to_remove = ['ID', 'SubjectID']  # Replace with the actual column names␣
 ↪to be removed
dataset1_csv = dataset1_csv.drop(columns=columns_to_remove, errors='ignore')

# Display the DataFrame after removing irrelevant data
print("\nDataFrame after removing irrelevant data:")
```

```python
print(dataset1_csv.head())
```

```
DataFrame after removing irrelevant data:
   Age_mean  Albumin_max  Albumin_median  Albumin_min  Albumin_range  \
0        65         57.0            40.5         38.0       0.066202
1        48         45.0            41.0         39.0       0.010453
2        38         50.0            47.0         45.0       0.008929
3        63         47.0            44.0         41.0       0.012111
4        63         47.0            45.5         42.0       0.008292

   ALSFRS_slope  ALSFRS_Total_max  ALSFRS_Total_median  ALSFRS_Total_min  \
0     -0.965608                30                 28.0                22
1     -0.921717                37                 33.0                21
2     -0.914787                24                 14.0                10
3     -0.598361                30                 29.0                24
4     -0.444039                32                 27.5                20

   ALSFRS_Total_range  …  Sodium_median  Sodium_min  Sodium_range  \
0            0.021164  …          145.5       143.0      0.017422
1            0.028725  …          138.0       136.0      0.010453
2            0.025000  …          143.0       140.0      0.008929
3            0.014963  …          139.0       138.0      0.012469
4            0.020374  …          140.0       138.0      0.008292

   trunk_max  trunk_median  trunk_min  trunk_range  Urine.Ph_max  \
0          8           7.0          7     0.002646           6.0
1          8           7.0          5     0.005386           7.0
2          5           0.0          0     0.008929           6.0
3          5           5.0          3     0.004988           7.0
4          6           4.0          1     0.008489           6.0

   Urine.Ph_median  Urine.Ph_min
0              6.0           6.0
1              5.0           5.0
2              5.0           5.0
3              6.0           5.0
4              5.0           5.0

[5 rows x 99 columns]
```

[39]:
```python
dataset1_csv.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2223 entries, 0 to 2222
Data columns (total 99 columns):
 #   Column                          Non-Null Count  Dtype
---  ------                          --------------  -----
```

```
0   Age_mean                          2223 non-null   int64
1   Albumin_max                       2223 non-null   float64
2   Albumin_median                    2223 non-null   float64
3   Albumin_min                       2223 non-null   float64
4   Albumin_range                     2223 non-null   float64
5   ALSFRS_slope                      2223 non-null   float64
6   ALSFRS_Total_max                  2223 non-null   int64
7   ALSFRS_Total_median               2223 non-null   float64
8   ALSFRS_Total_min                  2223 non-null   int64
9   ALSFRS_Total_range                2223 non-null   float64
10  ALT.SGPT._max                     2223 non-null   float64
11  ALT.SGPT._median                  2223 non-null   float64
12  ALT.SGPT._min                     2223 non-null   float64
13  ALT.SGPT._range                   2223 non-null   float64
14  AST.SGOT._max                     2223 non-null   int64
15  AST.SGOT._median                  2223 non-null   float64
16  AST.SGOT._min                     2223 non-null   float64
17  AST.SGOT._range                   2223 non-null   float64
18  Bicarbonate_max                   2223 non-null   float64
19  Bicarbonate_median                2223 non-null   float64
20  Bicarbonate_min                   2223 non-null   float64
21  Bicarbonate_range                 2223 non-null   float64
22  Blood.Urea.Nitrogen..BUN._max     2223 non-null   float64
23  Blood.Urea.Nitrogen..BUN._median  2223 non-null   float64
24  Blood.Urea.Nitrogen..BUN._min     2223 non-null   float64
25  Blood.Urea.Nitrogen..BUN._range   2223 non-null   float64
26  bp_diastolic_max                  2223 non-null   int64
27  bp_diastolic_median               2223 non-null   float64
28  bp_diastolic_min                  2223 non-null   int64
29  bp_diastolic_range                2223 non-null   float64
30  bp_systolic_max                   2223 non-null   int64
31  bp_systolic_median                2223 non-null   float64
32  bp_systolic_min                   2223 non-null   int64
33  bp_systolic_range                 2223 non-null   float64
34  Calcium_max                       2223 non-null   float64
35  Calcium_median                    2223 non-null   float64
36  Calcium_min                       2223 non-null   float64
37  Calcium_range                     2223 non-null   float64
38  Chloride_max                      2223 non-null   float64
39  Chloride_median                   2223 non-null   float64
40  Chloride_min                      2223 non-null   float64
41  Chloride_range                    2223 non-null   float64
42  Creatinine_max                    2223 non-null   float64
43  Creatinine_median                 2223 non-null   float64
44  Creatinine_min                    2223 non-null   float64
45  Creatinine_range                  2223 non-null   float64
46  Gender_mean                       2223 non-null   int64
47  Glucose_max                       2223 non-null   float64
```

```
48  Glucose_median                    2223 non-null   float64
49  Glucose_min                       2223 non-null   float64
50  Glucose_range                     2223 non-null   float64
51  hands_max                         2223 non-null   int64
52  hands_median                      2223 non-null   float64
53  hands_min                         2223 non-null   int64
54  hands_range                       2223 non-null   float64
55  Hematocrit_max                    2223 non-null   float64
56  Hematocrit_median                 2223 non-null   float64
57  Hematocrit_min                    2223 non-null   float64
58  Hematocrit_range                  2223 non-null   float64
59  Hemoglobin_max                    2223 non-null   float64
60  Hemoglobin_median                 2223 non-null   float64
61  Hemoglobin_min                    2223 non-null   float64
62  Hemoglobin_range                  2223 non-null   float64
63  leg_max                           2223 non-null   int64
64  leg_median                        2223 non-null   float64
65  leg_min                           2223 non-null   int64
66  leg_range                         2223 non-null   float64
67  mouth_max                         2223 non-null   int64
68  mouth_median                      2223 non-null   float64
69  mouth_min                         2223 non-null   int64
70  mouth_range                       2223 non-null   float64
71  onset_delta_mean                  2223 non-null   int64
72  onset_site_mean                   2223 non-null   int64
73  Platelets_max                     2223 non-null   int64
74  Platelets_median                  2223 non-null   float64
75  Platelets_min                     2223 non-null   float64
76  Potassium_max                     2223 non-null   float64
77  Potassium_median                  2223 non-null   float64
78  Potassium_min                     2223 non-null   float64
79  Potassium_range                   2223 non-null   float64
80  pulse_max                         2223 non-null   int64
81  pulse_median                      2223 non-null   float64
82  pulse_min                         2223 non-null   int64
83  pulse_range                       2223 non-null   float64
84  respiratory_max                   2223 non-null   int64
85  respiratory_median                2223 non-null   float64
86  respiratory_min                   2223 non-null   int64
87  respiratory_range                 2223 non-null   float64
88  Sodium_max                        2223 non-null   float64
89  Sodium_median                     2223 non-null   float64
90  Sodium_min                        2223 non-null   float64
91  Sodium_range                      2223 non-null   float64
92  trunk_max                         2223 non-null   int64
93  trunk_median                      2223 non-null   float64
94  trunk_min                         2223 non-null   int64
95  trunk_range                       2223 non-null   float64
```

```
 96  Urine.Ph_max                      2223 non-null   float64
 97  Urine.Ph_median                   2223 non-null   float64
 98  Urine.Ph_min                      2223 non-null   float64
dtypes: float64(75), int64(24)
memory usage: 1.7 MB
```

2. Apply a standard scalar to the data.

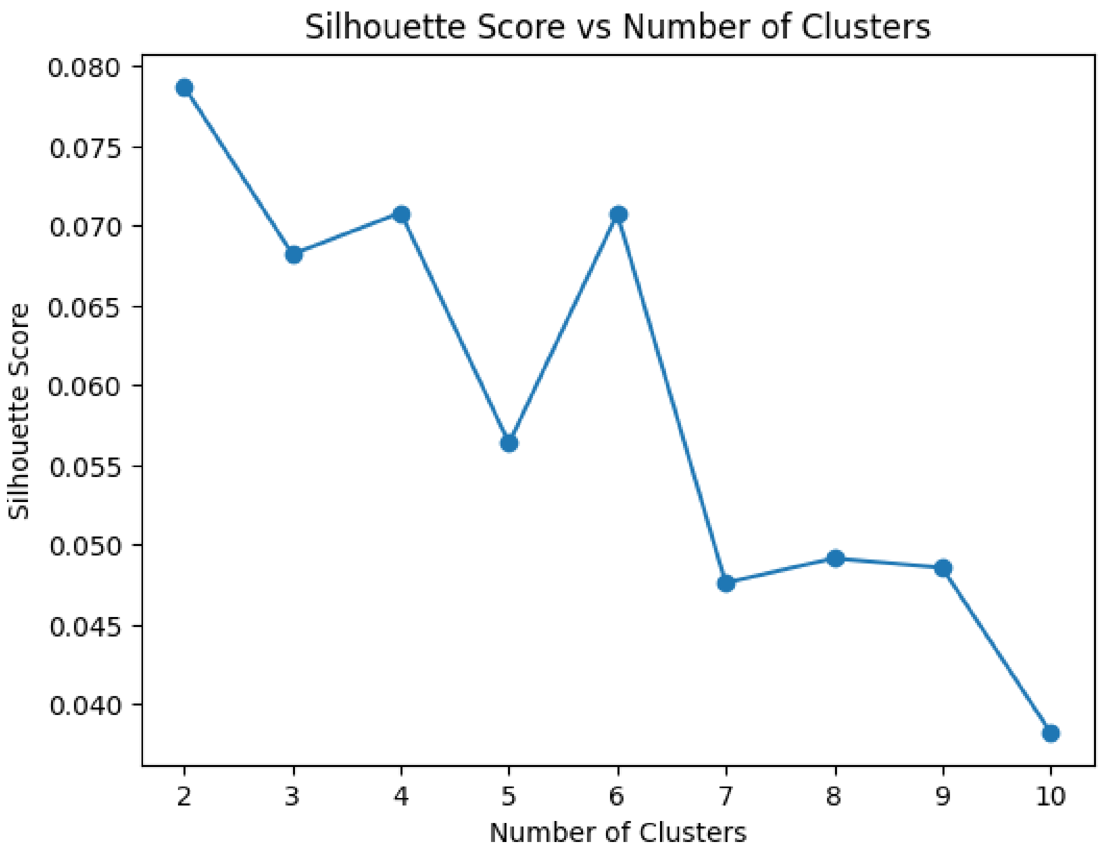
[40]:
```python
# 2. Apply a standard scalar to the data.
# Identify and extract all numeric columns
numeric_columns = dataset1_csv.select_dtypes(include=['number']).columns

# Extract data to be scaled
data_to_scale = dataset1_csv[numeric_columns]

# Apply Standard Scaling
scaler = StandardScaler()
scaled_data = scaler.fit_transform(data_to_scale)

# Replace the original numeric columns with the scaled data
dataset1_csv[numeric_columns] = scaled_data

# Display the DataFrame after applying Standard Scaling
print("\nDataFrame after applying Standard Scaling to all numeric columns:")
print(dataset1_csv.head())
```

```
DataFrame after applying Standard Scaling to all numeric columns:
   Age_mean  Albumin_max  Albumin_median  Albumin_min  Albumin_range  \
0  0.917137     3.089417       -1.300781    -0.866550       5.480929
1 -0.574879    -0.622016       -1.112401    -0.553303      -0.347725
2 -1.452535     0.924415        1.148162     1.326179      -0.507103
3  0.741606    -0.003443        0.017880     0.073191      -0.174361
4  0.741606    -0.003443        0.583021     0.386438      -0.573670

   ALSFRS_slope  ALSFRS_Total_max  ALSFRS_Total_median  ALSFRS_Total_min  \
0     -0.381450         -0.318520             0.134960          0.247368
1     -0.310907          0.998995             0.888863          0.130839
2     -0.299769         -1.447819            -1.975969         -1.150976
3      0.208801         -0.318520             0.285741          0.480425
4      0.456831          0.057913             0.059570          0.014311

   ALSFRS_Total_range  …  Sodium_median  Sodium_min  Sodium_range  \
0           -0.301588  …       2.992342    2.300470      0.260968
1            0.166537  …      -1.198812   -0.278144     -0.489913
2           -0.064100  …       1.595291    1.195350     -0.654169
3           -0.685524  …      -0.639992    0.458603     -0.272701
4           -0.350529  …      -0.081171    0.458603     -0.722774
```

```
   trunk_max  trunk_median  trunk_min  trunk_range  Urine.Ph_max  \
0   1.028018      0.981832   1.715365    -0.997420     -0.880376
1   1.028018      0.981832   0.867032    -0.388669      0.192665
2  -0.688950     -2.280669  -1.253800     0.398249     -0.880376
3  -0.688950      0.049689   0.018699    -0.477181      0.192665
4  -0.116627     -0.416383  -0.829634     0.300598     -0.880376

   Urine.Ph_median  Urine.Ph_min
0         0.463054      1.868532
1        -1.137208     -0.419151
2        -1.137208     -0.419151
3         0.463054     -0.419151
4        -1.137208     -0.419151

[5 rows x 99 columns]
```

3. Create a plot of the cluster silhouette score versus the number of clusters in a K-means cluster.

[41]:
```
# 3. Create a plot of the cluster silhouette score versus the number of␣
↪clusters in a K-means cluster.

# Range of cluster numbers to try
cluster_range = range(2, 11)  # considering the range 2 to 11

# List to store silhouette scores
silhouette_scores = []

# Perform K-means clustering for different numbers of clusters
for num_clusters in cluster_range:
    kmeans = KMeans(n_clusters=num_clusters, random_state=42)
    cluster_labels = kmeans.fit_predict(scaled_data)

    # Compute silhouette score and append to the list
    silhouette_avg = silhouette_score(scaled_data, cluster_labels)
    silhouette_scores.append(silhouette_avg)

# Plotting the results
plt.plot(cluster_range, silhouette_scores, marker='o')
plt.title('Silhouette Score vs Number of Clusters')
plt.xlabel('Number of Clusters')
plt.ylabel('Silhouette Score')
plt.show()
```



4. Use the plot created in (3) to choose on optimal number of clusters for K-means. Justify your choice. −> Using the elbow method for the “elbow” point, which is where the improvement in silhouette score starts to diminish. 7 is the optimal number of cluster.

5. Fit a K-means model to the data with the optimal number of clusters chosen in part (4).

[42]:
```
# 5. Fit a K-means model to the data with the optimal number of clusters chosen␣
  ↪in part (4).

# Replace 'optimal_num_clusters' with the number we have identified from the␣
  ↪silhouette score plot
optimal_num_clusters = 7  # Replace with determined optimal number of clusters

# Fit K-means model with the optimal number of clusters
kmeans = KMeans(n_clusters=optimal_num_clusters, random_state=42)
dataset1_csv['cluster_labels'] = kmeans.fit_predict(scaled_data)

# Display the DataFrame with cluster labels
print("DataFrame with Cluster Labels:")
```

```
dataset1_csv.head()
```

```
DataFrame with Cluster Labels:
```

[42]:
```
   Age_mean  Albumin_max  Albumin_median  Albumin_min  Albumin_range  \
0  0.917137     3.089417       -1.300781    -0.866550       5.480929
1 -0.574879    -0.622016       -1.112401    -0.553303      -0.347725
2 -1.452535     0.924415        1.148162     1.326179      -0.507103
3  0.741606    -0.003443        0.017880     0.073191      -0.174361
4  0.741606    -0.003443        0.583021     0.386438      -0.573670

   ALSFRS_slope  ALSFRS_Total_max  ALSFRS_Total_median  ALSFRS_Total_min  \
0     -0.381450         -0.318520             0.134960          0.247368
1     -0.310907          0.998995             0.888863          0.130839
2     -0.299769         -1.447819            -1.975969         -1.150976
3      0.208801         -0.318520             0.285741          0.480425
4      0.456831          0.057913             0.059570          0.014311

   ALSFRS_Total_range  …  Sodium_min  Sodium_range  trunk_max  trunk_median  \
0           -0.301588  …    2.300470      0.260968   1.028018      0.981832
1            0.166537  …   -0.278144     -0.489913   1.028018      0.981832
2           -0.064100  …    1.195350     -0.654169  -0.688950     -2.280669
3           -0.685524  …    0.458603     -0.272701  -0.688950      0.049689
4           -0.350529  …    0.458603     -0.722774  -0.116627     -0.416383

   trunk_min  trunk_range  Urine.Ph_max  Urine.Ph_median  Urine.Ph_min  \
0   1.715365    -0.997420     -0.880376         0.463054      1.868532
1   0.867032    -0.388669      0.192665        -1.137208     -0.419151
2  -1.253800     0.398249     -0.880376        -1.137208     -0.419151
3   0.018699    -0.477181      0.192665         0.463054     -0.419151
4  -0.829634     0.300598     -0.880376        -1.137208     -0.419151

   cluster_labels
0               0
1               6
2               5
3               2
4               6

[5 rows x 100 columns]
```

6. Fit a PCA transformation with two features to the scaled data.

[43]:
```
# 6. Fit a PCA transformation with two features to the scaled data.
# Fit PCA transformation with two features
pca = PCA(n_components=2)
pca_result = pca.fit_transform(scaled_data)
```

```
# Create a new DataFrame with the PCA results
pca_df = pd.DataFrame(data=pca_result, columns=['PC1', 'PC2'])

# Display the DataFrame with PCA results
print("DataFrame with PCA Results:")
pca_df.head()
```

```
DataFrame with PCA Results:
```

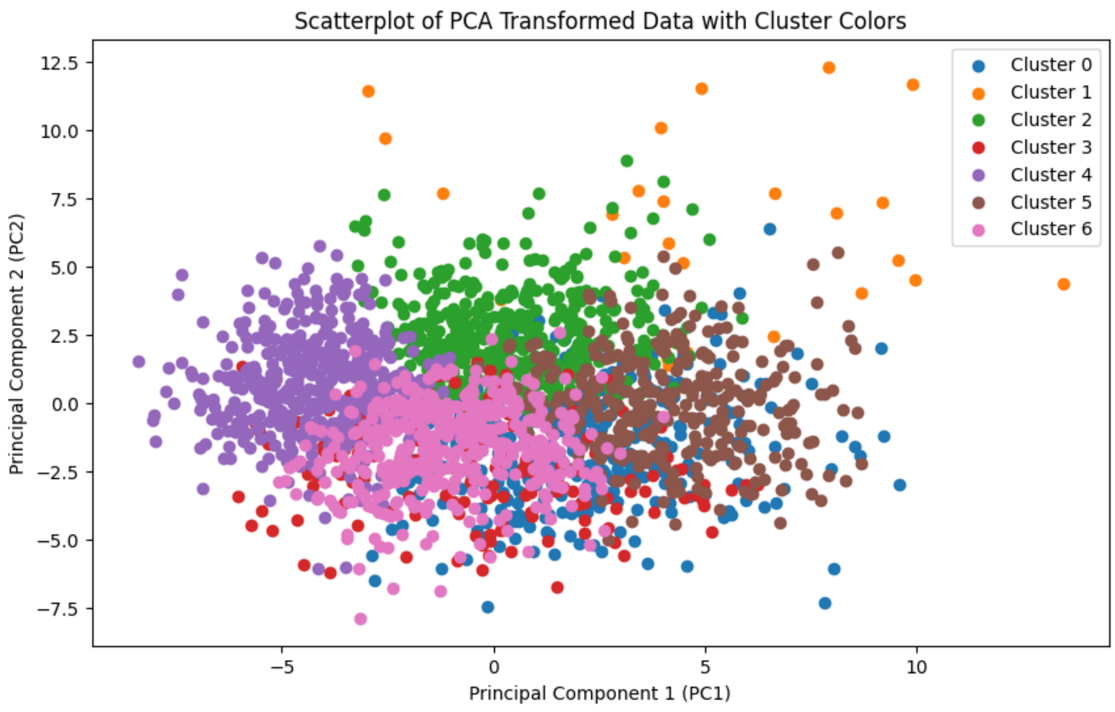
[43]:

```
        PC1       PC2
0 -1.426768 -2.320223
1 -1.440195 -4.870052
2  1.617824 -0.430010
3 -1.919997  2.096063
4  0.297701  0.166783
```

7. Make a scatterplot the PCA transformed data coloring each point by its cluster value.

[44]:

```
# 7. Make a scatterplot the PCA transformed data coloring each point by its␣
 ↪cluster value.

pca_df['Cluster'] = dataset1_csv['cluster_labels']
# Scatterplot with cluster colors
plt.figure(figsize=(10, 6))
for cluster_label in range(optimal_num_clusters):
    cluster_data = pca_df[pca_df['Cluster'] == cluster_label]
    plt.scatter(cluster_data['PC1'], cluster_data['PC2'], label=f'Cluster␣
 ↪{cluster_label}')

plt.title('Scatterplot of PCA Transformed Data with Cluster Colors')
plt.xlabel('Principal Component 1 (PC1)')
plt.ylabel('Principal Component 2 (PC2)')
plt.legend()
plt.show()
```



```
[45]: # Count of records in each cluster
      cluster_counts = dataset1_csv['cluster_labels'].value_counts()

      # Display the count of records in each cluster
      print("Record Count in Each Cluster:")
      print(cluster_counts)
```

```
Record Count in Each Cluster:
cluster_labels
4    472
2    466
6    419
0    338
5    331
3    171
1     26
Name: count, dtype: int64
```

8. Summarize your results and make a conclusion. **The analysis aimed to uncover patterns and relationships within ALS patient data by combining K-means clustering and PCA. The silhouette score plot was used to determine the optimal number of clusters, and a K-means model was applied to assign cluster labels to the data. PCA was then employed to reduce the dimensionality of the data for visualization. The scatterplot of the PCA-transformed data with cluster colors provides insights into the grouping of ALS patients based on the identified features.

The visual representation aids in understanding potential clusters or patterns that may exist in the data.

Cluster 2 ,4,5,6 –> Majority of the records are under these clusters, and they are well distributed. These clusters data provide the grouping of ALS patients based the diagnosis data. Which will help to do patterns analysis.

Cluster 0 & 3 –> records are spread out across another zone. Looks like more data cleanup required or we are considering unwanted rows/columns which causing the overlapping clustering.

Cluster 1 –> There are only 26 records out of 2.2k records, These may the rare scenarios or outlier.

**Further domain-specific knowledge and additional statistical assessments may be needed to draw meaningful conclusions and insights from the clustering and dimensionality reduction results

[ ]:
```

```