rwnwhtrl1

September 13, 2023

[2]:
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# Assignment: PCA Implementation
# Objective: The objective of this assignment is to implement PCA on a given␣
↪dataset and analyse the results.
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[1]:
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# Instructions:

# Download the wine dataset from the UCI Machine Learning Repository

# Load the dataset into a Pandas dataframe.

# Split the dataset into features and target variables.

# Perform data preprocessing (e.g., scaling, normalisation, missing value␣
↪imputation) as necessary.

# Implement PCA on the preprocessed dataset using the scikit-learn library.

# Determine the optimal number of principal components to retain based on the␣
↪explained variance ratio.

# Visualise the results of PCA using a scatter plot.

# Perform clustering on the PCA-transformed data using K-Means clustering␣
↪algorithm.

# Interpret the results of PCA and clustering analysis.
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# Deliverables:

# Jupyter notebook containing the code for the PCA implementation.

# A report summarising the results of PCA and clustering analysis.

# Scatter plot showing the results of PCA.

# A table showing the performance metrics for the clustering algorithm.

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# Additional Information:

# You can use the python programming language.

# You can use any other machine learning libraries or tools as necessary.

# You can use any visualisation libraries or tools as necessary.
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[7]:
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pip install requests
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Requirement already satisfied: requests in /opt/conda/lib/python3.10/site-
packages (2.28.1)
Requirement already satisfied: urllib3<1.27,>=1.21.1 in
/opt/conda/lib/python3.10/site-packages (from requests) (1.26.13)
Requirement already satisfied: certifi>=2017.4.17 in
/opt/conda/lib/python3.10/site-packages (from requests) (2022.12.7)
Requirement already satisfied: idna<4,>=2.5 in /opt/conda/lib/python3.10/site-
packages (from requests) (3.4)
Requirement already satisfied: charset-normalizer<3,>=2 in
/opt/conda/lib/python3.10/site-packages (from requests) (2.1.1)
Note: you may need to restart the kernel to use updated packages.
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import pandas as pd
import requests
from io import StringIO

# Url Of The Wine Dataset
url = "https://archive.ics.uci.edu/ml/machine-learning-databases/wine/wine.data"

# Send A GET Request To Download The Dataset
response = requests.get(url)

# Check If The Request Was Successful (Status Code 200)
if response.status_code == 200:
    # Create A Pandas Dataframe From The Downloaded Data
    wine_data = pd.read_csv(StringIO(response.text), header=None)
    # Add Column Names To Match The 14 Columns In The Dataset
    wine_data.columns = ["Target", "Alcohol", "Malic Acid", "Ash", "Alcalinity␣
↪of Ash", "Magnesium", "Total Phenols", "Flavanoids", "Nonflavanoid Phenols",␣
↪"Proanthocyanins", "Color Intensity", "Hue", "OD280/OD315 of Diluted Wines",␣
↪"Proline"]
    # Display The First Few Rows Of The Dataset
    print(wine_data.head())

    # Save The Dataframe As A CSV File
    wine_data.to_csv('wine_dataset.csv', index=False)
```

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    print("DataFrame saved as 'wine_dataset.csv'")
else:
    print("Failed to download the dataset.")
```

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   Target  Alcohol  Malic Acid   Ash  Alcalinity of Ash  Magnesium  \
0       1    14.23        1.71  2.43               15.6        127
1       1    13.20        1.78  2.14               11.2        100
2       1    13.16        2.36  2.67               18.6        101
3       1    14.37        1.95  2.50               16.8        113
4       1    13.24        2.59  2.87               21.0        118

   Total Phenols  Flavanoids  Nonflavanoid Phenols  Proanthocyanins  \
0           2.80        3.06                  0.28             2.29
1           2.65        2.76                  0.26             1.28
2           2.80        3.24                  0.30             2.81
3           3.85        3.49                  0.24             2.18
4           2.80        2.69                  0.39             1.82

   Color Intensity   Hue  OD280/OD315 of Diluted Wines  Proline
0             5.64  1.04                          3.92     1065
1             4.38  1.05                          3.40     1050
2             5.68  1.03                          3.17     1185
3             7.80  0.86                          3.45     1480
4             4.32  1.04                          2.93      735
DataFrame saved as 'wine_dataset.csv'
```

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# Import Necessary Libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.datasets import load_wine
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans





# Step 1: Load The Wine Dataset From The Saved CSV File
wine_df = pd.read_csv('wine_dataset.csv')

# Assuming You Want To Use The 'target' Column As Labels
wine_labels = wine_df['Target']
wine_df = wine_df.drop(columns=['Target'])  # Drop The 'target' Column From The
 ↪Features
```

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# Step 2: Data Preprocessing
# Standardize the features (scaling)
scaler = StandardScaler()
wine_scaled = scaler.fit_transform(wine_df)
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# Step 3: Implement PCA

# Choose The Number Of Components (You Can Adjust This)
n_components = 2
pca = PCA(n_components=n_components)
pca_result = pca.fit_transform(wine_scaled)

# Step 4: Determine the Optimal Number of Components
explained_variance = pca.explained_variance_ratio_
cumulative_explained_variance = explained_variance.cumsum()

print(explained_variance)
print(cumulative_explained_variance)

# Explained Variance Ratio Is An Attribute Of A PCA Model In Scikit-learn That
 ↪Provides An Array Of Values.
# Each Value In This Array Represents The Proportion Of The Total Variance
 ↪Explained By A Single Principal Component.

# Cumsum() Is A Function That Calculates The Cumulative Sum Of Values In An
 ↪Array.
# In The Context Of PCA, It's Typically Used With Explained Variance Ratio.
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[0.36198848 0.1920749 ]
[0.36198848 0.55406338]
```

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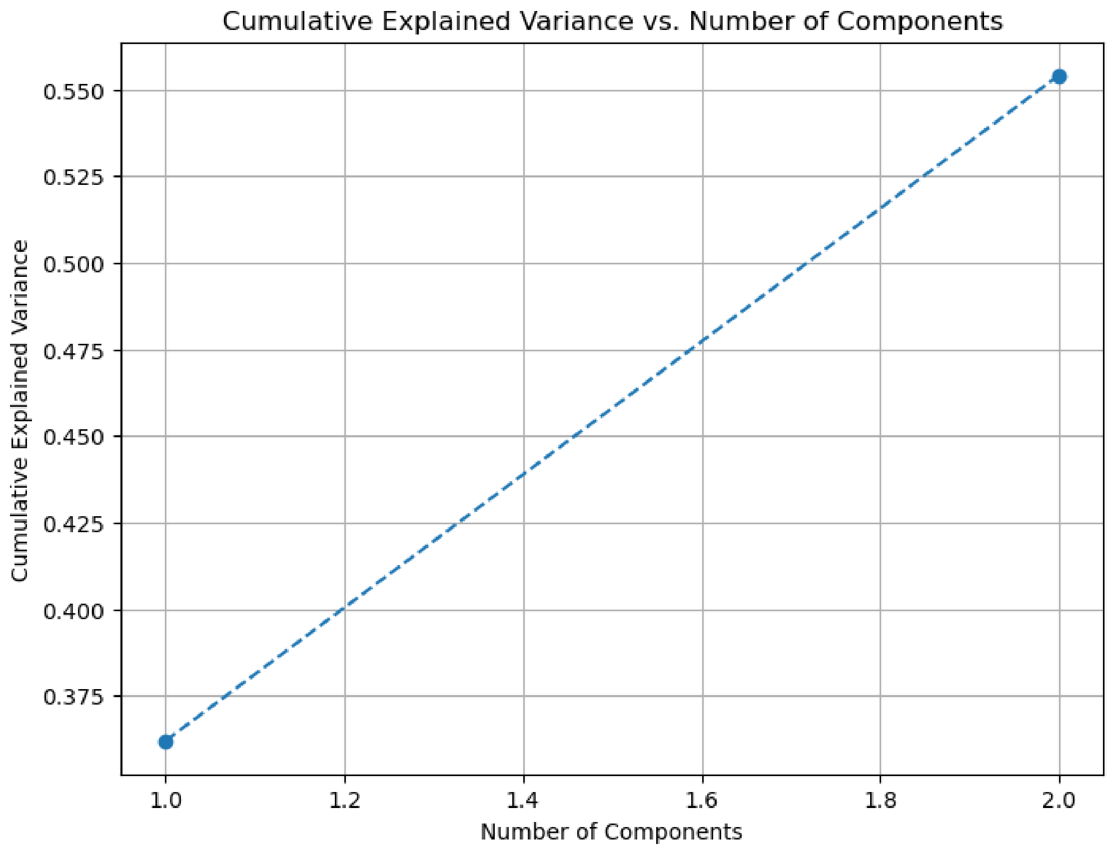
# Plot The Cumulative Explained Variance
plt.figure(figsize=(8, 6))
plt.plot(range(1, n_components + 1), cumulative_explained_variance, marker='o',
 ↪linestyle='--')
plt.xlabel('Number of Components')
plt.ylabel('Cumulative Explained Variance')
plt.title('Cumulative Explained Variance vs. Number of Components')
plt.grid(True)
plt.show()

# Based On The Plot, Determine The Optimal Number Of Components (E.g., Where
 ↪Explained Variance Saturates)
```



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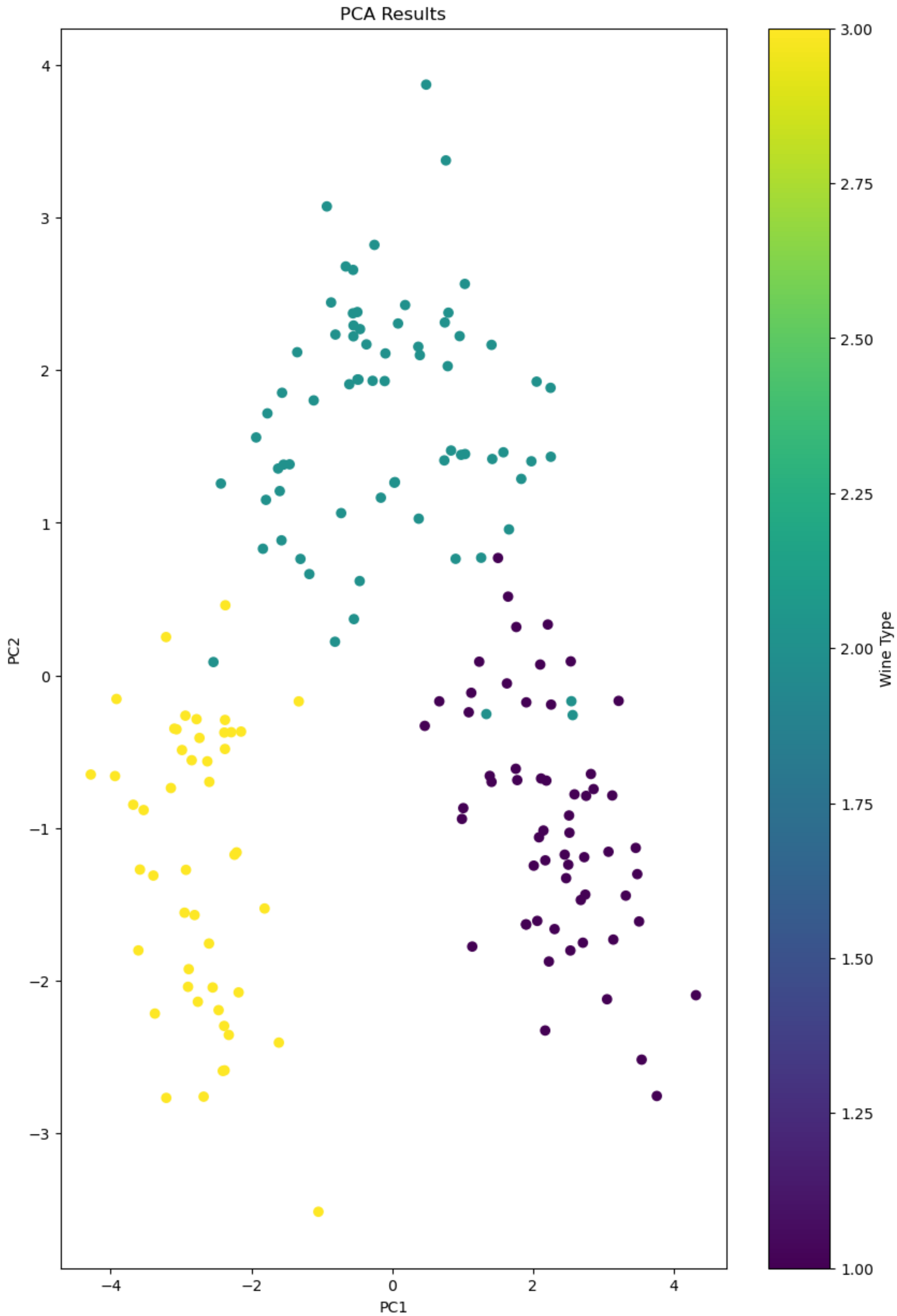
# Step 5: Visualize PCA Results
# Create A Scatter Plot Of The Data In The Reduced Dimensional Space
plt.figure(figsize=(10, 15))
plt.scatter(pca_result[:, 0], pca_result[:, 1], c=wine_labels, cmap='viridis')
plt.xlabel('PC1')
plt.ylabel('PC2')
plt.title('PCA Results')
plt.colorbar(label='Wine Type')
plt.show()
```


PCA Results
PC1
PC2
Wine Type
−4
−2
0
2
4
−3
−2
−1
0
1
2
3
4
1.00
1.25
1.50
1.75
2.00
2.25
2.50
2.75
3.00

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# Step 6: Perform Clustering (K-Means)
# Determine The Optimal Number Of Clusters Using Silhouette Score

from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score

# The Silhouette Score Is A Metric Used To Evaluate The Quality Of Clusters␣
↪Formed By A Clustering Algorithm, Such As K-means.

# Initialize An Empty List To Store Silhouette Scores
silhouette_scores = []

# Explore A Range Of Cluster Numbers From 2 To 10
for n_clusters in range(2, 11):
    # Create A K-means Clustering Model With The Current Number Of Clusters
    kmeans = KMeans(n_clusters=n_clusters, n_init=10) #  # Explicitly Set␣
↪n_init To 10


    # Fit The K-means Model To The Pca Result And Predict Cluster Labels
    cluster_labels = kmeans.fit_predict(pca_result)


    # Calculate The Silhouette Score For The Current Clustering
    silhouette_avg = silhouette_score(pca_result, cluster_labels)

    # Append The Silhouette Score To The List
    silhouette_scores.append(silhouette_avg)


print(silhouette_scores)
```

```
[0.46491409089201524, 0.5610505693103246, 0.4914213395710316,
0.45300766641841056, 0.430907848387192, 0.4234668858317838, 0.4071509089593133,
0.3966597727867158, 0.40126020559761083]
```

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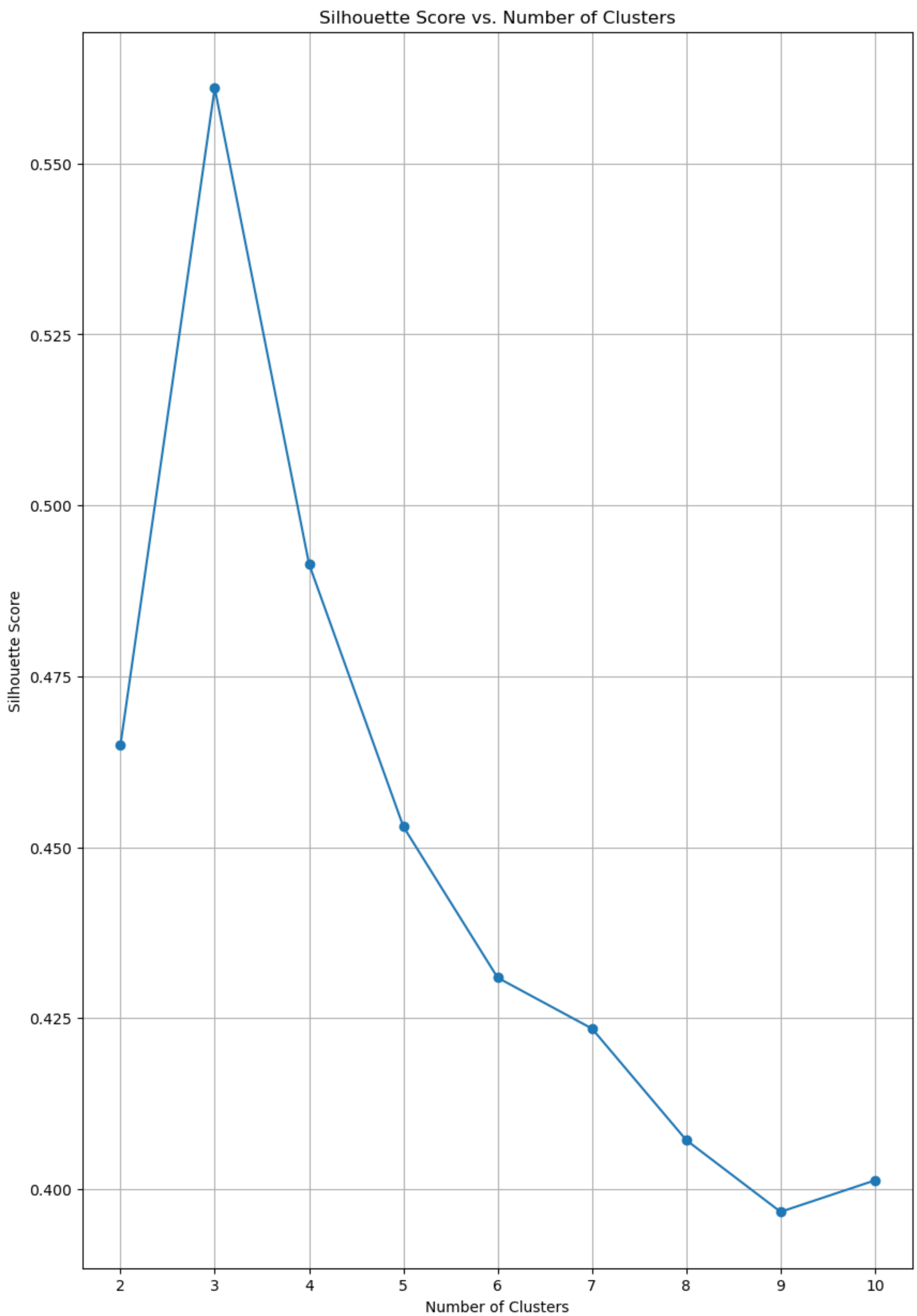
# Plot Silhouette Scores For Different Cluster Numbers
plt.figure(figsize=(10, 15))
plt.plot(range(2, 11), silhouette_scores, marker='o')
plt.xlabel('Number of Clusters')
plt.ylabel('Silhouette Score')
plt.title('Silhouette Score vs. Number of Clusters')
plt.grid(True)
plt.show()
```


Silhouette Score vs. Number of Clusters
Silhouette Score
0.550
0.525
0.500
0.475
0.450
0.425
0.400
2
3
4
5
6
7
8
9
10
Number of Clusters

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# Perform K-means Clustering With The Chosen Number Of Clusters

optimal_n_clusters = 3
kmeans = KMeans(n_clusters=optimal_n_clusters, n_init=10)
cluster_labels = kmeans.fit_predict(pca_result)
```

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# Step 7: Interpret Results
```