k-means-clustering-fl

April 11, 2025

```
[31]: import numpy as np
      import pandas as pd
      import matplotlib.pyplot as plt
      from sklearn.cluster import KMeans
      from sklearn.datasets import load_breast_cancer
      from sklearn.decomposition import PCA
      from sklearn.preprocessing import StandardScaler
[32]: # Load the Wisconsin Breast Cancer dataset
      data = load breast cancer()
      df = pd.DataFrame(data.data, columns=data.feature_names)
[33]: df.head
[33]: <bound method NDFrame.head of
                                          mean radius mean texture mean perimeter
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     worst concavity
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     worst fractal dimension
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3 0.17300
4 0.07678
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564 0.07115
565 0.06637
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567 0.12400
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```

[569 rows x 30 columns]>

[23]: df.keys()

[24]: df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 30 columns):

#	Column	Non-Null Count	Dtype
0	mean radius	569 non-null	float64
1	mean texture	569 non-null	float64
2	mean perimeter	569 non-null	float64
3	mean area	569 non-null	float64
4	mean smoothness	569 non-null	float64
5	mean compactness	569 non-null	float64
6	mean concavity	569 non-null	float64
7	mean concave points	569 non-null	float64
8	mean symmetry	569 non-null	float64
9	mean fractal dimension	569 non-null	float64
10	radius error	569 non-null	float64
11	texture error	569 non-null	float64
12	perimeter error	569 non-null	float64
13	area error	569 non-null	float64
14	smoothness error	569 non-null	float64
15	compactness error	569 non-null	float64

```
16 concavity error
                            569 non-null
                                            float64
   concave points error
                            569 non-null
                                            float64
17
18
   symmetry error
                            569 non-null
                                            float64
19 fractal dimension error
                            569 non-null
                                            float64
20 worst radius
                            569 non-null
                                            float64
21 worst texture
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                                            float64
22 worst perimeter
                            569 non-null
                                            float64
23 worst area
                            569 non-null
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24 worst smoothness
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                                            float64
25 worst compactness
                            569 non-null
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26 worst concavity
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                                            float64
27
   worst concave points
                            569 non-null
                                            float64
28 worst symmetry
                                            float64
                            569 non-null
29 worst fractal dimension
                            569 non-null
                                            float64
```

dtypes: float64(30) memory usage: 133.5 KB

[25]: df.isnull().sum()

[25]: mean radius 0 0 mean texture mean perimeter 0 mean area 0 mean smoothness 0 mean compactness 0 mean concavity mean concave points mean symmetry mean fractal dimension 0 radius error 0 texture error 0 perimeter error 0 area error 0 smoothness error compactness error concavity error 0 concave points error 0 symmetry error 0 fractal dimension error 0 worst radius 0 worst texture 0 worst perimeter worst area 0 worst smoothness 0 worst compactness 0 worst concavity 0 worst concave points 0

```
worst symmetry
                                 0
      worst fractal dimension
      dtype: int64
[26]: df.duplicated().sum()
[26]: 0
[27]: # Standardizing the features for better clustering performance
      scaler = StandardScaler()
      X_scaled = scaler.fit_transform(df)
[28]: # Apply K-Means Clustering
      num_clusters = 2 # We expect two clusters (malignant & benign)
      kmeans = KMeans(n clusters=num clusters, random state=42, n init=10)
      df['Cluster'] = kmeans.fit_predict(X_scaled)
[29]: # Reduce dimensionality to 2D using PCA for visualization
      pca = PCA(n_components=2)
      X_pca = pca.fit_transform(X_scaled)
      df['PCA1'] = X_pca[:, 0]
      df['PCA2'] = X_pca[:, 1]
[30]: # Transform centroids into PCA space
      centroids_pca = pca.transform(kmeans.cluster_centers_)
      # Plot clustering results
      plt.figure(figsize=(8, 6))
      plt.scatter(df['PCA1'], df['PCA2'], c=df['Cluster'], cmap='viridis', alpha=0.7,_
       ⇔edgecolors='k')
      plt.scatter(centroids_pca[:, 0], centroids_pca[:, 1], s=200, c='red',_
       →marker='X', label='Centroids')
      plt.xlabel('PCA Component 1')
      plt.ylabel('PCA Component 2')
      plt.title('K-Means Clustering on Breast Cancer Dataset')
      plt.legend()
      plt.show()
```



