Experiment 3: K-Means Clustering after PCA Dimensionality Reduction

Imports and Configuration

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%cd ..
from src.models.pca import PCA
from src.models.kmeans import KMeans, KMeansInit
from src.utils.metrics import *
from src.utils.utils import *

RANDOM_SEED = 42
np.random.seed(RANDOM_SEED)
```

```
c:\Users\ziade\OneDrive\Desktop\Term 7\ML\Lab 4\Assignment4-
Unsupervised-Clustering-Analysis
```

Data Loading and Preprocessing

```
X_scaled, y_true =
load_scale_data(data_path='./data/breast_cancer.csv')

print(f"Dataset shape: {X_scaled.shape}")
print(f"Labels shape: {y_true.shape}")
```

```
Dataset shape: (569, 30)
Labels shape: (569,)
```

Running PCA-KMeans

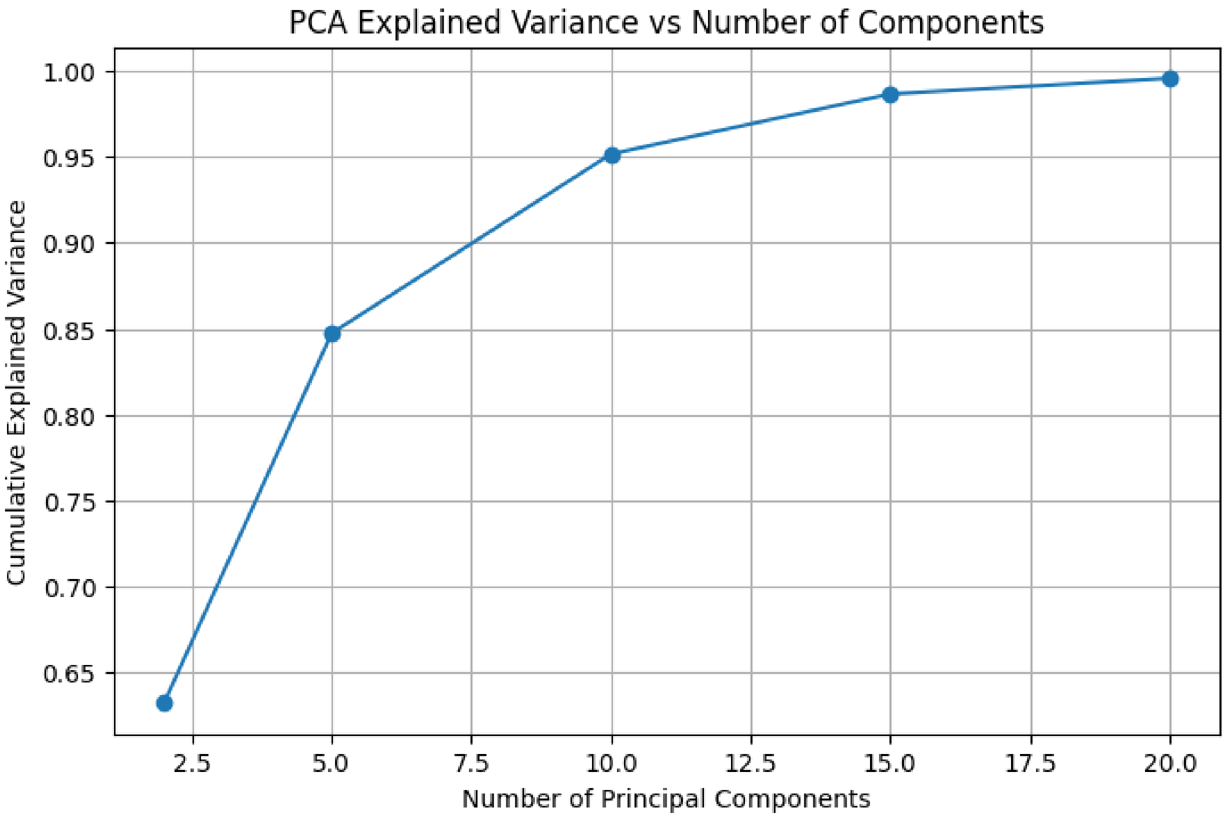
```
dims = [2, 5, 10, 15, 20]
exp3_results = []

for d in dims:
    # 1. Dimensionality Reduction
    pca = PCA(n_components=d)
    X_reduced = pca.fit_transform(X_scaled)
    recon_error = pca.reconstruction_error(X_scaled)
    var_ratio = np.sum(pca.explained_variance_ratio_)

    # 2. Clustering
    km = KMeans(K=2, init=KMeansInit.KMEANS_PLUS_PLUS,
random_state=42)
```

```
    km.fit(X_reduced)
    y_pred = km.clusters

    # 3. Validation Metrics
    sil = compute_silhouette_score(X_reduced, y_pred)
    db = compute_davies_bouldin(X_reduced, y_pred)
    ari = compute_ari(y_true, y_pred)
    purity = purity_score(y_true, y_pred)

    exp3_results.append({
        'Dimensions': d,
        'Reconstruction MSE': recon_error,
        'Explained Var': var_ratio,
        'Silhouette': sil,
        'Davies-Bouldin': db,
        'ARI': ari,
        'Purity': purity
    })

results_df = pd.DataFrame(exp3_results)
results_df
```

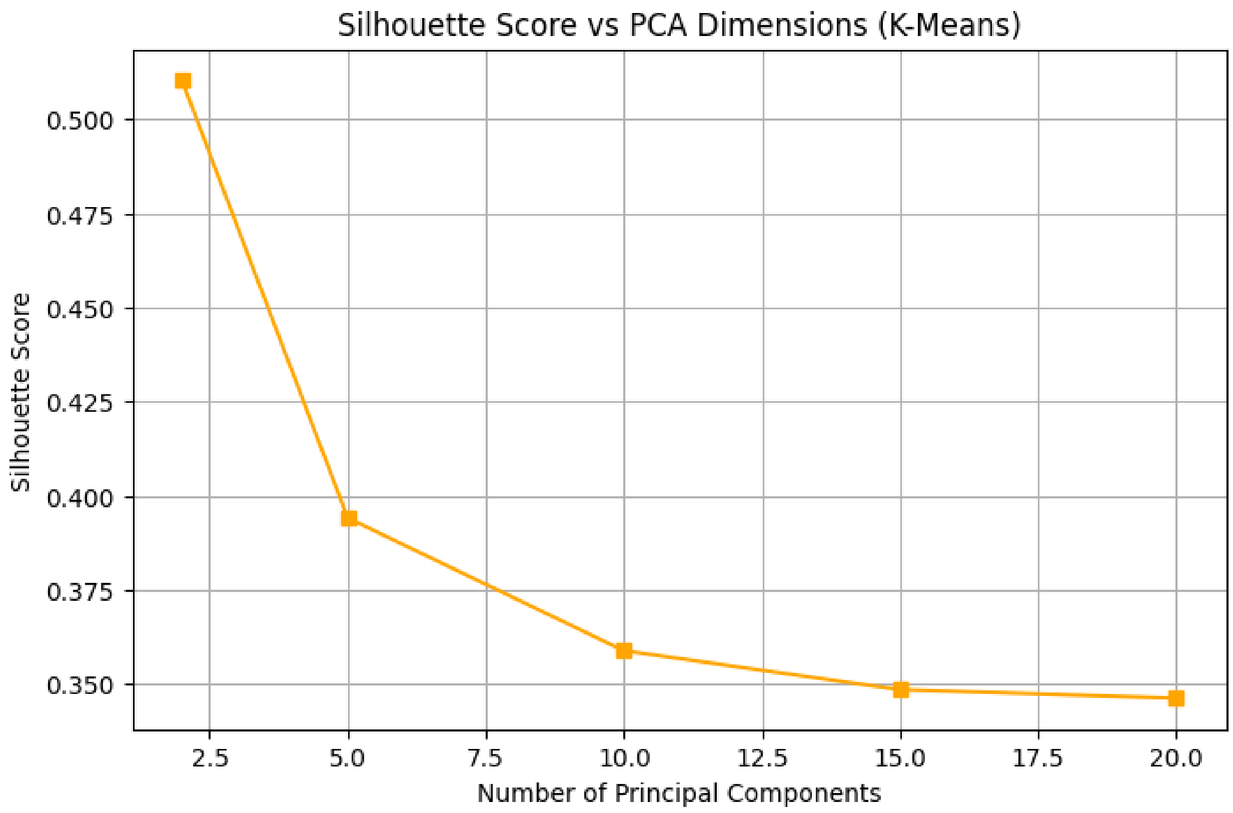
```
   Dimensions  Reconstruction MSE  Explained Var  Silhouette  Davies-
Bouldin  \
0           2            0.367567       0.632432    0.510358
0.846740
1           5            0.152657       0.847343    0.394124
1.148901
2          10            0.048431       0.951569    0.358843
1.267900
3          15            0.013512       0.986488    0.348497
1.306472
4          20            0.004428       0.995572    0.346259
1.315946

        ARI    Purity
0  0.659231  0.906854
1  0.653625  0.905097
2  0.653625  0.905097
3  0.659427  0.906854
4  0.659427  0.906854
```

Visualization - Reconstruction Error vs. Performance

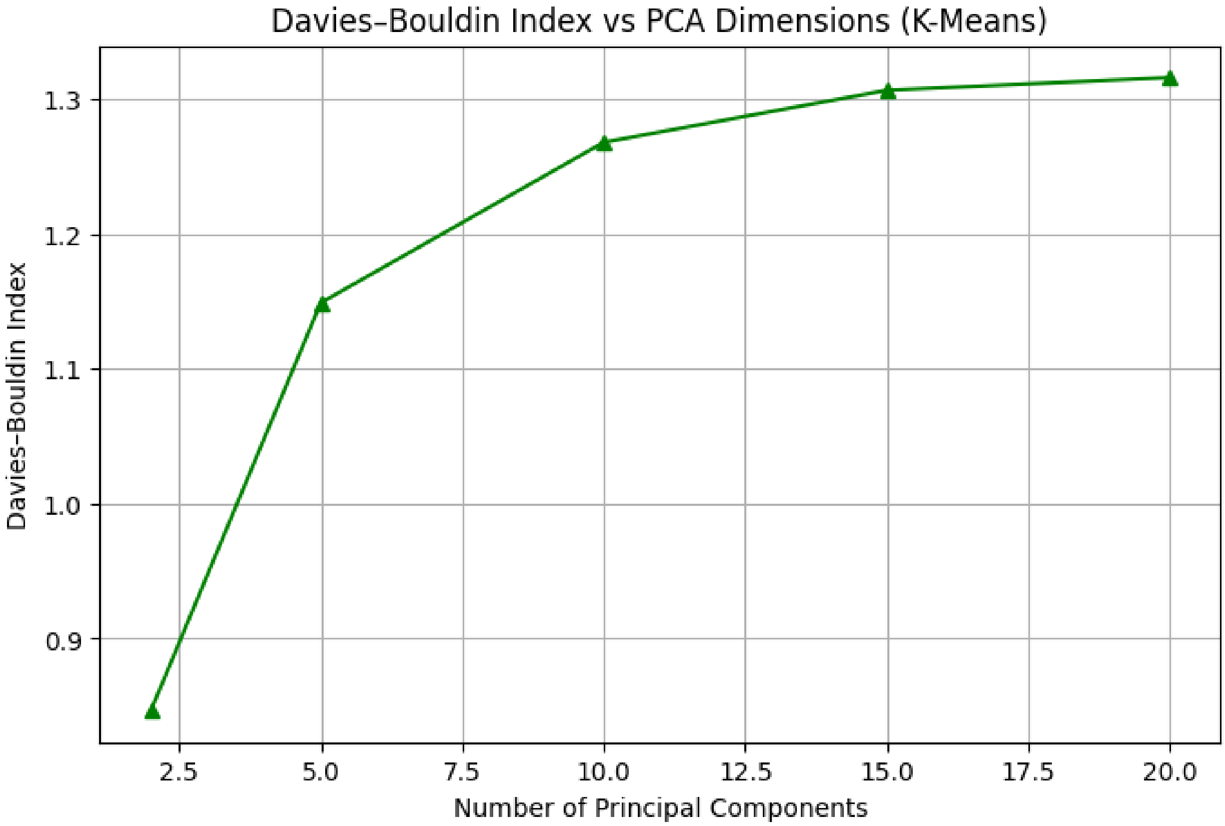
```
plt.figure(figsize=(8, 5))
plt.plot(dims, results_df['Explained Var'], marker='o')
plt.xlabel("Number of Principal Components")
plt.ylabel("Cumulative Explained Variance")
plt.title("PCA Explained Variance vs Number of Components")
plt.grid(True)
plt.show()
```



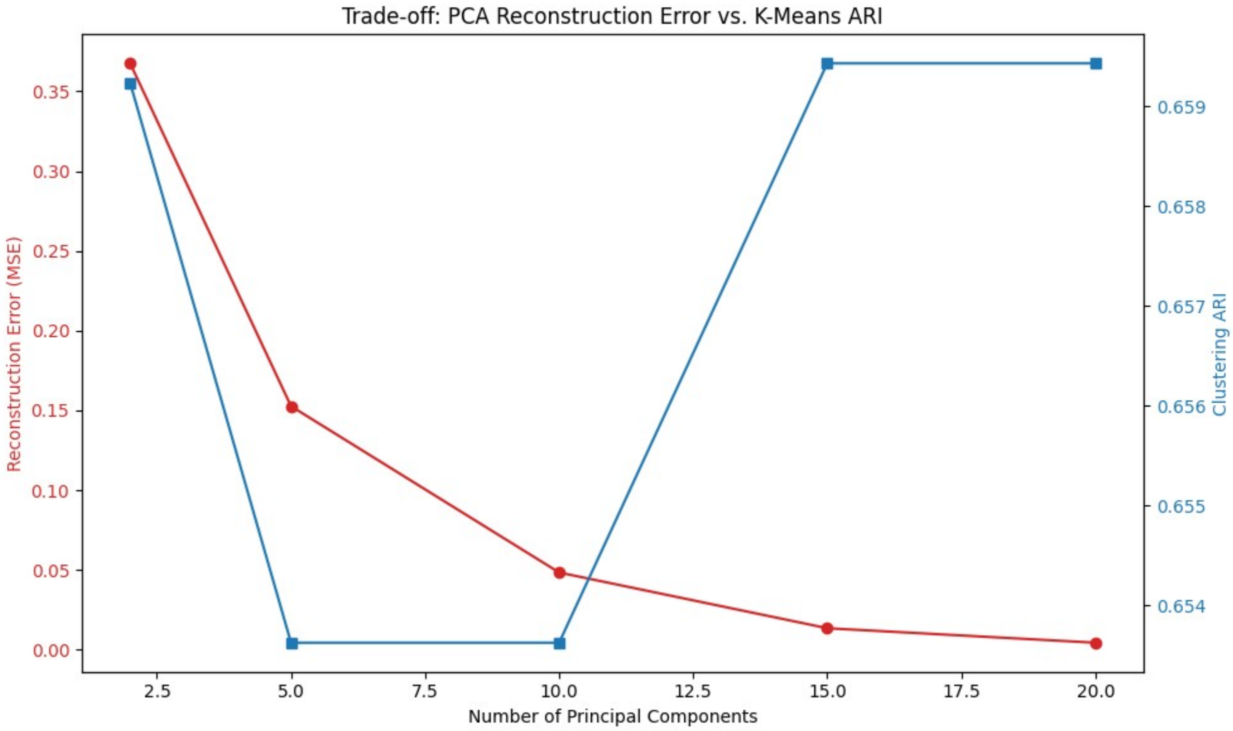
```
plt.figure(figsize=(8, 5))
plt.plot(dims, results_df['Silhouette'], marker='s', color='orange')
plt.xlabel("Number of Principal Components")
plt.ylabel("Silhouette Score")
plt.title("Silhouette Score vs PCA Dimensions (K-Means)")
plt.grid(True)
plt.show()
```



```python
plt.figure(figsize=(8, 5))
plt.plot(dims, results_df['Davies-Bouldin'], marker='^',
color='green')
plt.xlabel("Number of Principal Components")
plt.ylabel("Davies–Bouldin Index")
plt.title("Davies–Bouldin Index vs PCA Dimensions (K-Means)")
plt.grid(True)
plt.show()
```

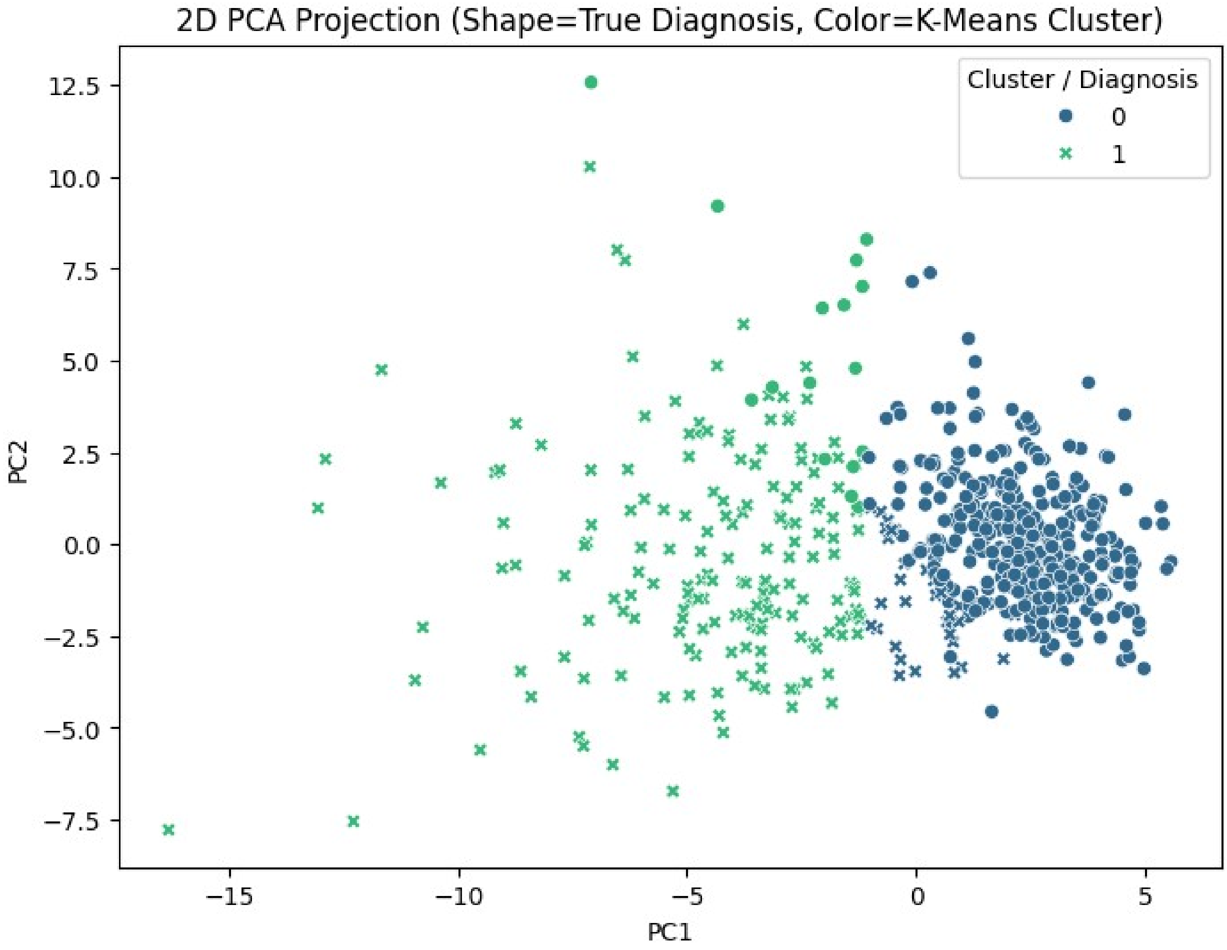


```
fig, ax1 = plt.subplots(figsize=(10, 6))

ax1.set_xlabel('Number of Principal Components')
ax1.set_ylabel('Reconstruction Error (MSE)', color='tab:red')
ax1.plot(dims, results_df['Reconstruction MSE'], marker='o',
color='tab:red', label='Reconstruction Error')
ax1.tick_params(axis='y', labelcolor='tab:red')

ax2 = ax1.twinx()
ax2.set_ylabel('Clustering ARI', color='tab:blue')
ax2.plot(dims, results_df['ARI'], marker='s', color='tab:blue',
label='ARI')
ax2.tick_params(axis='y', labelcolor='tab:blue')

plt.title('Trade-off: PCA Reconstruction Error vs. K-Means ARI')
fig.tight_layout()
plt.show()
```



2D Projection and Cluster Assignment

```
pca_2d = PCA(n_components=2)
X_2d = pca_2d.fit_transform(X_scaled)
km_2d = KMeans(K=2, init=KMeansInit.KMEANS_PLUS_PLUS, random_state=42)
km_2d.fit(X_2d)

plt.figure(figsize=(8, 6))
sns.scatterplot(x=X_2d[:, 0], y=X_2d[:, 1], hue=km_2d.clusters,
palette='viridis', style=y_true)
plt.title("2D PCA Projection (Shape=True Diagnosis, Color=K-Means
Cluster)")
plt.xlabel("PC1")
plt.ylabel("PC2")
plt.legend(title="Cluster / Diagnosis")
plt.show()
```


2D PCA Projection (Shape=True Diagnosis, Color=K-Means Cluster)
Cluster / Diagnosis
● 0
× 1
12.5
10.0
7.5
5.0
2.5
0.0
−2.5
−5.0
−7.5
PC2
−15
−10
−5
0
5
PC1