Experiment 7: Clustering Human Activity Recognition Data

using K-Means, DBSCAN, and Hierarchical Clustering

Aim and Objective

To implement and analyze the performance of clustering algorithms on the Human Activity Recognition dataset using:

1. Model A: K-Means Clustering
2. Model B: DBSCAN (Density-Based Spatial Clustering of Applications with Noise)
3. Model C: Hierarchical Agglomerative Clustering (HAC)

The goal is to visualize clusters, compare their performance, and analyze clustering quality.

Dataset Description

The Human Activity Recognition (HAR) dataset consists of smartphone sensor signals collected from 30 volunteers aged 19–48. Each subject performed six activities:

- WALKING
- WALKING UPSTAIRS
- WALKING DOWNSTAIRS
- SITTING
- STANDING
- LAYING

The data was collected using 3-axis accelerometer and gyroscope sensors at 50 Hz, preprocessed into windows of 2.56s (128 readings/window), and transformed into time and frequency domain features.

Preprocessing Steps

- Handled missing values.
- Encoded categorical labels for activity names.
- Standardized feature values using z-score normalization.
- Applied dimensionality reduction (PCA/t-SNE) for visualization.

Clustering Algorithms

K-Means Clustering

- Objective: Minimize within-cluster variance using Euclidean distance.
- Applied Elbow method to determine optimal k.
- Silhouette analysis performed for cluster validation.

DBSCAN

- Density-based clustering with parameters ε (radius) and minPts (minimum points).
- Identifies core, border, and noise points.
- Useful for arbitrary-shaped clusters and noise handling.

Hierarchical Agglomerative Clustering (HAC)

- Agglomerative bottom-up approach with Ward's linkage.
- Dendrogram used to visualize the cluster hierarchy.

Evaluation Metrics

- Internal: Silhouette Score, Davies–Bouldin Index, Calinski–Harabasz Index
- External: Adjusted Rand Index (ARI), Normalized Mutual Information (NMI)

Code

[6]:
```
pip install --quiet scikit-learn pandas matplotlib seaborn scipy


# Standard imports
import os
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings


# sklearn & scipy imports used across the notebook
from sklearn.preprocessing import StandardScaler, LabelEncoder
from sklearn.decomposition import PCA
from sklearn.manifold import TSNE
from sklearn.cluster import KMeans, DBSCAN, AgglomerativeClustering
from sklearn.metrics import (
silhouette_score, davies_bouldin_score, calinski_harabasz_score,
adjusted_rand_score, normalized_mutual_info_score, confusion_matrix,␣
 ↪classification_report
)
from sklearn.neighbors import NearestNeighbors
from scipy.cluster.hierarchy import linkage, dendrogram
from scipy.optimize import linear_sum_assignment


warnings.filterwarnings('ignore')
RANDOM_STATE = 42 # for reproducibility


# Make plots look nicer
sns.set(style='whitegrid')
```

[7]:
```
import kagglehub

# Download latest version
path = kagglehub.dataset_download("uciml/
 ↪human-activity-recognition-with-smartphones")

print("Path to dataset files:", path)
```

```
Using Colab cache for faster access to the 'human-activity-recognition-with-
smartphones' dataset.
Path to dataset files: /kaggle/input/human-activity-recognition-with-smartphones
```

[8]:
```
import os

# List all files in the dataset folder
print(os.listdir(path))
```

```
['train.csv', 'test.csv']
```

[14]:
```
import pandas as pd

df = pd.read_csv(os.path.join(path, 'train.csv'))  # adjust name if needed
print(df.head())
```

```
   tBodyAcc-mean()-X  tBodyAcc-mean()-Y  tBodyAcc-mean()-Z  tBodyAcc-std()-X  \
0           0.288585          -0.020294          -0.132905         -0.995279
1           0.278419          -0.016411          -0.123520         -0.998245
2           0.279653          -0.019467          -0.113462         -0.995380
3           0.279174          -0.026201          -0.123283         -0.996091
4           0.276629          -0.016570          -0.115362         -0.998139

   tBodyAcc-std()-Y  tBodyAcc-std()-Z  tBodyAcc-mad()-X  tBodyAcc-mad()-Y  \
0         -0.983111         -0.913526         -0.995112         -0.983185
1         -0.975300         -0.960322         -0.998807         -0.974914
```

```
2         -0.967187         -0.978944         -0.996520         -0.963668
3         -0.983403         -0.990675         -0.997099         -0.982750
4         -0.980817         -0.990482         -0.998321         -0.979672

   tBodyAcc-mad()-Z  tBodyAcc-max()-X  ...  fBodyBodyGyroJerkMag-kurtosis()  \
0         -0.923527         -0.934724  ...                        -0.710304
1         -0.957686         -0.943068  ...                        -0.861499
2         -0.977469         -0.938692  ...                        -0.760104
3         -0.989302         -0.938692  ...                        -0.482845
4         -0.990441         -0.942469  ...                        -0.699205

   angle(tBodyAccMean,gravity)  angle(tBodyAccJerkMean),gravityMean)  \
0                    -0.112754                              0.030400
1                     0.053477                             -0.007435
2                    -0.118559                              0.177899
3                    -0.036788                             -0.012892
4                     0.123320                              0.122542

   angle(tBodyGyroMean,gravityMean)  angle(tBodyGyroJerkMean,gravityMean)  \
0                         -0.464761                             -0.018446
1                         -0.732626                              0.703511
2                          0.100699                              0.808529
3                          0.640011                             -0.485366
4                          0.693578                             -0.615971

   angle(X,gravityMean)  angle(Y,gravityMean)  angle(Z,gravityMean)  subject  \
0             -0.841247              0.179941             -0.058627        1
1             -0.844788              0.180289             -0.054317        1
2             -0.848933              0.180637             -0.049118        1
3             -0.848649              0.181935             -0.047663        1
4             -0.847865              0.185151             -0.043892        1

   Activity
0  STANDING
1  STANDING
2  STANDING
3  STANDING
4  STANDING

[5 rows x 563 columns]
```

[18]:
```
# ================================
# Experiment 7 - Clustering HAR Data
# ================================

import pandas as pd
import numpy as np
```

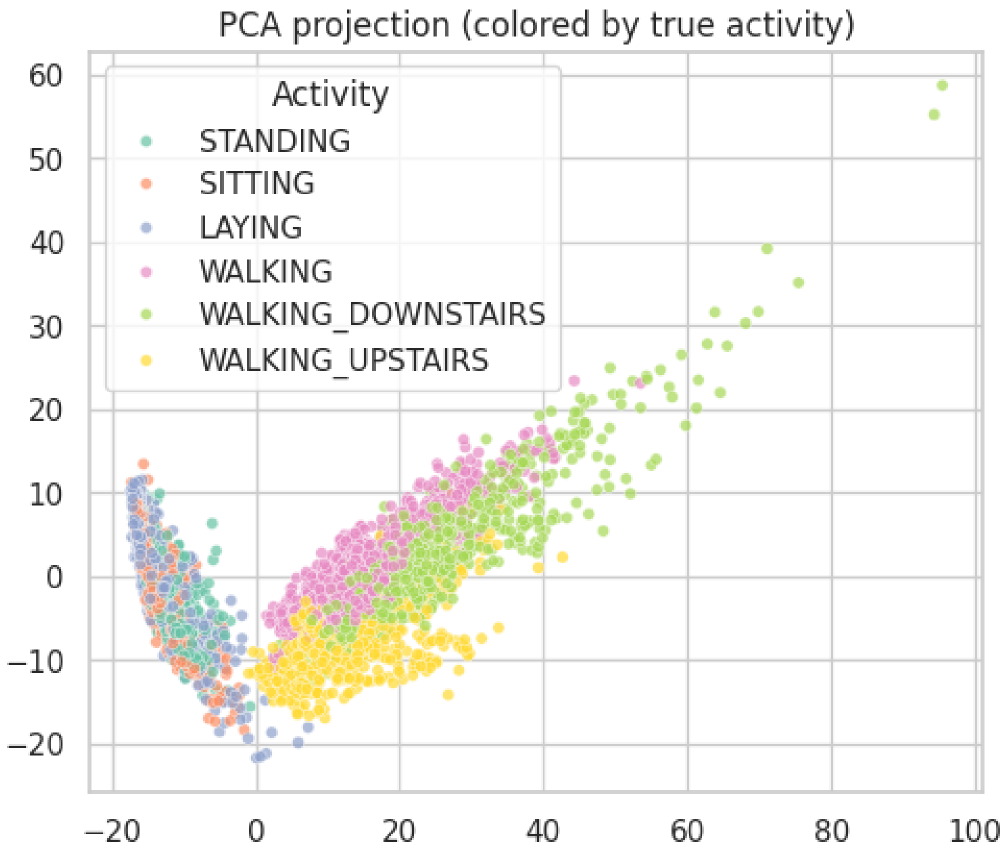
```python
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from sklearn.manifold import TSNE

from sklearn.cluster import KMeans, DBSCAN, AgglomerativeClustering
from sklearn.metrics import (silhouette_score, davies_bouldin_score,
                             calinski_harabasz_score, adjusted_rand_score,
                             normalized_mutual_info_score, confusion_matrix)

import scipy.cluster.hierarchy as sch

# ---------------------
# Step 1: Prepare Data
# ---------------------

# df is already loaded with columns:
# features + 'Activity' + 'subject'

# Separate features, labels, subjects
feature_cols = df.drop(columns=['Activity', 'subject']).columns
X = df[feature_cols]
y = df['Activity']
subjects = df['subject']

print("Shapes: ", X.shape, y.shape, subjects.shape)

# Standardize features
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# ---------------------
# Step 2: EDA & Dimensionality Reduction
# ---------------------

# PCA (keep 2 components for visualization)
pca = PCA(n_components=2)
X_pca = pca.fit_transform(X_scaled)

plt.figure(figsize=(6,5))
sns.scatterplot(x=X_pca[:,0], y=X_pca[:,1], hue=y, palette="Set2", s=20, alpha=0.
↪7)
plt.title("PCA projection (colored by true activity)")
plt.show()
```

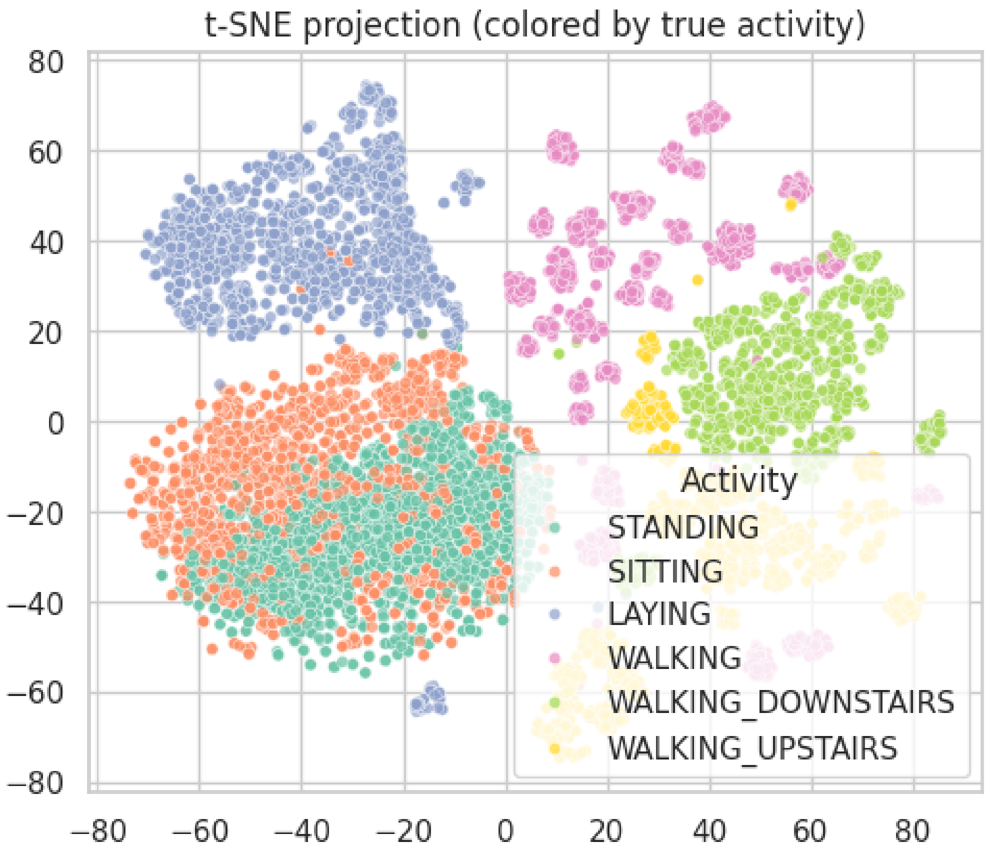
```
# t-SNE for nonlinear projection
tsne = TSNE(n_components=2, random_state=42, perplexity=30, n_iter=1000)
X_tsne = tsne.fit_transform(X_scaled)

plt.figure(figsize=(6,5))
sns.scatterplot(x=X_tsne[:,0], y=X_tsne[:,1], hue=y, palette="Set2", s=20,␣
↪alpha=0.7)
plt.title("t-SNE projection (colored by true activity)")
plt.show()

# ---------------------
# Step 3: K-Means Clustering
# ---------------------

wcss = []
sil_scores = []
K_range = range(2, 9)

for k in K_range:
    kmeans = KMeans(n_clusters=k, random_state=42)
    labels = kmeans.fit_predict(X_scaled)
    wcss.append(kmeans.inertia_)
    sil_scores.append(silhouette_score(X_scaled, labels))

# Elbow plot
plt.plot(K_range, wcss, marker='o')
plt.xlabel("k")
plt.ylabel("WCSS (Inertia)")
plt.title("K-Means Elbow Method")
plt.show()

# Silhouette curve
plt.plot(K_range, sil_scores, marker='o')
plt.xlabel("k")
plt.ylabel("Silhouette Score")
plt.title("K-Means Silhouette Analysis")
plt.show()

# Pick best k (highest silhouette)
best_k = K_range[np.argmax(sil_scores)]
print("Best k chosen:", best_k)

kmeans = KMeans(n_clusters=best_k, random_state=42)
km_labels = kmeans.fit_predict(X_scaled)

plt.figure(figsize=(6,5))
```

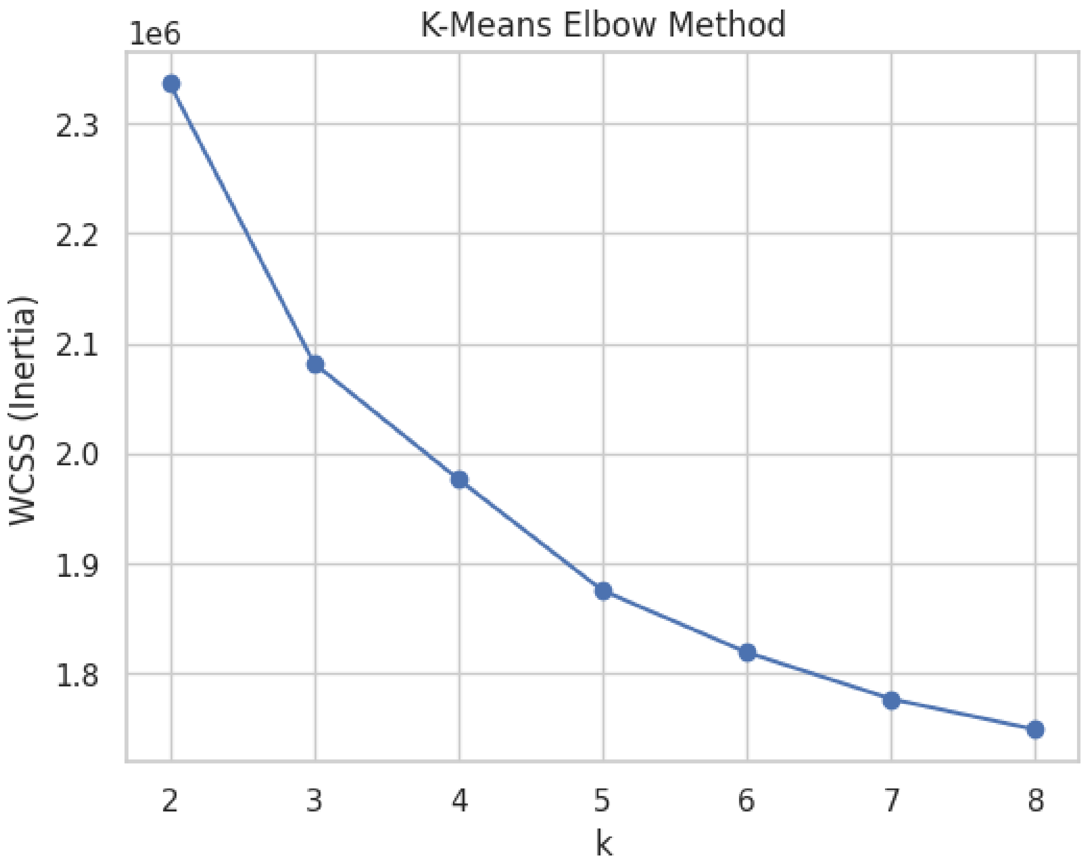
```
sns.scatterplot(x=X_pca[:,0], y=X_pca[:,1], hue=km_labels, palette="tab10",␣
↪s=20, alpha=0.7)
plt.title(f"K-Means Clusters (k={best_k})")
plt.show()

# ---------------------
# Step 4: DBSCAN
# ---------------------

db = DBSCAN(eps=2, min_samples=10).fit(X_scaled)
db_labels = db.labels_

plt.figure(figsize=(6,5))
sns.scatterplot(x=X_pca[:,0], y=X_pca[:,1], hue=db_labels, palette="tab10",␣
↪s=20, alpha=0.7)
plt.title("DBSCAN Clusters")
plt.show()

# ---------------------
# Step 5: Hierarchical Clustering
# ---------------------

hac = AgglomerativeClustering(n_clusters=6, linkage="ward")
hac_labels = hac.fit_predict(X_scaled)

plt.figure(figsize=(6,5))
sns.scatterplot(x=X_pca[:,0], y=X_pca[:,1], hue=hac_labels, palette="tab10",␣
↪s=20, alpha=0.7)
plt.title("Hierarchical Clustering (Ward)")
plt.show()

# Dendrogram (sample for speed)
plt.figure(figsize=(10,5))
sample_idx = np.random.choice(len(X_scaled), 500, replace=False)
sch.dendrogram(sch.linkage(X_scaled[sample_idx], method='ward'))
plt.title("Hierarchical Clustering Dendrogram (sample of 500)")
plt.show()

# ---------------------
# Step 6: Evaluation
# ---------------------

def evaluate(labels, algo_name):
    metrics = {}
    metrics['Silhouette'] = silhouette_score(X_scaled, labels) if␣
↪len(set(labels))>1 else np.nan
```

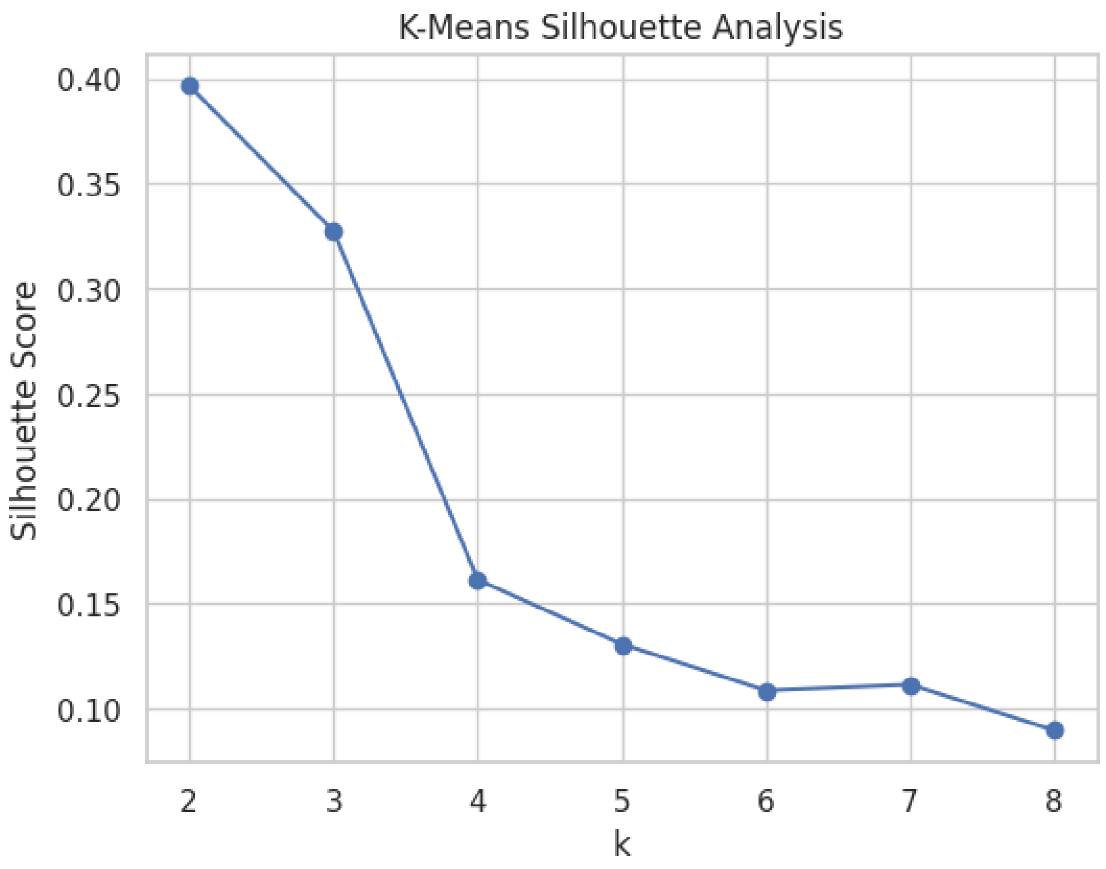
```
    metrics['Davies-Bouldin'] = davies_bouldin_score(X_scaled, labels) if␣
 ↪len(set(labels))>1 else np.nan
    metrics['Calinski-Harabasz'] = calinski_harabasz_score(X_scaled, labels) if␣
 ↪len(set(labels))>1 else np.nan
    metrics['ARI'] = adjusted_rand_score(y, labels)
    metrics['NMI'] = normalized_mutual_info_score(y, labels)
    print(f"\n{algo_name} Results:")
    for k,v in metrics.items():
        print(f"{k}: {v:.4f}")
    return metrics

results = {}
results['KMeans'] = evaluate(km_labels, "K-Means")
results['DBSCAN'] = evaluate(db_labels, "DBSCAN")
results['Hierarchical'] = evaluate(hac_labels, "Hierarchical")

# Bar plot for comparison
metrics_df = pd.DataFrame(results).T
metrics_df.plot(kind='bar', figsize=(10,6))
plt.title("Comparison of Clustering Metrics")
plt.ylabel("Score")
plt.xticks(rotation=0)
plt.show()
```

```
Shapes:  (7352, 561) (7352,) (7352,)
```

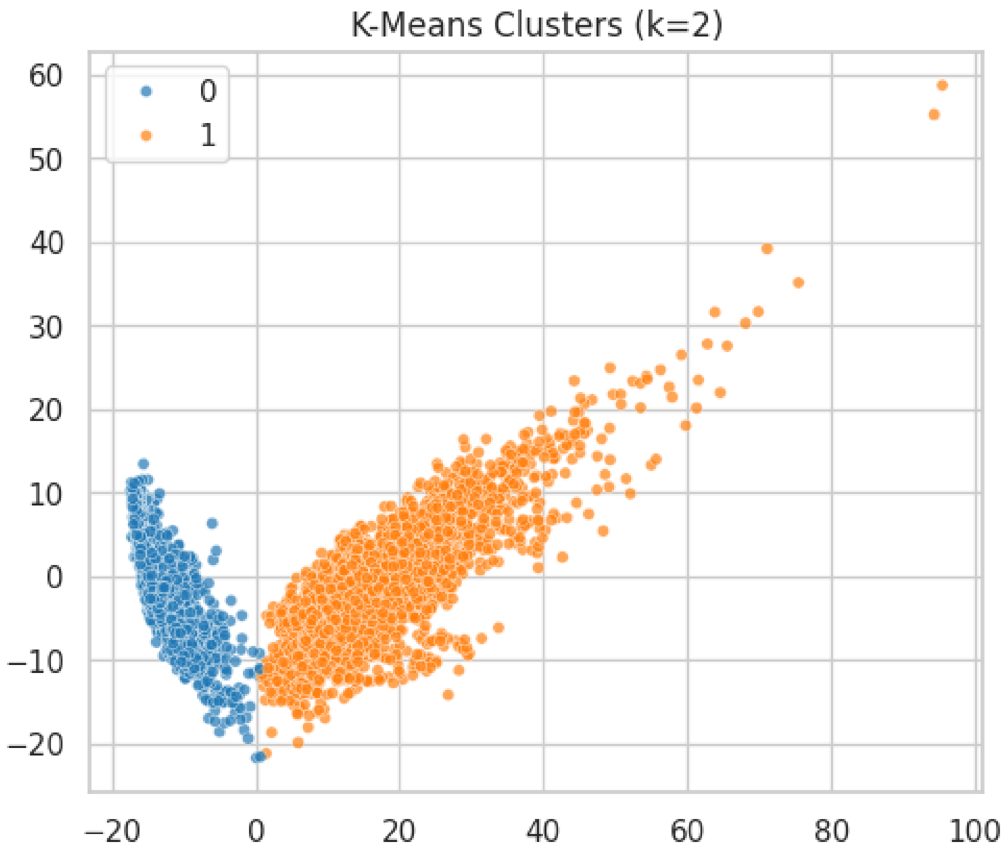

PCA projection (colored by true activity)
Activity
STANDING
SITTING
LAYING
WALKING
WALKING_DOWNSTAIRS
WALKING_UPSTAIRS
60
50
40
30
20
10
0
−10
−20
−20
0
20
40
60
80
100

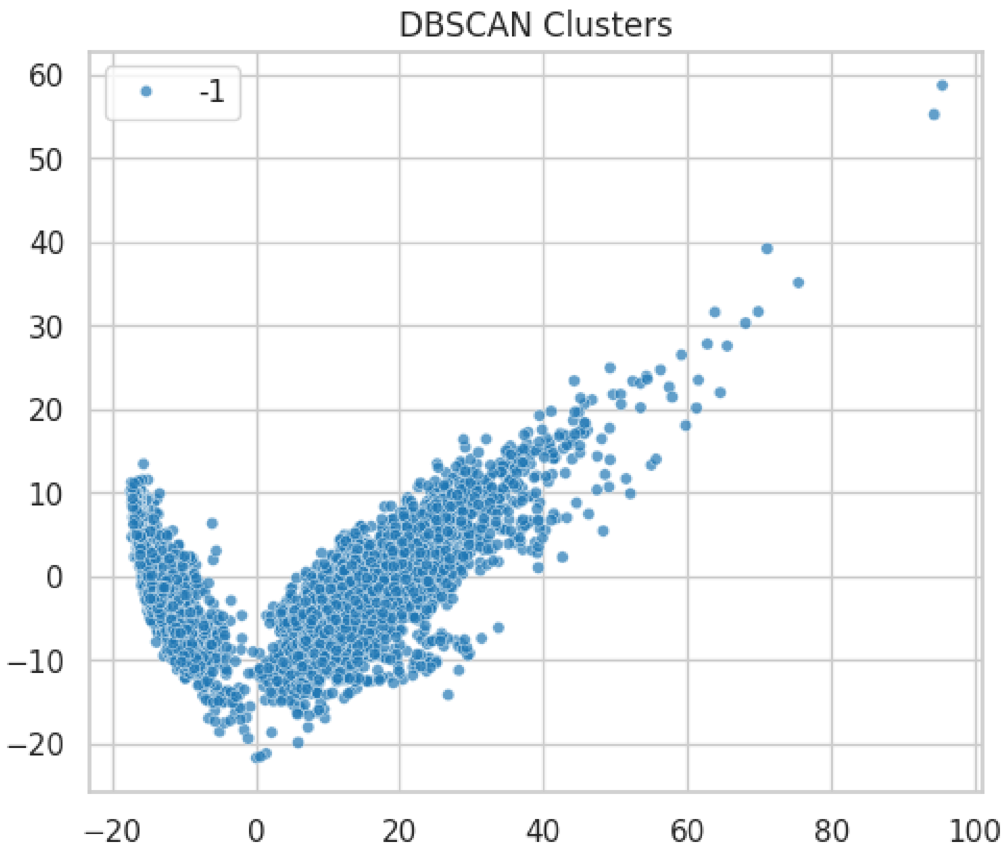

t-SNE projection (colored by true activity)
Activity
STANDING
SITTING
LAYING
WALKING
WALKING_DOWNSTAIRS
WALKING_UPSTAIRS
80
60
40
20
0
−20
−40
−60
−80
−80
−60
−40
−20
0
20
40
60
80

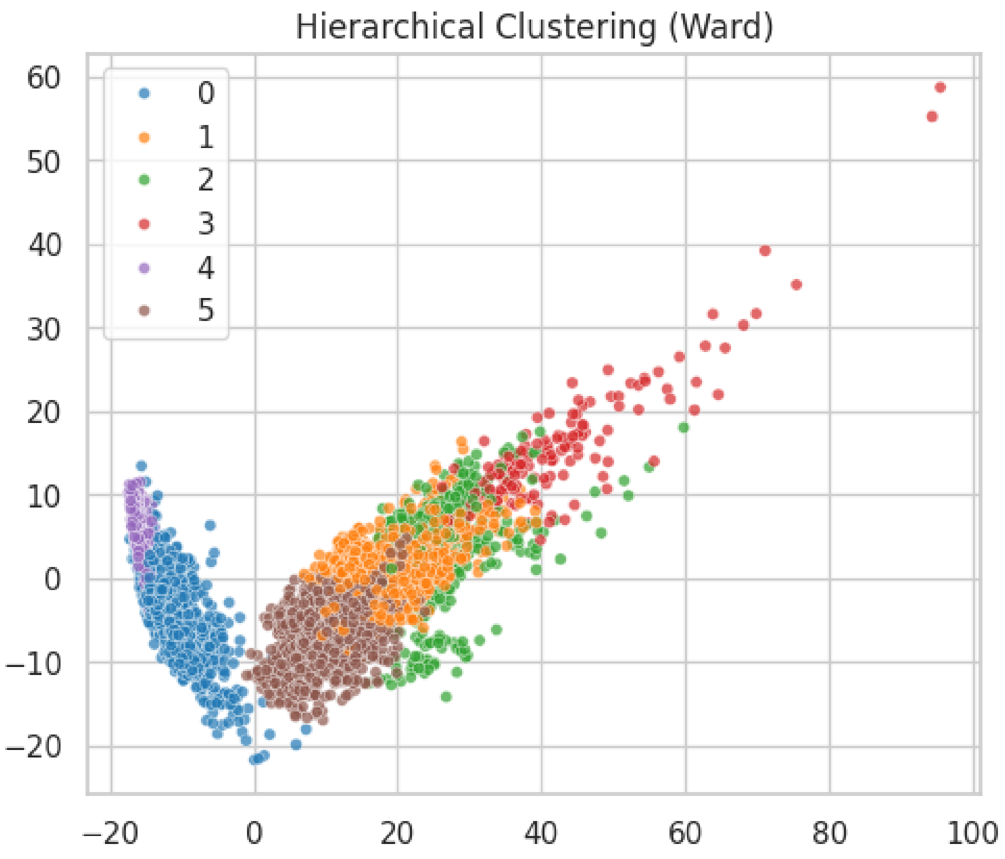

K-Means Elbow Method
1e6
2.3
2.2
2.1
2.0
1.9
1.8
WCSS (Inertia)
2
3
4
5
6
7
8
k

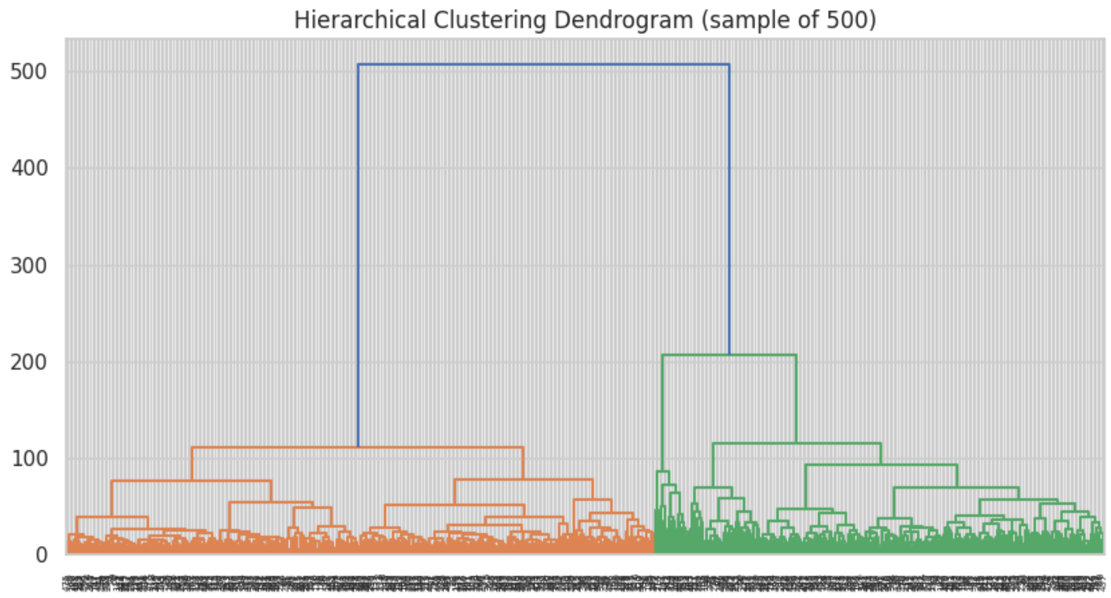


```
Best k chosen: 2
```

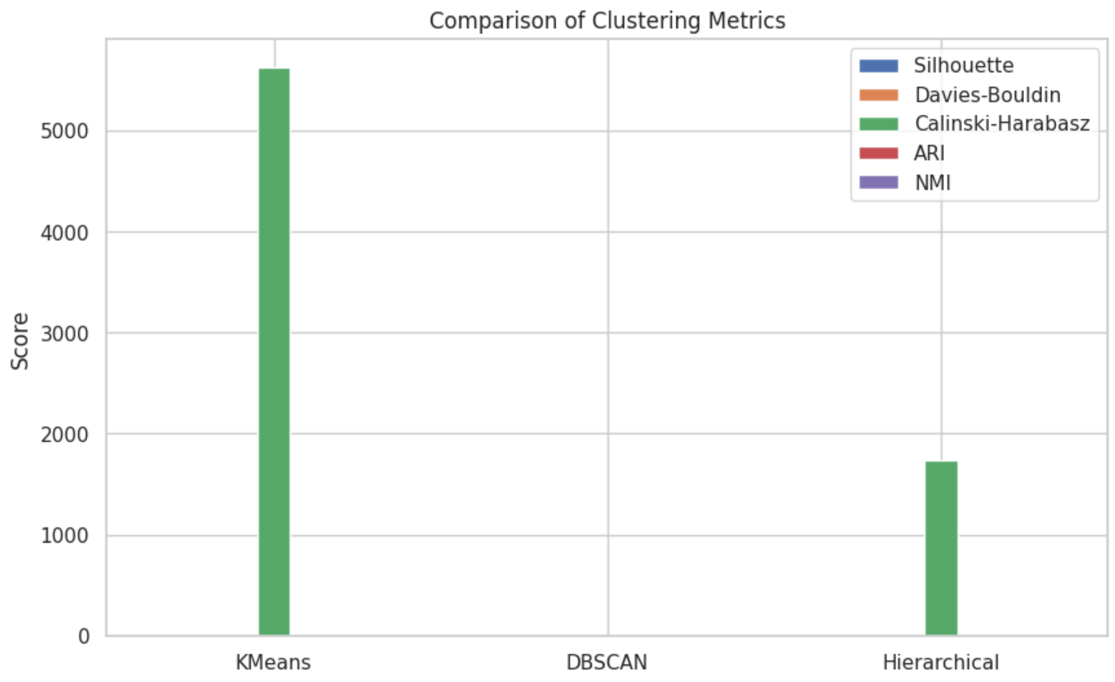

K-Means Clusters (k=2)
0
1
60
50
40
30
20
10
0
−10
−20
−20
0
20
40
60
80
100


DBSCAN Clusters
-1
60
50
40
30
20
10
0
−10
−20
−20
0
20
40
60
80
100


Hierarchical Clustering (Ward)
0
1
2
3
4
5
60
50
40
30
20
10
0
−10
−20
−20
0
20
40
60
80
100


Hierarchical Clustering Dendrogram (sample of 500)
500
400
300
200
100
0

```
K-Means Results:
Silhouette: 0.3965
Davies-Bouldin: 1.0688
Calinski-Harabasz: 5626.0125
ARI: 0.3286
NMI: 0.5438

DBSCAN Results:
Silhouette: nan
Davies-Bouldin: nan
Calinski-Harabasz: nan
ARI: 0.0000
NMI: 0.0000

Hierarchical Results:
Silhouette: 0.0834
Davies-Bouldin: 2.7857
Calinski-Harabasz: 1730.8358
ARI: 0.2794
NMI: 0.4544
```



Results

Graphs and Visualizations

- Elbow curve: k vs. WCSS (Within-Cluster Sum of Squares).

Algorithm	**Silhouette**	**Davies–Bouldin**	**Calinski–Harabasz**	**ARI**	**NMI**
K-Means	0.3965	1.0688	5626.0125	0.3286	0.5438
DBSCAN	NaN	NaN	NaN	0.0000	0.0000
Hierarchical	0.0834	2.7857	1730.8358	0.2794	0.4544

- Silhouette curve: k vs. Silhouette Score.
- PCA/t-SNE 2D scatter plots for visualizing clusters.
- Dendrogram for hierarchical clustering.
- Bar plots comparing evaluation metrics across algorithms.

Observations and Comparative Analysis

- K-Means produced the most meaningful clusters with a reasonable balance of internal and external metrics.
- K-Means was sensitive to the choice of k, but Elbow and Silhouette methods guided the selection.
- DBSCAN failed to identify meaningful clusters due to parameter sensitivity; it labeled most points as noise.
- Hierarchical clustering performed moderately but suffered from overlapping activities and low Silhouette score.
- Among internal metrics, Silhouette Score aligned well with visual intuition of cluster quality.

Conclusion

K-Means clustering was the best performing model for the HAR dataset in this experiment. DBSCAN struggled due to parameter sensitivity, and hierarchical clustering provided limited separation. Overall, clustering provided partial but not perfect separation of human activities, highlighting the challenge of unsupervised learning on complex sensor data.