data_mining_assignment4

December 11, 2024

1 Programming Assignment 4: Clustering Analysis

1.1 Imports and Settings

[1]:
```
import os
import ssl
import warnings
import xml.etree.ElementTree as ET
from pathlib import Path

import cv2
import matplotlib.pyplot as plt
import numpy as np
import torch
import torchvision.models as models
import torchvision.transforms as transforms
from PIL import Image
from sklearn.cluster import (
    DBSCAN,
    AgglomerativeClustering,
    BisectingKMeans,
    KMeans,
    SpectralClustering,
)
from sklearn.decomposition import PCA
from sklearn.metrics import fowlkes_mallows_score, silhouette_score
from sklearn.preprocessing import StandardScaler
from torch.utils.data import DataLoader

warnings.filterwarnings("ignore")
ssl._create_default_https_context = ssl._create_unverified_context
```

1.2 Define Constants and Directories

[2]:
```
base_image_directory = "./Dataset/Images"
base_annotation_directory = "./Dataset/Annotation"
grayscale_output_directory = "./Ass4/Grayscale_Images"
edge_histograms_output_directory = "./Ass4/EdgeHistograms"
```

```
cropped_images_output_directory = "./Ass4/Cropped"

crop_size = 224
dog_class_labels = [
    "n02087394-Rhodesian_ridgeback",
    "n02093256-Staffordshire_bullterrier",
    "n02097209-standard_schnauzer",
    "n02102318-cocker_spaniel",
]

Path(grayscale_output_directory).mkdir(parents=True, exist_ok=True)
Path(edge_histograms_output_directory).mkdir(parents=True, exist_ok=True)
Path(cropped_images_output_directory).mkdir(parents=True, exist_ok=True)
```

1.3 Define Helper Functions

[3]:
```
def extract_bounding_boxes(annotation_file):
    tree = ET.parse(annotation_file)
    root = tree.getroot()
    objects = root.findall("object")
    bounding_boxes = []
    for obj in objects:
        bbox = obj.find("bndbox")
        xmin = int(bbox.find("xmin").text)
        ymin = int(bbox.find("ymin").text)
        xmax = int(bbox.find("xmax").text)
        ymax = int(bbox.find("ymax").text)
        bounding_boxes.append((xmin, ymin, xmax, ymax))
    return bounding_boxes


def crop_and_resize_image(image_path, annotation_path, output_directory):
    image = Image.open(image_path)
    bounding_boxes = extract_bounding_boxes(annotation_path)
    cropped_images = []
    for bbox in bounding_boxes:
        cropped = image.crop(bbox)
        resized = cropped.resize((crop_size, crop_size), Image.Resampling.
 ↪LANCZOS)
        image_name = os.path.basename(image_path)
        save_path = os.path.join(output_directory, image_name)
        resized.convert("RGB").save(save_path)
        cropped_images.append(cropped)
    return image, cropped_images


def load_images(cropped_dir, classes):
```

```python
    image_paths = []
    labels = []
    transformation = transforms.Compose(
        [
            transforms.ToTensor(),
            transforms.Normalize(mean=[0.485, 0.456, 0.406], std=[0.229, 0.224,␣
↪0.225]),
        ]
    )
    for idx, dog_class in enumerate(classes):
        class_dir = os.path.join(cropped_dir, dog_class)
        if os.path.exists(class_dir):
            for img_file in os.listdir(class_dir):
                if img_file.endswith(".jpg"):
                    image_paths.append(os.path.join(class_dir, img_file))
                    labels.append(idx)
    return image_paths, labels, transformation


def extract_features(model, data_loader, device):
    feature_list = []
    label_list = []
    model.eval()
    with torch.no_grad():
        for images, batch_labels in data_loader:
            images = images.to(device)
            feature_maps = model(images)
            features = torch.mean(feature_maps, dim=[2, 3]).cpu().numpy()
            feature_list.extend(features)
            label_list.extend(batch_labels.numpy())
    return np.array(feature_list), np.array(label_list)


def compute_edge_histogram(image, bins=36):
    if len(image.shape) == 3:
        gray = cv2.cvtColor(image, cv2.COLOR_RGB2GRAY)
    else:
        gray = image
    sobelx = cv2.Sobel(gray, cv2.CV_64F, 1, 0, ksize=3)
    sobely = cv2.Sobel(gray, cv2.CV_64F, 0, 1, ksize=3)
    magnitude = np.sqrt(sobelx**2 + sobely**2)
    angle = np.arctan2(sobely, sobelx) * 180 / np.pi
    histogram = np.zeros(bins)
    for i in range(magnitude.shape[0]):
        for j in range(magnitude.shape[1]):
            if magnitude[i, j] > 30:
                bin_index = int((angle[i, j] + 180) * bins / 360)
```

```python
                if bin_index == bins:
                    bin_index = 0
                histogram[bin_index] += magnitude[i, j]
    if np.sum(histogram) > 0:
        histogram /= np.sum(histogram)
    return histogram


def process_images_and_pca(cropped_dir, classes):
    histograms = []
    labels = []
    for class_idx, dog_class in enumerate(classes):
        class_dir = os.path.join(cropped_dir, dog_class)
        if os.path.exists(class_dir):
            for img_file in os.listdir(class_dir):
                if img_file.endswith(".jpg"):
                    img_path = os.path.join(class_dir, img_file)
                    img = cv2.imread(img_path)
                    hist = compute_edge_histogram(img)
                    histograms.append(hist)
                    labels.append(class_idx)
    X = np.array(histograms)
    y = np.array(labels)
    scaler = StandardScaler()
    X_scaled = scaler.fit_transform(X)
    pca = PCA(n_components=2)
    X_pca = pca.fit_transform(X_scaled)
    return X_pca, y, pca.explained_variance_ratio_


def plot_pca(X, y, classes, title):
    plt.figure(figsize=(10, 8))
    colors = ["r", "g", "b", "y"]
    for i in range(len(classes)):
        mask = y == i
        plt.scatter(
            X[mask, 0],
            X[mask, 1],
            c=colors[i],
            label=classes[i].split("-")[1],
            alpha=0.6,
        )
    plt.xlabel("First Principal Component")
    plt.ylabel("Second Principal Component")
    plt.title(title)
    plt.legend()
    plt.show()
```

```python
def plot_clustering_results(X, cluster_labels, title):
    plt.figure(figsize=(10, 8))
    unique_labels = np.unique(cluster_labels)
    colors = plt.cm.viridis(np.linspace(0, 1, len(unique_labels)))
    for label, color in zip(unique_labels, colors):
        mask = cluster_labels == label
        label_name = "Noise" if label == -1 else f"Cluster {label}"
        plt.scatter(X[mask, 0], X[mask, 1], c=[color], label=label_name)
    plt.title(title)
    plt.xlabel("First Principal Component")
    plt.ylabel("Second Principal Component")
    plt.legend()
    plt.show()


def evaluate_clustering(method_name, predicted_labels, data, true_labels):
    if -1 in predicted_labels:
        mask = predicted_labels != -1
        fm = fowlkes_mallows_score(true_labels[mask], predicted_labels[mask])
        silhouette = silhouette_score(data[mask], predicted_labels[mask])
    else:
        fm = fowlkes_mallows_score(true_labels, predicted_labels)
        silhouette = silhouette_score(data, predicted_labels)
    return fm, silhouette
```

1.4 Image Processing and Feature Extraction

[4]:
```python
original_images = {}
cropped_images = {}
total_cropped = 0

for dog_class in dog_class_labels:
    image_dir = os.path.join(base_image_directory, dog_class)
    annotation_dir = os.path.join(base_annotation_directory, dog_class)
    output_dir = os.path.join(cropped_images_output_directory, dog_class)
    Path(output_dir).mkdir(parents=True, exist_ok=True)
    for img_file in os.listdir(image_dir):
        if img_file.endswith(".jpg"):
            image_path = os.path.join(image_dir, img_file)
            annotation_file = os.path.join(annotation_dir, img_file.replace(".
↪jpg", ""))
            if os.path.exists(annotation_file):
                orig_img, cropped = crop_and_resize_image(
                    image_path, annotation_file, output_dir
                )
```

```
                original_images[img_file] = orig_img
                cropped_images[img_file] = cropped
                total_cropped += len(cropped)
            else:
                print(f"Annotation missing for {img_file}, skipping.")

print(f"Total cropped images: {total_cropped}")
```

```
Total cropped images: 697
```

1.5 ResNet Feature Extraction

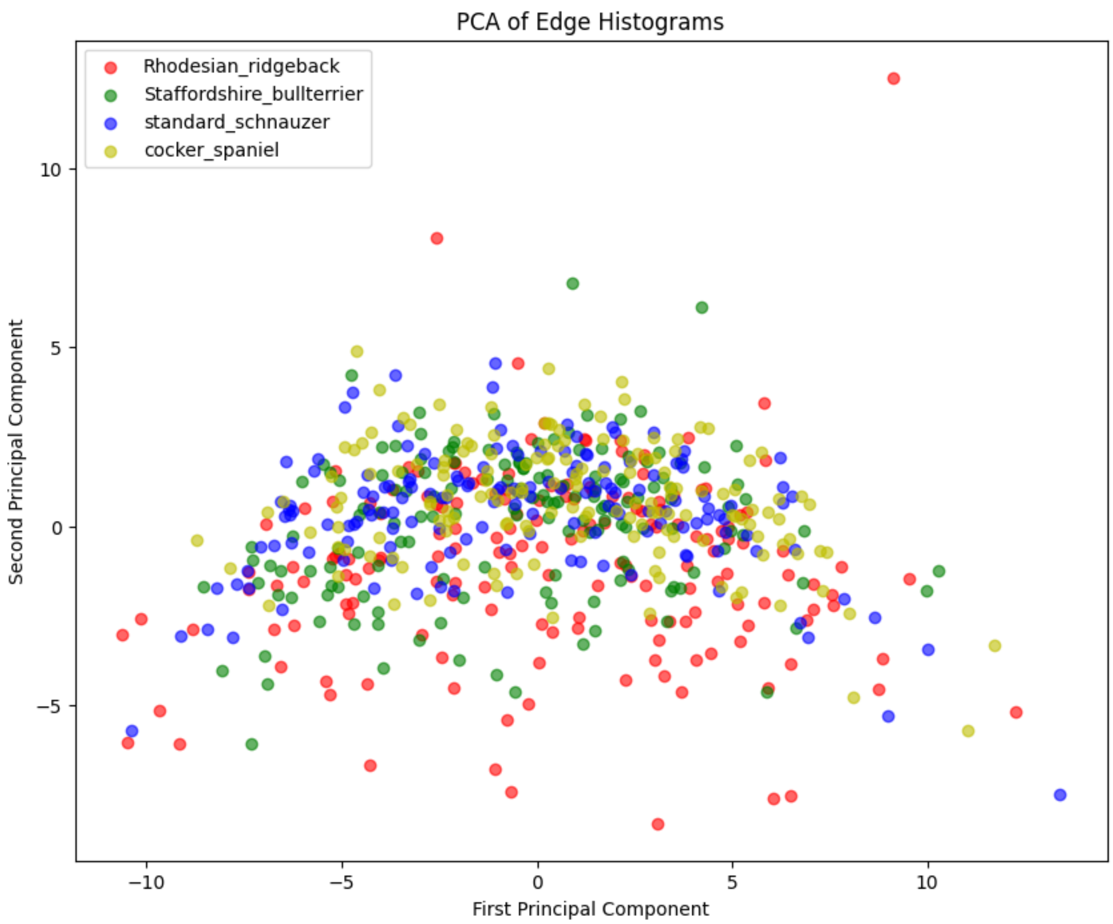
[5]:
```
device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
resnet_model = models.resnet18(pretrained=True)
resnet_model = torch.nn.Sequential(*(list(resnet_model.children())[:-2]))
resnet_model = resnet_model.to(device)

image_paths, image_labels, transform_pipeline = load_images(
    cropped_images_output_directory, dog_class_labels
)
dataset = [
    (
        transforms.ToPILImage()(transforms.ToTensor()(Image.open(path).
 ↪convert("RGB"))),
        label,
    )
    for path, label in zip(image_paths, image_labels)
]
tensor_images = torch.stack(
    [transform_pipeline(Image.open(path).convert("RGB")) for path in␣
 ↪image_paths]
)
tensor_labels = torch.tensor(image_labels)
data_loader = DataLoader(
    list(zip(tensor_images, tensor_labels)), batch_size=32, shuffle=False
)

print("Extracting ResNet features...")
resnet_features, resnet_labels = extract_features(resnet_model, data_loader,␣
 ↪device)
```

```
Extracting ResNet features…
```

1.6 Edge Histogram and PCA

[6]:
```
print("Computing edge histograms and performing PCA...")
edge_pca_features, edge_true_labels, explained_variance =␣
 ↪process_images_and_pca(
    cropped_images_output_directory, dog_class_labels
)
print("Explained variance ratio:", explained_variance)
plot_pca(
    edge_pca_features, edge_true_labels, dog_class_labels, "PCA of Edge␣
 ↪Histograms"
)
```

```
Computing edge histograms and performing PCA…
Explained variance ratio: [0.49122624 0.13395676]
```



1.7 Clustering Algorithms

[7]:
```python
def perform_kmeans(X, init_method, random_state=42):
    kmeans = KMeans(
        n_clusters=4, init=init_method, n_init=10, random_state=random_state
    )
    labels = kmeans.fit_predict(X)
    return labels


def perform_bisecting_kmeans(X, init_method, random_state=42):
    bisect_kmeans = BisectingKMeans(
        n_clusters=4, init=init_method, random_state=random_state
    )
    labels = bisect_kmeans.fit_predict(X)
    return labels


def perform_spectral_clustering(X, random_state=42):
    spectral = SpectralClustering(n_clusters=4, random_state=random_state)
    labels = spectral.fit_predict(X)
    return labels


def perform_dbscan(X, eps, min_samples):
    dbscan = DBSCAN(eps=eps, min_samples=min_samples)
    labels = dbscan.fit_predict(X)
    return labels


def perform_agglomerative_clustering(X, linkage):
    agglom = AgglomerativeClustering(n_clusters=4, linkage=linkage)
    labels = agglom.fit_predict(X)
    return labels


cluster_methods = {}

cluster_methods["K-means (Random Init)"] = perform_kmeans(
    edge_pca_features, init_method="random"
)
cluster_methods["K-means++"] = perform_kmeans(
    edge_pca_features, init_method="k-means++"
)
cluster_methods["Bisecting K-means"] = perform_bisecting_kmeans(
    edge_pca_features, init_method="random"
)
```

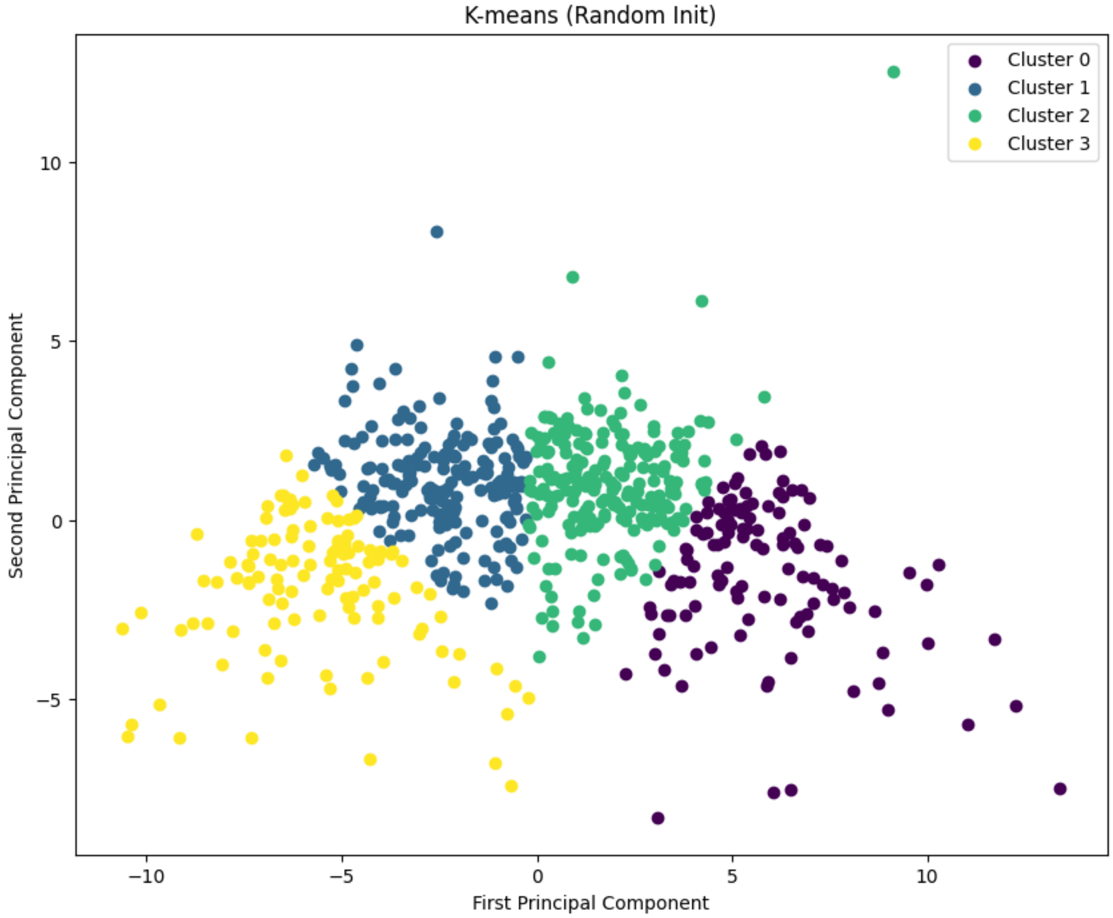
```
cluster_methods["Spectral Clustering"] =␣
↪perform_spectral_clustering(edge_pca_features)

# DBSCAN parameter selection
best_eps = 0
best_min_samples = 0
best_silhouette = -1
best_dbscan_labels = None

for eps in np.arange(0.1, 2.0, 0.1):
    for min_samples in range(2, 10):
        db_labels = perform_dbscan(edge_pca_features, eps, min_samples)
        unique_clusters = len(set(db_labels)) - (1 if -1 in db_labels else 0)
        if unique_clusters == 4:
            mask = db_labels != -1
            if np.sum(mask) > 1:
                score = silhouette_score(edge_pca_features[mask],␣
↪db_labels[mask])
                if score > best_silhouette:
                    best_silhouette = score
                    best_eps = eps
                    best_min_samples = min_samples
                    best_dbscan_labels = db_labels

if best_dbscan_labels is not None:
    cluster_methods["DBSCAN"] = best_dbscan_labels
    print(f"Best DBSCAN parameters: eps={best_eps},␣
↪min_samples={best_min_samples}")
else:
    print("No suitable DBSCAN parameters found for 4 clusters.")

linkage_methods = ["ward", "complete", "average", "single"]
for linkage in linkage_methods:
    agglom_labels = perform_agglomerative_clustering(edge_pca_features, linkage)
    cluster_methods[f"Agglomerative ({linkage})"] = agglom_labels
```

```
Best DBSCAN parameters: eps=0.2, min_samples=6
```

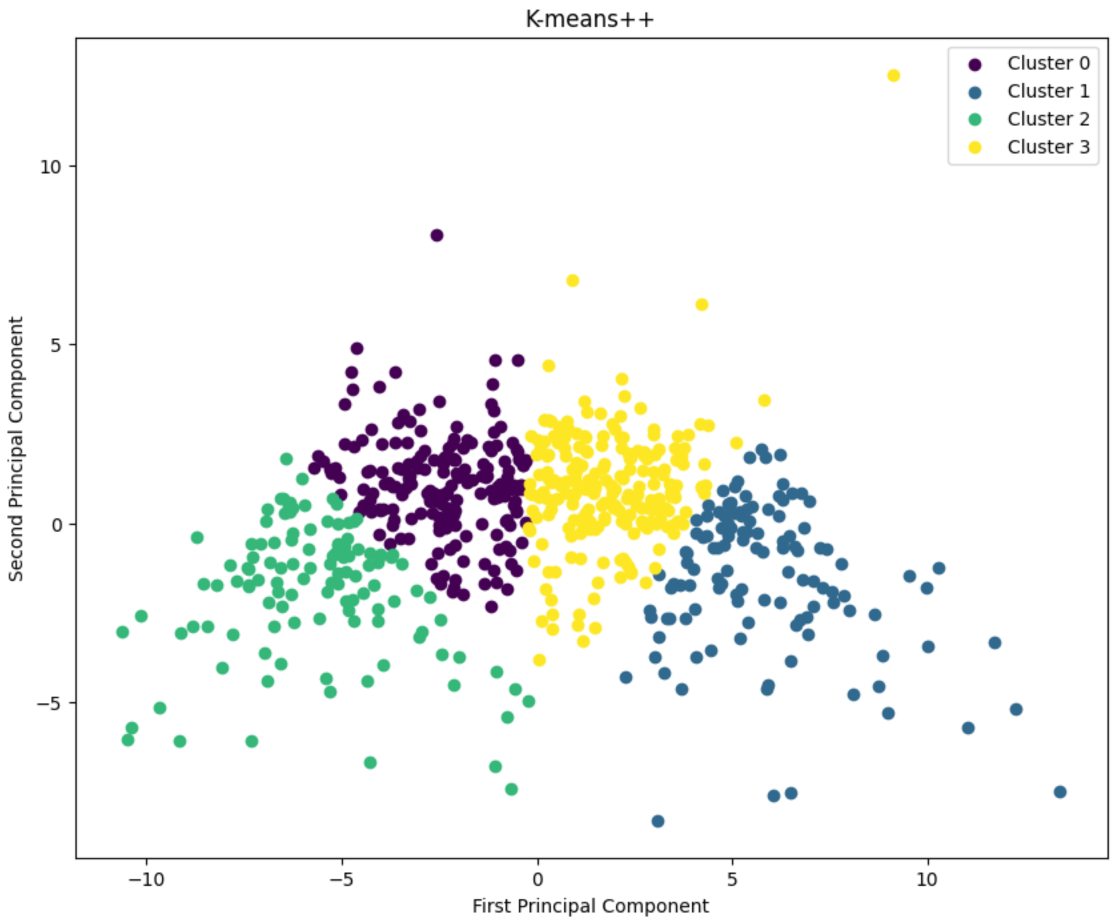
1.8 Plot Clustering Results

[8]:
```
for method, labels in cluster_methods.items():
    plot_clustering_results(edge_pca_features, labels, method)
    silhouette = (
        silhouette_score(edge_pca_features, labels)
        if -1 not in labels
        else silhouette_score(edge_pca_features[labels != -1], labels[labels !=␣
↪-1])
```

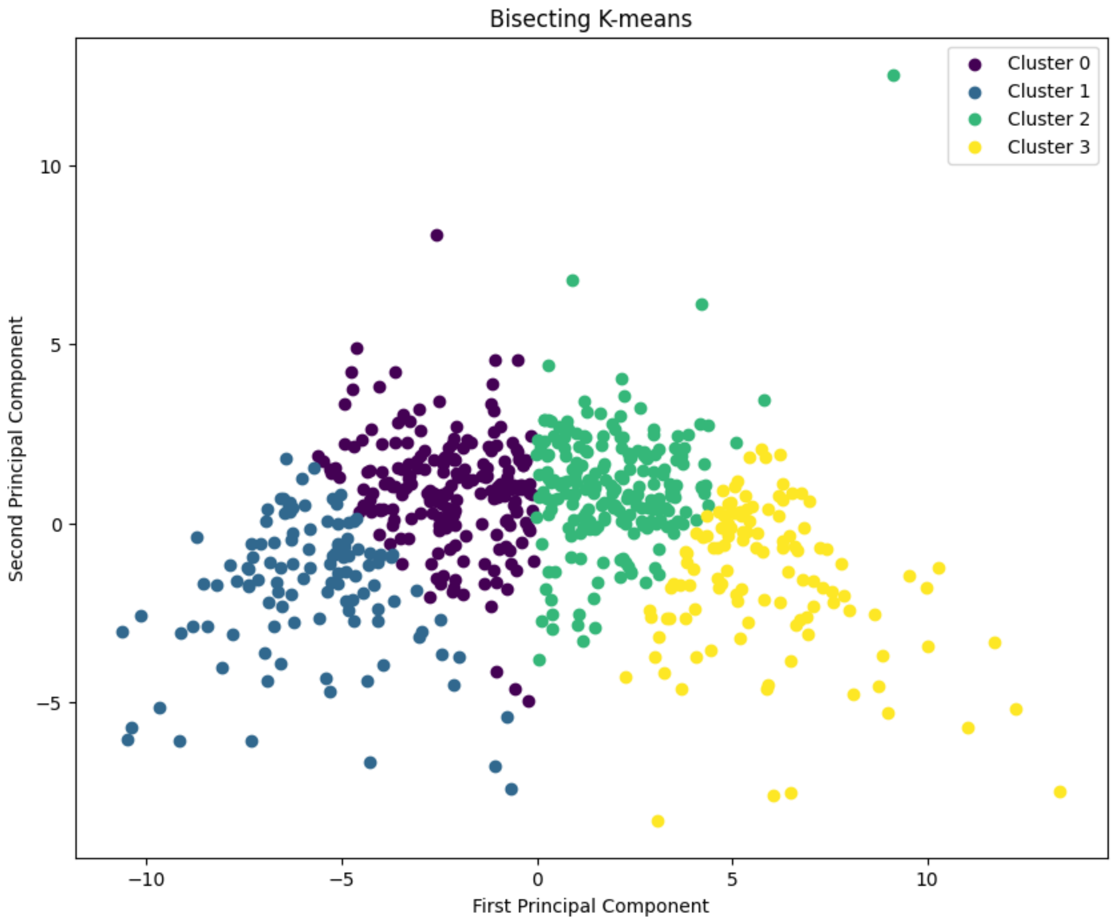
```
    )
    print(f"{method} Silhouette Score: {silhouette:.4f}")
```



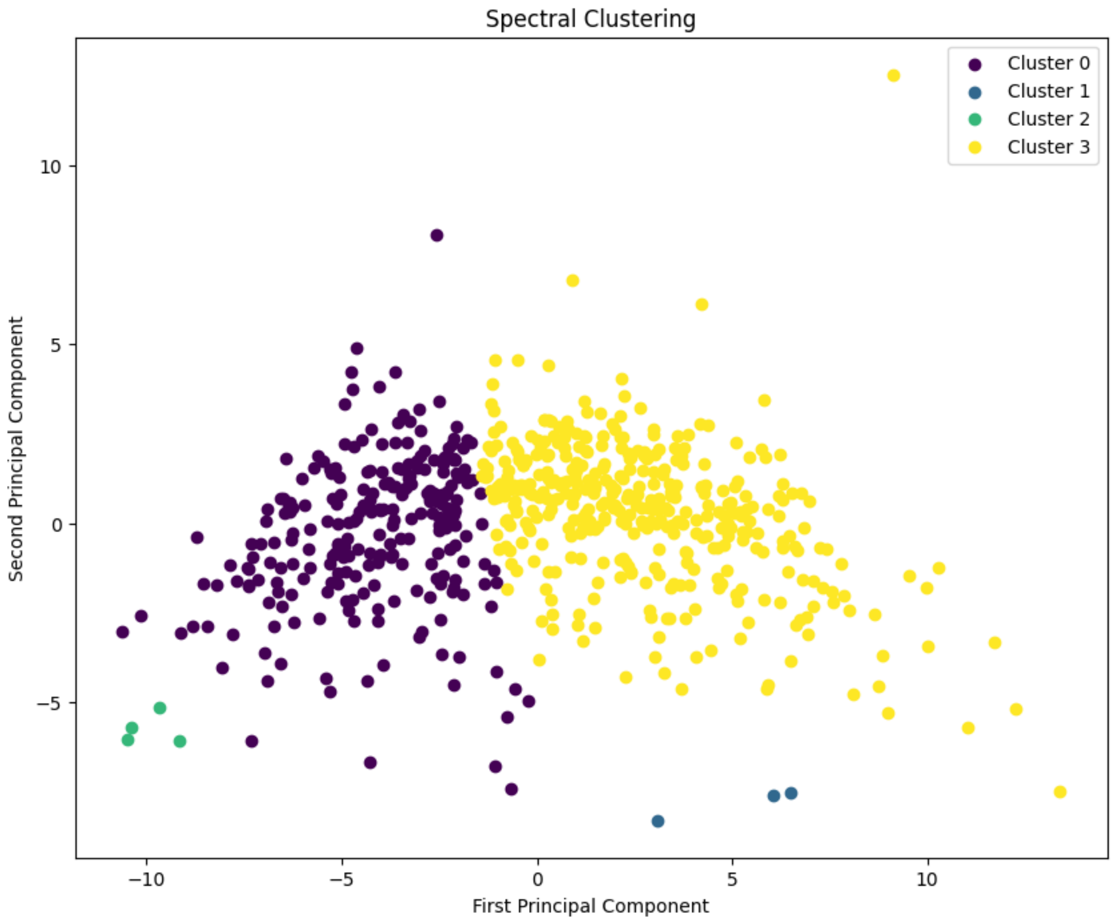

```
K-means (Random Init) Silhouette Score: 0.3477
```



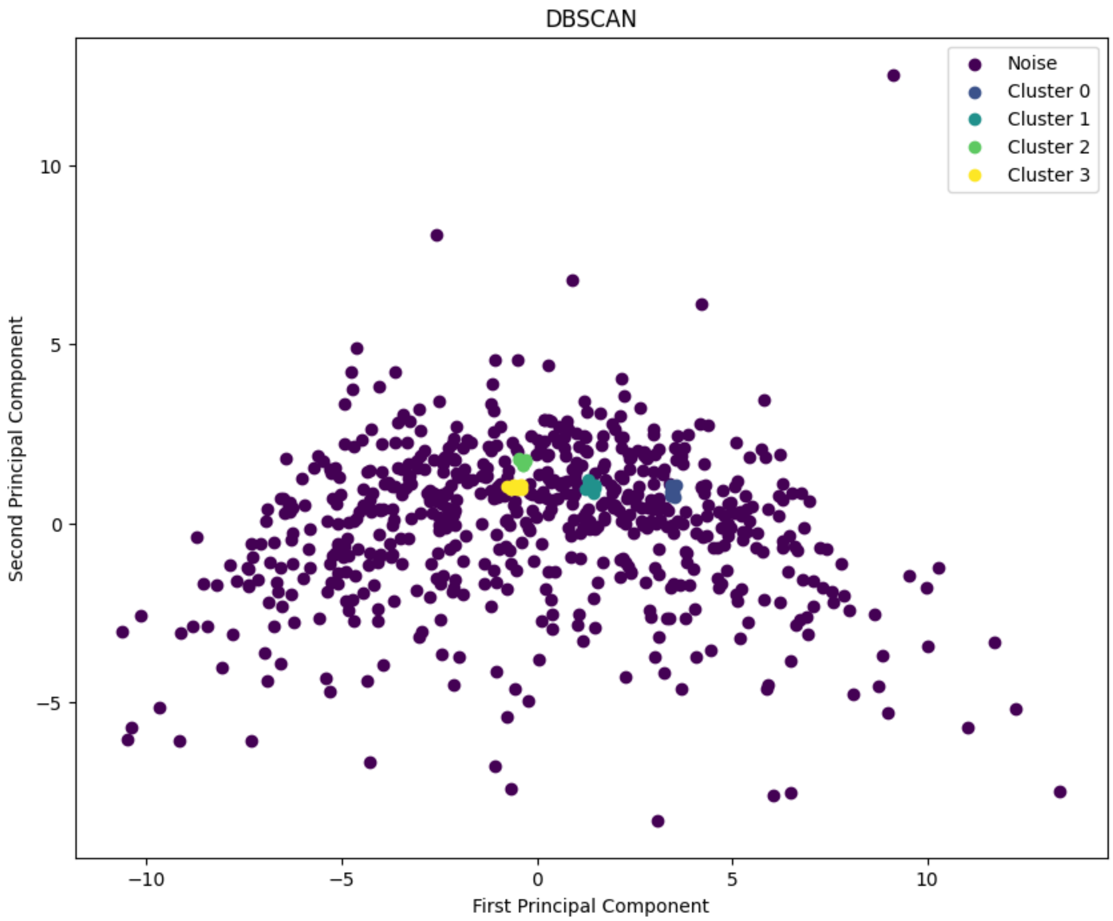

```
K-means++ Silhouette Score: 0.3477
```



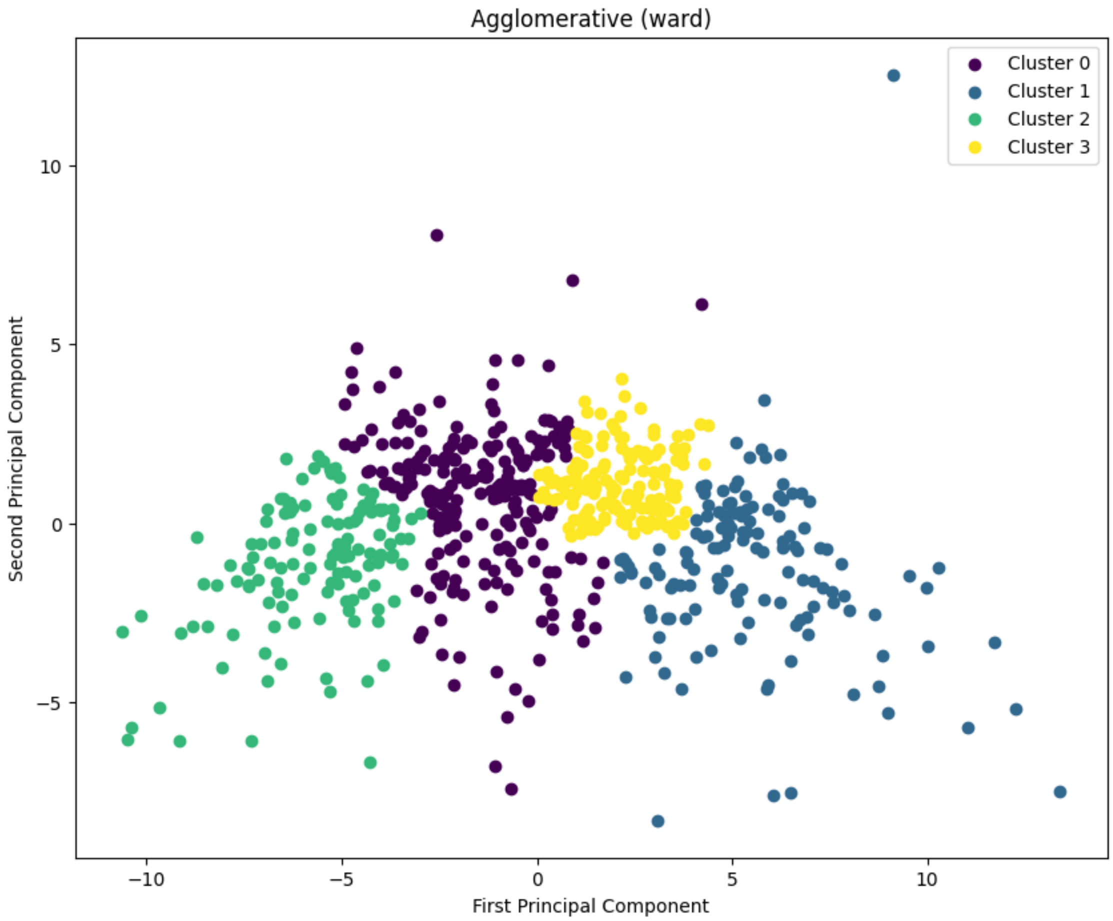

```
Bisecting K-means Silhouette Score: 0.3470
```



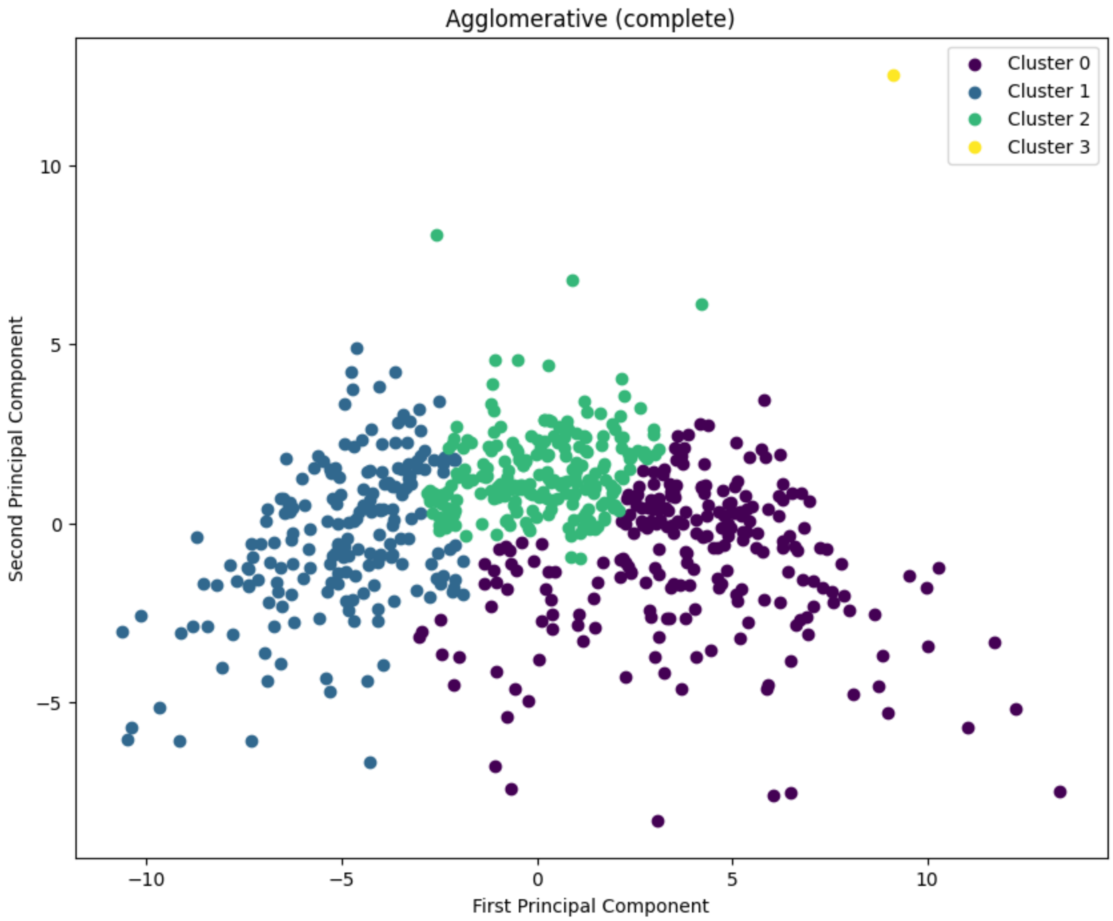
Spectral Clustering Silhouette Score: 0.3680



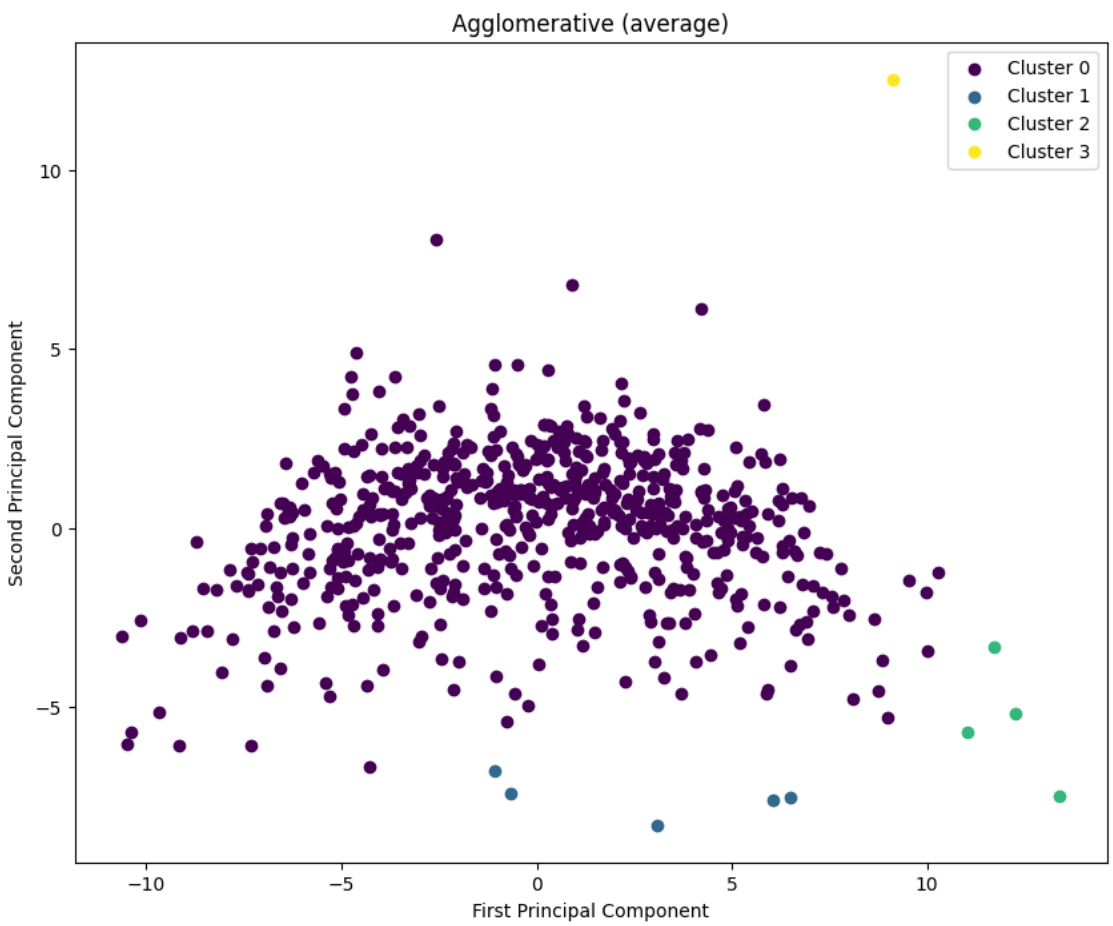
DBSCAN Silhouette Score: 0.8347



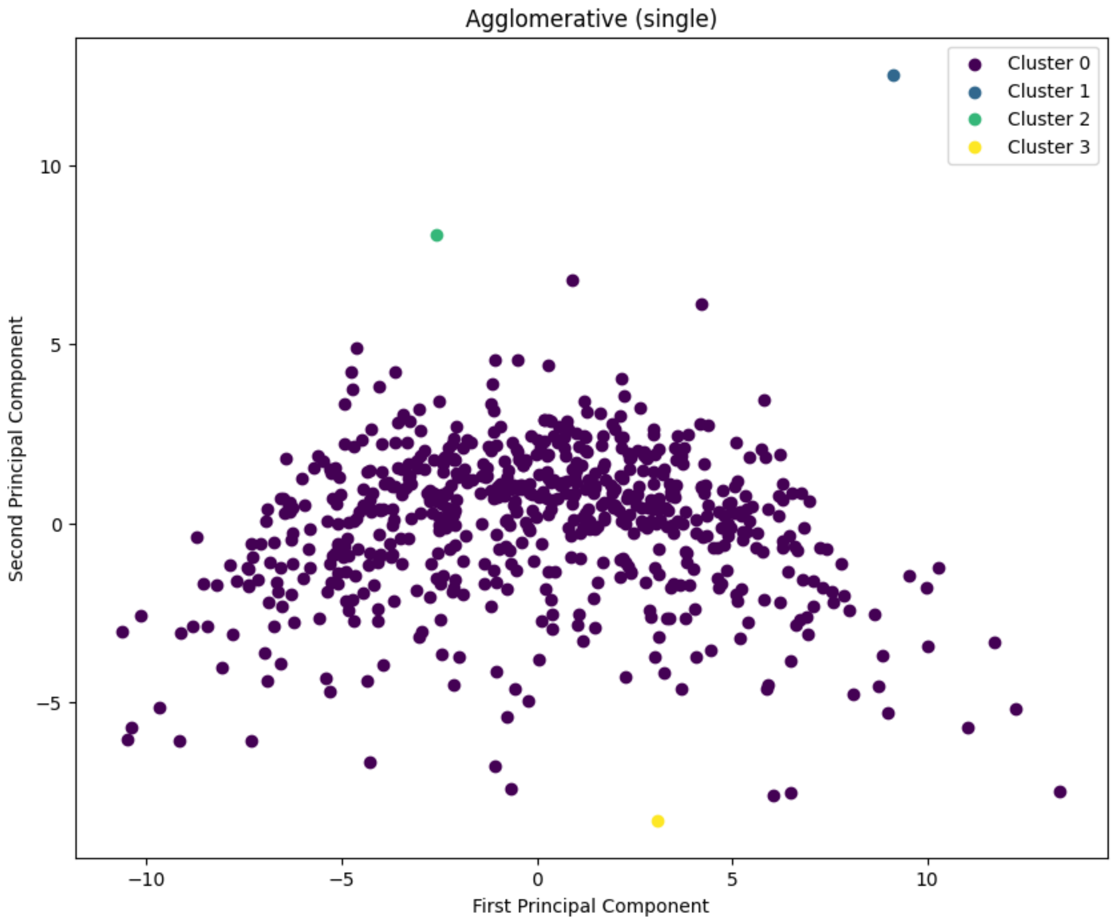
Agglomerative (ward) Silhouette Score: 0.2982




```
Agglomerative (complete) Silhouette Score: 0.3274
```




```
Agglomerative (average) Silhouette Score: 0.3865
```




```
Agglomerative (single) Silhouette Score: 0.2662
```

1.9 Clustering Evaluation

[9]:

```python
evaluation_results = {}

for method, labels in cluster_methods.items():
    fm, silhouette = evaluate_clustering(
        method, labels, edge_pca_features, edge_true_labels
    )
    evaluation_results[method] = (fm, silhouette)

print("\nDetailed Evaluation Results:")
print("-" * 80)
print(f"{'Method':<25} {'Fowlkes-Mallows':<20} {'Silhouette':<20}")
print("-" * 80)
for method, (fm, silhouette) in evaluation_results.items():
    print(f"{method:<25} {fm:<20.4f} {silhouette:<20.4f}")
```

```python
fm_ranking = sorted(evaluation_results.items(), key=lambda x: x[1][0],␣
↪reverse=True)
print("\nRanking based on Fowlkes-Mallows index:")
print("-" * 50)
for rank, (method, (fm, _)) in enumerate(fm_ranking, 1):
    print(f"{rank}. {method:<25} Score: {fm:.4f}")

silhouette_ranking = sorted(
    evaluation_results.items(), key=lambda x: x[1][1], reverse=True
)
print("\nRanking based on Silhouette Coefficient:")
print("-" * 50)
for rank, (method, (_, silhouette)) in enumerate(silhouette_ranking, 1):
    print(f"{rank}. {method:<25} Score: {silhouette:.4f}")
```

```
Detailed Evaluation Results:
--------------------------------------------------------------------------------
Method                    Fowlkes-Mallows     Silhouette
--------------------------------------------------------------------------------
K-means (Random Init)     0.2637              0.3477
K-means++                 0.2637              0.3477
Bisecting K-means         0.2649              0.3470
Spectral Clustering       0.3598              0.3680
DBSCAN                    0.2595              0.8347
Agglomerative (ward)      0.2622              0.2982
Agglomerative (complete)  0.2999              0.3274
Agglomerative (average)   0.4910              0.3865
Agglomerative (single)    0.4966              0.2662

Ranking based on Fowlkes-Mallows index:
--------------------------------------------------
1. Agglomerative (single)    Score: 0.4966
2. Agglomerative (average)   Score: 0.4910
3. Spectral Clustering       Score: 0.3598
4. Agglomerative (complete)  Score: 0.2999
5. Bisecting K-means         Score: 0.2649
6. K-means (Random Init)     Score: 0.2637
7. K-means++                 Score: 0.2637
8. Agglomerative (ward)      Score: 0.2622
9. DBSCAN                    Score: 0.2595

Ranking based on Silhouette Coefficient:
--------------------------------------------------
1. DBSCAN                    Score: 0.8347
2. Agglomerative (average)   Score: 0.3865
3. Spectral Clustering       Score: 0.3680
```

```
4. K-means (Random Init)      Score: 0.3477
5. K-means++                  Score: 0.3477
6. Bisecting K-means          Score: 0.3470
7. Agglomerative (complete)   Score: 0.3274
8. Agglomerative (ward)       Score: 0.2982
9. Agglomerative (single)     Score: 0.2662
```