```python
# Imports
import os
import xml.etree.ElementTree as ET
import glob
from PIL import Image
from pathlib import Path
from skimage import io
from skimage.transform import resize

from torch.utils.data import Dataset, DataLoader
import albumentations as A
from albumentations.pytorch import ToTensorV2

import torch
import torch.nn as nn
from torchvision import models, transforms
import timm

import numpy as np
import pandas as pd

from sklearn.decomposition import PCA

import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
from sklearn.cluster import BisectingKMeans
from sklearn.cluster import SpectralClustering
from sklearn.cluster import DBSCAN
from sklearn.cluster import AgglomerativeClustering
from sklearn.metrics import fowlkes_mallows_score, silhouette_score

# 1. Feature Extraction

# Resize each cropped image to a 224x224

# Get x and y coordinates from annotations for bounding box
information
def get_bounding_boxes(annot):
    xml = annot
    tree = ET.parse(xml)
    root = tree.getroot()
    objects = root.findall('object')
    bbox = []
    for o in objects:
        bndbox = o.find('bndbox')
        xmin = int(bndbox.find('xmin').text)
        ymin = int(bndbox.find('ymin').text)
        xmax = int(bndbox.find('xmax').text)
        ymax = int(bndbox.find('ymax').text)
        bbox.append((xmin, ymin, xmax, ymax))
    return bbox

# Get image path from annotation path
def get_image(annot):
    img_path = './images/'
    file = annot.split('\\')
    img_filename = img_path + file[-2] + '\\' + file[-1] + '.jpg'
    return img_filename

# Cropping and resizing images using bounding box info
def crop_and_resize(images, annotations):
    for i in range(len(images)):
        bbox = get_bounding_boxes(annotations[i])
        dog = get_image(annotations[i])
        im = Image.open(dog)
        for j in range(len(bbox)):
            im2 = im.crop(bbox[j])
            im2 = im2.resize((224,224), Image.Resampling.LANCZOS)
            new_path = dog.replace('./images/', './Processed_Data/')
            new_path = new_path.replace('.jpg', '-' + str(j) + '.jpg')
            im2 = im2.convert('RGB')
            head, tail = os.path.split(new_path)
            Path(head).mkdir(parents=True, exist_ok=True)
            im2.save(new_path)

# File paths
image_files = glob.glob('./images/*/*')
annotations = glob.glob('./annotations/*/*')

# Call crop_and_resize to get processed images
crop_and_resize(image_files, annotations)

# processed data path
processed = glob.glob('./Processed_Data/*/*')

# Normalize the data
    # Sources: https://kozodoi.me/blog/20210527/extracting-features
class ImageData(Dataset):
    def __init__(self, image_paths, transform=None):
        self.image_paths = image_paths
        self.transform = transform
    def __len__(self):
        return len(self.image_paths)
    def __getitem__(self, idx):
        img_path = self.image_paths[idx]
        img = Image.open(img_path).convert("RGB")
        if self.transform:
            img = self.transform(image=np.array(img))["image"]
        return img
```

```
def get_labels(image_files):
    labels = []
    for image_file in image_files:
        breed = os.path.basename(os.path.dirname(image_file))
        labels.append(breed)
    return labels

labels = get_labels(image_files)

unique_labels = np.unique(labels)
label_map = {label: i for i, label in enumerate(unique_labels)}
encoded_labels = np.array([label_map[label] for label in labels])

# Transforming data
transform = A.Compose([A.Resize(height=224,width=224),
                       A.Normalize(),
                       ToTensorV2()])
dataset = ImageData(image_paths=processed, transform=transform)
data_loader = DataLoader(dataset, batch_size=32, num_workers=0)

# Extract features for each image of layer resnet18
    # Sources: https://kozodoi.me/blog/20210527/extracting-features

# build the model
device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
model = timm.create_model(model_name="resnet18", pretrained=True)
model.fc = nn.Linear(512, 2)
model.to(device)

ResNet(
  (conv1): Conv2d(3, 64, kernel_size=(7, 7), stride=(2, 2),
padding=(3, 3), bias=False)
  (bn1): BatchNorm2d(64, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
  (act1): ReLU(inplace=True)
  (maxpool): MaxPool2d(kernel_size=3, stride=2, padding=1, dilation=1,
ceil_mode=False)
  (layer1): Sequential(
    (0): BasicBlock(
      (conv1): Conv2d(64, 64, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn1): BatchNorm2d(64, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (drop_block): Identity()
      (act1): ReLU(inplace=True)
      (aa): Identity()
      (conv2): Conv2d(64, 64, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn2): BatchNorm2d(64, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (act2): ReLU(inplace=True)
    )
    (1): BasicBlock(
      (conv1): Conv2d(64, 64, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn1): BatchNorm2d(64, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (drop_block): Identity()
      (act1): ReLU(inplace=True)
      (aa): Identity()
      (conv2): Conv2d(64, 64, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn2): BatchNorm2d(64, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (act2): ReLU(inplace=True)
    )
  )
  (layer2): Sequential(
    (0): BasicBlock(
      (conv1): Conv2d(64, 128, kernel_size=(3, 3), stride=(2, 2),
padding=(1, 1), bias=False)
      (bn1): BatchNorm2d(128, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (drop_block): Identity()
      (act1): ReLU(inplace=True)
      (aa): Identity()
      (conv2): Conv2d(128, 128, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn2): BatchNorm2d(128, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (act2): ReLU(inplace=True)
      (downsample): Sequential(
        (0): Conv2d(64, 128, kernel_size=(1, 1), stride=(2, 2),
bias=False)
        (1): BatchNorm2d(128, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      )
    )
    (1): BasicBlock(
      (conv1): Conv2d(128, 128, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn1): BatchNorm2d(128, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (drop_block): Identity()
      (act1): ReLU(inplace=True)
      (aa): Identity()
      (conv2): Conv2d(128, 128, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
```

```
      (bn2): BatchNorm2d(128, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (act2): ReLU(inplace=True)
    )
  )
  (layer3): Sequential(
    (0): BasicBlock(
      (conv1): Conv2d(128, 256, kernel_size=(3, 3), stride=(2, 2),
padding=(1, 1), bias=False)
      (bn1): BatchNorm2d(256, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (drop_block): Identity()
      (act1): ReLU(inplace=True)
      (aa): Identity()
      (conv2): Conv2d(256, 256, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn2): BatchNorm2d(256, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (act2): ReLU(inplace=True)
      (downsample): Sequential(
        (0): Conv2d(128, 256, kernel_size=(1, 1), stride=(2, 2),
bias=False)
        (1): BatchNorm2d(256, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      )
    )
    (1): BasicBlock(
      (conv1): Conv2d(256, 256, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn1): BatchNorm2d(256, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (drop_block): Identity()
      (act1): ReLU(inplace=True)
      (aa): Identity()
      (conv2): Conv2d(256, 256, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn2): BatchNorm2d(256, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (act2): ReLU(inplace=True)
    )
  )
  (layer4): Sequential(
    (0): BasicBlock(
      (conv1): Conv2d(256, 512, kernel_size=(3, 3), stride=(2, 2),
padding=(1, 1), bias=False)
      (bn1): BatchNorm2d(512, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (drop_block): Identity()
      (act1): ReLU(inplace=True)
      (aa): Identity()
      (conv2): Conv2d(512, 512, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn2): BatchNorm2d(512, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (act2): ReLU(inplace=True)
      (downsample): Sequential(
        (0): Conv2d(256, 512, kernel_size=(1, 1), stride=(2, 2),
bias=False)
        (1): BatchNorm2d(512, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      )
    )
    (1): BasicBlock(
      (conv1): Conv2d(512, 512, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn1): BatchNorm2d(512, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (drop_block): Identity()
      (act1): ReLU(inplace=True)
      (aa): Identity()
      (conv2): Conv2d(512, 512, kernel_size=(3, 3), stride=(1, 1),
padding=(1, 1), bias=False)
      (bn2): BatchNorm2d(512, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
      (act2): ReLU(inplace=True)
    )
  )
  (global_pool): SelectAdaptivePool2d(pool_type=avg,
flatten=Flatten(start_dim=1, end_dim=-1))
  (fc): Linear(in_features=512, out_features=2, bias=True)
)
```

```python
# Hook function - from: https://kozodoi.me/blog/20210527/extracting-
features
def get_features(name):
    def hook(model, input, output):
        features[name] = output.detach()
    return hook
model.global_pool.register_forward_hook(get_features("feats"))
```

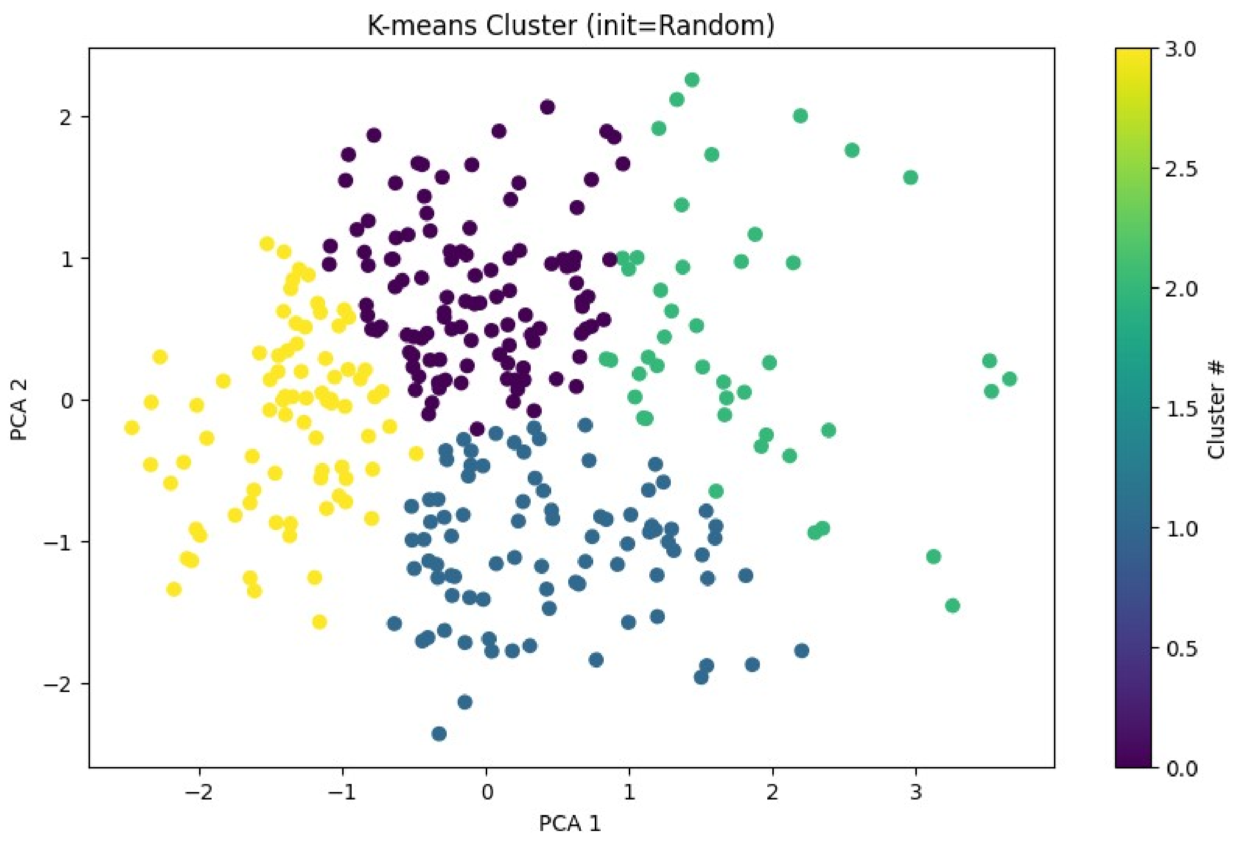
```
<torch.utils.hooks.RemovableHandle at 0x1f7b41b3350>
```

```python
# Extracting features - from:
https://kozodoi.me/blog/20210527/extracting-features
# placeholders
PREDS = []
FEATS = []

# placeholder for batch features
```

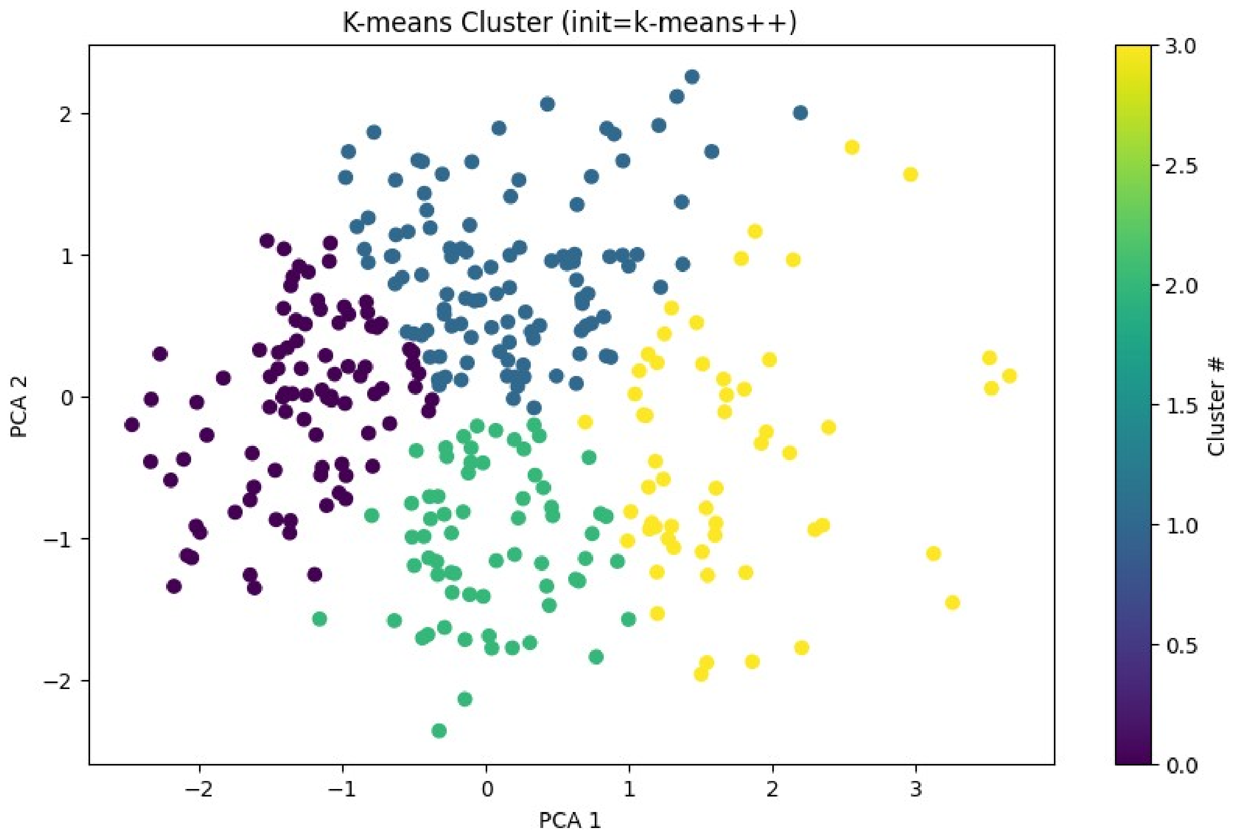
```
features = {}

# loop through batches
for idx, inputs in enumerate(data_loader):
    # move to device
    inputs = inputs.to(device)

    # forward pass [with feature extraction]
    preds = model(inputs)

    # add feats and preds to lists
    PREDS.append(preds.detach().cpu().numpy())
    FEATS.append(features["feats"].cpu().numpy())

    # early stop
    if idx == 9:
        break

# Inspect features
PREDS = np.concatenate(PREDS)
FEATS = np.concatenate(FEATS)

print("- preds shape:", PREDS.shape)
print("- feats shape:", FEATS.shape)
```

```
- preds shape: (320, 2)
- feats shape: (320, 512)
```

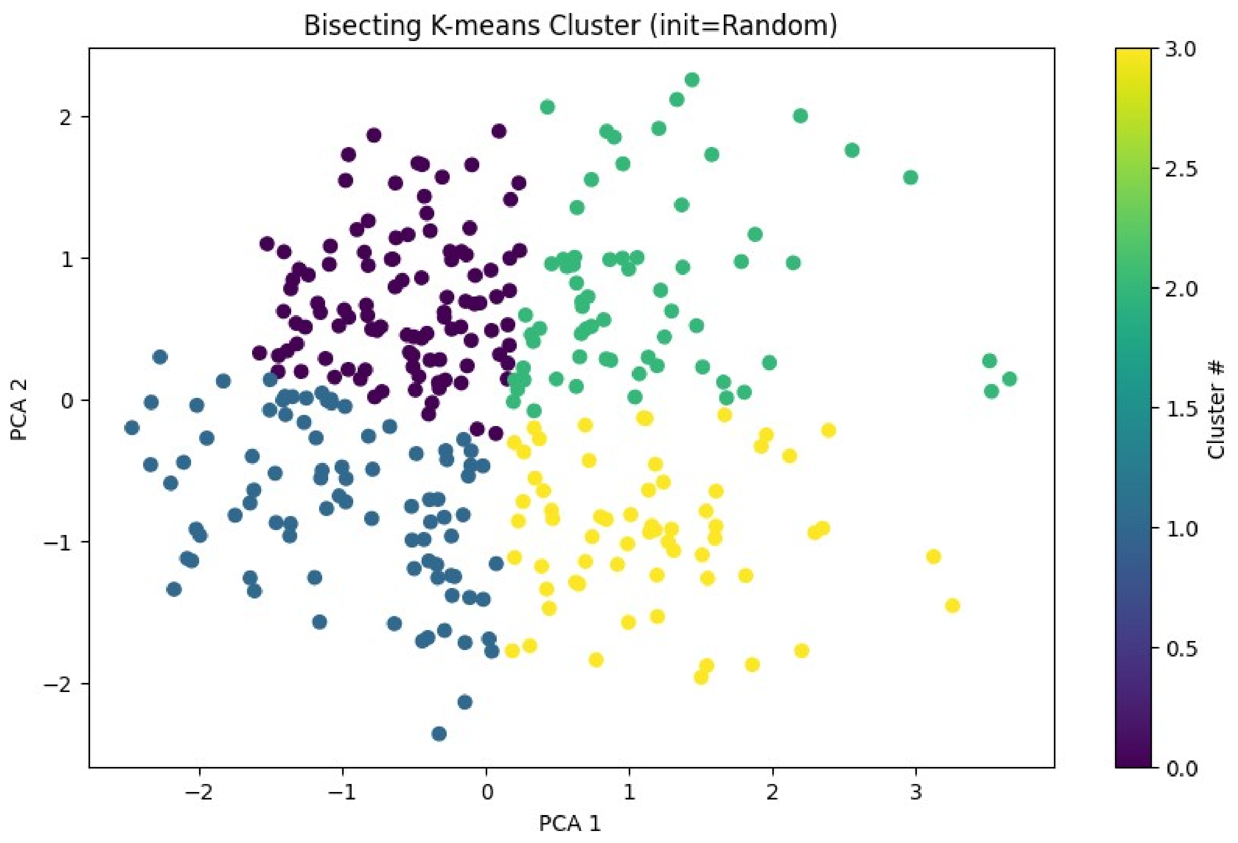
```
# 2) Dimensionality Reduction
pca = PCA(n_components=2)
reduced_data = pca.fit_transform(FEATS)

# 3) Clustering Algorithm

# K-mean cluster K=4
    # a. K-means with init=Random
k_random = KMeans(n_clusters=4, init='random', random_state=42)
k_random_cluster = k_random.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1],
c=k_random_cluster)
plt.title("K-means Cluster (init=Random)")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()
```



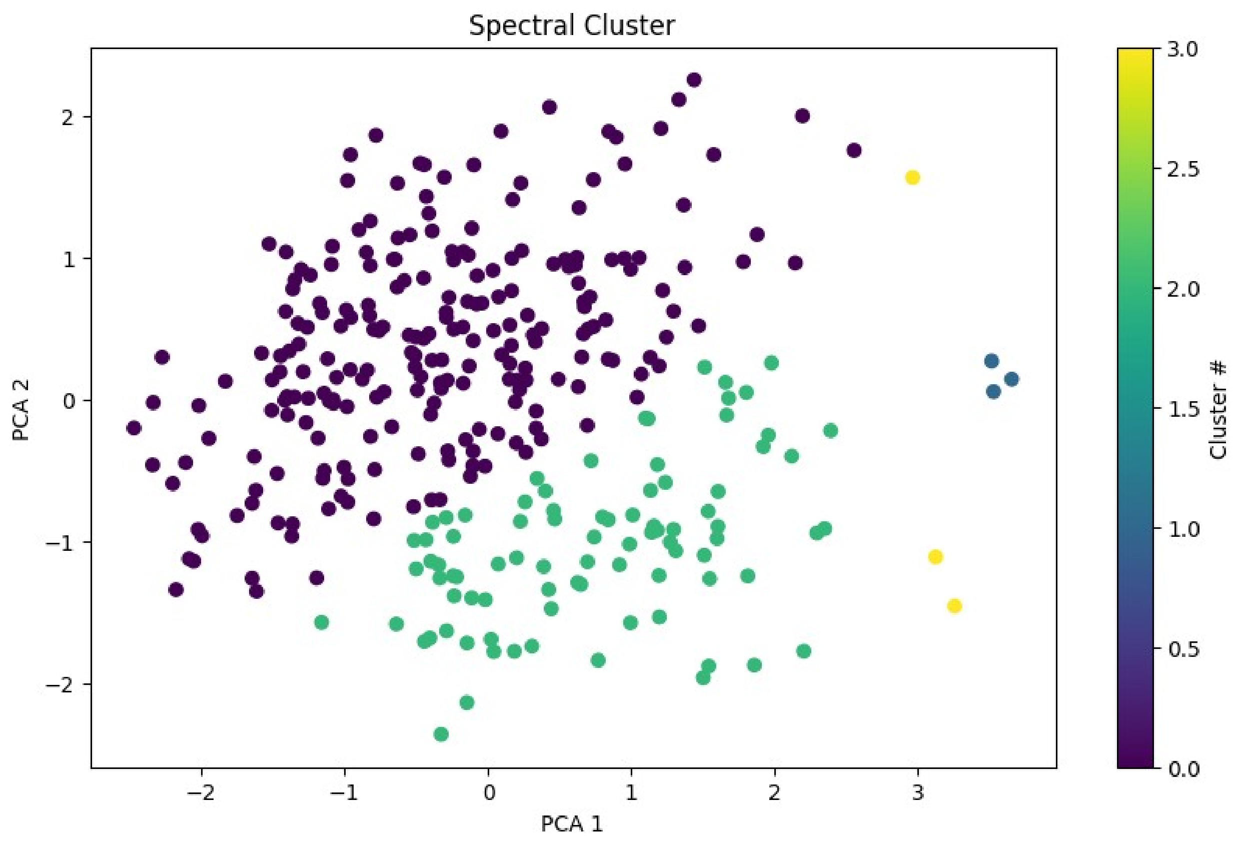
```
    # b. K-means with init=k-means++
k_plus = KMeans(n_clusters=4, init='k-means++', random_state=42)
k_plus_cluster = k_plus.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1], c=k_plus_cluster)
plt.title("K-means Cluster (init=k-means++)")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()
```



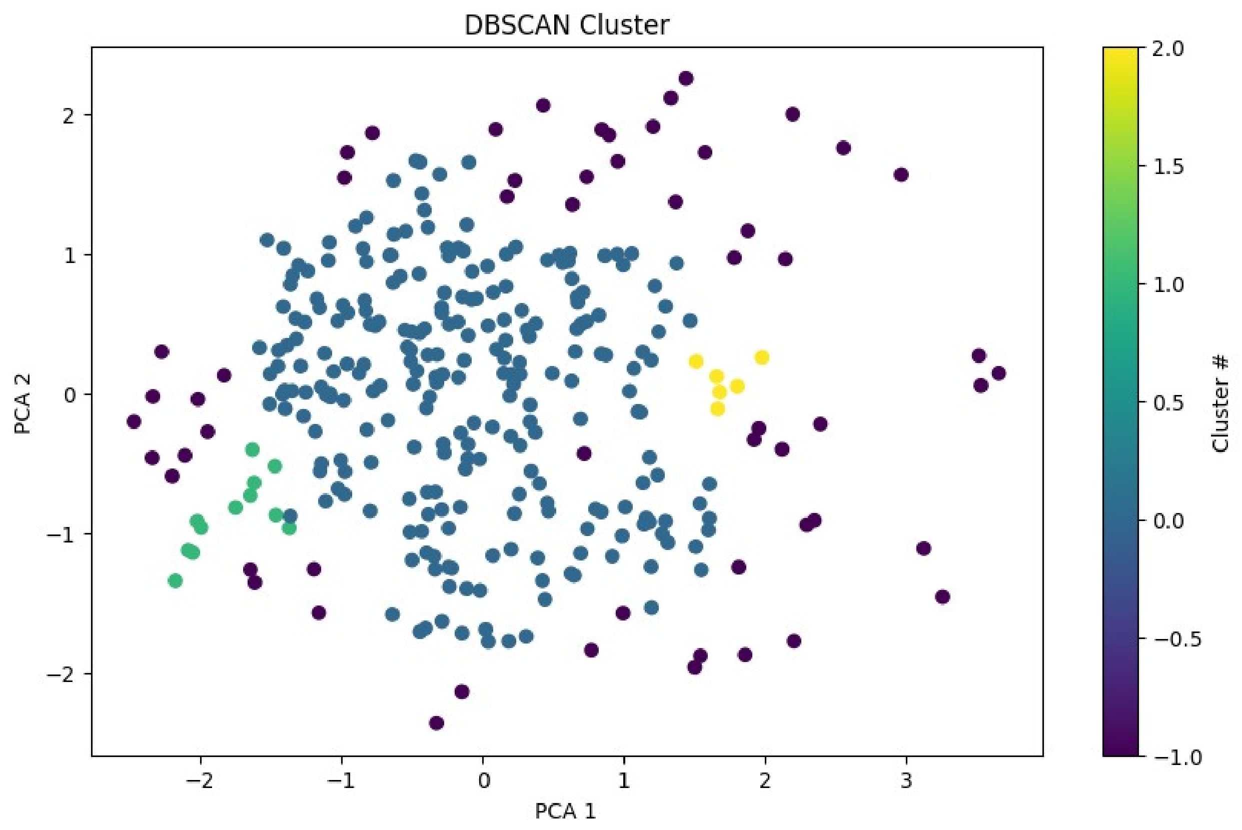
```
    # c. Bisecting K-means with init=random
bisect_k = BisectingKMeans(n_clusters=4, init='random',
random_state=42)
bisect_k_cluster = bisect_k.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1],
c=bisect_k_cluster)
plt.title("Bisecting K-means Cluster (init=Random)")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()
```



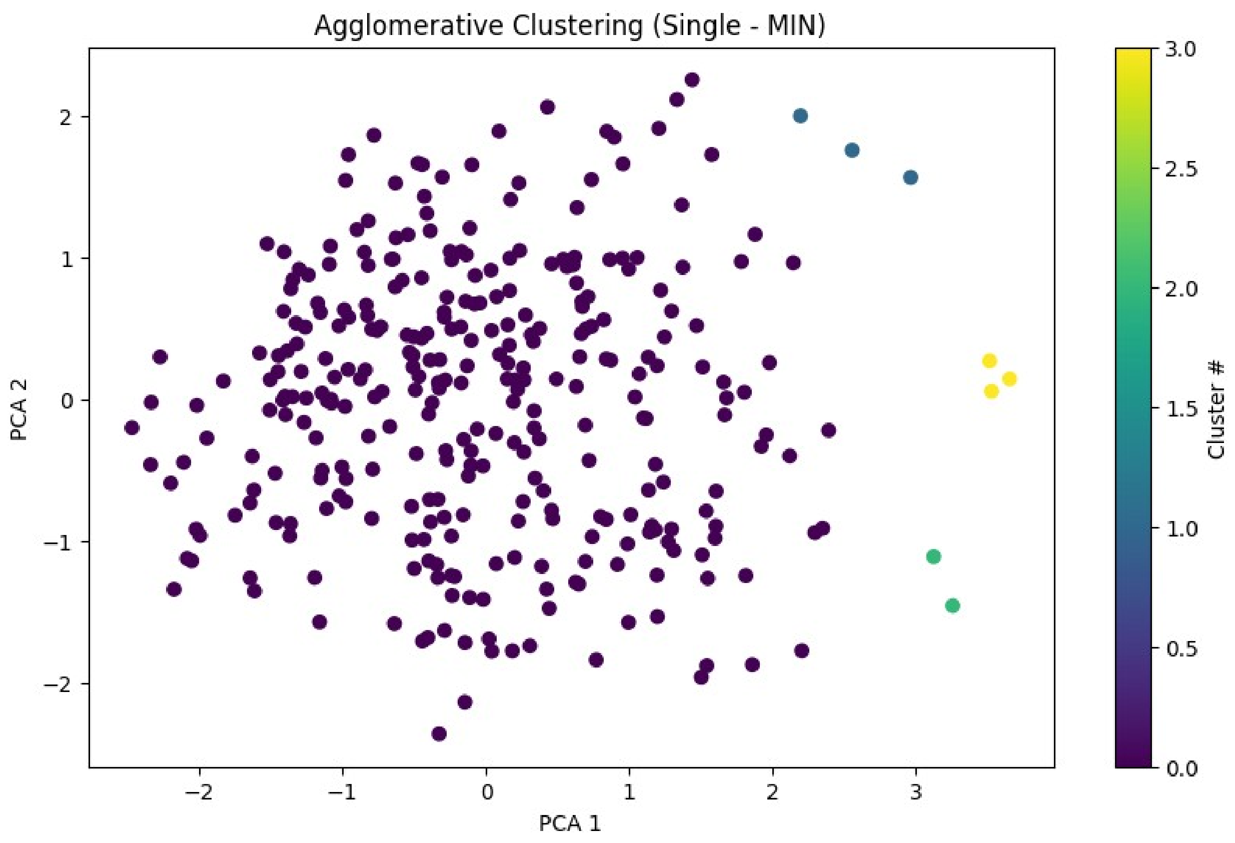
```
    # d. Spectral Clustering
spectral = SpectralClustering(n_clusters=4, random_state=42)
spectral_cluster = spectral.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1],
c=spectral_cluster)
plt.title("Spectral Cluster")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()
```



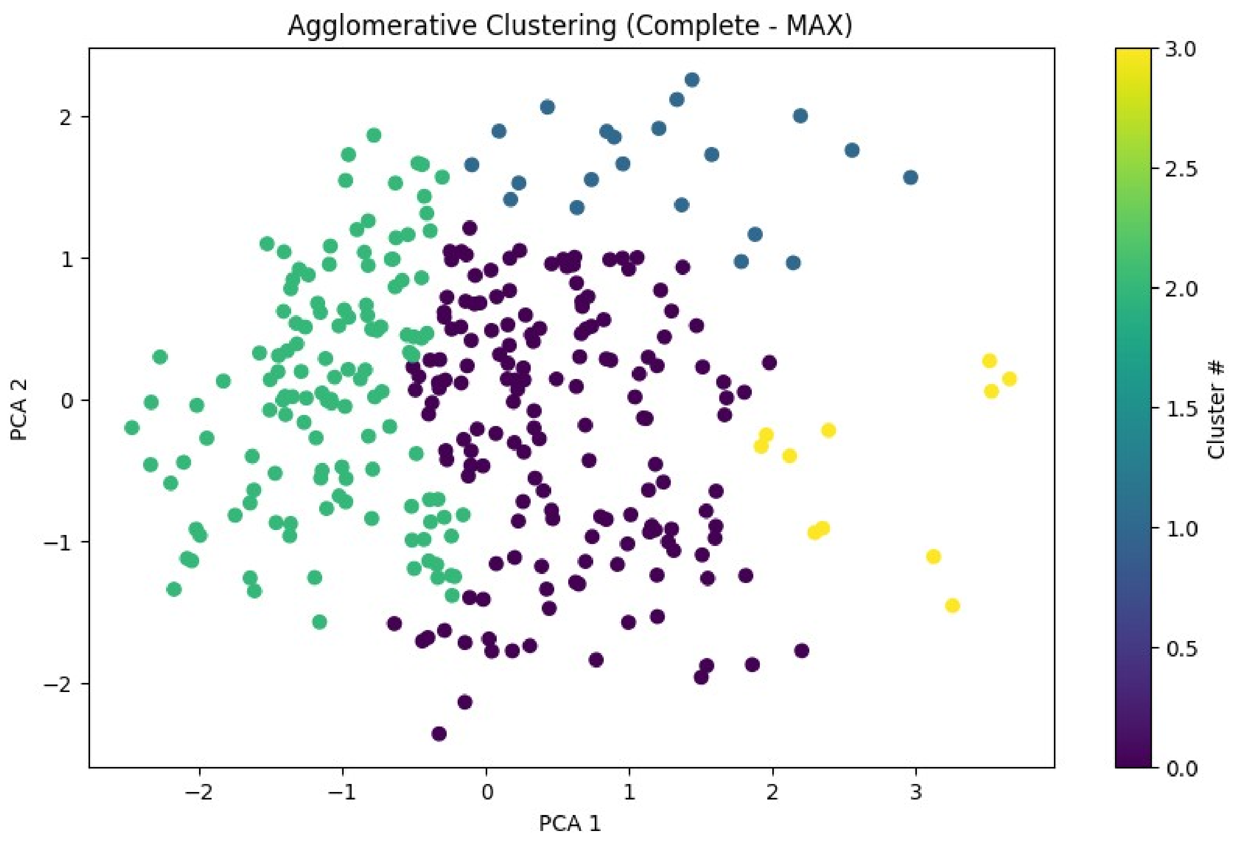
```
# DBSCAN
dbscan = DBSCAN(eps=0.3, min_samples=5)
dbscan_cluster = dbscan.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1], c=dbscan_cluster)
plt.title("DBSCAN Cluster")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()

# What eps and min_samples values did you use to get 4 clusters?
    # eps=0.3 and min_samples=5 to get 4 clusters
```



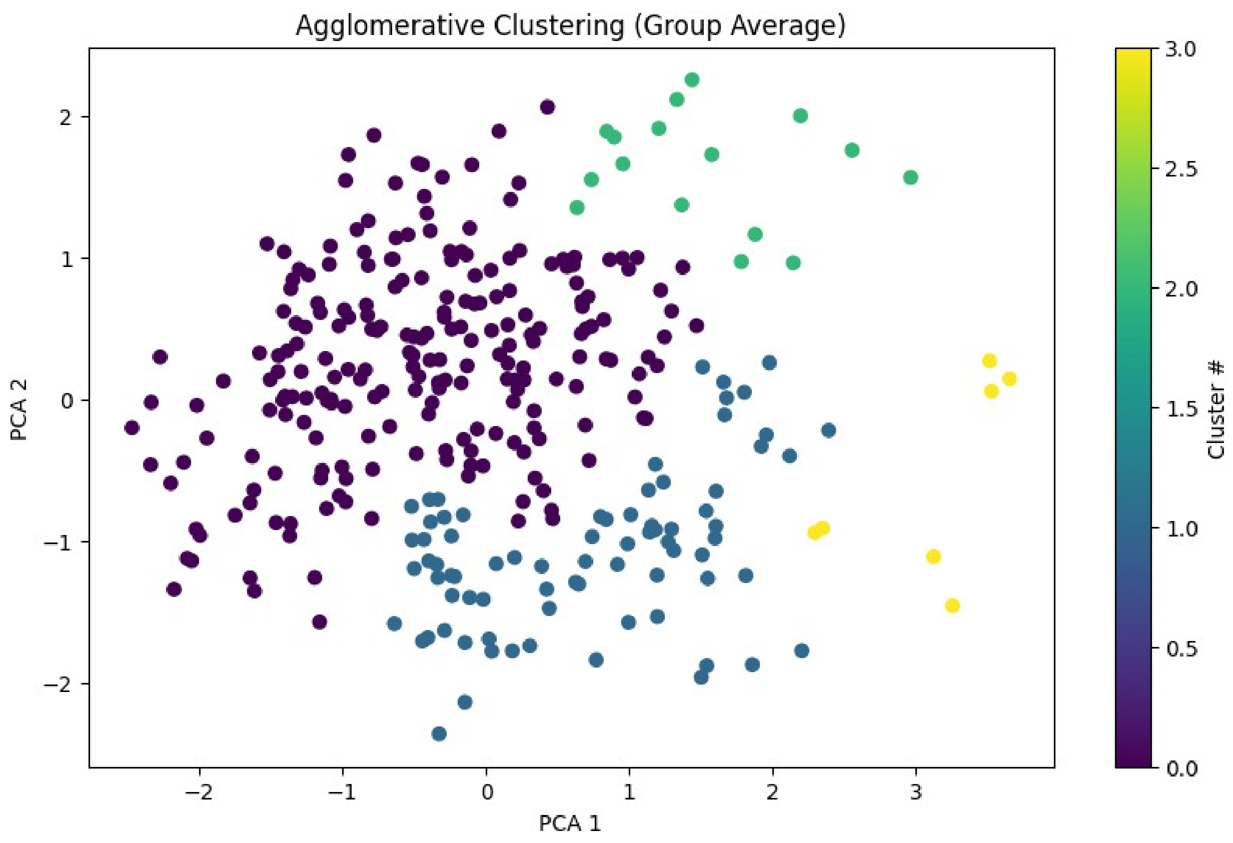
```
# Agglomerative Clustering

    # a. Single link (MIN)
agg_min = AgglomerativeClustering(n_clusters=4, linkage='single')
agg_min_cluster = agg_min.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1], c=agg_min_cluster)
plt.title("Agglomerative Clustering (Single - MIN)")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()
```



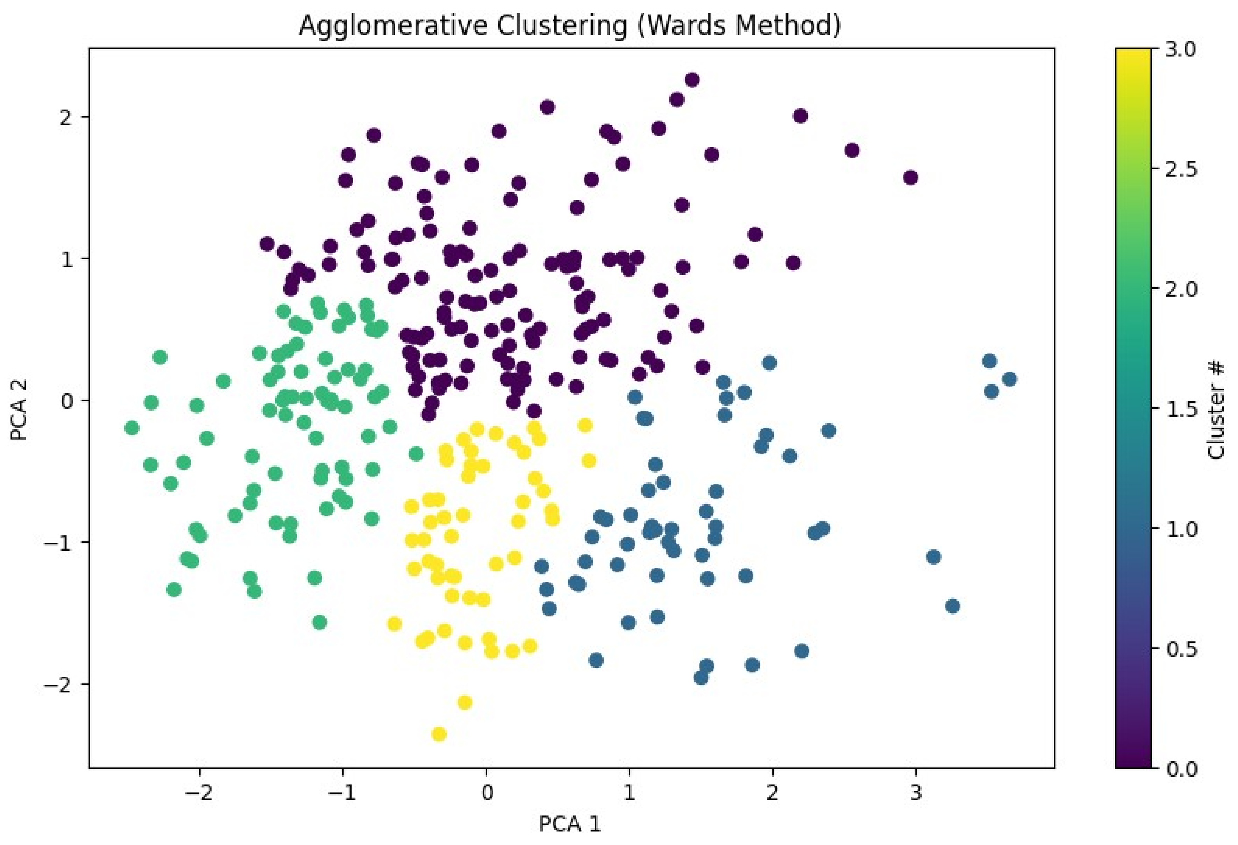
```python
    # b. Complete link (MAX)
agg_max = AgglomerativeClustering(n_clusters=4, linkage='complete')
agg_max_cluster = agg_max.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1], c=agg_max_cluster)
plt.title("Agglomerative Clustering (Complete - MAX)")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()
```



```
    # c. Group Average
agg_avg = AgglomerativeClustering(n_clusters=4, linkage='average')
agg_avg_cluster = agg_avg.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1], c=agg_avg_cluster)
plt.title("Agglomerative Clustering (Group Average)")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()
```



```
    # d. Wards method
agg_ward = AgglomerativeClustering(n_clusters=4, linkage='ward')
agg_ward_cluster = agg_ward.fit_predict(reduced_data)

plt.figure(figsize=(10, 6))
plt.scatter(reduced_data[:, 0], reduced_data[:, 1],
c=agg_ward_cluster)
plt.title("Agglomerative Clustering (Wards Method)")
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.colorbar(label="Cluster #")
plt.show()
```



```
# 4) Clustering Evaluations

    # a. perform clusteing eval using Fowlkes-Mallows for each method
in #3
k_random_fms = fowlkes_mallows_score(encoded_labels, k_random_cluster)
k_plus_fms = fowlkes_mallows_score(encoded_labels, k_plus_cluster)
bisect_k_fms = fowlkes_mallows_score(encoded_labels,bisect_k_cluster)
spectral_fms = fowlkes_mallows_score(encoded_labels, spectral_cluster)
dbscan_fms = fowlkes_mallows_score(encoded_labels, dbscan_cluster)
agg_min_fms = fowlkes_mallows_score(encoded_labels, agg_min_cluster)
agg_max_fms = fowlkes_mallows_score(encoded_labels, agg_max_cluster)
agg_avg_fms = fowlkes_mallows_score(encoded_labels, agg_avg_cluster)
agg_ward_fms = fowlkes_mallows_score(encoded_labels, agg_ward_cluster)

fms = {
    "K-Means init=Random": k_random_fms,
    "K-Means init=k-means++": k_plus_fms,
    "Bisecting K-Means": bisect_k_fms,
    "Spectral": spectral_fms,
    "DBSCAN": dbscan_fms,
    "Single (MIN)": agg_min_fms,
    "Complete (MAX)": agg_max_fms,
    "Group AVG": agg_avg_fms,
    "Wards Method": agg_ward_fms
}

----------------------------------------------------------------------
-----
ValueError                                Traceback (most recent call
last)
Cell In[76], line 4
      1 # 4) Clustering Evaluations
      2 
      3     # a. perform clusteing eval using Fowlkes-Mallows for each
method in #3
----> 4 k_random_fms = fowlkes_mallows_score(encoded_labels,
k_random_cluster)
      5 k_plus_fms = fowlkes_mallows_score(encoded_labels,
k_plus_cluster)
      6 bisect_k_fms =
fowlkes_mallows_score(encoded_labels,bisect_k_cluster)

File ~\AppData\Local\Programs\Python\Python312\Lib\site-packages\
sklearn\utils\_param_validation.py:213, in
validate_params.<locals>.decorator.<locals>.wrapper(*args, **kwargs)
    207 try:
    208     with config_context(
    209         skip_parameter_validation=(
    210             prefer_skip_nested_validation or
global_skip_validation
    211         )
    212     ):
--> 213         return func(*args, **kwargs)
    214 except InvalidParameterError as e:
    215     # When the function is just a wrapper around an estimator,
we allow
    216     # the function to delegate validation to the estimator,
but we replace
    217     # the name of the estimator by the name of the function in
the error
    218     # message to avoid confusion.
    219     msg = re.sub(
    220         r"parameter of \w+ must be",
    221         f"parameter of {func.__qualname__} must be",
    222         str(e),
    223     )

File ~\AppData\Local\Programs\Python\Python312\Lib\site-packages\
sklearn\metrics\cluster\_supervised.py:1251, in
fowlkes_mallows_score(labels_true, labels_pred, sparse)
   1176 @validate_params(
   1177     {
   1178         "labels_true": ["array-like"],
   (...)
   1183 )
   1184 def fowlkes_mallows_score(labels_true, labels_pred, *,
sparse=False):
   1185     """Measure the similarity of two clusterings of a set of
points.
   1186
   1187     .. versionadded:: 0.18
   (...)
   1249       0.0
   1250     """
-> 1251     labels_true, labels_pred = check_clusterings(labels_true,
labels_pred)
   1252     (n_samples,) = labels_true.shape
   1254     c = contingency_matrix(labels_true, labels_pred,
sparse=True)

File ~\AppData\Local\Programs\Python\Python312\Lib\site-packages\
sklearn\metrics\cluster\_supervised.py:73, in
check_clusterings(labels_true, labels_pred)
     71 if labels_pred.ndim != 1:
     72     raise ValueError("labels_pred must be 1D: shape is %r" %
(labels_pred.shape,))
---> 73 check_consistent_length(labels_true, labels_pred)
     75 return labels_true, labels_pred

File ~\AppData\Local\Programs\Python\Python312\Lib\site-packages\
sklearn\utils\validation.py:457, in check_consistent_length(*arrays)
    455 uniques = np.unique(lengths)
    456 if len(uniques) > 1:
--> 457     raise ValueError(
    458         "Found input variables with inconsistent numbers of
samples: %r"
    459         % [int(l) for l in lengths]
    460     )

ValueError: Found input variables with inconsistent numbers of
samples: [654, 320]

    # Silhouette Coeefficient for each method
silhouette_scores = {
    "K-means init=random": silhouette_score(reduced_data,
k_random_cluster),
    "K-means init=k-means++": silhouette_score(reduced_data,
k_plus_cluster),
    "Bisecting K-means": silhouette_score(reduced_data,
bisect_k_cluster),
    "Spectral": silhouette_score(reduced_data, spectral_cluster),
    "DBSCAN": silhouette_score(reduced_data, dbscan_cluster),
    "Single (MIN)": silhouette_score(reduced_data, agg_min_cluster),
    "Complete (MAX)": silhouette_score(reduced_data, agg_max_cluster),
    "Group AVG": silhouette_score(reduced_data, agg_avg_cluster),
    "Wards method": silhouette_score(reduced_data, agg_ward_cluster)
}

    # c. Rank Fowlkes-Mallows

    # d. Rank Silhouette Coefficient
ranked_sil = sorted(silhouette_scores.items(), key=lambda x: x[1])
print("Silhouette Score Rankings:")
for method, score in ranked_sil:
        print(f"{method}: {score:.3f}")
```

```
Silhouette Score Rankings:
DBSCAN: -0.028
Complete (MAX): 0.244
Group AVG: 0.283
Spectral: 0.319
Wards method: 0.320
Bisecting K-means: 0.328
K-means init=k-means++: 0.352
K-means init=random: 0.356
Single (MIN): 0.371
```