PROBLEM 5

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt

from google.colab import drive
drive.mount('/content/drive')

Drive already mounted at /content/drive; to attempt to forcibly
remount, call drive.mount("/content/drive", force_remount=True).
```

Part (a)

```
# Function to get principle components
def get_pc(x):
    u, s, vt = np.linalg.svd(x)
    principle_components = vt.T
    return principle_components

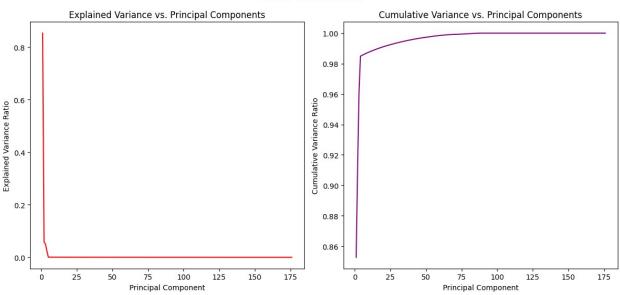
# Function to get the explained variance for the Scree plot
def exp_var(X):
    eigenvalues = np.linalg.eigvals(np.cov(X.T))
    explained_variance_ratio = eigenvalues / np.sum(eigenvalues)
    return explained_variance_ratio
```

InsA Analysis

```
dataA = pd.read csv('/content/drive/MyDrive/sem 7/ID5055/Assignment
1/Problem 5/InsA.csv')
# Centering the data
mean = np.mean(dataA, axis=0)
scaled data = dataA - mean
# Getting the principle components
pca = scaled data@get pc(scaled data)
# Scree plot to visualize explained variance by each principal
component
explained variance = exp var(pca)
cumulative variance = np.cumsum(explained variance)
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(12, 6))
# Subplot 1: Explained Variance vs. Principal Components
ax1.plot(range(1, len(explained variance) + 1), explained variance,
color='red')
ax1.set xlabel('Principal Component')
```

```
ax1.set ylabel('Explained Variance Ratio')
ax1.set title('Explained Variance vs. Principal Components')
# Subplot 2: Cumulative Variance vs. Principal Components
ax2.plot(range(1, len(cumulative variance) + 1), cumulative variance,
color='purple')
ax2.set_xlabel('Principal Component')
ax2.set ylabel('Cumulative Variance Ratio')
ax2.set title('Cumulative Variance vs. Principal Components')
fig.suptitle('Scree Plot of InsA', fontsize=16)
plt.tight_layout()
plt.show()
# Implementing the "knee" point detection algorithm
total variance = np.sum(explained variance)
knee threshold = 0.9 # adjustable
num components = np.argmax(cumulative variance >= knee threshold *
total variance) + 1
print(f"Number of components selected: {num components}")
/usr/local/lib/python3.10/dist-packages/matplotlib/cbook/
  init .py:1335: ComplexWarning: Casting complex values to real
discards the imaginary part
  return np.asarray(x, float)
```

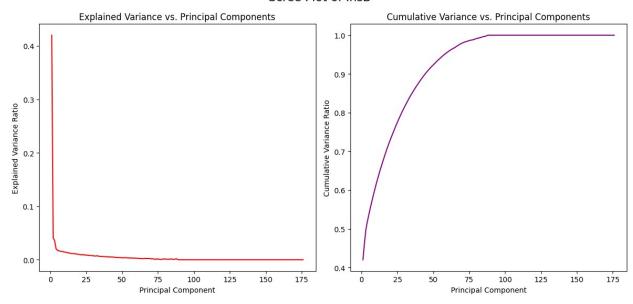
Scree Plot of InsA



Number of components selected: 2

```
dataB = pd.read csv('/content/drive/MyDrive/sem 7/ID5055/Assignment
1/Problem 5/InsB.csv')
# Centering the data
mean = np.mean(dataB, axis=0)
scaled data = dataB - mean
# Getting the principle components
pca = scaled data@get pc(scaled data)
# Scree plot to visualize explained variance by each principal
component
explained variance = exp var(pca)
cumulative variance = np.cumsum(explained variance)
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(12, 6))
# Subplot 1: Explained Variance vs. Principal Components
ax1.plot(range(1, len(explained variance) + 1), explained variance,
color='red')
ax1.set xlabel('Principal Component')
ax1.set ylabel('Explained Variance Ratio')
ax1.set title('Explained Variance vs. Principal Components')
# Subplot 2: Cumulative Variance vs. Principal Components
ax2.plot(range(1, len(cumulative variance) + 1), cumulative variance,
color='purple')
ax2.set xlabel('Principal Component')
ax2.set ylabel('Cumulative Variance Ratio')
ax2.set title('Cumulative Variance vs. Principal Components')
fig.suptitle('Scree Plot of InsB', fontsize=16)
plt.tight layout()
plt.show()
# Implementing the "knee" point detection algorithm
total variance = np.sum(explained variance)
knee threshold = 0.9 # adjustable
num components = np.argmax(cumulative variance >= knee threshold *
total variance) + 1
print(f"Number of components selected: {num components}")
/usr/local/lib/python3.10/dist-packages/matplotlib/cbook/
init .py:1335: ComplexWarning: Casting complex values to real
discards the imaginary part
  return np.asarray(x, float)
```

Scree Plot of InsB



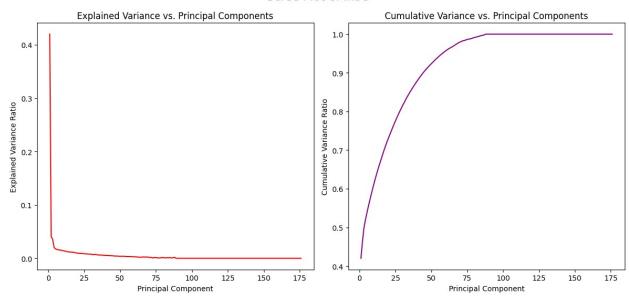
Number of components selected: 45

```
InsC Analysis
```

```
dataC = pd.read csv('/content/drive/MyDrive/sem 7/ID5055/Assignment
1/Problem 5/InsC.csv')
# Centering the data
mean = np.mean(dataC, axis=0)
scaled data = dataC - mean
# Getting the principle components
pca = scaled data@get pc(scaled data)
# Scree plot to visualize explained variance by each principal
component
explained variance = exp var(pca)
cumulative variance = np.cumsum(explained variance)
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(12, 6))
# Subplot 1: Explained Variance vs. Principal Components
ax1.plot(range(1, len(explained variance) + 1), explained variance,
color='red')
ax1.set xlabel('Principal Component')
ax1.set ylabel('Explained Variance Ratio')
ax1.set_title('Explained Variance vs. Principal Components')
# Subplot 2: Cumulative Variance vs. Principal Components
ax2.plot(range(1, len(cumulative variance) + 1), cumulative variance,
color='purple')
```

```
ax2.set xlabel('Principal Component')
ax2.set ylabel('Cumulative Variance Ratio')
ax2.set title('Cumulative Variance vs. Principal Components')
fig.suptitle('Scree Plot of InsC', fontsize=16)
plt.tight_layout()
plt.show()
# Implementing the "knee" point detection algorithm
total variance = np.sum(explained variance)
knee threshold = 0.9 # adjustable
num components = np.argmax(cumulative variance >= knee threshold *
total variance) + 1
print(f"Number of components selected: {num components}")
/usr/local/lib/python3.10/dist-packages/matplotlib/cbook/
  init .py:1335: ComplexWarning: Casting complex values to real
discards the imaginary part
  return np.asarray(x, float)
```

Scree Plot of InsC



Number of components selected: 45

```
Part (b)
```

```
# Load the new test data
test_data = pd.read_csv('/content/drive/MyDrive/sem
7/ID5055/Assignment 1/Problem 5/Test_data.csv')
mean = np.mean(test_data, axis=0)
```

```
test_data_centered = test_data - mean

# Perform PCA on the test data using the same PCA object
pca = get_pc(test_data_centered)[:, :9]

# Using the rule of thumb I opted to use first 9 principle components

transformed_data = test_data_centered @ pca
reconstructed_data = np.dot(transformed_data, pca.T)
reconstructed_data = reconstructed_data + mean.values

# Calculate the reconstruction error for each test sample
reconstruction_errors = np.mean(np.square(test_data -
reconstructed_data), axis=1)

# Identify the contaminated sample
contaminated_sample_index = np.argmax(reconstruction_errors)
print(f"The contaminated sample is at index:
{contaminated_sample_index}")

The contaminated sample is at index: 3
```

The contaminated sample might have higher residuals compared to the rest of the samples. So I looked for samples with significantly larger residuals than the others. This could be indicative of the sample with contaminants and it turned out that sample at index 3 has the highest residual.