PATTERN PROCESSING USING AI

PRACTICAL FILE

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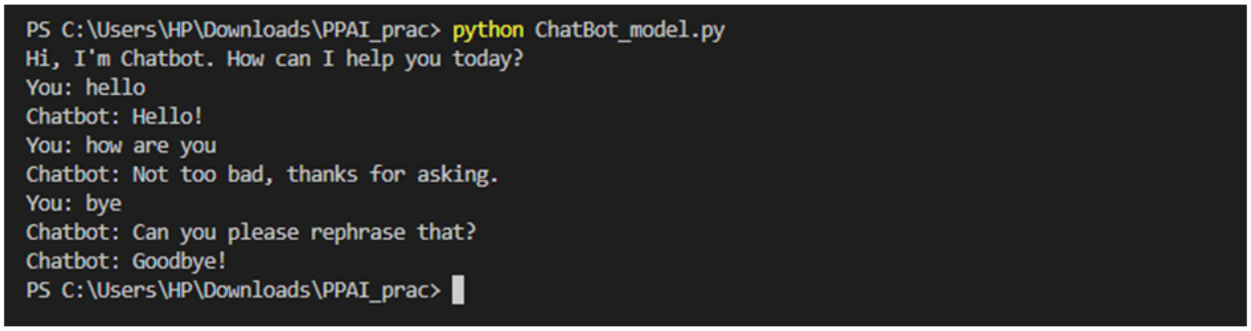
1. Write a python program to implement a simple Chatbot.

Code

```
import random

responses = {
        "hello": ["Hi there!", "Hello!", "Hey!"],
        "how are you": ["I'm doing well, thank you.", "Not too bad, thanks for asking.", "I'm just
fine."],
        "what's your name": ["My name is Chatbot.", "I go by Chatbot.", "You can call me Chatbot."],
        "default": ["I'm sorry, I didn't understand what you said.", "Can you please rephrase that?",
"I'm not sure what you mean."],
}

def get_response(user_input):
        user_input = user_input.lower().strip()

        if user_input in responses:
        return random.choice(responses[user_input])
        else:
        return random.choice(responses["default"])


def run_chatbot():
        print("Hi, I'm Chatbot. How can I help you today?")

        while True:
        user_input = input("You: ")

        bot_response = get_response(user_input)

        print("Chatbot: " + bot_response)

        if user_input.lower().strip() == "bye":
        print("Chatbot: Goodbye!")
        break

run_chatbot()
```

Output



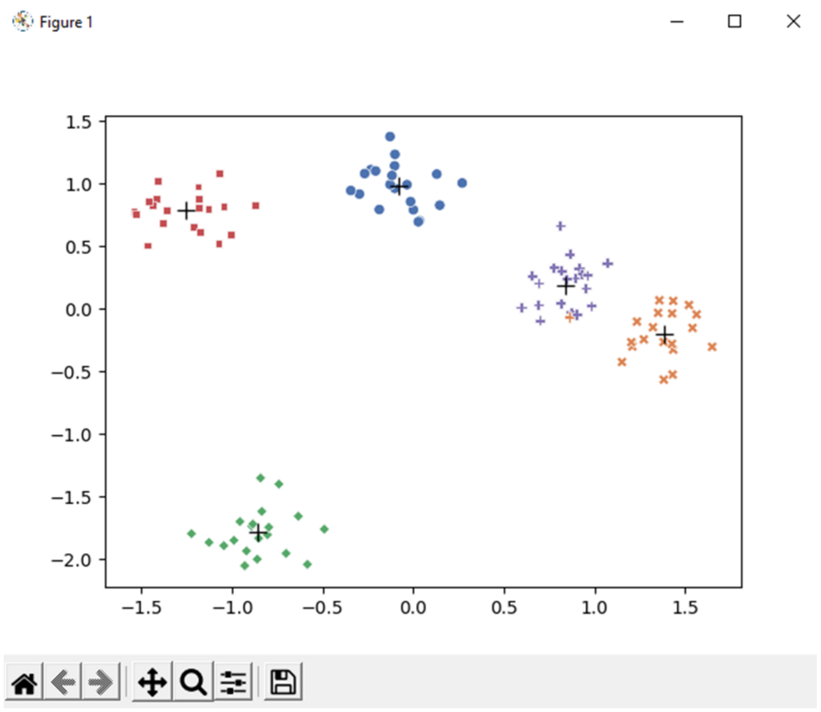
```
PS C:\Users\HP\Downloads\PPAI_prac> python ChatBot_model.py
Hi, I'm Chatbot. How can I help you today?
You: hello
Chatbot: Hello!
You: how are you
Chatbot: Not too bad, thanks for asking.
You: bye
Chatbot: Can you please rephrase that?
Chatbot: Goodbye!
PS C:\Users\HP\Downloads\PPAI_prac>
```

2. Write a program to implement k-means clustering from scratch.

Code

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.preprocessing import StandardScaler
from numpy.random import uniform
from sklearn.datasets import make_blobs
import seaborn as sns
import random
def euclidean(point, data):
        """
    Euclidean distance between point & data.
        Point has dimensions (m,), data has dimensions (n,m), and output will be of size (n,).
    """
        return np.sqrt(np.sum((point - data)**2, axis=1))
class KMeans:
        def __init__(self, n_clusters=8, max_iter=300):
        self.n_clusters = n_clusters
        self.max_iter = max_iter
        def fit(self, X_train):

        self.centroids = [random.choice(X_train)]
        for _ in range(self.n_clusters-1):
        # Calculate distances from points to the centroids
        dists = np.sum([euclidean(centroid, X_train) for centroid in self.centroids], axis=0)
        # Normalize the distances
        dists /= np.sum(dists)
        # Choose remaining points based on their distances
        new_centroid_idx, = np.random.choice(range(len(X_train)), size=1, p=dists)
        self.centroids += [X_train[new_centroid_idx]]

        iteration = 0
        prev_centroids = None
        while np.not_equal(self.centroids, prev_centroids).any() and iteration < self.max_iter:
        # Sort each datapoint, assigning to nearest centroid
        sorted_points = [[] for _ in range(self.n_clusters)]
        for x in X_train:
                dists = euclidean(x, self.centroids)
                centroid_idx = np.argmin(dists)
                sorted_points[centroid_idx].append(x)

        prev_centroids = self.centroids
        self.centroids = [np.mean(cluster, axis=0) for cluster in sorted_points]
        for i, centroid in enumerate(self.centroids):
                if np.isnan(centroid).any():
                    self.centroids[i] = prev_centroids[i]
        iteration += 1
        def evaluate(self, X):
        centroids = []
        centroid_idxs = []
        for x in X:
        dists = euclidean(x, self.centroids)
        centroid_idx = np.argmin(dists)
        centroids.append(self.centroids[centroid_idx])
        centroid_idxs.append(centroid_idx)
        return centroids, centroid_idxs

centers = 5
X_train, true_labels = make_blobs(n_samples=100, centers=centers, random_state=42)
X_train = StandardScaler().fit_transform(X_train)
# Fit centroids to dataset
kmeans = KMeans(n_clusters=centers)
kmeans.fit(X_train)

class_centers, classification = kmeans.evaluate(X_train)
sns.scatterplot(x=[X[0] for X in X_train],
                y=[X[1] for X in X_train],
                hue=true_labels,
                style=classification,
                palette="deep",
                legend=None
                )
plt.plot([x for x, _ in kmeans.centroids],
        [y for _, y in kmeans.centroids],
        'k+',
        markersize=10,
        )
plt.show()
```

Output

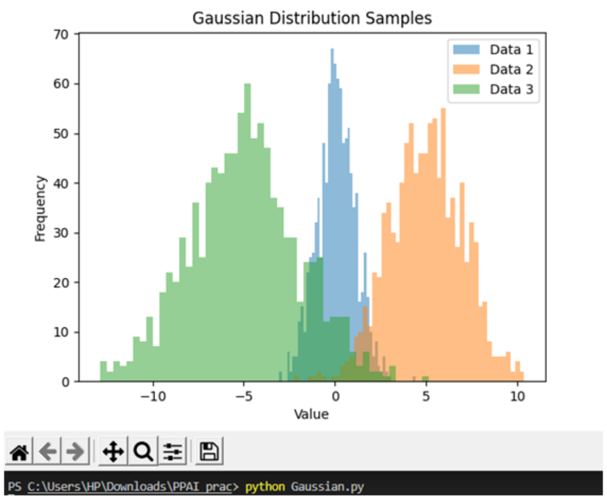


3. Generating samples of Gaussian (normal) distributions and plotting them for visualization.

Code

```python
import numpy as np
import matplotlib.pyplot as plt

mean1, mean2, mean3 = 0, 5, -5
std1, std2, std3 = 1, 2, 3

data1 = np.random.normal(mean1, std1, 1000)
data2 = np.random.normal(mean2, std2, 1000)
data3 = np.random.normal(mean3, std3, 1000)

fig, ax = plt.subplots()

ax.hist(data1, bins=50, alpha=0.5, label='Data 1')
ax.hist(data2, bins=50, alpha=0.5, label='Data 2')
ax.hist(data3, bins=50, alpha=0.5, label='Data 3')

ax.legend(loc='upper right')
ax.set_title('Gaussian Distribution Samples')
ax.set_xlabel('Value')
ax.set_ylabel('Frequency')
plt.show()
```

Output



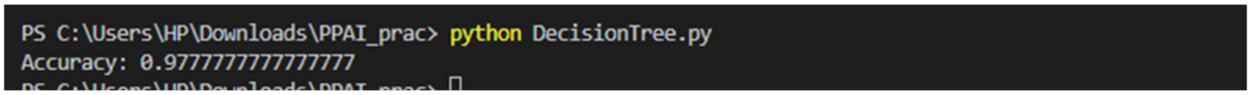
```
PS C:\Users\HP\Downloads\PPAI_prac> python Gaussian.py
```

4. Implement Decision Tree algorithms.

Code

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split

class DecisionTree:
      def __init__(self, max_depth=5, min_samples_split=2):
      self.max_depth = max_depth
      self.min_samples_split = min_samples_split

      def fit(self, X, y):
      class Node:
             def __init__(self, feature_idx=None, threshold=None, left=None,
right=None, is_leaf=False, label=None):
                self.feature_idx = feature_idx
                self.threshold = threshold
                self.left = left
                self.right = right
                self.is_leaf = is_leaf
                self.label = label

      def entropy(y):
             _, counts = np.unique(y, return_counts=True)
             p = counts / len(y)
             return -np.sum(p * np.log2(p))

      def info_gain(X, y, feature_idx, threshold):
             left_idx = X[:, feature_idx] < threshold
             left_y = y[left_idx]
             right_y = y[~left_idx]
             p_left = len(left_y) / len(y)
             p_right = 1 - p_left
             ig = entropy(y) - p_left * entropy(left_y) - p_right *
entropy(right_y)
             return ig

      def split(X, y, depth):
             if depth >= self.max_depth or len(X) < self.min_samples_split or
len(np.unique(y)) == 1:
                label = np.bincount(y).argmax()
                return Node(is_leaf=True, label=label)

             best_feature_idx, best_threshold, best_ig = None, None, 0
             for feature_idx in range(X.shape[1]):
                thresholds = np.unique(X[:, feature_idx])
                for threshold in thresholds:
                    ig = info_gain(X, y, feature_idx, threshold)
                    if ig > best_ig:
                          best_feature_idx, best_threshold, best_ig = feature_idx,
threshold, ig

             left_idx = X[:, best_feature_idx] < best_threshold
             right_idx = ~left_idx
             left_node = split(X[left_idx], y[left_idx], depth+1)
             right_node = split(X[right_idx], y[right_idx], depth+1)
             return Node(feature_idx=best_feature_idx, threshold=best_threshold,
left=left_node, right=right_node)

      self.root = split(X, y, depth=0)

      def predict(self, X):
      def traverse(node, x):
             if node.is_leaf:
                return node.label
             if x[node.feature_idx] < node.threshold:
                return traverse(node.left, x)
             else:
                return traverse(node.right, x)

      y_pred = np.array([traverse(self.root, x) for x in X])
      return y_pred

iris = load_iris()
X, y = iris.data, iris.target

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3,
random_state=42)

dt = DecisionTree()
dt.fit(X_train, y_train)

y_pred = dt.predict(X_test)

accuracy = np.sum(y_pred == y_test) / len(y_test)
print("Accuracy:", accuracy)
```

Output



```
PS C:\Users\HP\Downloads\PPAI_prac> python DecisionTree.py
Accuracy: 0.9777777777777777
PS C:\Users\HP\Downloads\PPAI_prac>
```

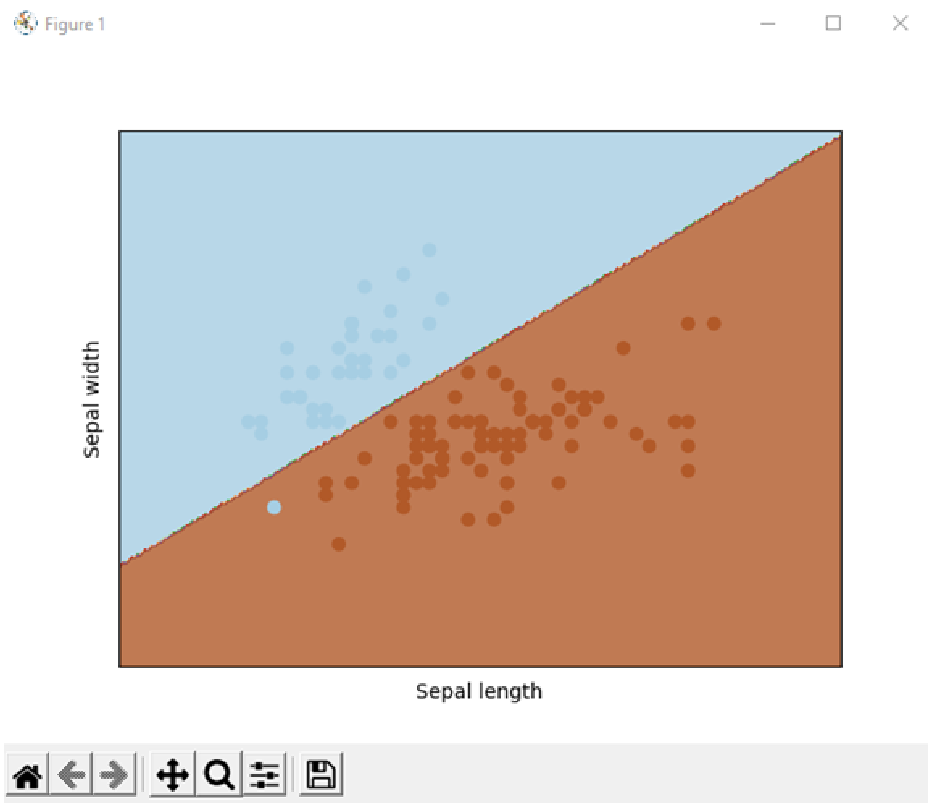
5. Implement SVM.

Code

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split
import matplotlib.pyplot as plt

class SVM:
      def __init__(self, learning_rate=0.001, regularization=0.01,
num_iterations=1000):
      self.lr = learning_rate
      self.reg = regularization
      self.num_iters = num_iterations
      self.w = None
      self.b = None

      def fit(self, X, y):
      self.w = np.zeros(X.shape[1])
      self.b = 0

      for i in range(self.num_iters):
            margins = y * (np.dot(X, self.w) + self.b)
            hinge_loss = np.maximum(0, 1 - margins)

            dw = self.reg * self.w - np.dot(X.T, y * (hinge_loss > 0))
            db = -np.sum(y * (hinge_loss > 0))

            self.w -= self.lr * dw
            self.b -= self.lr * db

      def predict(self, X):
      scores = np.dot(X, self.w) + self.b

      return np.sign(scores)

iris = load_iris()
X = iris.data[:, :2]  # Select only the first two features
y = np.where(iris.target == 0, -1, 1)  # Convert labels to -1 or 1
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)
```

```
svm = SVM()
svm.fit(X_train, y_train)

x_min, x_max = X[:, 0].min() - 1, X[:, 0].max() + 1
y_min, y_max = X[:, 1].min() - 1, X[:, 1].max() + 1
xx, yy = np.meshgrid(np.arange(x_min, x_max, 0.02),
                     np.arange(y_min, y_max, 0.02))

Z = svm.predict(np.c_[xx.ravel(), yy.ravel()])
Z = Z.reshape(xx.shape)
plt.contourf(xx, yy, Z, cmap=plt.cm.Paired, alpha=0.8)
plt.scatter(X_train[:, 0], X_train[:, 1], c=y_train, cmap=plt.cm.Paired)
plt.xlabel('Sepal length')
plt.ylabel('Sepal width')
plt.xlim(xx.min(), xx.max())
plt.ylim(yy.min(), yy.max())
plt.xticks(())
plt.yticks(())
plt.show()
```

Output

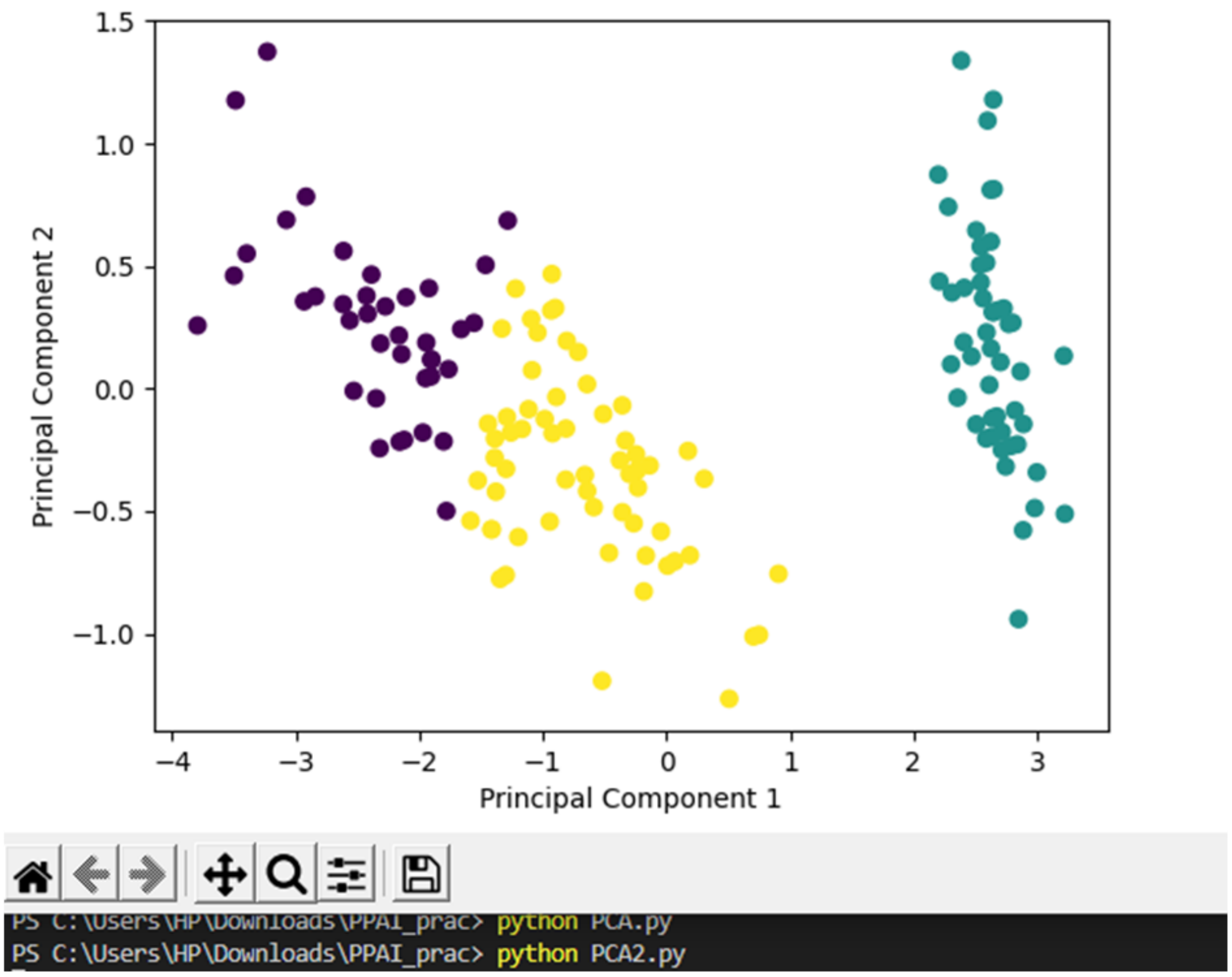


6. Implement Principal component analysis and use it for unsupervised learning

Code

```
import numpy as np

def pca(X, num_components):
      mean_X = np.mean(X, axis=0)

      X_centered = X - mean_X

      cov_X = np.cov(X_centered, rowvar=False)

      eigenvalues, eigenvectors = np.linalg.eigh(cov_X)

      sorted_indices = np.argsort(eigenvalues)[::-1]
      sorted_eigenvalues = eigenvalues[sorted_indices]
      sorted_eigenvectors = eigenvectors[:, sorted_indices]

      top_eigenvectors = sorted_eigenvectors[:, :num_components]

      X_transformed = np.dot(X_centered, top_eigenvectors)

      return X_transformed, top_eigenvectors

from sklearn.datasets import load_iris
iris = load_iris()
X = iris.data

X_transformed, top_eigenvectors = pca(X, num_components=2)

from sklearn.cluster import KMeans
kmeans = KMeans(n_clusters=3, random_state=42)
kmeans.fit(X_transformed)
labels = kmeans.labels_


import matplotlib.pyplot as plt
plt.scatter(X_transformed[:, 0], X_transformed[:, 1], c=labels)
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.show()
```

Output



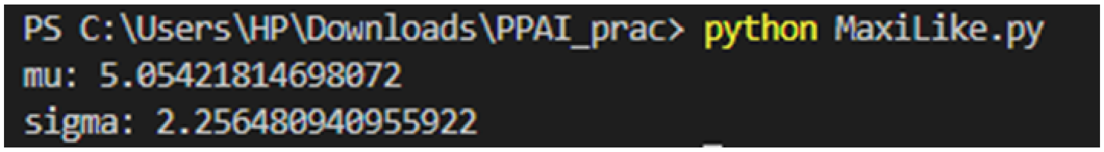
```
PS C:\Users\HP\Downloads\PPAI_prac> python PCA.py
PS C:\Users\HP\Downloads\PPAI_prac> python PCA2.py
```

7. Implement Maximum-Likelihood estimation.

Code

```
import numpy as np
def likelihood(x, mu, sigma):
        n = len(x)
        log_likelihood = -n/2*np.log(2*np.pi*sigma**2) -
np.sum((x-mu)**2)/(2*sigma**2)
        return log_likelihood

def d_likelihood_mu(x, mu, sigma):
        n = len(x)
        d_log_likelihood_mu = np.sum((mu-x)/(sigma**2))
        return d_log_likelihood_mu

def d_likelihood_sigma(x, mu, sigma):
        n = len(x)
        d_log_likelihood_sigma = -n/(2*sigma**2) + np.sum((x-mu)**2)/(2*sigma**4)
        return d_log_likelihood_sigma

def maximum_likelihood_estimation(x):
        mu = np.mean(x)
        sigma = np.std(x)

        alpha = 0.1
        epsilon = 1e-5

        while True:
        d_mu = d_likelihood_mu(x, mu, sigma)
        d_sigma = d_likelihood_sigma(x, mu, sigma)
        mu -= alpha*d_mu
        sigma -= alpha*d_sigma

        if np.abs(d_mu) < epsilon and np.abs(d_sigma) < epsilon:
                break

        return mu, sigma

np.random.seed(123)
x = np.random.normal(loc=5, scale=2, size=100)

mu, sigma = maximum_likelihood_estimation(x)

print('mu:', mu)
print('sigma:', sigma)
```

Output



```
PS C:\Users\HP\Downloads\PPAI_prac> python MaxiLike.py
mu: 5.05421814698072
sigma: 2.256480940955922
```

8. Implement agglomerative Hierarchical clustering.

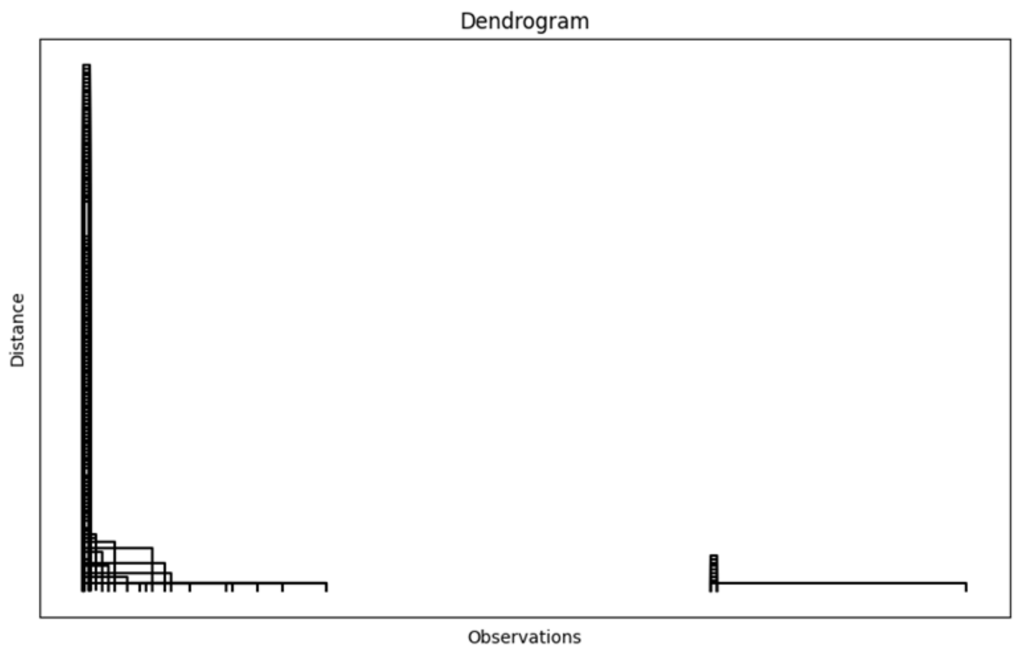
Code

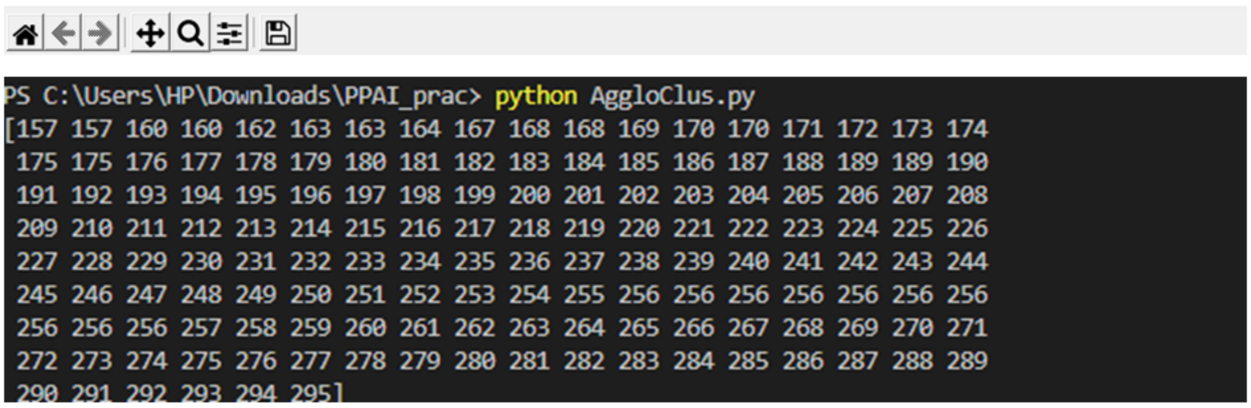
```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.datasets import load_iris

class AgglomerativeClustering:
      def __init__(self, n_clusters):
      self.n_clusters = n_clusters

      def fit(self, X):
      clusters = [[i] for i in range(X.shape[0])]
      dist_matrix = np.zeros((X.shape[0], X.shape[0]))
      for i in range(X.shape[0]):
            for j in range(i+1, X.shape[0]):
                dist_matrix[i,j] = np.linalg.norm(X[i,:] - X[j,:])
      dendrogram = np.zeros((X.shape[0]-1, 4))
      for i in range(X.shape[0]-1):
            min_dist = np.inf
            for j in range(len(clusters)):
                for k in range(j+1, len(clusters)):
                    dist =
np.min(dist_matrix[clusters[j],:][:,clusters[k]])
                    if dist < min_dist:
                        min_dist = dist
                        merge_clusters = (j,k)
            dendrogram[i,0] = merge_clusters[0]
            dendrogram[i,1] = merge_clusters[1]
            dendrogram[i,2] = min_dist
            dendrogram[i,3] = len(clusters[merge_clusters[0]]) +
len(clusters[merge_clusters[1]])
```

```
            clusters[merge_clusters[0]] += clusters[merge_clusters[1]]
            del clusters[merge_clusters[1]]
            # Update the distance matrix
            for j in range(len(clusters)-1):
                for k in range(j+1, len(clusters)):
                    min_dists = []
                    for l in clusters[j]:
                        for m in clusters[k]:
                              min_dists.append(dist_matrix[l,m])
                    dist_matrix[j,k] = min(min_dists)
                    dist_matrix[k,j] = dist_matrix[j,k]
      self.labels_ = np.zeros(X.shape[0], dtype=np.int32)
      for i in range(X.shape[0]):
            for j in range(dendrogram.shape[0]):
                if dendrogram[j,0] <= i < dendrogram[j,3]:
                    self.labels_[i] = j + X.shape[0] - self.n_clusters
                    break
      self.dendrogram = dendrogram


      def plot_dendrogram(self):
      # Plot the dendrogram
      plt.figure(figsize=(10,6))
      plt.title('Dendrogram')
      plt.xlabel('Observations')
      plt.ylabel('Distance')
      plt.xticks([])
      plt.yticks([])
      for i in range(self.dendrogram.shape[0]):
            x1 = self.dendrogram[i,0]
            x2 = self.dendrogram[i,1]
            y1 = self.dendrogram[i,2]
            y2 = self.dendrogram[i,3]
            plt.plot([x1,x1,x2,x2], [y1,y2,y2,y1], 'k-')
      plt.show()


iris = load_iris()
X = iris.data

n_clusters = 3
model = AgglomerativeClustering(n_clusters)
```

```
model.fit(X)
model.plot_dendrogram()

print(model.labels_)
```

Output





```
PS C:\Users\HP\Downloads\PPAI_prac> python AggloClus.py
[157 157 160 160 162 163 163 164 167 168 168 169 170 170 171 172 173 174
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 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289
 290 291 292 293 294 295]
```