proj4_aa10108

October 21, 2024

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1.1 Applied Machine Learning - ENGR-UH 3332 - Project 4

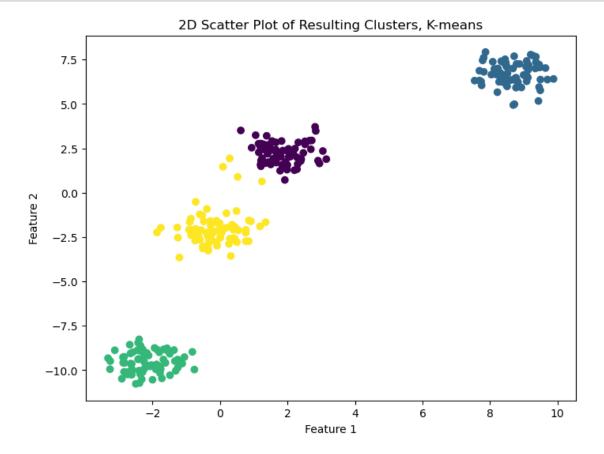
```
[138]: import sklearn
   import numpy as np
   import pandas as pd
   from matplotlib import pyplot as plt
   from sklearn.datasets import make_blobs
   from mpl_toolkits import mplot3d
   from sklearn.metrics import pairwise_distances_argmin
   import cv2
   import scipy.cluster.hierarchy as sch
```

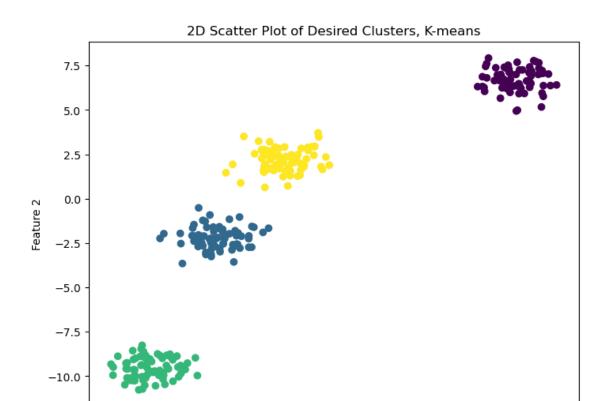
1.2 K-Means

```
[139]: class Kmeans:
           def __init__(self, X, k, tol):
               self.X = X
               self.n_centers = k
               self.tolerance = tol
               self.n_points = self.X.shape[0]
               self.n_dimensions = self.X.shape[1]
               self.centers = self.X[np.random.randint(low = 0, high = self.n_points,_
        ⇒size = self.n centers)]
               self.labels = pairwise_distances_argmin(X, self.centers)
           def update(self):
               for i in range(self.n_centers):
                   labeli = []
                   for j in range(len(self.labels)):
                       if self.labels[j] == i:
                           labeli.append(self.X[j])
                   if labeli != []:
                       self.centers[i] = np.mean(labeli)
               self.labels = pairwise_distances_argmin(self.X, self.centers)
           def recursive(self):
```

```
y1 = self.centers
      self.update()
      y2 = self.centers
      diff = np.sqrt(np.sum((y2 - y1) ** 2))
      while diff > self.tolerance:
          y1 = self.centers
          self.update()
          y2 = self.centers
          diff = np.sqrt(np.sum((y2 - y1) ** 2))
  def plot(self, y, method):
      plt.figure(figsize = (8, 6))
      plt.scatter(self.X[:, 0], self.X[:, 1], c = self.labels, cmap =_
⇔'viridis', marker = 'o')
      plt.title('2D Scatter Plot of Resulting Clusters, ' + method)
      plt.xlabel('Feature 1')
      plt.ylabel('Feature 2')
      plt.show()
      plt.figure(figsize = (8, 6))
      plt.scatter(self.X[:, 0], self.X[:, 1], c = y, cmap = 'viridis', marker_
plt.title('2D Scatter Plot of Desired Clusters, ' + method)
      plt.xlabel('Feature 1')
      plt.ylabel('Feature 2')
      plt.show()
  def kmeanspp_centers(self):
      self.centers = np.random.uniform(self.X.min(axis = 0), self.X.max(axis_
G= 0), size = (1, self.n_dimensions))
      for i in range(1, self.n_centers):
          prob = []
          self.labels = pairwise_distances_argmin(self.X, self.centers)
          for j in range(len(self.labels)):
              prob.append(sum((self.X[j] - self.centers[self.labels[j]]) **
⇒2))
          prob = prob / sum(prob)
          self.centers = np.vstack([self.centers, self.X[np.argmax(prob)]])
  def kmeans(self, y):
      self.recursive()
      self.plot(y, "K-means")
  def kmeanspp(self, y):
      self.kmeanspp_centers()
      self.recursive()
      self.plot(y, "K-means++")
```

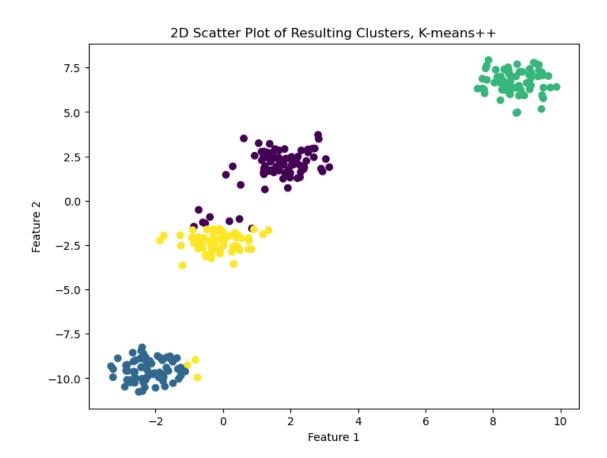
```
def recolor(self):
    X = self.X
    indices = [[] for _ in range(self.n_centers)]
    for i in range(len(self.X)):
        indices[self.labels[i]].append(i)
    for i in range(self.n_centers):
        if indices[i] != []:
            X[indices[i]] = np.mean(X[indices[i]], axis = 0)
    return X
```

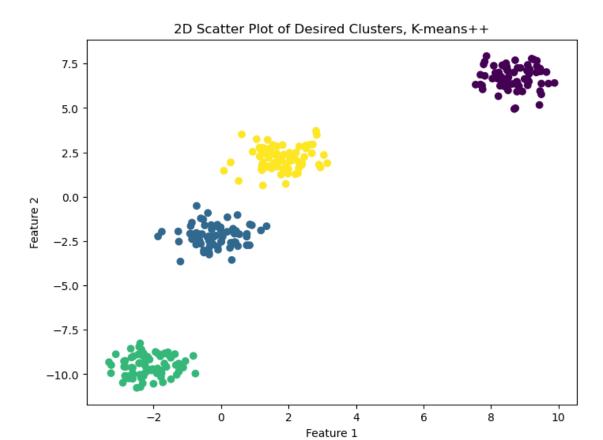


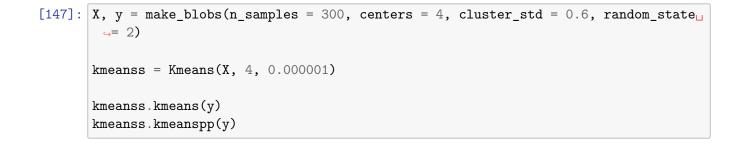


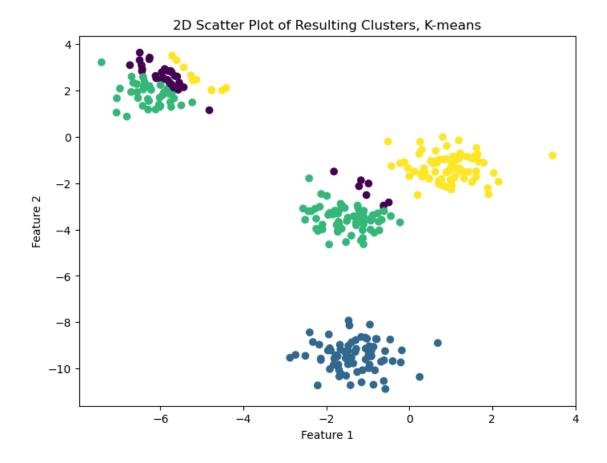
Ó

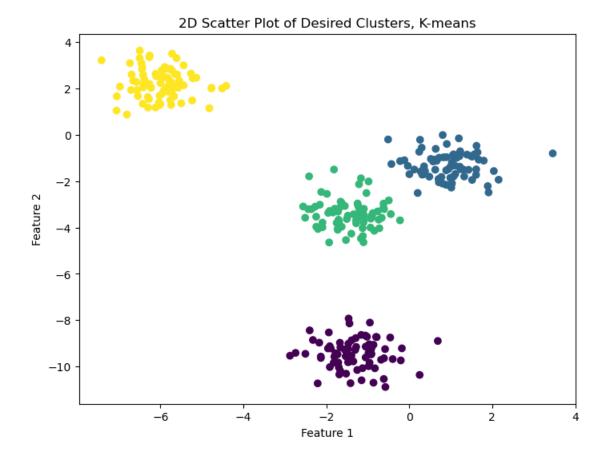
Feature 1

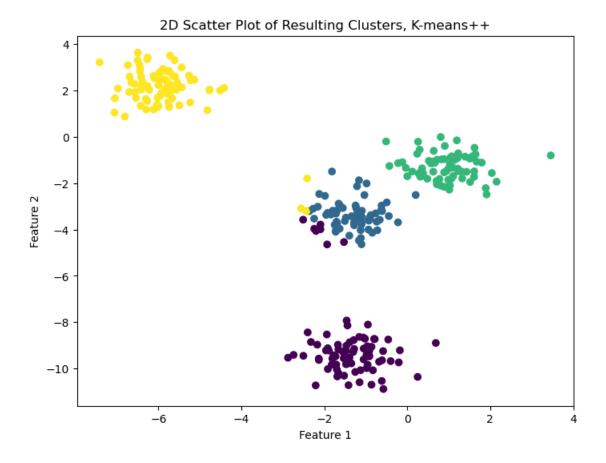




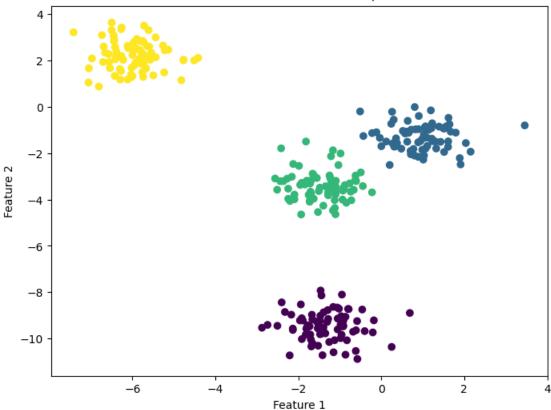












1.2.1 Comparing results from different seeds:

Seed = 2 seems to give pleasant results. I feel like the random seed sometimes sees a completely different way of clustering that is not necessarily not valid, but just doesn't fit the expected labels.

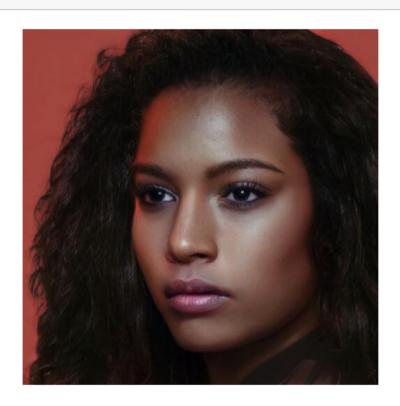
```
[142]: img = cv2.imread('cropped.jpg')
   img_rgb = cv2.cvtColor(img, cv2.COLOR_BGR2RGB)
   shape = img_rgb.shape
   plt.imshow(img_rgb)
   plt.axis('off')
   plt.show()
   img_rgb = img_rgb.reshape(-1, 3)

kme = Kmeans(img_rgb, 4, 0.000001)
   kme.kmeanspp_centers()
   kme.recursive()

img_rgb_edit = kme.recolor().reshape(shape)

plt.imshow(img_rgb_edit)
```

plt.axis('off')
plt.show()





1.2.2 Comparing all results from different methods and seeds:

K-means++ does not always provide better results, but it usually does at least. If the clusters are not very separate, both K-means and K-means++ don't provide nice clusters. But both are working fine for most seeds. K-means++ is much better at not having mixed clusters, although it causes two clusters to be the same sometimes.

1.3 Hierarchical

```
[143]: class Hierarchical:
           def __init__(self, X):
               self.X = X
               self.clusters = [np.array(c) for c in X]
               self.matrix = []
               self.clustersid = list(range(len(self.clusters)))
           def merge(self, clusterA_id, clusterB_id):
               clusterA = self.clusters[clusterA_id]
               clusterB = self.clusters[clusterB_id]
               min_dist = self.ward_distance(clusterA_id, clusterB_id)
               self.clusters.append(np.vstack([clusterA, clusterB]))
               self.clusters[clusterA id] = None
               self.clusters[clusterB id] = None
               self.clusters = [cluster for cluster in self.clusters if cluster is not_
        →Nonel
               self.clustersid.append(max(self.clustersid) + 1)
               clusterA_id_new = self.clustersid[clusterA_id]
               clusterB_id_new = self.clustersid[clusterB_id]
               self.clustersid[clusterA_id] = -1
               self.clustersid[clusterB_id] = -1
               self.clustersid = [id for id in self.clustersid if id != -1]
               self.matrix.append([clusterA_id_new, clusterB_id_new, np.
        ⇔sqrt(min_dist), 0])
           def ward_distance(self, clusterA_id, clusterB_id):
               clusterA = self.clusters[clusterA_id]
               clusterB = self.clusters[clusterB_id]
```

```
if clusterA.ndim == 1:
            centroidA = clusterA
        else:
            centroidA = np.mean(clusterA, axis = 0)
        if clusterB.ndim == 1:
            centroidB = clusterB
        else:
            centroidB = np.mean(clusterB, axis = 0)
        sizeA = len(clusterA)
        sizeB = len(clusterB)
        centroid_distance = np.sum((centroidA - centroidB) ** 2)
        return (sizeA * sizeB) / (sizeA + sizeB) * centroid_distance
    def recursive(self):
        while len(self.clusters) > 1:
            min_dist = float("inf")
            i_max, j_max = 0, 0
            for i in range(len(self.clusters)):
                for j in range(i + 1, len(self.clusters)):
                    dist = self.ward_distance(i, j)
                    if(dist < min dist):</pre>
                        min_dist = dist
                        i_max, j_max = i, j
            self.merge(i_max, j_max)
    def hierarchical(self):
        self.recursive()
        den = sch.dendrogram(np.array(self.matrix))
with pd.option_context('future.no_silent_downcasting', True):
    df["Gender"] = df["Gender"].replace(to_replace = ['Male', 'Female'], value_
```

