

I. Pen-and-paper [12v]

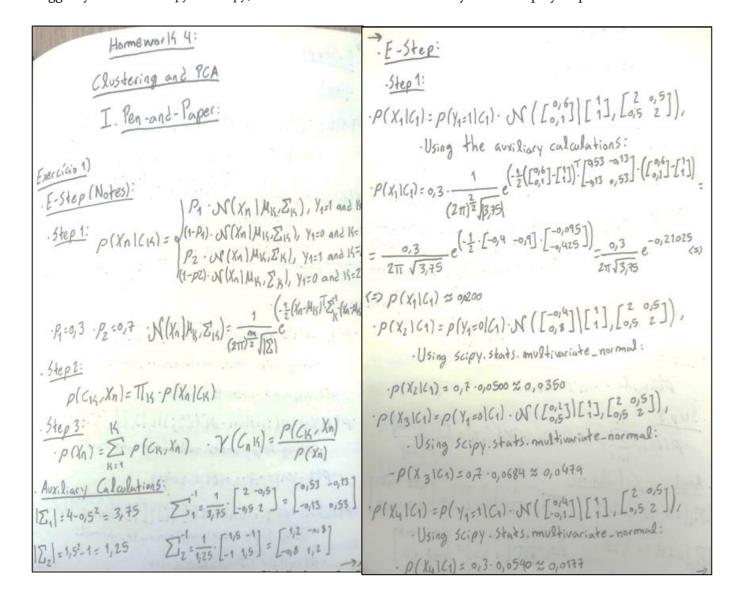
Given the following observations,
$$\left\{ \begin{pmatrix} 1\\0.6\\0.1 \end{pmatrix}, \begin{pmatrix} 0\\-0.4\\0.8 \end{pmatrix}, \begin{pmatrix} 0\\0.2\\0.5 \end{pmatrix}, \begin{pmatrix} 1\\0.4\\-0.1 \end{pmatrix} \right\}$$
.

Consider a Bayesian clustering that assumes $\{y_1\} \perp \{y_2, y_3\}$, two clusters following a Bernoulli distribution on y_1 (p_1 and p_2), a multivariate Gaussian on $\{y_2, y_3\}$ (N_1 and N_2), and the following initial mixture:

$$\begin{aligned} \pi_1 &= 0.5, \pi_2 = 0.5 \\ p_1 &= P(y_1 = 1) = 0.3, \ p_2 = P(y_1 = 1) = 0.7 \\ N_1 \left(\mathbf{u}_1 = \begin{pmatrix} 1 \\ 1 \end{pmatrix}, \mathbf{\Sigma}_1 = \begin{pmatrix} 2 & 0.5 \\ 0.5 & 2 \end{pmatrix} \right), \ N_2 \left(\mathbf{u}_2 = \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{\Sigma}_2 = \begin{pmatrix} 1.5 & 1 \\ 1 & 1.5 \end{pmatrix} \right). \end{aligned}$$

Note: you can solve this exercise by neglecting *y*₁ and still scoring up to 70% of its grade.

1) [6v] Perform one epoch of the EM clustering algorithm and determine the new parameters. Hint: we suggest you to use numpy and scipy, however disclose the intermediary results step by step.





· P(X1,62) = T2 · P(X162) & 0,0419 · P(X2,62) = T72 · P(X2162) & 0,0002 7. p(X162) = p(Y1=162) · N([0,6][0], [1,5]), · p(x3,62) = T(2 · p(x3/62) % 0,0194 · p(x4,62) = T(2 · p(x4/62) % 0,0436 . Using the auxiliary culculations: $\cdot \rho(\chi_1 | \mathcal{L}_2) = o_1 7. \frac{1}{(2^{\pi})^{\frac{2}{2}} \sqrt{|1,25|}} e^{\left(-\frac{1}{2} \left(\int_{0,1}^{o_1 6} \right] - \int_{0}^{o} \right)^{T} \cdot \left[\int_{-o_1 \delta}^{1/2} - o_1 \delta \right] \cdot \left(\int_{0,1}^{o_1 6} \left[\int_{0}^{o} \left(\int_{0}^{o} \left$ $P(X_1) = \sum_{K=1}^{K} \rho(C_K, X_1) = \rho(C_1, X_1) + \rho(C_2, X_1) \approx 0,0519$ $P(X_2) = \sum_{K=1}^{14} \rho(C_K, X_2) = \rho(C_1, X_2) + \rho(C_2, X_2) \approx 0,02777$ $= \frac{0.7}{2\pi\sqrt{1,25}} e^{\left(-\frac{1}{2}\cdot\left[0,6-91\right]\cdot\left[\frac{0,64}{-0,36}\right]\right)} = \frac{0.7}{2\pi\sqrt{1,25}} e^{-0.774}$ €7 p(X1162) 2000837 -p(x4) = [p(C1, X4) = p(C1, X4) + p(C2, X4) = 0,0524 . p(x2(2) = p(y1=0(2) - N([-0,4][0],[1,5]), . Using scipy. stats. multivariate_normal: ·P(X21C2)=0,3·0,0682 ≈ 0,0205 · Y (C11) = P(C1 | X1) = P(C1 / X1) = 0,193 · p(x3162) = p(y150162) · W([0,5])[0],[1,5 1]), . Y(C12) = p(C2 | X1) = p(C2, X1) = 0,807 . Using Scipy. Stuts. multivariate normal: · P(X3162)=0,3.0,130 \$ 0,0389 · Y((21) = P(C1 | X2) = D(C1 | X2) = 0,631 · p(x4162) = p(x4=1162)· N([0,4][0],[1,5]), · Y (622) = p(621×2) = P(62,×2) = 0,369 · Using scipy- stats. multivariate_normal: · p(X4162) = 0,7 · 0,125 \$ 0,0872 · Y (C31) = P(C1 | X3) = P(C1 | X3) = 0,552 Step 2: - TT = 0,5 . TT = 0,5 P(X1,C1)=TT1.p(X1)C1) = 0,00999 .p(X2,C1)=TT1.p(X2/C1) = 0,0175 Y(C32) = P(C2/X3) = P(C2, X3) = 0,448 P(X3,C1) = TT1 · P(X3|C1) \$20,0239 · P(X4,C1)=TT1 · P(X4|C1) \$20,00886



$$\frac{3}{\sqrt{(C_{41})}} = p(C_{1}|X_{4}) = \frac{p(C_{1}|X_{4})}{p(X_{4})} \approx 0,169$$

$$\frac{1}{\sqrt{(C_{42})}} = p(C_{2}|X_{4}) = \frac{p(C_{2}|X_{4})}{p(X_{4})} \approx 0,831$$

$$\frac{1}{\sqrt{(C_{41})}} = \frac{1}{\sqrt{(C_{41})}} \times \frac{$$



$$\frac{1}{N_{1}} \cdot \frac{1}{N_{1}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}1)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{1}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}1)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{1}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}1)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{1}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}1)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{1}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}1)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{1}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}1)(\chi_{n} - M_{1})(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n} - M_{1})(\chi_{n} - M_{1})^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n}2)(\chi_{n}2)(\chi_{n}2)(\chi_{n}2)^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n}2)(\chi_{n}2)(\chi_{n}2)(\chi_{n}2)^{T} = \frac{1}{N_{2}} \cdot \sum_{n=1}^{N_{1}} \gamma(\zeta_{n}2)(\chi_{n}2)(\chi_{n}2)(\chi_{n}2)(\chi_{n}2)^{T} = \frac{1}{N_{2}} \gamma(\zeta_{n}2)(\chi_{n}2$$



2) [2v] Given the new observation, $\mathbf{x}_{new} = \begin{pmatrix} 1 \\ 0.3 \\ 0.7 \end{pmatrix}$, determine the cluster memberships (posteriors).

$$\frac{\sum_{P \in V(C)} \sum_{i=1}^{N} \sum_{N \in N} \sum_{i=1}^{N} \sum_{P \in N} \sum_{n \in N} \sum$$



3) [2.5v] Performing a hard assignment of observations to clusters under a ML assumption, identify the silhouette of the larger cluster under a Manhattan distance.

```
. For the following calculations we will be using

$cipy. Stats. multivariate -normal.

\(\text{X_1|C_1} = \text{N(\begin{array}{c} \lefta \cdot \lefta \lef
```

```
-> . Under ML assumption we want:

. Mg Mmax P(X1|W) = C2

WE & C11626

. arg max P(X2|W) = C1

WE & C1,626

. arg max P(X3|W) = C1

WE & C1,626

. clusters = & C1 = & M2, M36, C2 = & X1, M466

. So both clusters have the same site.

. a (X1) = | X1-X4| = 0,44

. b (X1) = (|X1-X2|+|X1-X3|) = (2,7+1,8) = 2,25

. a (X2) = |X2-X3| = 0,9

. b (X2) = (|X2-X3|+|X3-X4|) = (1,8+1,8) = 1,8

. a (X3) = |X3-X2| = 0,9

. b (X3) = |X3-X2| = 0,9

. b (X3) = |X3-X2| = 0,9

. b (X3) = |X3-X2| = 0,9

. c (X4) = (|X4-X2|+|X4-X3|) = (2,7+1,8) = 2,25

. a (X4) = |X4-X1| = 0,4

. b (X3) = |X3-X2| = 0,9

. b (X3) = |X3-X2| = 0,9

. c (X4) = |X4-X1| = 0,4

. c (X4) = |X4-X1| = 0,4

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. c (X3) = |X3-X2| = 0,6667

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. c (X4) = 1
```



4) [0.5v] Knowing the purity of the clustering solution is 0.75, identify the number of possible classes (ground truth).

Exercises

Nowing that purity = 0,75 and the formula is

purity = \frac{1}{n} \sum_{\text{max}} (1C_{\text{K}} \text{n L}_{\text{j}}), For this statement, n=4

(number of observations) and there are 2 clusters (C1 and G1:

0,75 = \frac{1}{4} \sum_{\text{K-1}}^2 \max (1C_{\text{K}} \text{n L}_{\text{j}}) (=)

(=) \sum_{\text{max}}^2 \max (1C_{\text{K}} \text{n L}_{\text{j}}) (=)

(2 = d \text{max} \text{n L}_{\text{j}} \text{n let} \tex



Programming and critical analysis [8v]

Recall the column_diagnosis.arff dataset from previous homework's. For the following exercises, normalize the data using sklearn's MinMaxScaler.

1) [4v] Using sklearn, apply k-means clustering fully unsupervised Ly on the normalized data with $k \in \{2,3,4,5\}$ (random=0 and remaining parameters as default). Assess the silhouette and purity of the produced solutions.

```
import pandas as pd
import numpy as np
from scipy.io.arff import loadarff
from sklearn.preprocessing import MinMaxScaler
from sklearn.cluster import KMeans
from sklearn.metrics.cluster import contingency_matrix
from sklearn.metrics import silhouette_score
# Read ARFF file
data = loadarff('column_diagnosis.arff')
df = pd.DataFrame(data[0])
df['class'] = df['class'].str.decode('utf-8')
X = df.drop('class', axis=1)
  = df['class']
X_scaled = MinMaxScaler().fit_transform(X)
k_{values} = [2, 3, 4, 5]
for k in k_values:
    # Perform K-means clustering
    kmeans = KMeans(n_clusters=k, random_state=0).fit(X_scaled)
    if (k==3):
        kmeans3 = kmeans
    # Calculate silhouette scores and purity scores
    s_score = silhouette_score(X_scaled, kmeans.labels_)
    confusion_matrix = contingency_matrix(y, kmeans.labels_)
    p_score = np.sum(np.amax(confusion_matrix, axis=0)) / np.sum(confusion_matrix)
    print('For K =', k)
    print('Silhouete score:', s_score)
    print('Purity score:', p_score,
```

Output:

For K = 2

Silhouete score: 0.36044124340441114 Purity score: 0.632258064516129

For K = 3

Silhouete score: 0.29579055730002257 Purity score: 0.667741935483871

For K = 4

Silhouete score: 0.27442402122340176 Purity score: 0.6612903225806451

For K = 5

Silhouete score: 0.23823928397844843 Purity score: 0.6774193548387096



i. Identify the variability explained by the top two principal components.

```
from sklearn.decomposition import PCA

pca = PCA(n_components=2)
principal_components = pca.fit(X_scaled)

# Compute the explained variance for the top two components
explained_variance = pca.explained_variance_ratio_
print('Explained variance of the top two components:', explained_variance)
```

Output:

Explained variance of the top two components: [0.56181445 0.20955953]

ii. For each one of these two components, sort the input variables by relevance by inspecting the absolute weights of the linear projection.

```
# Get the absolute weights
component_weights = abs(pca.components_)

# Sort the input variables by relevance
relevance_df = pd.DataFrame(component_weights, columns=X.columns, index=['Component 1', 'Component 2']).T
relevance_df = relevance_df.sort_values(by=['Component 1', 'Component 2'], ascending=False)
print('Sorted relevance of input variables in the top two components:')
print(relevance_df)
```

Output:

Sorted relevance of input variables in the top two components:

	Component 1	Component 2
<pre>pelvic_incidence</pre>	0.591621	0.100037
<pre>lumbar_lordosis_angle</pre>	0.515085	0.080047
pelvic_tilt	0.467039	0.670373
sacral_slope	0.325689	0.443303
degree_spondylolisthesis	0.216930	0.004583
pelvic_radius	0.115824	0.581074



3) [2v] Visualize side-by-side the data using: i) the ground diagnoses, and ii) the *previously* learned k = 3 clustering solution. To this end, projected the normalized data onto a 2-dimensional data space using PCA and then color observations using the reference and cluster annotations.

```
import matplotlib.pyplot as plt
# Reduce the dimensionality of data
pca = PCA(n_components=2)
X_pca = pca.fit_transform(X_scaled)
# Real labels as inetegers to compare with kmeans labels
codes = {'Hernia':0, 'Normal':1, 'Spondylolisthesis':2}
y_pred = y.map(codes).tolist()
plt.figure(figsize=(14, 5))
plt.subplot(121)
plt.scatter(X_pca[:,0], X_pca[:,1], c=y_pred)
plt.title('Ground Diagnoses')
plt.subplot(122)
plt.scatter(X_pca[:,0], X_pca[:,1], c=kmeans3.labels_)
plt.title('K-means Clustering (k=3)')
plt.show()
                     Ground Diagnoses
                                                                           K-means Clustering (k=3)
  0.6
                                                          0.6
  0.2
                                                          0.2
  0.0
                                                          0.0
 -0.2
                                                          -0.2
 -0.4
                                                          -0.4
                                                  0.8
   -0.6
                                                            -0.6
```

4) [1v] Considering the results from questions (1) and (3), identify two ways on how clustering can be used to characterize the population of ill and healthy individuals.

Answer: Clustering can be used to identify groups of patients with similar medical characteristics to discover potential causes of the disease or define groups at higher risk of developing the disease.