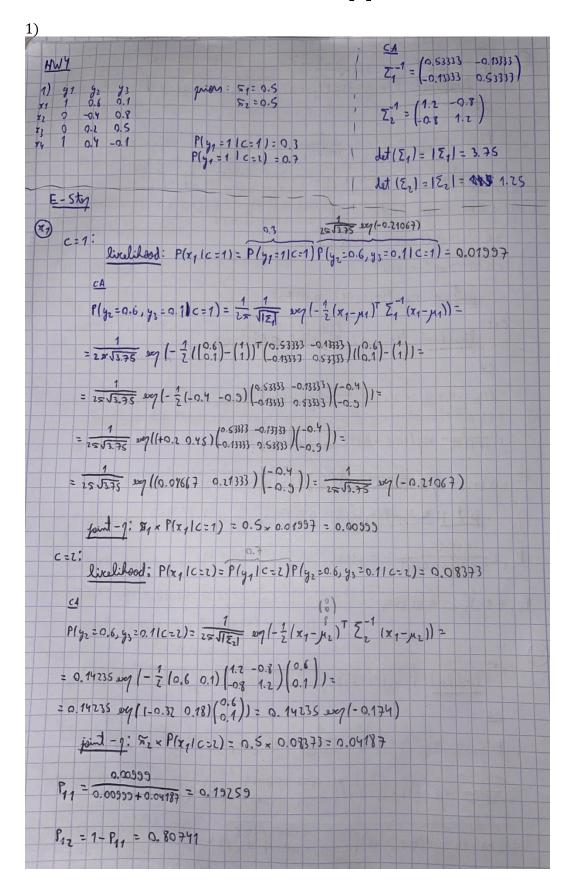
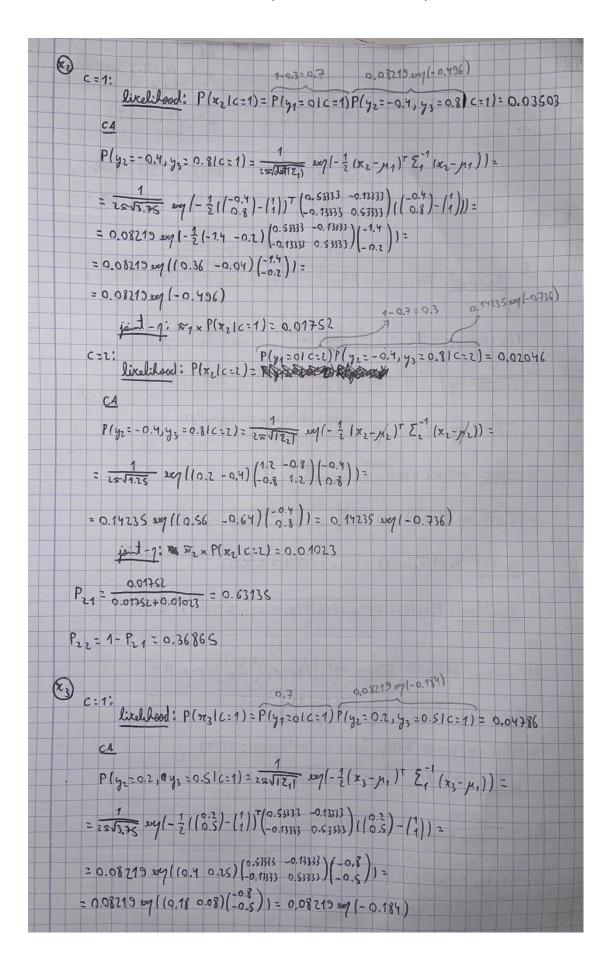
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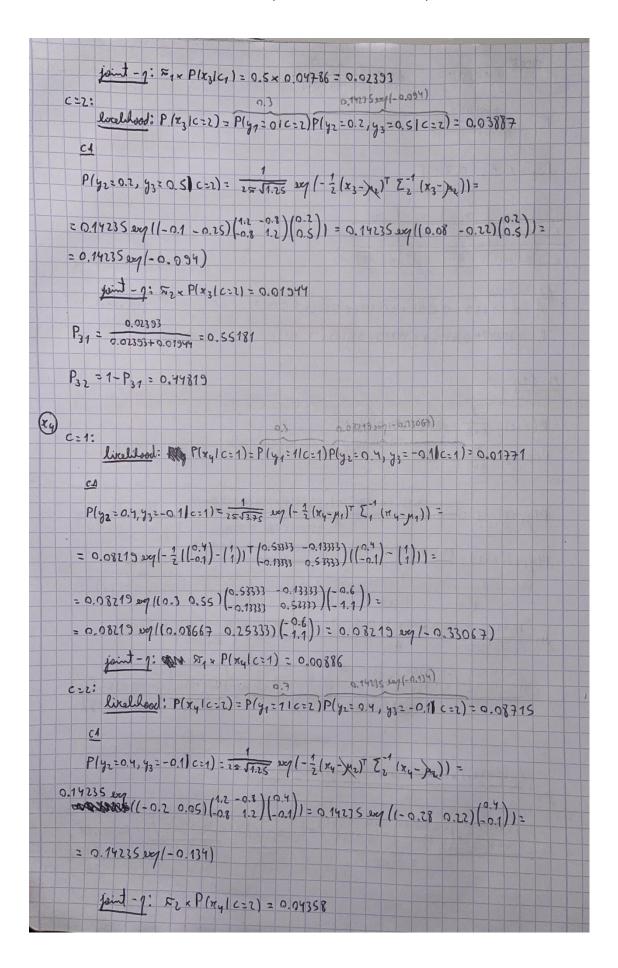
I. Pen-and-paper



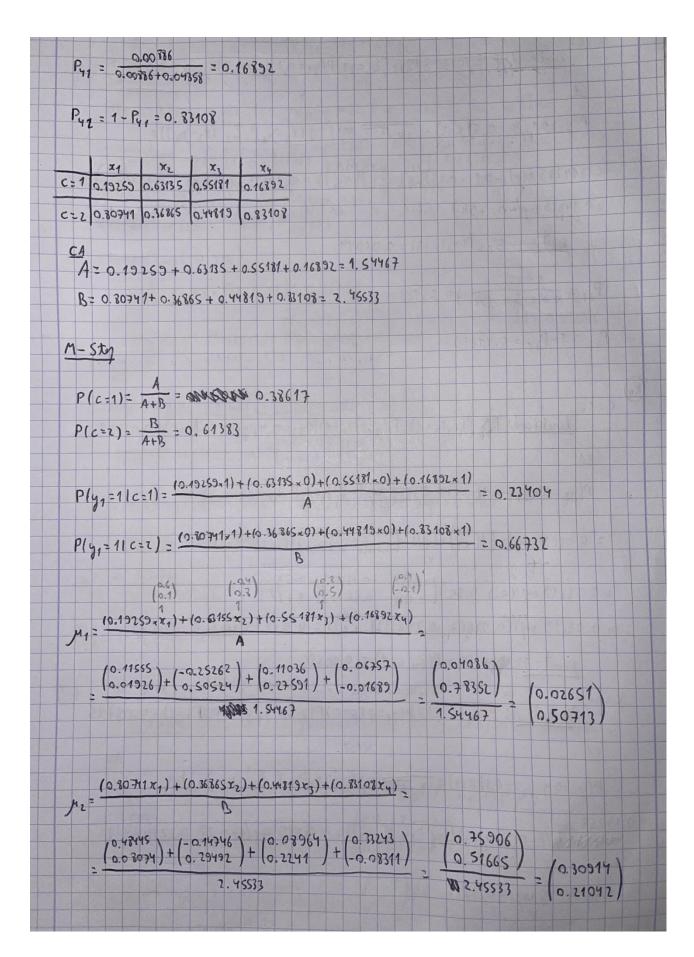
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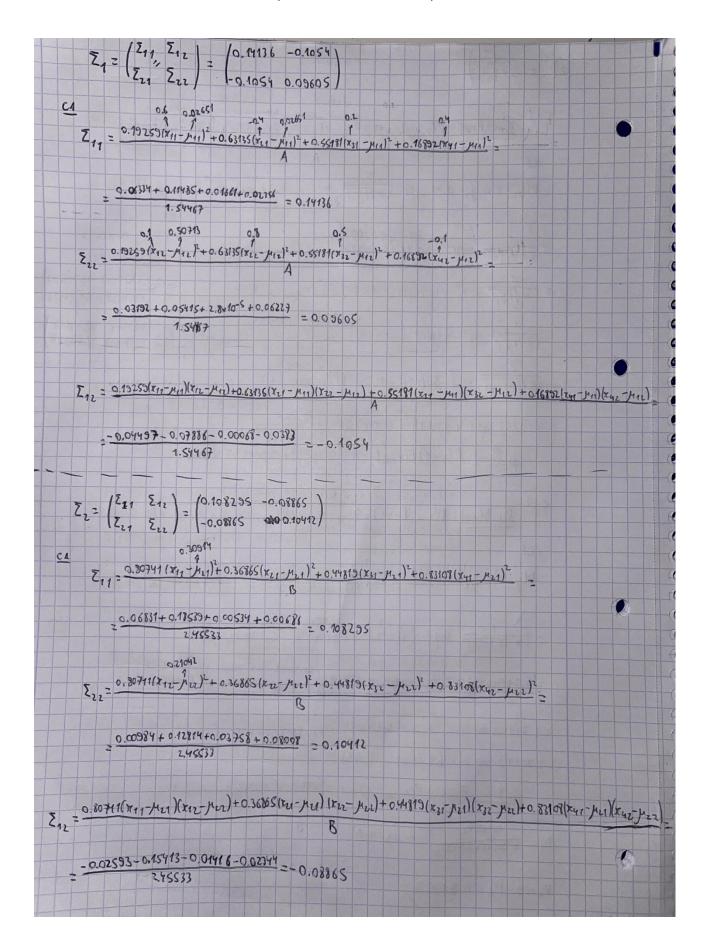
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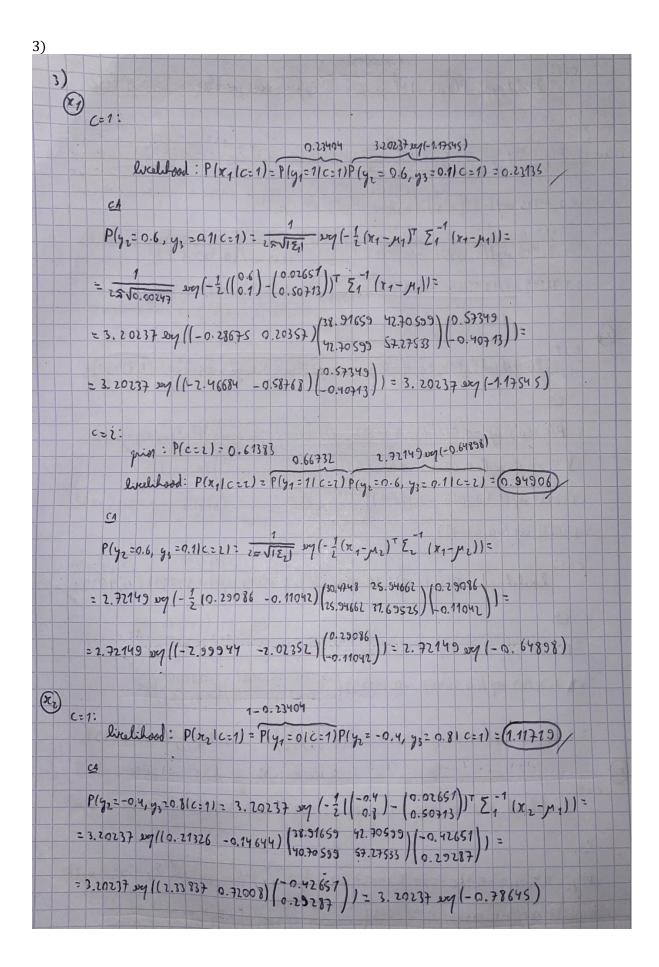


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 $x_{max} = \begin{pmatrix} 1 \\ 0.3 \\ 0.7 \end{pmatrix}$ C=1: likelihood: P(xmu |c=1) = P(y=11 |c=1)P(y=0.3, y=0.7 |c=1) = 0.00633 P(y=0.3, y=0.71 c=1)= 25 151 voj (- 2 (xmy-y=) = 21 (xmy-y=))= = 1 my (-2((0.3) - (0.02651)) T \(\frac{1}{2}\) (\(\text{X}_{man}\) - \(\psi_1\)) = \(\frac{1}{2}\) \(\frac{1}{2}\) = 0.00247 = 1 27 (- 2 (0.27345 0.1927) [1 (row-ma)) = | [1 38.91659 42.70595 57.27533 = 2510.00243 27 ((-9.44041 -11.36368) (0.27349))= = 3.20257 mg (-4.77367) = 0.02706 pint - 7: P(c=1) P(xmulc=1)= 0.38617x 0.00633= 0.00245 C22: likelihood: Plx mulc 22) = P(gy = 11C22) P(gy=0.3, y, = 0.71C=2) = 0.04564 P(y=03, y=0.71022) = 25 JI = 20/- 2 (xnow- pe) = (xnow- pe) = = 2.72149 oy (-1 (-0.00914 0.48 35) (30.4748 25, 94662) (-0.00974) = 2.72749 009 (1-6.2122 -7.6401) (-0.00014)) = = 2.72149 00 (-3.683) = 0.06839 joint -9: P(c=2) P(x mulczz) = 0.61383 x 0.04564 = 0.02802 P1 = 0.00245 = 0.08041 P2=1-P1= 0.91959

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```
ciz:
          likelihood: P(x216=2)=P(y1=016=2)P(y2=-0.4, y3=0.816=2)=0.088636
       = 2.72149 wy (- 2 ((-0.4) - (0.30914)) [ 2-1 (x1-12))=
    22.72149 my (10.35457 -0.29479) (30.4747 25.94662) (-0.70914) = 22.72149 my (10.35457 -0.29479) (25.94662 31.69525) (0.58958) ] = 2.72149 my (-2.32314)
(E)
          luchilood: P(7, 1c=1)=P(y,=0,c=1)P(y=0.2, y=0.5(c=1)=(1.43404)
     c=1:
      Ply2=0.2, y3=0.5(c=1)=3.20237 ωσ/-2((0.2)-(0.50713)) Σ, (π3-μ1)=

3.20237 ωσ/-0.08675 0.00357) (38.91659 40.70599) (π3-μ1)=
     = 3.20237 sxy ((-3.23060 -3.32677) (0.17349)) =
     = 3.20237 20 (-0.53677)
      c:2: livelihood: P(x31c=1)= (1-0.66732) x 2.72149 erg (-0.69039)= 0.45394
         CA
       P(y220.2, y320.5(222) = 272149 wg (-2((0.5) - (0.30.914))) = -1 (x3-µ2))=
= 2.72149 wg ((0.05457 -0.14479) (30.4748 25.54662) (-0.10.914))=
       = 2.72149 eg/1-20938 -3.17325)(-0.10914))= 2.72149 eg/1-0.69039)
 Ry
     C=1: livellood: P(xy (C=1)= 0.23404 x 3.20237 sq (-3.58653)=0.02076
       P(y2 = 0.4, y3 = -0.1)(21) = 3. 20237 wy (- 2 ((-0.4) - (0.50713)) = 1 (x4 - 41)=
     = 3. 2023+ sep ((-0.18675 0.30357) (38.91659 42.70599) (24-11))=
     = 3.20237 my ((5.69658 9,41173) (0.37349) = 3.20237 my (-3.58653)
```

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| CA | | | |
|---------------------|--|--|-----------------------|
| P(yz=0 | .4, 73 = - 0.11 (= 2) = | 72149 wy (- 2 ((0.4)) - (0. | 1092) T Ez (x4-12) = |
| = 2.7214 | 9 207 11-0.04543 0.15 | 21) (30.4948 25.94662) (x | 4-12)]= |
| | |) (0.09086)) = 2.72149 ve | |
| angone | nts: x ₁ > C ₂ | $S(x_1) = 1 - \frac{ x_1 }{\frac{1}{2}(x_1-x_2 }$ | |
| | 23 >> C1 23 >> C1 24 >> C2 | | |
| 1 | | =1- 1 (2.7 + 1.8) = 1- | 2.25 = 0.82222 |
| 86-1-1 | x1-x1 1 | | |
| 3(47) - (| = = = = = = = = = = = = = = = = = = = | $= 1 - \frac{0.9}{\frac{7}{2}(2.7 + 2.7)} = 1 - \frac{0}{2}$ | 7 - 0.6667 |
| S(x3)=1 | 1123-2211 | 1- 1.8 - 1- 0.9 | -05 |
| | 2 (11 1/3- x-1/1/1 + 1/1/23 - x-1/1/1) | 1.8+1.8) 1.8 | |
| S(x4)=1- | 11 24- 27 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 1- {2(2.7+1.8) = 1- 2.75 | = 0.82222 |
| s(c ₇)= | S(x2)+S(x3) = 0.66667 | 0.5 = 0.58333 | |
| S(cz)= | $\frac{1}{2}$ = 0.822 | | |

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| 4) | Puni | Gy= | 0.7 | 5 - | 57 | 5% | , of | the | oh | ental | idus | an | 2 | come | etly | a | rign | ed | | |
|-----|--------|---------|-------|-----|------|-----|------|-------|-------|----------------|------|--------------|-----|------|------|----|-------------------|--|---------------|---|
| Clu | ten 1: | 5 x 5 x | 2, X3 | } | 5 3 | q | ove | don | rigum | nentr | on | d | 1 2 | ~con | neit | on | 2. | | | |
| | 4 | 71 | is | in | core | thy | · a | nigna | J: | c, | 2 2 | 171, 1746 | XI, | 236 | on | | CZZ | 3×11 | | |
| | 7 | π | À | inc | ovei | tly | ani | ged | | C | - 3 | r3} | L,X | 48 | ol | | C12 C22 C3= | 8 x 3 | } , \ru\} | |
| | | | | | | | | ned . | | c ₁ | 29: | x_ } | 3.7 | 4 | on | | C12 C22 C32 | \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\ | rub | |
| | 4 | πη | M | ine | onei | tly | ani | gued | 2 | c, | - 4 | 72, Y | 3,7 | rut | en | | C1 = C2 = C3 | 9×2 | , 23 b | |
| | | | | | | | | | | | | | | lan | ible | gr | ome | 人力 | inths | 1 |
| | | | | | | | | | | | | | 1~ | mb | n og | d | nter | 0 4 | inths in h | L |



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II. Programming and critical analysis

1)

```
from scipy.io import arff
import pandas as pd
from sklearn.preprocessing import MinMaxScaler
from sklearn.cluster import KMeans
from sklearn.metrics import silhouette score
from sklearn.preprocessing import LabelEncoder
from sklearn.metrics import pairwise_distances_argmin_min
# Load the ARFF dataset
data, meta = arff.loadarff("column_diagnosis.arff")
df = pd.DataFrame(data)
# Convert the "class" column to numeric using LabelEncoder
label_encoder = LabelEncoder()
df['class'] = label_encoder.fit_transform(df['class'])
# Normalize the data using MinMaxScaler
scaler = MinMaxScaler()
normalized_data = scaler.fit_transform(df.drop(columns=['class']))
# Values of k to be tested
k_{values} = [2, 3, 4, 5]
silhouette_scores = []
purity_scores = []
for k in k_values:
   # Apply K-means clustering
    kmeans = KMeans(n_clusters=k, random_state=0)
    cluster_labels = kmeans.fit_predict(normalized_data)
   # Compute silhouette score
    silhouette = silhouette_score(normalized_data, cluster_labels)
    # Calculate purity
    closest_to_centers = pairwise_distances_argmin_min(kmeans.cluster_centers_,
                                                       normalized_data)[0]
    cluster_purity = 0
    for i in range(k):
        cluster_mask = (cluster_labels == i)
        majority_class = df['class'][cluster_mask].value_counts().max()
       cluster_purity += majority_class
```



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```
cluster_purity /= len(cluster_labels)

silhouette_scores.append(silhouette)
purity_scores.append(cluster_purity)

# Print the results
for k, silhouette, purity in zip(k_values, silhouette_scores, purity_scores):
    print(f'K={k}: Silhouette Score = {silhouette:.15f}, Purity = {purity:.15f}')

K=2: Silhouette Score = 0.360441243404411, Purity = 0.632258064516129
K=3: Silhouette Score = 0.295790557300023, Purity = 0.667741935483871
K=4: Silhouette Score = 0.274424021223402, Purity = 0.661290322580645
K=5: Silhouette Score = 0.238239283978448, Purity = 0.677419354838710
```

2)

```
#Ex2
from scipy.io import arff
import pandas as pd
from sklearn.preprocessing import MinMaxScaler
from sklearn.decomposition import PCA
# Load the ARFF dataset
data, meta = arff.loadarff("column_diagnosis.arff")
df = pd.DataFrame(data)
# Convert the "class" column to numeric using LabelEncoder
df['class'] = df['class'].str.decode('utf-8')
# Normalize the data using MinMaxScaler
scaler = MinMaxScaler()
normalized_data = scaler.fit_transform(df.drop(columns=['class']))
# Perform PCA to extract the top two principal components
pca = PCA(n_components=2)
principal_components = pca.fit_transform(normalized_data)
# i. Explained variance by the top two principal components
explained_variance = pca.explained_variance_ratio_
print(f"Explained Variance by the Top Two Principal Components:
{explained_variance}")
```

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```
# ii. Sort input variables by relevance for each of the top two components
component 1 loadings = pca.components [0]
component 2_loadings = pca.components_[1]
# Sort variables by absolute loadings for component 1
sorted_vars_component_1 = df.columns[abs(component_1_loadings).argsort()[::-1]]
sorted_loadings_component_1 =
component 1 loadings[abs(component 1 loadings).argsort()[::-1]]
# Sort variables by absolute loadings for component 2
sorted vars component 2 = df.columns[abs(component 2 loadings).argsort()[::-1]]
sorted loadings component 2 =
component_2_loadings[abs(component_2_loadings).argsort()[::-1]]
# Print the sorted variables and their loadings for the top two components
print("\nTop Two Principal Components - Sorted Variables and Loadings:")
print("Principal Component 1:")
for var, loading in zip(sorted vars component 1, sorted loadings component 1):
   print(f"{var}: {loading:.4f}")
print("\nPrincipal Component 2:")
for var, loading in zip(sorted_vars_component_2, sorted_loadings_component_2):
   print(f"{var}: {loading:.4f}")
```

Top Two Principal Components - Sorted Variables and Loadings:

Principal Component 1: pelvic_incidence: 0.5916 lumbar_lordosis_angle: 0.5151

pelvic_tilt: 0.4670 sacral_slope: 0.3257

degree_spondylolisthesis: 0.2169

pelvic_radius: -0.1158

Principal Component 2: pelvic_tilt: -0.6704 pelvic_radius: -0.5811 sacral_slope: 0.4433 pelvic_incidence: 0.1000 lumbar_lordosis_angle: 0.0800 degree_spondylolisthesis: 0.0046



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3)

```
#Ex3
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.preprocessing import MinMaxScaler
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans
import seaborn as sns
from scipy.io import arff
# Load the ARFF file
data, meta = arff.loadarff('column_diagnosis.arff')
df = pd.DataFrame(data)
# Normalize the data using MinMaxScaler
scaler = MinMaxScaler()
normalized_data = scaler.fit_transform(df.iloc[:, :-1])
# Perform PCA to reduce the data to 2 dimensions
pca = PCA(n components=2)
pca_result = pca.fit_transform(normalized_data)
# Create a new DataFrame with the PCA results
pca_df = pd.DataFrame(data=pca_result, columns=['PC1', 'PC2'])
# Add the diagnosis labels to the PCA DataFrame
pca_df['Diagnosis'] = df['class'].str.decode('utf-8') # Decode bytes to strings
# Create a palette of colors based on unique values in the 'Diagnosis' column
value_palette = sns.color_palette("husl", len(pca_df['Diagnosis'].unique()))
# Map colors to values in the 'Diagnosis' column
value_colors = {value: color for value, color in
# Visualize the data side-by-side
plt.figure(figsize=(12, 6))
plt.subplot(1, 2, 1)
sns.scatterplot(x='PC1', y='PC2', hue='Diagnosis', data=pca_df,
palette=value_colors)
plt.title('Ground Diagnoses')
```

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```
# Perform k-means clustering with k=3
kmeans = KMeans(n_clusters=3, random_state=0)
cluster_labels = kmeans.fit_predict(normalized_data)

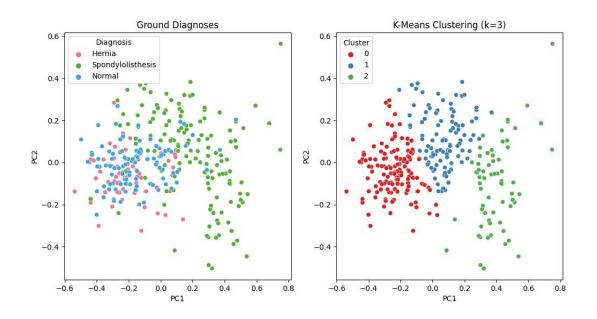
# Create a palette of colors based on unique values in the 'cluster_labels' array
cluster_palette = sns.color_palette("Set1", len(np.unique(cluster_labels)))

# Map colors to values in the 'cluster_labels' array
cluster_colors = {cluster: color for cluster, color in
zip(np.unique(cluster_labels), cluster_palette)}

# Add cluster labels to the PCA DataFrame
pca_df['Cluster'] = cluster_labels

plt.subplot(1, 2, 2)
sns.scatterplot(x='PC1', y='PC2', hue='Cluster', data=pca_df,
palette=cluster_colors)
plt.title('K-Means Clustering (k=3)')

plt.savefig("Ex3GRAPH")
```



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4)

Ao usarmos clusters podemos criar "grupos" que representam diferentes condições e grupos de risco. Por exemplo, como no exercício 3, tendo um clustering de k=3, pode originar-se 3 clusters, em que cada um identifica um tipo diferente de condição. Um pode ser para pessoas que sejam saudáveis enquanto que as outras duas categorias são para pessoas com problemas diferentes de saúde. Esta distinção é importante e útil porque facilita na escolha de tratamento de paciente para paciente. Para além dessa vantagem, os clusters podem também associar certas categorias de risco a certos problemas (Exemplo hipotético: Se a pelvic_tilt for superior a 20, o paciente é mais propício a ter uma hérnia) .

Outra vantagem de usarmos clusters é que estes ajudam-nos a encontrar outliers, ou seja, indivíduos com padrões de saúde incomuns e raros. Estes casos podem ser revistos e investigados com mais pormenor de forma a dar o tratamento mais adequado à pessoa.

END