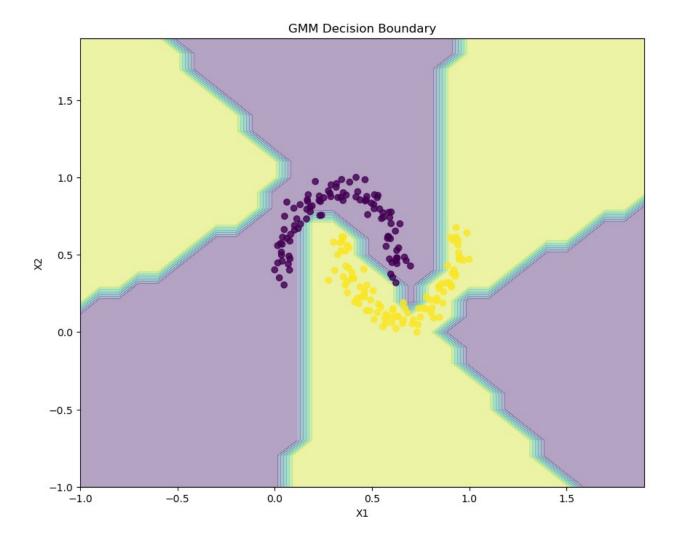
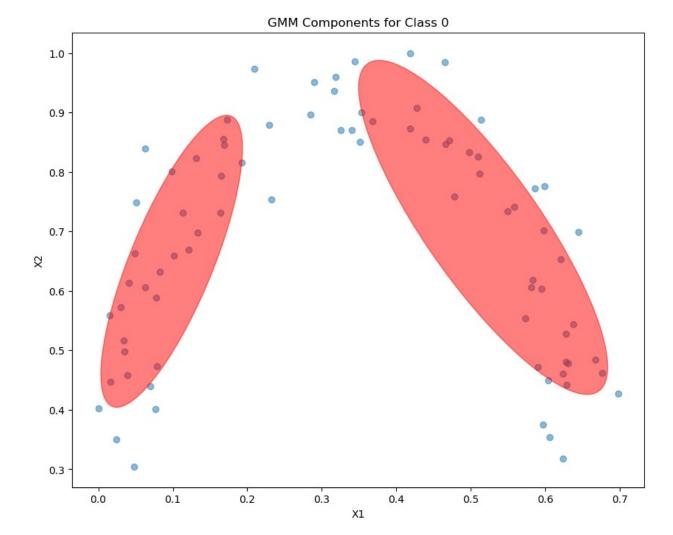
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model selection import train test split
from sklearn.metrics import accuracy score, confusion matrix
# Load the data
data = pd.read_csv('datasets/moonDataset.csv')
df normalized = (data - data.min()) / (data.max() - data.min())
data= df normalized
X = data[['X1', 'X2', 'X3']].values
y = data['label'].values
# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y,
test size=0.2, random state=42)
class GaussianMixture:
    def init (self, n components, n features, max iter=100, tol=1e-
3):
        self.n components = n components
        self.n features = n features
        self.max iter = max iter
        self.tol = tol
    def initialize_parameters(self, X):
        n \text{ samples} = X.shape[0]
        self.weights = np.ones(self.n components) / self.n components
        self.means = X[np.random.choice(n samples, self.n components,
replace=False)1
        self.covariances = np.array([np.eye(self.n features)] *
self.n components)
    def gaussian pdf(self, X, mean, cov):
        n = X.shape[1]
        diff = X - mean
        return np.exp(-0.5 * np.sum(np.dot(diff, np.linalg.inv(cov)) *
diff, axis=1)) / np.sqrt((2 * np.pi)**n * np.linalg.det(cov))
    def expectation step(self, X):
        weighted likelihood = np.zeros((X.shape[0],
self.n components))
        for k in range(self.n_components):
            weighted likelihood[:, k] = self.weights[k] *
self.gaussian pdf(X, self.means[k], self.covariances[k])
        return weighted likelihood / weighted likelihood.sum(axis=1,
```

```
keepdims=True)
    def maximization_step(self, X, responsibilities):
        total resp = responsibilities.sum(axis=0)
        self.weights = total resp / X.shape[0]
        self.means = np.dot(responsibilities.T, X) / total resp[:,
        for k in range(self.n components):
            diff = X - self.means[k]
            self.covariances[k] = np.dot(responsibilities[:, k] *
diff.T, diff) / total resp[k]
    def fit(self, X):
        self.initialize parameters(X)
        for in range(self.max iter):
            prev log likelihood = self.log likelihood(X)
            responsibilities = self.expectation step(X)
            self.maximization step(X, responsibilities)
            curr log likelihood = self.log likelihood(X)
            if np.abs(curr log likelihood - prev log likelihood) <</pre>
self.tol:
                break
    def log likelihood(self, X):
        weighted likelihood = np.zeros((X.shape[0],
self.n components))
        for k in range(self.n components):
            weighted_likelihood[:, k] = self.weights[k] *
self.gaussian_pdf(X, self.means[k], self.covariances[k])
        return np.sum(np.log(weighted likelihood.sum(axis=1)))
    def predict(self, X):
        responsibilities = self.expectation step(X)
        return np.argmax(responsibilities, axis=1)
# Train GMMs for each class
gmm class 0 = GaussianMixture(n components=2, n features=3)
gmm class 1 = GaussianMixture(n components=2, n features=3)
X train 0 = X train[y_train == 0]
X train 1 = X train[y train == 1]
gmm class 0.fit(X train 0)
gmm_class_1.fit(X train 1)
# Predict on test set
def predict gmm(X):
    log likelihood 0 =
```

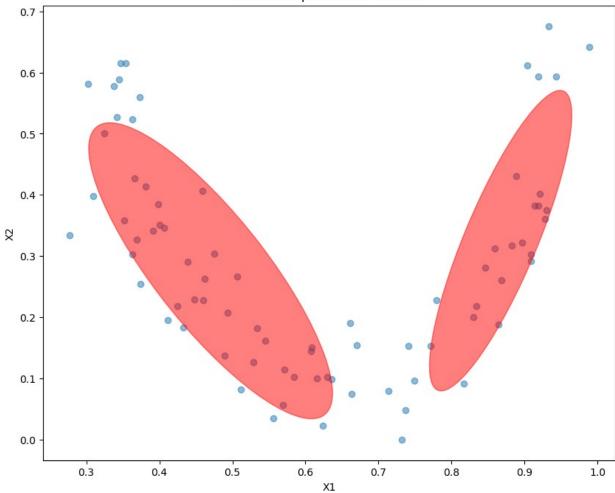
```
np.array([qmm class 0.log likelihood(x.reshape(1, -1)) for x in X])
    log likelihood 1 =
np.array([gmm_class_1.log_likelihood(x.reshape(1, -1)) for x in X])
    return (log likelihood 1 > log likelihood 0).astype(int)
y pred = predict gmm(X test)
# Evaluate the model
accuracy = accuracy score(y test, y pred)
conf matrix = confusion matrix(y test, y pred)
print(f"Accuracy: {accuracy: .4f}")
print(np.mean(y pred == y test))
print("Confusion Matrix:")
print(conf matrix)
# Visualize the results
def plot_decision_boundary(X, y, gmm_0, gmm_1, title):
    x \min, x \max = X[:, 0].\min() - 1, X[:, 0].\max() + 1
    y_{min}, y_{max} = X[:, 1].min() - 1, <math>X[:, 1].max() + 1
    xx, yy = np.meshgrid(np.arange(x min, x max, <math>0.1),
                         np.arange(y min, y max, 0.1))
    mesh points = np.c [xx.ravel(), yy.ravel(),
np.zeros like(xx.ravel())]
    Z = predict gmm(mesh points)
    Z = Z.reshape(xx.shape)
    plt.figure(figsize=(10, 8))
    plt.contourf(xx, yy, Z, alpha=0.4)
    plt.scatter(X[:, 0], X[:, 1], c=y, alpha=0.8)
    plt.title(title)
    plt.xlabel("X1")
    plt.ylabel("X2")
    plt.show()
plot_decision_boundary(X, y, gmm_class_0, gmm_class_1, "GMM Decision
Boundary")
# Plot GMM components
def plot gmm components(X, gmm, title):
    plt.figure(figsize=(10, 8))
    plt.scatter(X[:, 0], X[:, 1], alpha=0.5)
    for k in range(gmm.n components):
        mean = gmm.means[k][:2]
        cov = gmm.covariances[k][:2, :2]
        v, w = np.linalg.eigh(cov)
        v = 2. * np.sqrt(2.) * np.sqrt(v)
        u = w[0] / np.linalg.norm(w[0])
```

```
angle = np.arctan2(u[1], u[0])
        angle = 180. * angle / np.pi
        ell = plt.matplotlib.patches.Ellipse(xy=mean, width=v[0],
height=v[1], angle=angle, color='r')
        ell.set clip_box(plt.gca().bbox)
        ell.set alpha(0.5)
        plt.gca().add artist(ell)
    plt.title(title)
    plt.xlabel("X1")
    plt.ylabel("X2")
    plt.show()
plot_gmm_components(X_train_0, gmm_class_0, "GMM Components for Class
plot gmm components(X train 1, gmm class 1, "GMM Components for Class
1")
Accuracy: 1.0000
Confusion Matrix:
[[19 0]
[ 0 21]]
```





GMM Components for Class 1



```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler

# Load the data
data = pd.read_csv('datasets/moonDataset.csv')
df_normalized = (data - data.min()) / (data.max() - data.min())

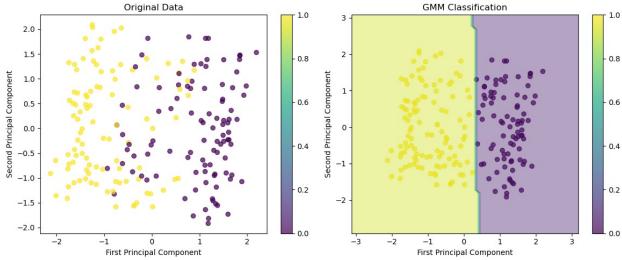
data= df_normalized
X = data[['X1', 'X2', 'X3']].values
y = data['label'].values

# Standardize the features
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# Perform PCA
```

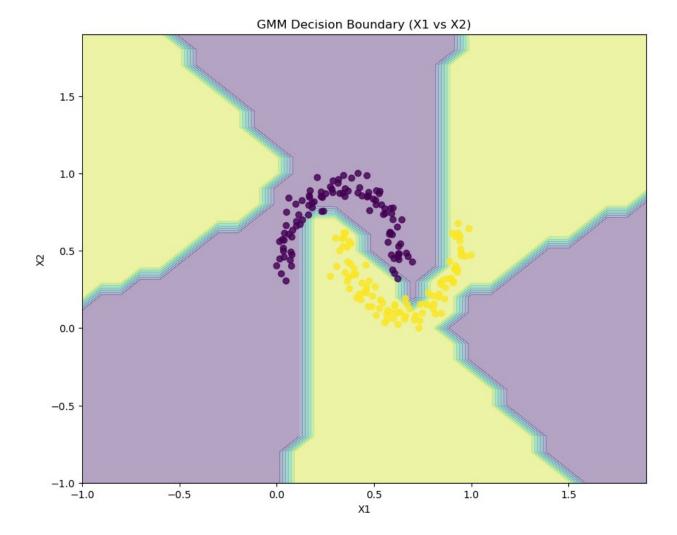
```
pca = PCA(n components=2)
X pca = pca.fit transform(X scaled)
# print(X pca)
# Implement GMM from scratch
class GMM:
    def __init__(self, n_components, n_iterations=100):
        self.n components = n components
        self.n iterations = n iterations
    def initialize parameters(self, X):
        n samples, n features = X.shape
        self.weights = np.ones(self.n components) / self.n components
        self.means = X[np.random.choice(n_samples, self.n_components,
replace=False)1
        self.covariances = [np.eye(n features) for in
range(self.n components)]
    def gaussian pdf(self, X, mean, cov):
        n features = X.shape[1]
        det = np.linalg.det(cov)
        inv cov = np.linalg.inv(cov)
        diff = X - mean
        exponent = -0.5 * np.sum(diff.dot(inv cov) * diff, axis=1)
        normalizer = 1 / (np.sqrt((2 * np.pi) ** n features * det))
        return normalizer * np.exp(exponent)
    def expectation step(self, X):
        weighted likelihoods = np.zeros((X.shape[0],
self.n components))
        for i in range(self.n components):
            weighted likelihoods[:, i] = self.weights[i] *
self.gaussian pdf(X, self.means[i], self.covariances[i])
        total likelihood = np.sum(weighted likelihoods, axis=1)
        return weighted likelihoods / total likelihood[:, np.newaxis]
    def maximization step(self, X, responsibilities):
        n \text{ samples} = X.shape[0]
        self.weights = np.sum(responsibilities, axis=0) / n samples
        self.means = responsibilities.T.dot(X) /
np.sum(responsibilities, axis=0)[:, np.newaxis]
        for i in range(self.n components):
            diff = X - self.means[i]
            self.covariances[i] = (responsibilities[:, i][:,
np.newaxis] * diff).T.dot(diff) / np.sum(responsibilities[:, i])
    def fit(self, X):
        self.initialize parameters(X)
        for in range(self.n iterations):
            responsibilities = self.expectation step(X)
            self.maximization step(X, responsibilities)
```

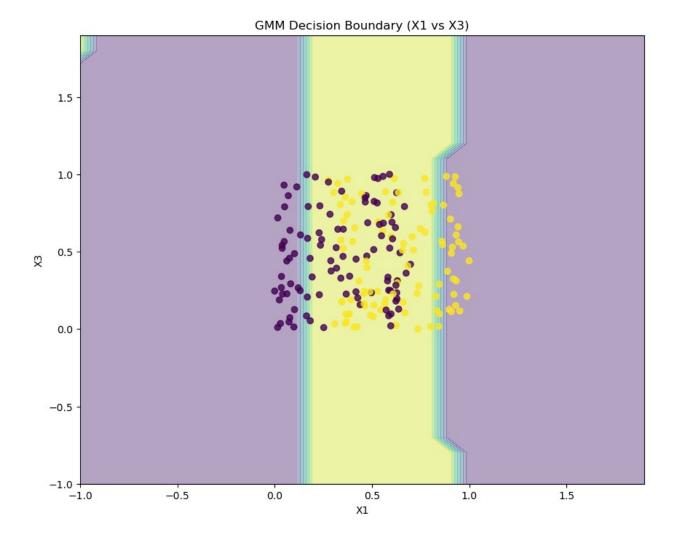
```
def predict(self, X):
        responsibilities = self.expectation step(X)
        return np.argmax(responsibilities, axis=1)
# Train the GMM model
gmm = GMM(n components=2, n iterations=10000)
gmm.fit(X pca)
# Make predictions
y pred = gmm.predict(X pca)
# Evaluate the model's performance
accuracy = np.mean(y pred == y)
print(f"Accuracy: {accuracy:.4f}")
# Visualize the results
plt.figure(figsize=(12, 5))
# Plot the original data
plt.subplot(121)
scatter = plt.scatter(X_pca[:, 0], X_pca[:, 1], c=y, cmap='viridis',
alpha=0.7)
plt.title("Original Data")
plt.xlabel("First Principal Component")
plt.ylabel("Second Principal Component")
plt.colorbar(scatter)
# Plot the GMM classification
plt.subplot(122)
scatter = plt.scatter(X pca[:, 0], X pca[:, 1], c=y pred,
cmap='viridis', alpha=0.7)
plt.title("GMM Classification")
plt.xlabel("First Principal Component")
plt.ylabel("Second Principal Component")
plt.colorbar(scatter)
# Plot decision boundaries
x \min, x \max = X pca[:, 0].min() - 1, X pca[:, 0].max() + 1
y \min, y \max = X pca[:, 1].min() - 1, X pca[:, 1].max() + 1
xx, yy = np.meshgrid(np.arange(x min, x max, 0.1),
                     np.arange(y min, y max, 0.1))
Z = gmm.predict(np.c [xx.ravel(), yy.ravel()])
Z = Z.reshape(xx.shape)
plt.contourf(xx, yy, Z, alpha=0.4, cmap='viridis')
plt.tight layout()
plt.show()
Accuracy: 0.8400
```

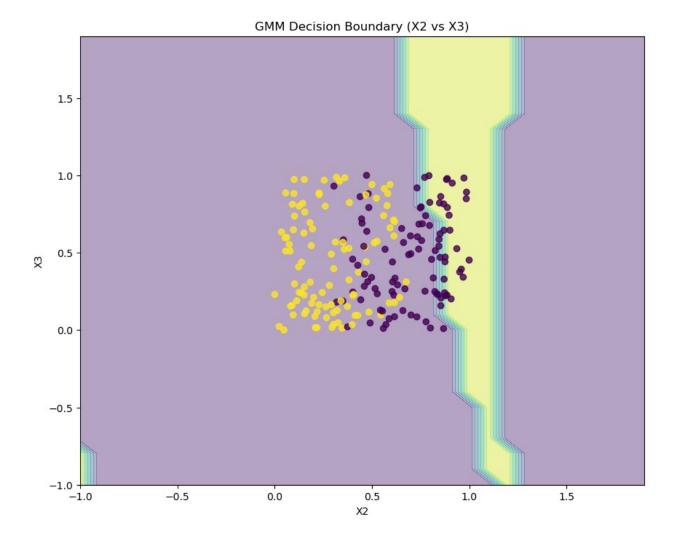


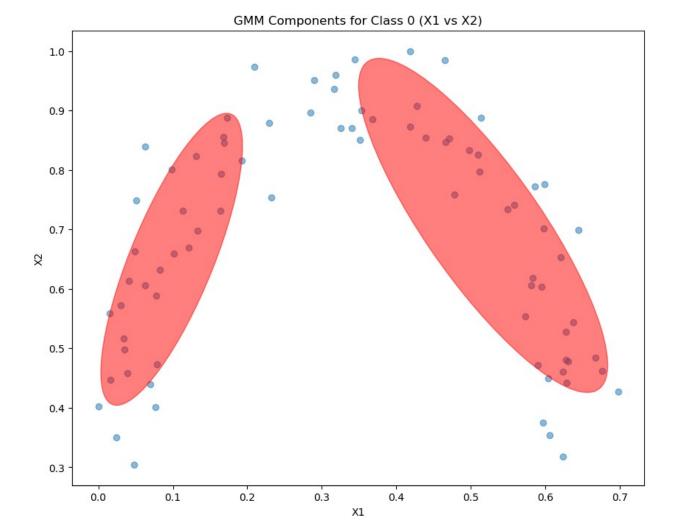
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model selection import train test split
from sklearn.metrics import accuracy score, confusion matrix
# ... (previous code remains the same)
def plot decision boundary 2d(X, y, gmm 0, gmm 1, title, feature1,
feature2):
    x \min, x \max = X[:, feature1].\min() - 1, X[:, feature1].\max() + 1
    y_{min}, y_{max} = X[:, feature2].min() - 1, <math>X[:, feature2].max() + 1
    xx, yy = np.meshgrid(np.arange(x min, x max, 0.1),
                         np.arange(y_min, y_max, 0.1))
    mesh points = np.zeros((xx.ravel().shape[0], 3))
    mesh points[:, feature1] = xx.ravel()
    mesh_points[:, feature2] = yy.ravel()
    Z = predict gmm(mesh points)
    Z = Z.reshape(xx.shape)
    plt.figure(figsize=(10, 8))
    plt.contourf(xx, yy, Z, alpha=0.4)
    plt.scatter(X[:, feature1], X[:, feature2], c=y, alpha=0.8)
    plt.title(title)
    plt.xlabel(f"X{feature1+1}")
    plt.ylabel(f"X{feature2+1}")
    plt.show()
# Plot decision boundaries for all feature pairs
feature pairs = [(0, 1), (0, 2), (1, 2)]
for i, j in feature pairs:
```

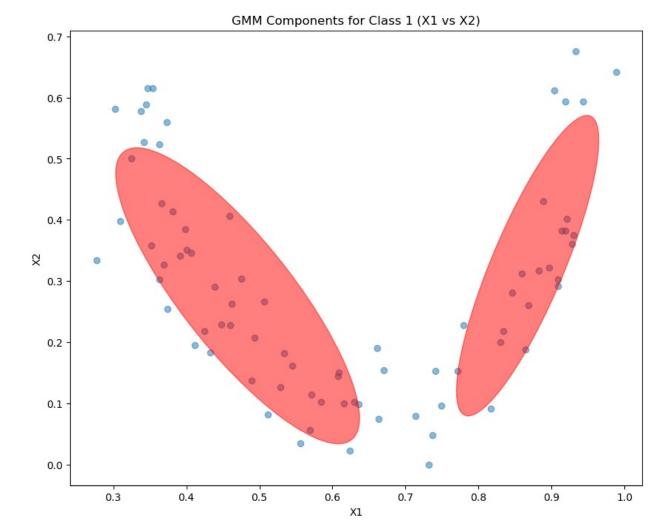
```
plot_decision_boundary_2d(X, y, gmm_class_0, gmm_class_1, f"GMM
Decision Boundary (X\{i+1\} \ vs \ X\{j+1\})", i, j)
def plot_gmm_components_2d(X, gmm, title, feature1, feature2):
    plt.figure(figsize=(10, 8))
    plt.scatter(X[:, feature1], X[:, feature2], alpha=0.5)
    for k in range(gmm.n components):
        mean = gmm.means[k][[feature1, feature2]]
        cov = gmm.covariances[k][[feature1, feature2]][:, [feature1,
feature211
        v, w = np.linalg.eigh(cov)
        v = 2. * np.sqrt(2.) * np.sqrt(v)
        u = w[0] / np.linalg.norm(w[0])
        angle = np.arctan2(u[1], u[0])
        angle = 180. * angle / np.pi
        ell = plt.matplotlib.patches.Ellipse(xy=mean, width=v[0],
height=v[1], angle=angle, color='r')
        ell.set clip box(plt.gca().bbox)
        ell.set alpha(0.5)
        plt.gca().add artist(ell)
    plt.title(title)
    plt.xlabel(f"X{feature1+1}")
    plt.ylabel(f"X{feature2+1}")
    plt.show()
# Plot GMM components for all feature pairs for both classes
for i, j in feature pairs:
    plot_gmm_components_2d(X_train_0, gmm_class_0, f"GMM Components
for Class 0 (X{i+1} vs X{j+1})", i, j)
    plot_gmm_components_2d(X_train_1, gmm_class_1, f"GMM Components
for Class 1 (X{i+1} vs X{j+1})", i, j)
```

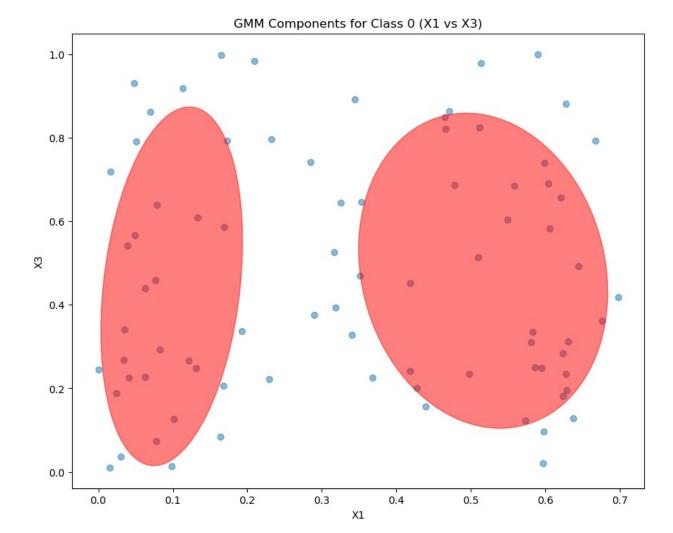


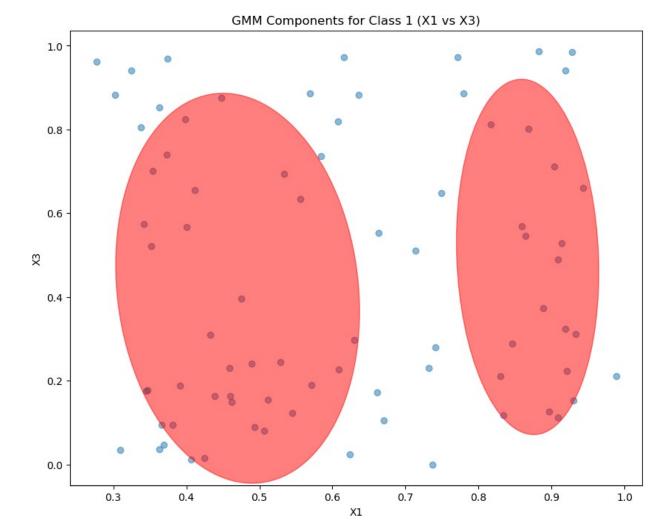


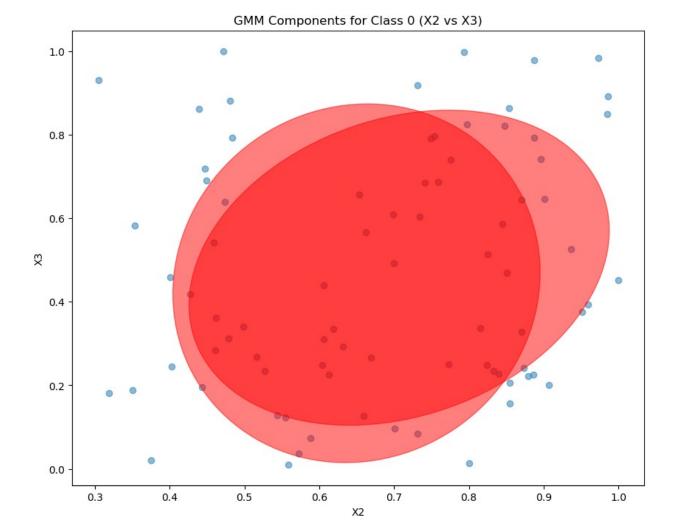




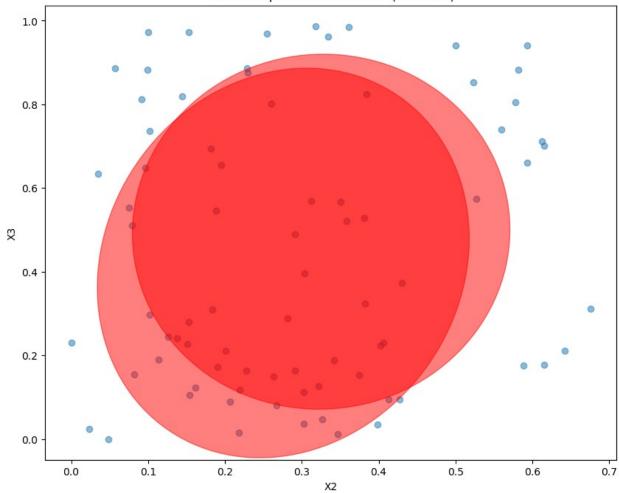












```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, confusion_matrix

# Load the data
data = pd.read_csv('datasets/moonDataset.csv')

df_normalized = (data - data.min()) / (data.max() - data.min())
data= df_normalized

X = data[['X1', 'X2', 'X3']].values
y = data['label'].values

pca = PCA(n_components=2)
X_pca = pca.fit_transform(X)
```

```
print(len(X pca))
# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_pca, y,
test size=0.2, random state=42)
class GaussianMixture:
    def __init__(self, n_components, n_features, max_iter=100, tol=1e-
3):
        self.n components = n components
        self.n features = n features
        self.max iter = max iter
        self.tol = tol
    def initialize parameters(self, X):
        n \text{ samples} = X.\text{shape}[0]
        self.weights = np.ones(self.n components) / self.n components
        self.means = X[np.random.choice(n samples, self.n components,
replace=False)]
        self.covariances = np.array([np.eye(self.n features)] *
self.n_components)
    def gaussian_pdf(self, X, mean, cov):
        n = X.shape[1]
        diff = X - mean
        return np.exp(-0.5 * np.sum(np.dot(diff, np.linalg.inv(cov)) *
diff, axis=1)) / np.sqrt((2 * np.pi)**n * np.linalg.det(cov))
    def expectation step(self, X):
        weighted likelihood = np.zeros((X.shape[0],
self.n components))
        for k in range(self.n components):
            weighted likelihood[:, k] = self.weights[k] *
self.gaussian pdf(X, self.means[k], self.covariances[k])
        return weighted likelihood / weighted likelihood.sum(axis=1,
keepdims=True)
    def maximization_step(self, X, responsibilities):
        total resp = responsibilities.sum(axis=0)
        self.weights = total resp / X.shape[0]
        self.means = np.dot(responsibilities.T, X) / total resp[:,
np.newaxis]
        for k in range(self.n components):
            diff = X - self.means[k]
            self.covariances[k] = np.dot(responsibilities[:, k] *
diff.T, diff) / total resp[k]
    def fit(self, X):
        self.initialize parameters(X)
```

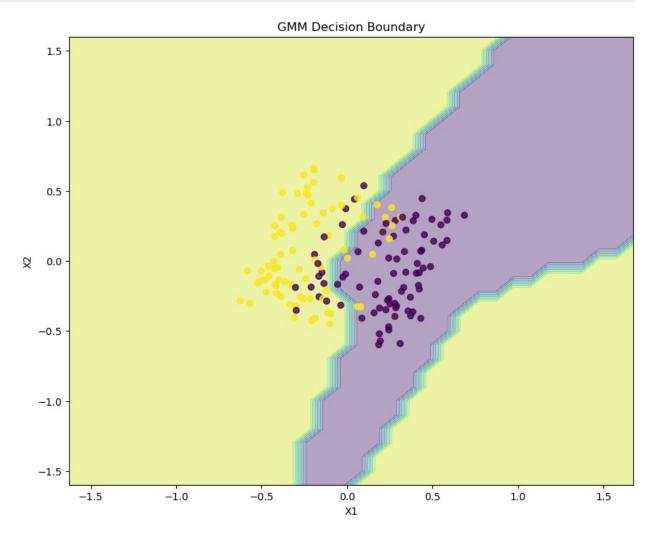
```
for in range(self.max iter):
            prev log likelihood = self.log likelihood(X)
            responsibilities = self.expectation step(X)
            self.maximization step(X, responsibilities)
            curr log likelihood = self.log likelihood(X)
            if np.abs(curr log likelihood - prev log likelihood) <</pre>
self.tol:
                break
    def log likelihood(self, X):
        weighted likelihood = np.zeros((X.shape[0],
self.n components))
        for k in range(self.n components):
            weighted_likelihood[:, k] = self.weights[k] *
self.gaussian pdf(X, self.means[k], self.covariances[k])
        return np.sum(np.log(weighted likelihood.sum(axis=1)))
    def predict(self, X):
        responsibilities = self.expectation step(X)
        return np.argmax(responsibilities, axis=1)
# Train GMMs for each class
gmm class 0 = GaussianMixture(n components=2, n features=2)
gmm class 1 = GaussianMixture(n components=2, n features=2)
X train 0 = X train[y train == 0]
X train 1 = X train[y train == 1]
gmm class 0.fit(X train 0)
gmm class 1.fit(X train 1)
# Predict on test set
def predict qmm(X):
    log\ likelihood\ 0 =
np.array([gmm class 0.log likelihood(x.reshape(1, -1)) for x in X])
    log likelihood 1 =
np.array([gmm class 1.log likelihood(x.reshape(\frac{1}{1}, -\frac{1}{1})) for x in X])
    return (log likelihood 1 > log likelihood 0).astype(int)
y pred = predict gmm(X test)
# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
conf matrix = confusion matrix(y test, y pred)
print(f"Accuracy: {accuracy:.4f}")
print(np.mean(y pred == y test))
print("Confusion Matrix:")
print(conf matrix)
```

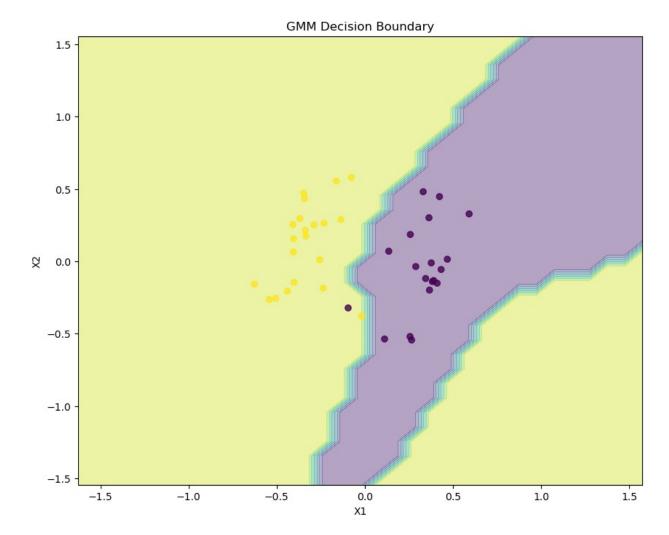
```
# Visualize the results
def plot_decision_boundary(X, y, gmm_0, gmm_1, title):
    x_{min}, x_{max} = X[:, 0].min() - 1, <math>X[:, \overline{0}].max() + 1
    y \min, y \max = X[:, 1].\min() - 1, X[:, 1].\max() + 1
    xx, yy = np.meshgrid(np.arange(x_min, x_max, 0.1),
                         np.arange(y_min, y_max, 0.1))
    # Create meshgrid points in 2D (matching the PCA-reduced data)
    mesh_points = np.c_[xx.ravel(), yy.ravel()]
    # Predict the class for each point in the meshgrid
    Z = predict gmm(mesh points)
    Z = Z.reshape(xx.shape)
    plt.figure(figsize=(10, 8))
    plt.contourf(xx, yy, Z, alpha=0.4)
    plt.scatter(X[:, 0], X[:, 1], c=y, alpha=0.8)
    plt.title(title)
    plt.xlabel("X1")
    plt.ylabel("X2")
    plt.show()
plot decision boundary(X train, y train, gmm class 0, gmm class 1,
"GMM Decision Boundary")
plot decision boundary(X test, y test, gmm class 0, gmm class 1, "GMM
Decision Boundary")
# Plot GMM components
def plot gmm components(X, gmm, title):
    plt.figure(figsize=(10, 8))
    plt.scatter(X[:, 0], X[:, 1], alpha=0.5)
    for k in range(gmm.n components):
        mean = qmm.means[k][:2]
        cov = gmm.covariances[k][:2, :2]
        v, w = np.linalg.eigh(cov)
        v = 2. * np.sqrt(2.) * np.sqrt(v)
        u = w[0] / np.linalg.norm(w[0])
        angle = np.arctan2(u[1], u[0])
        angle = 180. * angle / np.pi
        ell = plt.matplotlib.patches.Ellipse(xy=mean, width=v[0],
height=v[1], angle=angle, color='r')
        ell.set clip box(plt.gca().bbox)
        ell.set alpha(0.5)
        plt.gca().add artist(ell)
```

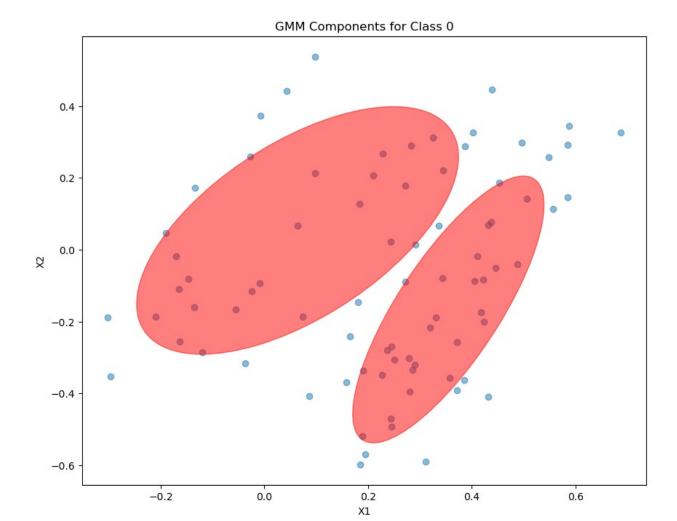
```
plt.title(title)
  plt.xlabel("X1")
  plt.ylabel("X2")
  plt.show()

plot_gmm_components(X_train_0, gmm_class_0, "GMM Components for Class 0")
  plot_gmm_components(X_train_1, gmm_class_1, "GMM Components for Class 1")

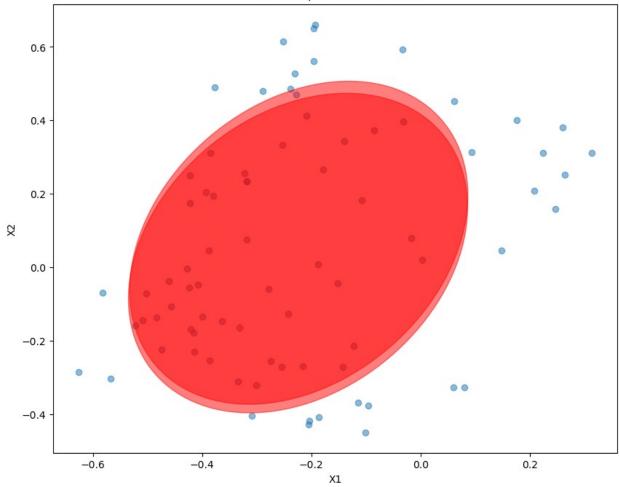
200
Accuracy: 0.9750
0.975
Confusion Matrix:
[[18  1]
  [ 0 21]]
```











```
# WHY GMMS? EACH CLASS IS A NORMAL DISTRIBUTION?
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy import stats

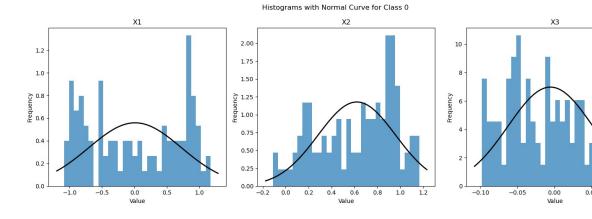
# Load the data
data = pd.read_csv('datasets/moonDataset.csv')

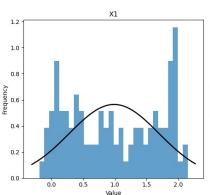
# Separate the data points by class
class_0 = data[data['label'] == 0][['X1', 'X2', 'X3']]
class_1 = data[data['label'] == 1][['X1', 'X2', 'X3']]

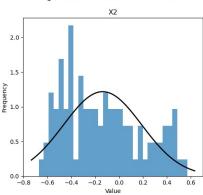
def plot_histogram_with_normal(data, class_name):
    fig, axes = plt.subplots(1, 3, figsize=(15, 5))
    fig.suptitle(f'Histograms with Normal Curve for Class
{class_name}')

for i, feature in enumerate(['X1', 'X2', 'X3']):
```

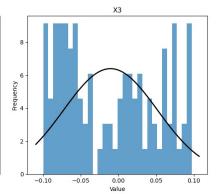
```
ax = axes[i]
        ax.hist(data[feature], bins=30, density=True, alpha=0.7)
        # Fit a normal distribution to the data
        mu, std = stats.norm.fit(data[feature])
        # Plot the normal curve
        xmin, xmax = ax.get xlim()
        x = np.linspace(xmin, xmax, 100)
        p = stats.norm.pdf(x, mu, std)
        ax.plot(x, p, 'k', linewidth=2)
        ax.set title(f'{feature}')
        ax.set_xlabel('Value')
        ax.set ylabel('Frequency')
    plt.tight layout()
    plt.show()
# Plot histograms with normal curves
plot histogram with normal(class 0, 0)
plot_histogram_with_normal(class_1, 1)
# Perform Shapiro-Wilk test
def shapiro wilk test(data, class name):
    print(f"Shapiro-Wilk Test Results for Class {class_name}")
    for feature in ['X1', 'X2', 'X3']:
        statistic, p value = stats.shapiro(data[feature])
        print(f"{feature}: statistic={statistic:.4f}, p-
value={p value:.4f}")
    print()
shapiro wilk test(class 0, 0)
shapiro wilk test(class 1, 1)
```







Histograms with Normal Curve for Class 1



```
Shapiro-Wilk Test Results for Class 0
X1: statistic=0.9065, p-value=0.0000
X2: statistic=0.9434, p-value=0.0003
X3: statistic=0.9555, p-value=0.0020
Shapiro-Wilk Test Results for Class 1
X1: statistic=0.9218, p-value=0.0000
X2: statistic=0.9464, p-value=0.0005
X3: statistic=0.9175, p-value=0.0000
# WHY GMMS? EACH CLASS IS A NORMAL DISTRIBUTION?
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy import stats
# Load the data
data = pd.read csv('datasets/moonDataset.csv')
df normalized = (data - data.min()) / (data.max() - data.min())
data= df normalized
X = data[['X1', 'X2', 'X3']].values
y = data['label'].values
pca = PCA(n_components=2)
X pca = pca.fit transform(X)
# X pca
labels = data['label']
labeled array = np.column stack((X pca, labels))
# labeled array
# Separate the data points by class
class 0 = labeled array[labeled array[:, 2] == 0][:, :2]
class_1 = labeled_array[labeled_array[:, 2] == 1][:, :2]
```

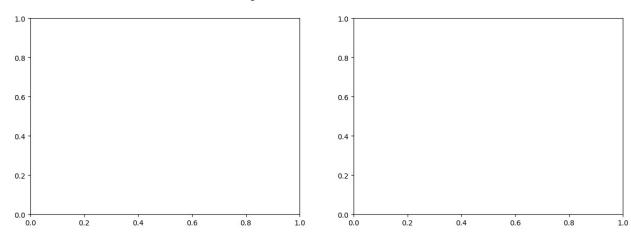
```
def plot histogram with normal(data, class name):
    fig, axes = plt.subplots(1, 2, figsize=(15, 5))
    fig.suptitle(f'Histograms with Normal Curve for Class
{class name}')
    for i, feature in enumerate(X pca):
        ax = axes[i]
        ax.hist(data[feature], bins=30, density=True, alpha=0.7)
        # Fit a normal distribution to the data
        mu, std = stats.norm.fit(data[feature])
        # Plot the normal curve
        xmin, xmax = ax.get xlim()
        x = np.linspace(xmin, xmax, 100)
        p = stats.norm.pdf(x, mu, std)
        ax.plot(x, p, 'k', linewidth=2)
        ax.set title(f'{feature}')
        ax.set xlabel('Value')
        ax.set_ylabel('Frequency')
    plt.tight layout()
    plt.show()
# Plot histograms with normal curves
plot histogram with normal(class 0, 0)
plot histogram with normal(class 1, 1)
# Perform Shapiro-Wilk test
def shapiro wilk test(data, class name):
    print(f"Shapiro-Wilk Test Results for Class {class name}")
    for feature in X pca:
        statistic, p value = stats.shapiro(data[feature])
        print(f"{feature}: statistic={statistic:.4f}, p-
value={p value:.4f}")
    print()
shapiro wilk test(class 0, 0)
shapiro wilk test(class 1, 1)
IndexError
                                          Traceback (most recent call
last)
Cell In[28], line 54
            plt.show()
     51
     53 # Plot histograms with normal curves
---> 54 plot histogram with normal(class 0, 0)
```

```
55 plot_histogram_with_normal(class_1, 1)
57 # Perform Shapiro-Wilk test

Cell In[28], line 35, in plot_histogram_with_normal(data, class_name)
33 for i, feature in enumerate(X_pca):
34          ax = axes[i]
---> 35          ax.hist(data[feature], bins=30, density=True, alpha=0.7)
37          # Fit a normal distribution to the data
38          mu, std = stats.norm.fit(data[feature])

IndexError: arrays used as indices must be of integer (or boolean)
type
```

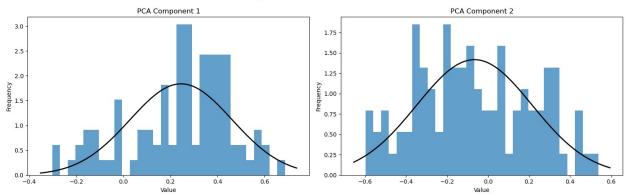
Histograms with Normal Curve for Class 0



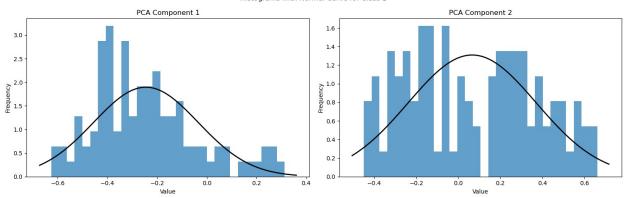
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy import stats
from sklearn.decomposition import PCA
from sklearn.preprocessing import MinMaxScaler
# Load and preprocess the data
data = pd.read csv('datasets/moonDataset.csv')
# scaler = MinMaxScaler()
# X normalized = scaler.fit transform(data[['X1', 'X2', 'X3']])
X = data[['X1', 'X2', 'X3']].values
y = data['label'].values
# Apply PCA
pca = PCA(n components=2)
X pca = pca.fit transform(X normalized)
# Separate the data points by class
class 0 = X pca[y == 0]
class 1 = X pca[y == 1]
```

```
def plot histogram with normal(data, class name):
    fig, axes = plt.subplots(1, 2, figsize=(15, 5))
    fig.suptitle(f'Histograms with Normal Curve for Class
{class name}')
    for i in range(2):
        ax = axes[i]
        ax.hist(data[:, i], bins=30, density=True, alpha=0.7)
        # Fit a normal distribution to the data
        mu, std = stats.norm.fit(data[:, i])
        # Plot the normal curve
        xmin, xmax = ax.get xlim()
        x = np.linspace(xmin, xmax, 100)
        p = stats.norm.pdf(x, mu, std)
        ax.plot(x, p, 'k', linewidth=2)
        ax.set title(f'PCA Component {i+1}')
        ax.set xlabel('Value')
        ax.set_ylabel('Frequency')
    plt.tight layout()
    plt.show()
# Plot histograms with normal curves
plot histogram with normal(class 0, 0)
plot histogram with normal(class 1, 1)
# Perform Shapiro-Wilk test
def shapiro wilk test(data, class name):
    print(f"Shapiro-Wilk Test Results for Class {class name}")
    for i in range(2):
        statistic, p_value = stats.shapiro(data[:, i])
        print(f"PCA Component {i+1}: statistic={statistic:.4f}, p-
value={p value:.4f}")
    print()
shapiro wilk test(class 0, 0)
shapiro wilk test(class 1, 1)
```

Histograms with Normal Curve for Class 0



Histograms with Normal Curve for Class 1



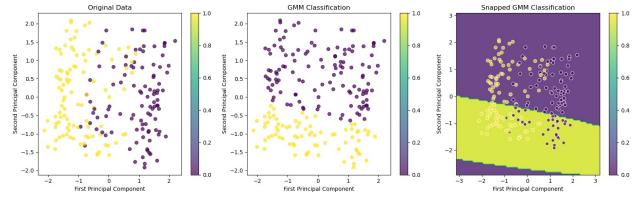
```
Shapiro-Wilk Test Results for Class 0
PCA Component 1: statistic=0.9525, p-value=0.0012
PCA Component 2: statistic=0.9771, p-value=0.0789
Shapiro-Wilk Test Results for Class 1
PCA Component 1: statistic=0.9516, p-value=0.0011
PCA Component 2: statistic=0.9561, p-value=0.0021
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
# Load and preprocess the data
data = pd.read_csv('datasets/moonDataset.csv')
X = data[['X1', 'X2', 'X3']].values
y = data['label'].values
scaler = StandardScaler()
X scaled = scaler.fit transform(X)
pca = PCA(n components=2)
```

```
X pca = pca.fit transform(X scaled)
# Implement GMM from scratch (same as before)
class GMM:
    def init (self, n components, n iterations=100):
        self.n_components = n_components
        self.n iterations = n iterations
    def initialize parameters(self, X):
        n_samples, n_features = X.shape
        self.weights = np.ones(self.n components) / self.n components
        self.means = X[np.random.choice(n samples, self.n_components,
replace=False)]
        self.covariances = [np.eye(n features) for in
range(self.n components)]
    def gaussian pdf(self, X, mean, cov):
        n features = X.shape[1]
        det = np.linalq.det(cov)
        inv cov = np.linalg.inv(cov)
        diff = X - mean
        exponent = -0.5 * np.sum(diff.dot(inv cov) * diff, axis=1)
        normalizer = 1 / (np.sqrt((2 * np.pi) ** n_features * det))
        return normalizer * np.exp(exponent)
    def expectation step(self, X):
        weighted_likelihoods = np.zeros((X.shape[0],
self.n components))
        for i in range(self.n_components):
            weighted likelihoods[:, i] = self.weights[i] *
self.gaussian pdf(X, self.means[i], self.covariances[i])
        total_likelihood = np.sum(weighted_likelihoods, axis=1)
        return weighted likelihoods / total likelihood[:, np.newaxis]
    def maximization step(self, X, responsibilities):
        n \text{ samples} = X.shape[0]
        self.weights = np.sum(responsibilities, axis=0) / n_samples
        self.means = responsibilities.T.dot(X) /
np.sum(responsibilities, axis=0)[:, np.newaxis]
        for i in range(self.n components):
            diff = X - self.means[i]
            self.covariances[i] = (responsibilities[:, i][:,
np.newaxis] * diff).T.dot(diff) / np.sum(responsibilities[:, i])
    def fit(self, X):
        self.initialize_parameters(X)
        for in range(self.n iterations):
            responsibilities = self.expectation step(X)
            self.maximization step(X, responsibilities)
```

```
def predict(self, X):
        responsibilities = self.expectation step(X)
        return np.argmax(responsibilities, axis=1)
# Train the GMM model
gmm = GMM(n components=2, n iterations=100)
gmm.fit(X pca)
# Implement snap functionality
def create snap grid(gmm, x_range, y_range, resolution=100):
    x = np.linspace(x range[0], x range[1], resolution)
    y = np.linspace(y_range[0], y_range[1], resolution)
    xx, yy = np.meshgrid(x, y)
    positions = np.vstack([xx.ravel(), yy.ravel()]).T
    responsibilities = gmm.expectation step(positions)
    labels = np.argmax(responsibilities, axis=1)
    return xx, yy, labels.reshape(xx.shape)
# Visualize the results with snap
plt.figure(figsize=(16, 5))
# Original data
plt.subplot(131)
scatter = plt.scatter(X pca[:, 0], X pca[:, 1], c=y, cmap='viridis',
alpha=0.7
plt.title("Original Data")
plt.xlabel("First Principal Component")
plt.ylabel("Second Principal Component")
plt.colorbar(scatter)
# GMM classification
plt.subplot(132)
y_pred = gmm.predict(X pca)
scatter = plt.scatter(X pca[:, 0], X pca[:, 1], c=y pred,
cmap='viridis', alpha=0.7)
plt.title("GMM Classification")
plt.xlabel("First Principal Component")
plt.ylabel("Second Principal Component")
plt.colorbar(scatter)
# Snapped GMM
plt.subplot(133)
x \text{ range} = (X \text{ pca}[:, 0].min() - 1, X \text{ pca}[:, 0].max() + 1)
y_range = (X_pca[:, 1].min() - 1, X_pca[:, 1].max() + 1)
xx, yy, Z = \text{create snap grid(gmm, x range, y range, resolution=} 100)
plt.contourf(xx, yy, Z, alpha=0.8, cmap='viridis')
scatter = plt.scatter(X pca[:, 0], X pca[:, 1], c=y, cmap='viridis',
```

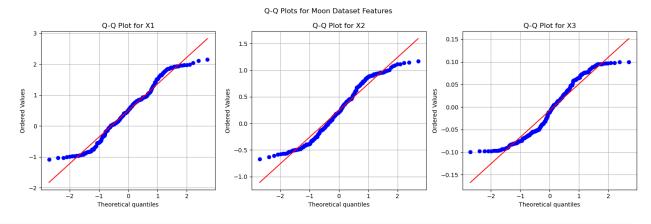
```
alpha=0.7, edgecolors='w')
plt.title("Snapped GMM Classification")
plt.xlabel("First Principal Component")
plt.ylabel("Second Principal Component")
plt.colorbar(scatter)

plt.tight_layout()
plt.show()
```



```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats
# Read the data
data = pd.read csv('datasets/moonDataset.csv')
# Create Q-Q plots for each feature
fig, axes = plt.subplots(1, 3, figsize=(15, 5))
fig.suptitle('Q-Q Plots for Moon Dataset Features')
features = ['X1', 'X2', 'X3']
for idx, feature in enumerate(features):
    # Get the data for the current feature
    feature data = data[feature]
    # Create 0-0 plot
    stats.probplot(feature_data, dist="norm", plot=axes[idx])
    # Customize the plot
    axes[idx].set title(f'Q-Q Plot for {feature}')
    axes[idx].grid(True)
# Adjust layout
plt.tight layout()
plt.show()
```

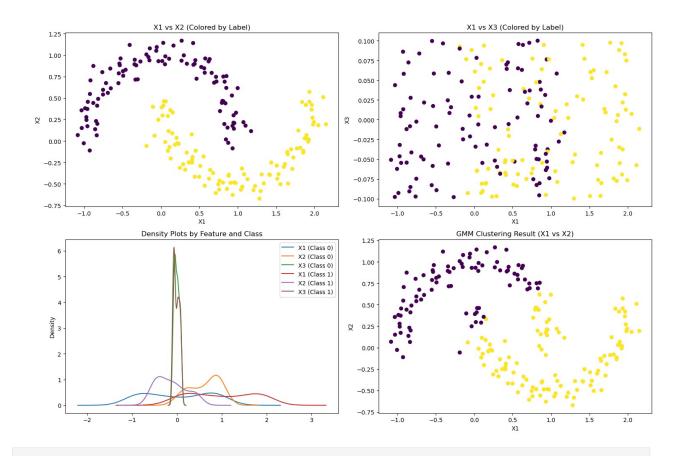
```
# Calculate and print additional statistics
print("\nNormality Test Results (Shapiro-Wilk):")
print("-" * 50)
for feature in features:
    statistic, p_value = stats.shapiro(data[feature])
    print(f"{feature}:")
    print(f"Statistic: {statistic:.4f}")
    print(f"P-value: {p_value:.4f}")
    print("-" * 50)
```



```
Normality Test Results (Shapiro-Wilk):
X1:
Statistic: 0.9685
P-value: 0.0002
X2:
Statistic: 0.9565
P-value: 0.0000
X3:
Statistic: 0.9398
P-value: 0.0000
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats
from sklearn.mixture import GaussianMixture
from sklearn.preprocessing import StandardScaler
# Read and prepare the data
data = pd.read_csv('datasets/moonDataset.csv')
```

```
X = data[['X1', 'X2', 'X3']].values
y = data['label'].values
# 1. Visualize the data distribution
fig = plt.figure(figsize=(15, 10))
# 2D scatter plot with different views
ax1 = fig.add subplot(221)
ax1.scatter(X[:, 0], X[:, 1], c=y, cmap='viridis')
ax1.set title('X1 vs X2 (Colored by Label)')
ax1.set xlabel('X1')
ax1.set ylabel('X2')
ax2 = fig.add subplot(222)
ax2.scatter(X[:, 0], X[:, 2], c=y, cmap='viridis')
ax2.set title('X1 vs X3 (Colored by Label)')
ax2.set xlabel('X1')
ax2.set ylabel('X3')
# Density plots for each feature
ax3 = fig.add subplot(223)
for label in [0, 1]:
    for i, feature in enumerate(['X1', 'X2', 'X3']):
        data[data['label'] == label][feature].plot.density(ax=ax3,
label=f'{feature} (Class {label})')
ax3.set title('Density Plots by Feature and Class')
ax3.legend()
# Fit GMM and plot clusters
ax4 = fig.add subplot(224)
gmm = GaussianMixture(n components=2, random state=42)
gmm_labels = gmm.fit_predict(X)
ax4.scatter(X[:, 0], X[:, 1], c=gmm_labels, cmap='viridis')
ax4.set_title('GMM Clustering Result (X1 vs X2)')
ax4.set xlabel('X1')
ax4.set ylabel('X2')
plt.tight layout()
plt.show()
# Statistical tests and metrics
print("\nGMM Justification Analysis:")
print("-" * 50)
# 1. Test for multimodality using Hartigan's dip test
from scipy.stats import median abs deviation
def hartigan dip test(x):
    mad = median abs deviation(x)
    if mad == 0:
```

```
return 0
    return np.mean(np.abs(x - np.median(x))) / mad
for feature in ['X1', 'X2', 'X3']:
    dip value = hartigan dip test(data[feature])
    print(f"Hartigan's dip test for {feature}: {dip value:.4f}")
# 2. BIC scores for different numbers of components
n components range = range(1, 6)
bic = []
for n components in n components range:
    gmm = GaussianMixture(n components=n components, random state=42)
    qmm.fit(X)
    bic.append(gmm.bic(X))
print("\nBIC scores for different numbers of components:")
for n, score in zip(n components range, bic):
    print(f"n components = {n}: BIC = {score:.2f}")
# 3. Calculate average silhouette score for GMM clustering
from sklearn.metrics import silhouette score
gmm = GaussianMixture(n components=2, random state=42)
labels = gmm.fit predict(X)
silhouette avg = silhouette score(X, labels)
print(f"\nSilhouette Score for GMM clustering: {silhouette avg:.4f}")
# 4. Anderson-Darling test for normality within clusters
print("\nAnderson-Darling test for normality within clusters:")
for cluster in [0, 1]:
    cluster data = X[labels == cluster]
    print(f"\nCluster {cluster}:")
    for i, feature in enumerate(['X1', 'X2', 'X3']):
        stat, crit, sig = stats.anderson(cluster data[:, i])
        print(f"{feature}: statistic = {stat:.4f}")
```



```
GMM Justification Analysis:
Hartigan's dip test for X1: 1.2869
Hartigan's dip test for X2: 0.9445
Hartigan's dip test for X3: 1.0414
BIC scores for different numbers of components:
n_{components} = 1: BIC = 246.28
n_{components} = 2: BIC = 226.38
n components = 3: BIC = 202.75
n_{components} = 4: BIC = 151.13
n components = 5: BIC = 155.45
Silhouette Score for GMM clustering: 0.4556
Anderson-Darling test for normality within clusters:
Cluster 0:
X1: statistic = 1.3683
X2: statistic = 1.8933
X3: statistic = 1.0332
Cluster 1:
X1: statistic = 1.5085
```

X2: statistic = 1.2152 X3: statistic = 2.7840