**10. Develop a program to implement k-means clustering using Wisconsin Breast Cancer data set and visualize the clustering result.**

import numpy as np

import pandas as pd

import matplotlib.pyplot as plt

from sklearn.datasets import load\_breast\_cancer

from sklearn.cluster import KMeans

from sklearn.decomposition import PCA

from sklearn.metrics import confusion\_matrix, accuracy\_score

from sklearn.preprocessing import StandardScaler

data = load\_breast\_cancer()

X = data.data

y = data.target

feature\_names = data.feature\_names

target\_names = data.target\_names

print("Data Shape:", X.shape)

print("Classes:", target\_names)

scaler = StandardScaler()

X\_scaled = scaler.fit\_transform(X)

kmeans = KMeans(n\_clusters=2, random\_state=42, n\_init=10)

clusters = kmeans.fit\_predict(X\_scaled)

labels\_mapped = np.where(clusters == 1, 0, 1)

print("\nConfusion Matrix:")

print(confusion\_matrix(y, labels\_mapped))

print("Accuracy:", accuracy\_score(y, labels\_mapped))

pca = PCA(n\_components=2)

X\_pca = pca.fit\_transform(X\_scaled)

plt.figure(figsize=(10, 6))

plt.scatter(X\_pca[:, 0], X\_pca[:, 1], c=clusters, cmap='viridis', alpha=0.6)

plt.scatter(kmeans.cluster\_centers\_[:, 0], kmeans.cluster\_centers\_[:, 1],

s=250, marker='X', c='red', label='Centroids')

plt.title("K-Means Clustering of Breast Cancer Dataset (PCA-2D)")

plt.xlabel("PCA Component 1")

plt.ylabel("PCA Component 2")

plt.legend()

plt.grid(True)

plt.show()

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**Output:**

Output:

Data Shape: (569, 30)

Classes: ['malignant' 'benign']

Confusion Matrix:

[[176 36]

[ 18 339]]

Accuracy: 0.9050966608084359

