**ML EXPERIMENT 11**

**import pandas as pd**

**from sklearn.decomposition import PCA**

**import matplotlib.pyplot as plt**

**# Load the dataset**

**column\_names = [**

**"Class",**

**"Alcohol",**

**"Malic\_Acid",**

**"Ash",**

**"Ash\_Alcanity",**

**"Magnesium",**

**"Total\_Phenols",**

**"Flavanoids",**

**"Nonflavanoid\_Phenols",**

**"Proanthocyanins",**

**"Color\_Intensity",**

**"Hue",**

**"OD280",**

**"Proline"**

**]**

**data = pd.read\_csv("wine.data", names=column\_names)**

**# Separate features (X) and target (y)**

**X = data.drop("Class", axis=1)**

**y = data["Class"]**

**# Perform PCA**

**pca = PCA(n\_components=2)  # Reduce to 2 dimensions for visualization**

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

**# Plot the PCA-reduced data**

**plt.figure(figsize=(10, 8))**

**plt.scatter(X\_pca[:, 0], X\_pca[:, 1], c=y, cmap='viridis')**

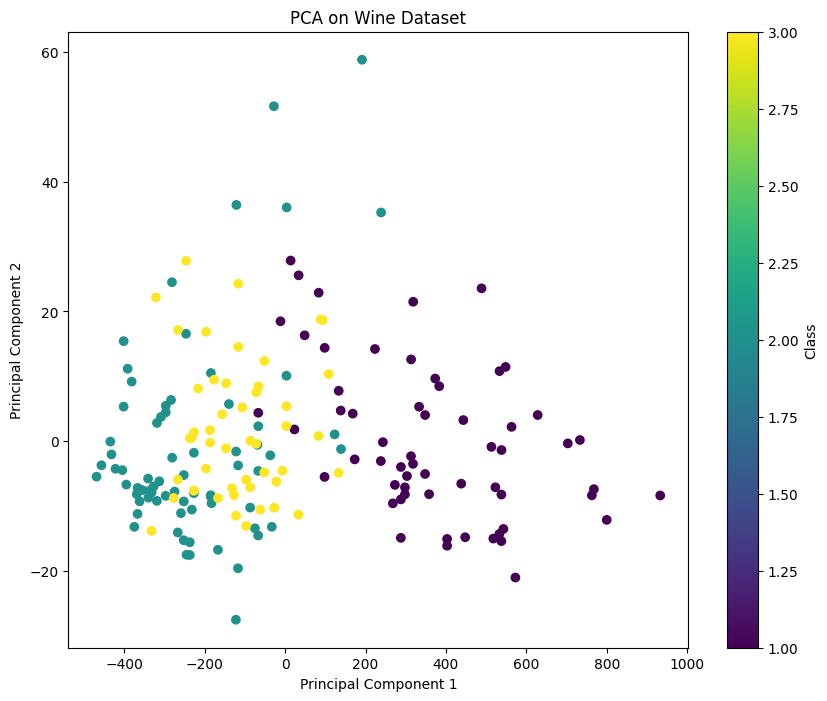
**plt.xlabel("Principal Component 1")**

**plt.ylabel("Principal Component 2")**

**plt.title("PCA on Wine Dataset")**

**plt.colorbar(label='Class')**

**plt.show()**



**# Add the transformed features back to the original DataFrame**

**data["PCA\_Component\_1"] = X\_pca[:, 0]**

**data["PCA\_Component\_2"] = X\_pca[:, 1]**

**# Display the new dataset**

**print(data.head())**

