Darshan
UNIVERSITY
योग: कर्मसु कौशलम्

Data Mining

Lab - 6

Raj Vekariya | 23010101298

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# Dimensionality Reduction using NumPy
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🔍 What is Data Reduction?

Data reduction refers to the process of reducing the amount of data that needs to be processed and stored, while preserving the essential patterns in the data.

Why do we reduce data?

- To reduce computational cost.
- To remove noise and redundant features.
- To improve model performance and training time.
- To visualize high-dimensional data in 2D or 3D.

Common data reduction techniques include:

- Principal Component Analysis (PCA)
- Feature selection
- Sampling

📉 What is Principal Component Analysis (PCA)?

PCA is a **dimensionality reduction technique** that transforms a dataset into a new coordinate system. It identifies the **directions (principal components)** where the variance of the data is maximized.

Key Concepts:

- **Principal Components**: New features (linear combinations of original features) capturing most variance.
- **Eigenvectors & Eigenvalues**: Used to compute these principal directions.
- **Covariance Matrix**: Measures how features vary with each other.

PCA helps in **visualizing high-dimensional data**, **noise reduction**, and **speeding up algorithms**.

🧠 NumPy Functions Summary for PCA

Function	Purpose
`np.mean(X, axis=0)`	Compute mean of each column (feature-wise mean).
`X - np.mean(X, axis=0)`	Centering the data (zero mean).
`np.cov(X, rowvar=False)`	Compute covariance matrix for features.
`np.linalg.eigh(cov_mat)`	Get eigenvalues and eigenvectors (for symmetric matrices).
`np.argsort(values)[::-1]`	Sort values in descending order.
`np.dot(X, eigenvectors)`	Project original data onto new axes.

Step 1: Load the Iris Dataset

In [4]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
df= pd.read_csv('iris.csv')
df
```

Out[4]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.1	3.5	1.4	0.2	setosa
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa
...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	virginica
146	6.3	2.5	5.0	1.9	virginica
147	6.5	3.0	5.2	2.0	virginica
148	6.2	3.4	5.4	2.3	virginica
149	5.9	3.0	5.1	1.8	virginica

150 rows × 5 columns

In [5]:

```
df.shape
```

Out[5]:

```
(150, 5)
```

Step 2: Standardize the data (zero mean)

In [6]:

```
X=df.drop(columns='species')
Y=df['species'].map({'setosa': 0, 'virginica': 1, 'versicolor': 2})
print("Dimension of X:", X.shape)
```

```
Dimension of X: (150, 4)
```

In [7]:

```
X_meaned=X-np.mean(X,axis=0)
print("Data after centering(first 5 rows):\n",X_meaned[:5])
print(X_meaned.shape)
```

```
Data after centering(first 5 rows):
    sepal_length  sepal_width  petal_length  petal_width
0     -0.743333     0.442667        -2.358    -0.999333
1     -0.943333    -0.057333        -2.358    -0.999333
2     -1.143333     0.142667        -2.458    -0.999333
3     -1.243333     0.042667        -2.258    -0.999333
4     -0.843333     0.542667        -2.358    -0.999333
(150, 4)
```

Step 3: Compute the Covariance Matrix

In [8]:

```
cov_mat=np.cov(X_meaned, rowvar=False)
print("Covariance matrix shape:", cov_mat.shape)
print("Covariance matrix:\n", cov_mat)
```

```
Covariance matrix shape: (4, 4)
Covariance matrix:
 [[ 0.68569351 -0.042434    1.27431544  0.51627069]
 [-0.042434    0.18997942 -0.32965638 -0.12163937]
 [ 1.27431544 -0.32965638  3.11627785  1.2956094 ]
 [ 0.51627069 -0.12163937  1.2956094   0.58100626]]
```

Step 4: Compute eigenvalues and eigenvectors

In [9]:

```
eigen_values, eigen_vectors = np.linalg.eig(cov_mat)
print("Eigenvalues:\n", eigen_values)
print("Eigenvectors:\n", eigen_vectors)
```

```
Eigenvalues:
 [4.22824171 0.24267075 0.0782095  0.02383509]
Eigenvectors:
 [[ 0.36138659 -0.65658877 -0.58202985  0.31548719]
 [-0.08452251 -0.73016143  0.59791083 -0.3197231 ]
 [ 0.85667061  0.17337266  0.07623608 -0.47983899]
 [ 0.3582892   0.07548102  0.54583143  0.75365743]]
```

Step 5: Compute eigenvalues and eigenvectors

In [11]:

```
sorted_index=np.argsort(eigen_values)[::-1]
sorted_eigenvalues = eigen_values[sorted_index]
sorted_eigenvectors=eigen_vectors[:, sorted_index]
print("Sort Index:", sorted_index)
print("Sorted Eigenvalues:\n", sorted_eigenvalues)
print("Sorted Eigenvectors:\n", sorted_eigenvectors)
```

```
Sort Index: [0 1 2 3]
Sorted Eigenvalues:
 [4.22824171 0.24267075 0.0782095  0.02383509]
Sorted Eigenvectors:
 [[ 0.36138659 -0.65658877 -0.58202985  0.31548719]
 [-0.08452251 -0.73016143  0.59791083 -0.3197231 ]
 [ 0.85667061  0.17337266  0.07623608 -0.47983899]
 [ 0.3582892   0.07548102  0.54583143  0.75365743]]
```

Step 6: Select the top k eigenvectors (top 2)

In [12]:

```
k=2
eigenvector_subset=sorted_eigenvectors[:,0:k]
print(eigenvector_subset.shape)
```

```
(4, 2)
```

Step 7: Project the data onto the top k eigenvectors

In [13]:

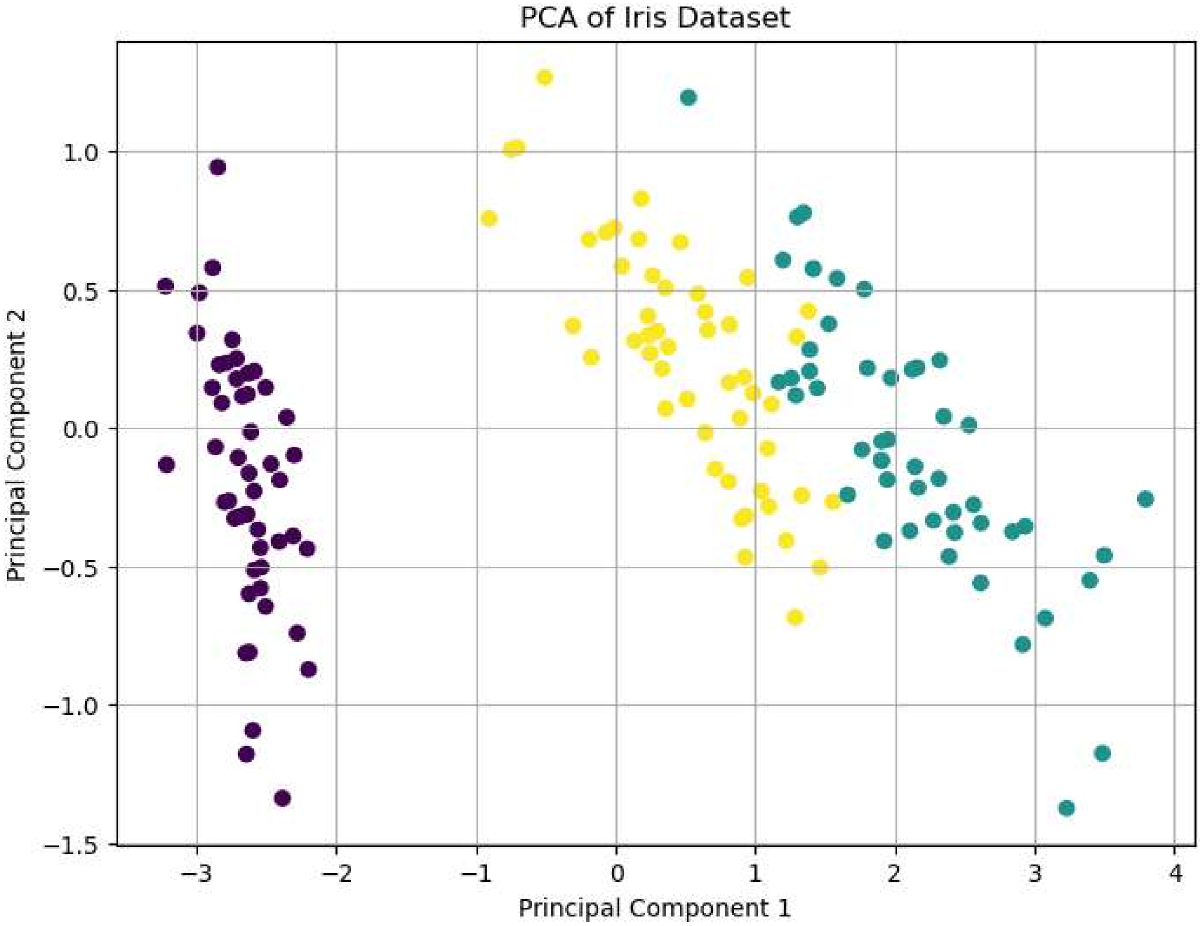
```
X_reduced=np.dot(X_meaned, eigenvector_subset)
print("Reduced data shape:", X_reduced.shape)
```

```
Reduced data shape: (150, 2)
```

Step 8: Plot the PCA-Reduced Data

In [14]:

```
plt.figure(figsize=(8, 6))
plt.scatter(X_reduced[:,0], X_reduced[:,1], c=Y, cmap='viridis')
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.title('PCA of Iris Dataset')
plt.grid(True)
plt.show()
```



Extra - Bining Method

5,10,11,13,15,35,50,55,72,92,204,215.

Partition them into three bins by each of the following methods: (a) equal-frequency (equal-depth) partitioning (b) equal-width partitioning

In [23]:

```
Sorted Data: [5, 10, 11, 13, 15, 35, 50, 55, 72, 92, 204, 215]

(a) Equal-Frequency Bins:
Bin 1: [5, 10, 11, 13]
Bin 2: [15, 35, 50, 55]
Bin 3: [72, 92, 204, 215]

(b) Equal-Width Bins:
Bin 1: [5, 10, 11, 13, 15, 35, 50, 55, 72]
Bin 2: [92]
Bin 3: [204, 215]
```

In [ ]: