

Data Mining

Lab - 6

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Dimensionality Reduction using NumPy



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



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

Step 1: Load the Iris Dataset

```
In [1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt

In [2]: iris = pd.read_csv('iris.csv')
iris.shape

Out[2]: (150, 5)

In [3]: iris
```

Out[3]:		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

Step 2: Standardize the data (zero mean)

```
In [4]: x = iris.drop(columns='species')
        y = iris['species'].map({
           'setosa' : 0,
           'versicolor' : 1,
           'virginica' : 2
        })
In [5]: print("Original shape : ", x.shape)
      Original shape: (150, 4)
In [6]: x_{meaned} = x - np.mean(x, axis = 0)
        print("Data after centering ( first 5 rows ) : \n",x_meaned[:5])
      Data after centering (first 5 rows):
          sepal_length sepal_width petal_length petal_width
            -0.743333
      0
                        0.442667
                                       -2.358
                                                -0.999333
            -0.943333 -0.057333
                                       -2.358 -0.999333
      1
      2
           -1.143333 0.142667
                                       -2.458 -0.999333
      3
                                        -2.258 -0.999333
           -1.243333 0.042667
            -0.843333
                         0.542667
                                        -2.358
                                               -0.999333
```

Step 3: Compute the Covariance Matrix

Step 4: Compute eigenvalues and eigenvectors

```
In [8]: eigen_values, eigen_vectors = np.linalg.eigh(cov_mat)
    print("Eigenvalues:\n", eigen_values)
    print("Eigenvectors (first 2):\n",eigen_vectors[:,:2])

Eigenvalues:
    [0.02383509 0.0782095 0.24267075 4.22824171]
Eigenvectors (first 2):
    [[ 0.31548719 0.58202985]
    [-0.3197231 -0.59791083]
    [-0.47983899 -0.07623608]
    [ 0.75365743 -0.54583143]]
```

Step 5: Sort eigenvalues and eigenvectors in descending order

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

```
In [11]: k = 2
    eigenvector_subset = sorted_eigenvectors[:, 0:k]
    print(eigenvector_subset);

[[-0.36138659    0.65658877]
       [ 0.08452251    0.73016143]
       [-0.85667061    -0.17337266]
       [-0.3582892    -0.07548102]]
```

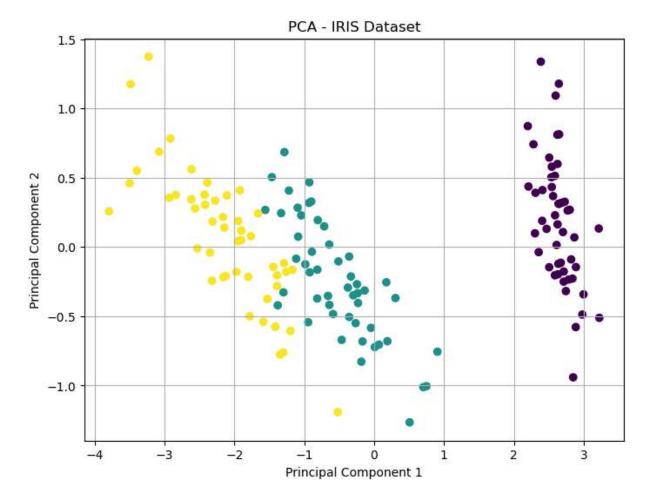
Step 7: Project the data onto the top k eigenvectors

```
In [12]: 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 [13]: plt.figure(figsize=(8, 6))
    plt.scatter(x_reduced[:, 0],x_reduced[:, 1], c=y)
    plt.xlabel("Principal Component 1")
    plt.ylabel("Principal Component 2")
    plt.title("PCA - 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 [14]: values = np.array([5,10,11,13,15,35,50,55,72,92,204,215])

# (a) Equal-Frequency Bins:
    equal_freq_bins = pd.qcut(values, q=3, labels=["Bin 1","Bin 2","Bin 3"])

# (b) Equal-Width Bins:
    # max - min / noOfBins
    equal_width_bins = pd.cut(values, bins=3, labels=["Bin 1","Bin 2","Bin 3"])

# Combine results
binning_results = pd.DataFrame({
        "Value": values,
        "Equal-Frequency Bin": equal_freq_bins,
        "Equal-Width Bin": equal_width_bins
```

})
binning_results

Out[14]:

	Value	Equal-Frequency Bin	Equal-Width Bin
0	5	Bin 1	Bin 1
1	10	Bin 1	Bin 1
2	11	Bin 1	Bin 1
3	13	Bin 1	Bin 1
4	15	Bin 2	Bin 1
5	35	Bin 2	Bin 1
6	50	Bin 2	Bin 1
7	55	Bin 2	Bin 1
8	72	Bin 3	Bin 1
9	92	Bin 3	Bin 2
10	204	Bin 3	Bin 3
11	215	Bin 3	Bin 3

In []: