```
import numpy as np
import pandas as pd
import plotly.express as px
import seaborn as sns
import matplotlib.pyplot as plt
```

Data preparation

```
df = pd.read_csv('../data/processed/cleaned_dataset.csv',
thousands=',', index_col=0)

df.head()

   Household_Weekly_Expenditure  Monthly_Household_Income  \
0                        391.15                   1000.00
1                        553.82                   4958.45
2                        710.45                   6459.93
3                        639.76                   6871.41
4                        473.14                   4783.66

   Number_of_Household_Dependents  Age_of_Head_of_Household
Household_Size  \
0                             5.0                      38.0
7.000000
1                             3.0                      59.0
6.037438
2                             6.0                      53.0
8.000000
3                             3.0                      36.0
5.000000
4                             7.0                      42.0
9.000000

  Education_Level Employment_Status  Location  Savings_Rate
Weekly_Savings  \
0     High School        Unemployed     Urban          0.26
376.26
1        Master's          Employed  Suburban          0.29
351.83
2        Master's          Employed     Urban          0.29
431.85
3       Doctorate        Unemployed  Suburban          0.26
480.82
4      Bachelor's          Employed  Suburban          0.05
61.29

   Monthly_Rent  Loan_Repayment  Transport_Expenses  Utility_Bills
0       1790.00          404.60          131.170000         193.06
1       1408.59          492.12          296.120000         269.79
2       1000.42          549.64          174.825609         240.01
```

```
3         862.12           239.42            61.830000            306.85
4        1602.23           378.17            61.250000            374.29
```

We need to discretize the continuous values existing in our discrete columns because of preprocessing procedures

```
discrete_cols = ['Number_of_Household_Dependents',
"Age_of_Head_of_Household", "Household_Size"]

df[discrete_cols] = df[discrete_cols].apply(round)

cat = df.nunique()[df.nunique() < 10]
cat = cat.index.tolist()
cat

['Number_of_Household_Dependents',
 'Household_Size',
 'Education_Level',
 'Employment_Status',
 'Location']

pca_df = df.drop(columns=cat)
data_matrix = pca_df.to_numpy()
```

PCA

Principal Component Analysis (PCA) is the process of reducing a space of variables into a smaller space with little variance loss. It is achieved in a set of steps as follows.

1. Standardization

The first step is so center our data so that the *mean* μ equals zero, and scale it so that the *standard deviation* σ equals one, using Z-score normalization, for which the formula is:

$$X_{\text{scaled}} = \frac{X - \mu}{\sigma}$$

Where X is our sample space, μ and σ are the mean and standard deviation of X, respectively.

```
def scale(X):
  return (X - X.mean()) / X.std()

scaled_data_matrix = np.apply_along_axis(scale, 0, data_matrix)

scaled_data_matrix

array([[-5.51998727e-01, -1.71315790e+00, -7.16189002e-01, ...,
        -3.37920239e-01, -6.29225640e-01, -6.92227498e-01],
       [ 4.01235003e-01,  1.81969841e-01,  9.80462437e-01, ...,
        -1.69032451e-02,  1.76191411e+00,  2.44737515e-01],
```

```
       [ 1.31907480e+00,  9.00810901e-01,  4.95704883e-01, ...,
         1.94075931e-01,  3.61257087e-03, -1.18911880e-01],
       ...,
       [-4.63865480e-01,  7.75434897e-04, -1.50638523e-01, ...,
        -1.01325901e+00, -4.85713767e-01, -5.61934044e-01],
       [ 1.77146088e+00,  1.46127981e+00,  1.46521999e+00, ...,
        -1.71548368e+00, -1.23748405e+00,  1.36963282e+00],
       [ 3.66192661e-01,  1.08868739e-01,  6.57290734e-01, ...,
        -1.18376438e-03, -4.44162595e-03,  1.33971539e+00]],
      shape=(3941, 9))
```

We can verify by checking the mean and standard deviation for our new, scaled data columns

```
print(np.apply_along_axis(lambda col: {'mean': col.mean(), 'std':
col.std()}, 0, scaled_data_matrix))
```

```
[{'mean': np.float64(2.1635404286021829e-16), 'std': np.float64(1.0)}
 {'mean': np.float64(-7.211801428673942e-17), 'std':
np.float64(0.9999999999999999)}
 {'mean': np.float64(2.4520124857491404e-16), 'std': np.float64(1.0)}
 {'mean': np.float64(1.0231743276931156e-16), 'std': np.float64(1.0)}
 {'mean': np.float64(-1.1674103562665945e-16), 'std': np.float64(1.0)}
 {'mean': np.float64(8.811919870660974e-16), 'std': np.float64(1.0)}
 {'mean': np.float64(-2.7044255357527286e-17), 'std': np.float64(1.0)}
 {'mean': np.float64(9.104899303700852e-17), 'std':
np.float64(0.9999999999999999)}
 {'mean': np.float64(-3.0650156071864255e-17), 'std':
np.float64(1.0)}]
```

2. Covariance Matrix

PCA captures the direction that maximize variance, we therefore need to compute the *covariance matrix*, given by the formula:

$$\Sigma = \frac{1}{n-1} X^T X$$

Where n is the number of samples (observations)

```
sigma = (1 / scaled_data_matrix.shape[0]) * scaled_data_matrix.T @
scaled_data_matrix
sigma.shape
```

```
(9, 9)
```

We get a 9×9 matrix in which each number lying on the i^{th} row and the j^{th} column, is the covariance between components (features) i and j

3. Eigenvalues and Eigenvectors

The eigenvalues of the covariance matrix represent the variance explained by each principal component. The corresponding eigenvector represents the direction of the component

```
eigenvalues, eigenvectors = np.linalg.eig(sigma)
```

4. Choosing the top-K Principal Components

The magnitudes of our eigenvalues determine how much variance the corresponding component explains on its own. We will therefore sort them in descending order.

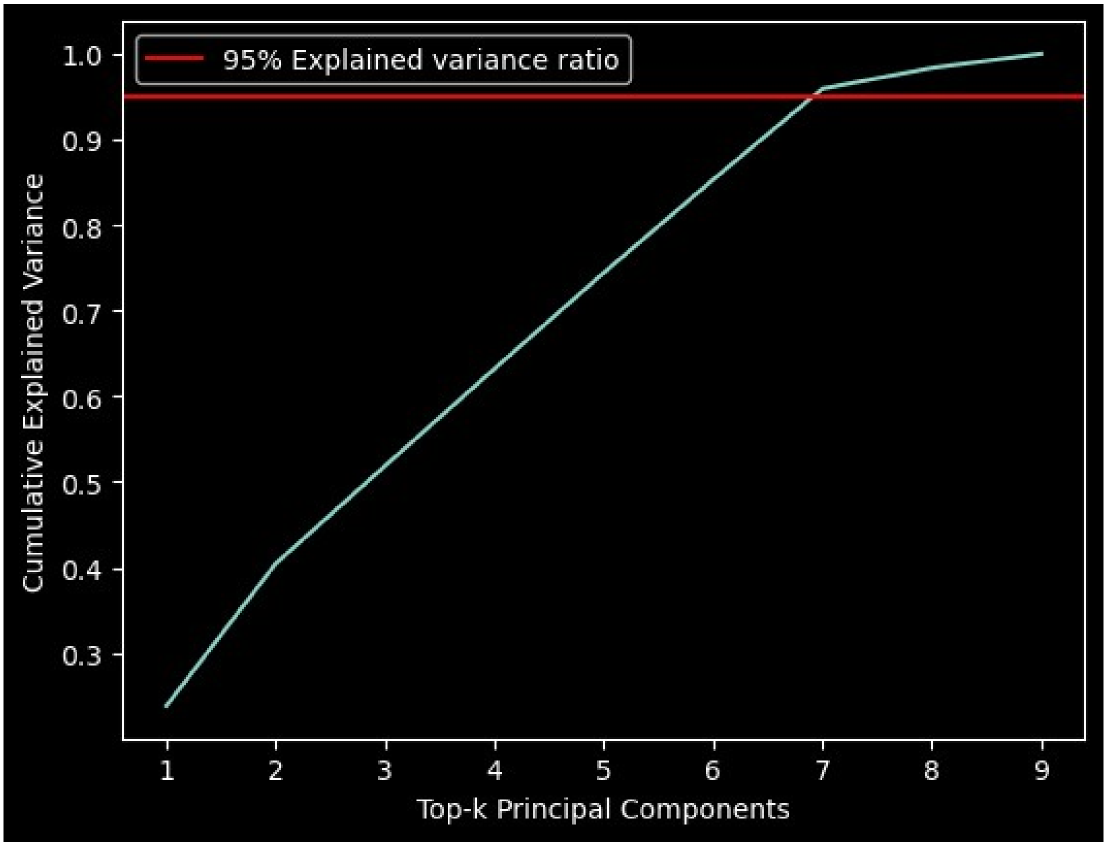
```
eigenvalues_sorted_idx = np.argsort(eigenvalues)[::-1]
eigenvalues = eigenvalues[eigenvalues_sorted_idx]
eigenvectors = eigenvectors[:, eigenvalues_sorted_idx]
```

In practice, we keep enough components to explain atleast 95% variance, thus, we will calculate the cumulative variance for our components.

```
explained_variance_ratio = eigenvalues / eigenvalues.sum()
cumulative_var = np.cumsum(explained_variance_ratio)
k = len(cumulative_var[cumulative_var < 0.95]) + 1
k
```

```
7
```

```
plt.plot(np.arange(1, len(explained_variance_ratio) + 1),
cumulative_var)
plt.axhline(0.95, c="r", label="95% Explained variance ratio")
plt.xlabel("Top-k Principal Components")
plt.ylabel("Cumulative Explained Variance")
plt.legend()
plt.show()
```



We can see that in our case, the top 7 principal components explain 95% of the variance, we will therefore set $k=7$

5. Projection onto Principal Components

We will now represent our features in a space consisting only of the top-k principal components, with the formula:

$$X_{\text{new}} = X_{\text{scaled}} \cdot V_k$$

Where V_k contains the top-k eigenvectors.

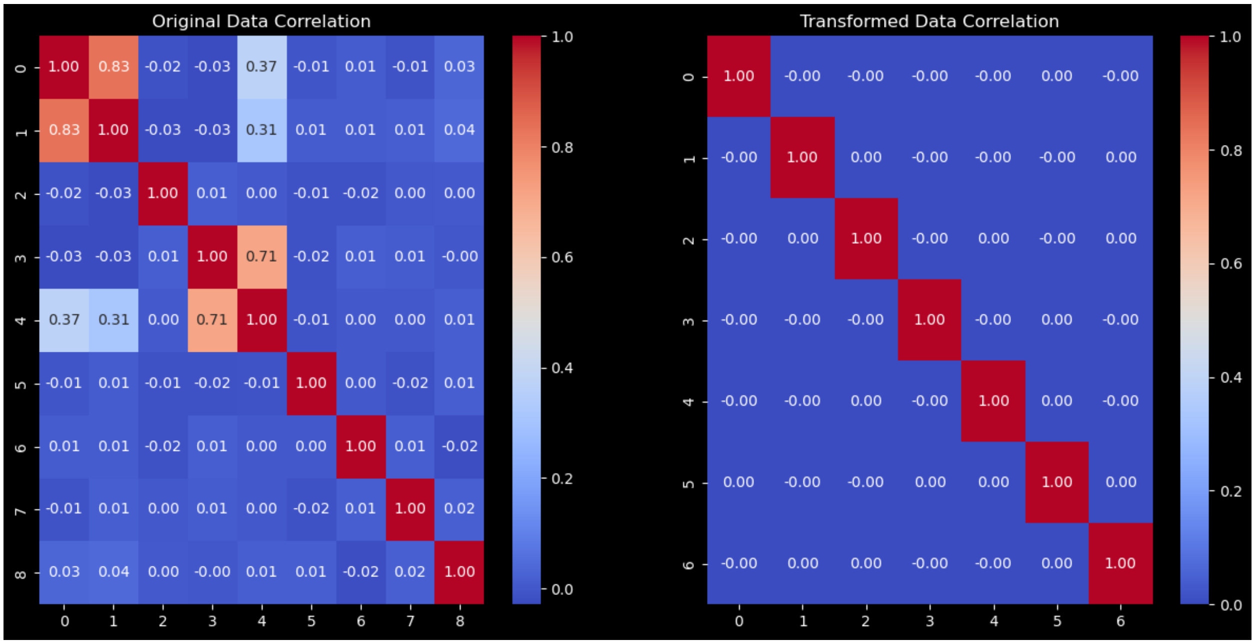
```
v_k = eigenvectors[:, :k]
X_new = scaled_data_matrix @ v_k
```

Final Results

```
plt.style.use('dark_background')

corr_ = np.corrcoef(data_matrix.T)
corr = np.corrcoef(X_new.T)
fig, axes = plt.subplots(1, 2, figsize=(15, 7))
axes[0].set_title('Original Data Correlation')
```

```python
sns.heatmap(corr_, cmap='coolwarm', annot=True, fmt='.2f', ax=axes[0])
axes[1].set_title('Transformed Data Correlation')
sns.heatmap(corr, cmap='coolwarm', annot=True, fmt='.2f', ax=axes[1])
plt.show()
```



As we can see, there are relatively stronger absolute correlations in our original data matrix in comparison to the final matrix with the top 7 principal components, indicating stronger variance in the latter.