```
from IPython.display import Image
             Requirement already satisfied: IPython in c:\users\user\anaconda3\lib\site-packages (7.12.0)
             Requirement already satisfied: setuptools>=18.5 in c:\users\user\anaconda3\lib\site-packages
             (from IPython) (45.2.0.post20200210)
             Requirement already satisfied: backcall in c:\users\user\anaconda3\lib\site-packages (from IP
             ython) (0.1.0)
             Requirement already satisfied: colorama; sys_platform == "win32" in c:\user\user\anaconda3\l
             ib\site-packages (from IPython) (0.4.3)
             Requirement already satisfied: pygments in c:\users\user\anaconda3\lib\site-packages (from IP
             ython) (2.5.2)
             Requirement already satisfied: pickleshare in c:\users\user\anaconda3\lib\site-packages (from
             IPython) (0.7.5)
             Requirement already satisfied: decorator in c:\users\user\anaconda3\lib\site-packages (from I
             Python) (4.4.1)
             Requirement already satisfied: prompt-toolkit!=3.0.0,!=3.0.1,<3.1.0,>=2.0.0 in c:\users\user
             \anaconda3\lib\site-packages (from IPython) (3.0.3)
             Requirement already satisfied: jedi>=0.10 in c:\users\user\anaconda3\lib\site-packages (from
             IPython) (0.14.1)
             Requirement already satisfied: traitlets>=4.2 in c:\users\user\anaconda3\lib\site-packages (f
             rom IPython) (4.3.3)
             Requirement already satisfied: wcwidth in c:\users\user\anaconda3\lib\site-packages (from pro
             mpt-toolkit!=3.0.0,!=3.0.1,<3.1.0,>=2.0.0->IPython) (0.1.8)
             Requirement already satisfied: parso>=0.5.0 in c:\user\user\anaconda3\lib\site-packages (fro
             m jedi>=0.10->IPython) (0.5.2)
             Requirement already satisfied: ipython-genutils in c:\users\user\anaconda3\lib\site-packages
             (from traitlets>=4.2->IPython) (0.2.0)
             Requirement already satisfied: six in c:\users\user\anaconda3\lib\site-packages (from traitle
             ts>=4.2->IPython) (1.14.0)
In [32]: Image("C:/Users/Users/Desktop/KakaoTalk_20210819_104918768.jpg")
Out[32]:
                           \max_{\Sigma} Var(S^TX) = S^TVar(X)S S.t. ||S|| = 1 \Leftrightarrow S^TS = 1
                          \frac{\partial L_0}{\partial S} = 2\Sigma S - 2\lambda S = 0 \Leftrightarrow \Sigma S = \lambda S
\sum_{n=1}^{\infty} \sum_{n=1
                           STX S = X STS = X (:: MOFY MH STF = 1)
             HW 2
 In [1]: import numpy as np
             import pandas as pd
             from sklearn.preprocessing import StandardScaler
             import matplotlib.pyplot as plt
              Import Seaborn as sns
             Bounus : PCA examples
             Eigenfaces : PCA as feature selector
 In [3]: from sklearn.datasets import fetch_lfw_people
              from sklearn.decomposition import PCA
              faces = fetch_lfw_people(min_faces_per_person=60)
             print(faces.target_names)
             print(faces.images.shape)
             Downloading LFW metadata: https://ndownloader.figshare.com/files/5976012
             Downloading LFW metadata: https://ndownloader.figshare.com/files/5976009
             Downloading LFW metadata: https://ndownloader.figshare.com/files/5976006
             Downloading LFW data (~200MB): https://ndownloader.figshare.com/files/5976015
              ['Ariel Sharon' 'Colin Powell' 'Donald Rumsfeld' 'George W Bush'
               'Gerhard Schroeder' 'Hugo Chavez' 'Junichiro Koizumi' 'Tony Blair']
              (1348, 62, 47)
 In [4]: # number of features (pixels)
 Out[4]: 2914
             Let's take a look at the principal axes that span this dataset. Because this is a large dataset, we will use RandomizedPCA—it
             contains a randomized method to approximate the first N principal components much more quickly than the standard PCA
             estimator, and thus is very useful for high-dimensional data (here, a dimensionality of nearly 3,000). We will take a look at the
             first 150 components:
 In [5]: pca = PCA(n_components=150, svd_solver='randomized')
             pca.fit(faces.data)
 Out[5]: PCA(copy=True, iterated_power='auto', n_components=150, random_state=None,
                   svd_solver='randomized', tol=0.0, whiten=False)
             Now, let's take a look at first 24 basis components/features of images. 처음 몇 개의 eigenface들은 빛의 각도 등 전반적인
             feature라면 뒤로 갈수록 더 자세한 feature들(눈코입)의 map이 뽑아짐을 확인할 수 있다.
 In [6]: fig, axes = plt.subplots(3, 8, figsize=(9, 4),
                                                 subplot_kw={'xticks':[], 'yticks':[]},
                                                 gridspec_kw=dict(hspace=0.1, wspace=0.1))
             for i, ax in enumerate(axes.flat):
                   ax.imshow(pca.components_[i].reshape(62, 47), cmap='bone')
 In [7]: # how many components to choose?
              plt.plot(np.cumsum(pca.explained_variance_ratio_))
              plt.xlabel('number of components')
             plt.ylabel('cumulative explained variance');
                 0.9
              0.8 0.7 0.6 0.5 0.4 0.3
                 0.2
                                                                120
                                                                      140
                       0
                             20
                                                  80
                                                         100
                                       number of components
 In [8]: # Compute the components and projected faces
              pca = PCA(150, svd_solver = 'randomized').fit(faces.data)
             components = pca.transform(faces.data)
             projected = pca.inverse_transform(components) # reconstruction
 In [9]: # Plot the results
              fig, ax = plt.subplots(2, 10, figsize=(10, 2.5),
                                              subplot_kw={'xticks':[], 'yticks':[]},
                                              gridspec_kw=dict(hspace=0.1, wspace=0.1))
              for i in range(10):
                   ax[0, i].imshow(faces.data[i].reshape(62, 47), cmap='binary_r')
                   ax[1, i].imshow(projected[i].reshape(62, 47), cmap='binary_r')
             ax[0, 0].set_ylabel('full-dim\ninput')
             ax[1, 0].set_ylabel('150-dim\nreconstruction');
             HW: PCA from scratch
               • iris 데이터에 numpy만을 사용해서 PCA를 해봅시다!
               · We can find PCA makes visualization easier!
In [10]: | df = pd.read_csv('https://raw.githubusercontent.com/uiuc-cse/data-fa14/gh-pages/data/iris.cs
             v')
             df.head()
Out[10]:
                 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
                           5.0
                                         3.6
                                                       1.4
                                                                     0.2 setosa
In [11]: X = df.iloc[:,:-1]
             label = df.iloc[:,-1]
             X.head()
Out[11]:
                 sepal_length sepal_width petal_length petal_width
                           5.1
                                         3.5
                                                       1.4
                                                                     0.2
              1
                           4.9
                                         3.0
                                                       1.4
                                                                     0.2
              2
                                                                     0.2
                           4.7
                                         3.2
                                                       1.3
                           4.6
                                                       1.5
                                                                     0.2
                                         3.1
                           5.0
                                         3.6
                                                       1.4
                                                                     0.2
             Using Covariance Matrix
In [12]: # Step 1. Center Data
             X_scaled = StandardScaler().fit_transform(X)
             X_scaled[:5]
Out[12]: array([[-0.90068117, 1.03205722, -1.3412724 , -1.31297673],
                       [-1.14301691, -0.1249576 , -1.3412724 , -1.31297673],
                       [-1.38535265, 0.33784833, -1.39813811, -1.31297673],
                       [-1.50652052, 0.10644536, -1.2844067, -1.31297673],
                       [-1.02184904, 1.26346019, -1.3412724, -1.31297673]])
In [14]: # Step 2. Compute Covariance Matrix
             cov_matrix = np.cov(X_scaled.T)
             cov_matrix
Out[14]: array([[ 1.00671141, -0.11010327, 0.87760486, 0.82344326],
                       [-0.11010327, 1.00671141, -0.42333835, -0.358937],
                       [\ 0.87760486,\ -0.42333835,\ 1.00671141,\ 0.96921855],
                       [ 0.82344326, -0.358937 , 0.96921855, 1.00671141]])
In [20]: # Step 3. Eigenvalue decomposition
             eigvals, eigvecs = np.linalg.eig(cov_matrix)
             print("Eigenvalues:", eigvals)
             print("")
             print("Eigenvectors:", eigvecs)
             Eigenvalues: [2.93035378 0.92740362 0.14834223 0.02074601]
             Eigenvectors: [[ 0.52237162 -0.37231836 -0.72101681 0.26199559]
              [-0.26335492 -0.92555649 0.24203288 -0.12413481]
               [ 0.58125401 -0.02109478  0.14089226 -0.80115427]
               [ 0.56561105 -0.06541577  0.6338014  0.52354627]]
In [21]: # Ratio of explained variance per PC
              explained_variances = []
              for i in range(len(eigvals)):
                   explained_variances.append(eigvals[i] / np.sum(eigvals))
             print(np.sum(explained_variances), '\n', explained_variances)
             0.99999999999999
              [0.7277045209380132, 0.23030523267680636, 0.03683831957627389, 0.0051519268089063935]
             첫 번쨰, 두 번째 PC가 이미 variance의 95% 이상을 설명함!
In [24]: # Visualization (Embedding)
             pc1 = np.dot(X_scaled, eigvecs[:,0])
             pc2 = np.dot(X_scaled, eigvecs[:, 1])
             res = pd.DataFrame(pc1, columns=['PC1'])
             res['PC2'] = pc2
              res['label'] = label
             res.head()
Out[24]:
                                  PC2 label
                       PC1
              0 -2.264542 -0.505704 setosa
              1 -2.086426 0.655405 setosa
                             0.318477 setosa
              2 -2.367950
              3 -2.304197 0.575368 setosa
              4 -2.388777 -0.674767 setosa
In [25]: # Projection on 1-dim subspace
              plt.figure(figsize=(20, 10))
             sns.scatterplot(res['PC1'], [0] * len(res), hue=res['label'], s=200)
Out[25]: <matplotlib.axes._subplots.AxesSubplot at 0x193cdc65a08>
                                                                                                                                         setosa
                                                                                                                                           versicolo
                                                                                                                                         virginica
               0.005
              -0.005
              -0.010
              -0.015
In [26]: # Projection on 2-dim subspace
             plt.figure(figsize=(20, 10))
             sns.scatterplot(res['PC1'], res['PC2'], hue=res['label'], s=100)
Out[26]: <matplotlib.axes._subplots.AxesSubplot at 0x193cf8a0cc8>
                                                                                                                                          setosa

    versicolo

              δ.
              Shortcut
In [27]: from sklearn.decomposition import PCA as sklearnPCA
              sklearn_pca = sklearnPCA(n_components=2)
             projection = sklearn_pca.fit_transform(X, y=label)
             sklearn_pca.explained_variance_ratio_
Out[27]: array([0.92461621, 0.05301557])
In [28]: sklearn_pca.components_
Out[28]: array([[ 0.36158968, -0.08226889,  0.85657211,  0.35884393],
                       [0.65653988, 0.72971237, -0.1757674, -0.07470647]])
In [29]: with plt.style.context('seaborn-whitegrid'):
                   plt.figure(figsize=(6, 4))
                   projection[label==lab, 1],
                                          label=lab,
                                          c=col)
                   plt.xlabel('PC 1')
                   plt.ylabel('PC 2')
                   plt.legend(loc='lower right')
                   plt.tight_layout()
                   plt.show()
                  1.0
```

**HW 1** 

In [31]: !pip install IPython

-0.5

-1.0

versicolor