ENEL503_lab5

April 14, 2025

#

ENEL 503: Computer Vision (W2025)

#

Lab5: Face Recognition

General Notes:

- This lab can be done in groups of 2 students. Only one submission with both names on the report
- The due date to submit this lab is April 11 at 11:59 pm
- Read the lab instructions carefully and make sure you respond to all the open questions and coding tasks.
- After finishing your work, ensure all the outputs are there. Then, run the Notebook "collect_submission.ipynb", which will generate two files for you "lab5_code_submission.zip" and "lab5_inline_submission.pdf". Finally, upload both files should be uploaded to D2L Dropbox.
- Don't forget to write your names and student IDs below.

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0.1 Objectives

In this lab, you will learn the following:

- Face recognition usnig raw data + KNN classifier
- Face recognition using PCA + KNN classifier
- Face recognition using LDA + KNN classifier

This lab is adapted from: - Assignments of the CSE 445 course at University of Washington

0.2 Setup

0.2.1 Step 1

[1]:
```
# Run this part if you want to mount your Google Drive to Colab VM and
# work on your lab folder directly. Make sure to enter the correct path to your
# folder. Otherwise, you can work on the realtime workspace but you will need
# to upload your images.

from google.colab import drive
drive.mount('/content/drive')

# TODO: Enter the foldername in your Drive where you have saved the unzipped
# lab folder, e.g. 'Colab Notebooks/ENEL503/Lab5'
FOLDERNAME = 'Colab Notebooks/ENEL_503_Lab5' #None
assert FOLDERNAME is not None, "[!] Enter the foldername."
FullPath = '/content/drive/MyDrive/' + FOLDERNAME
print(FullPath)

import os
os.chdir(FullPath)
!pwd # check that your folder is the current working directory

# Now that we've mounted your Drive, this ensures that
# the Python interpreter of the Colab VM can load
# python files from within it.
import sys
sys.path.append(FullPath)
```

```
Mounted at /content/drive
/content/drive/MyDrive/Colab Notebooks/ENEL_503_Lab5
/content/drive/MyDrive/Colab Notebooks/ENEL_503_Lab5
```

0.2.2 Step 2

Next, run the cells below to install the necessary libraries and packages.

[2]:
```
# Check the Python version
!python --version

# Install the required packages (uncomment if not on Google Colab or not␣
 ↪already installed on your env)
# %pip install numpy
# %pip install matplotlib
# %pip install opencv-python
# %pip install scikit-image
# %pip install scipy
```

```
Python 3.11.12
```

[3]:
```
# Imports the print function from newer versions of python
from __future__ import print_function

# Numpy is the main package for scientific computing with Python.
# This will be one of our most used libraries in this class
import numpy as np

# skimage (Scikit-Image) is a library for image processing
# from skimage import io

import cv2 as cv

# Matplotlib is a useful plotting library for python
import matplotlib.pyplot as plt

# This code is to make matplotlib figures appear inline in the
# notebook rather than in a new window.
%matplotlib inline

plt.rcParams['figure.figsize'] = (12.0, 10.0) # set default size of plots
plt.rcParams['image.interpolation'] = 'nearest'
plt.rcParams['image.cmap'] = 'gray'

# Some more magic so that the notebook will reload external python modules;
# see http://stackoverflow.com/questions/1907993/
  ↪autoreload-of-modules-in-ipython
%load_ext autoreload
%autoreload 2
```

1 Part 1: Face Recognition

In this section, we will implement face recognition with a simple kNN classifier. We will explore the dimensionality reduction using both PCA and LDA methods.

1.1 Face Dataset

We will use a dataset of faces of celebrities. Download the dataset using the following command in a code block (will be called in the next code cell):

```
!bash get_dataset.sh
```

The directory containing the dataset has the following structure:

```
faces/
    train/
        angelina jolie/
        anne hathaway/
        ...
```

```
test/
    angelina jolie/
    anne hathaway/
    ...
```

Each class has 50 training images and 10 testing images.

[ ]:
```
# # Use this cell one time to download the data. You can comment it after the␣
 ↪data is downloaded.
# !bash get_dataset.sh
```

[4]:
```
from utils import load_dataset

X_train, y_train, classes_train = load_dataset('faces', train=True,␣
 ↪as_gray=True)
X_test, y_test, classes_test = load_dataset('faces', train=False, as_gray=True)

assert classes_train == classes_test
classes = classes_train

print('Class names:', classes)
print('Training data shape:', X_train.shape)
print('Training labels shape: ', y_train.shape)
print('Test data shape:', X_test.shape)
print('Test labels shape: ', y_test.shape)
```

```
Class names: ['angelina jolie', 'anne hathaway', 'barack obama', 'brad pitt',
'cristiano ronaldo', 'emma watson', 'george clooney', 'hillary clinton',
'jennifer aniston', 'johnny depp', 'justin timberlake', 'leonardo dicaprio',
'natalie portman', 'nicole kidman', 'scarlett johansson', 'tom cruise']
Training data shape: (800, 64, 64)
Training labels shape:  (800,)
Test data shape: (160, 64, 64)
Test labels shape:  (160,)
```

[ ]:
```
# Visualize some examples from the dataset.
# We show a few examples of training images from each class.
num_classes = len(classes)
samples_per_class = 10
for y, cls in enumerate(classes):
    idxs = np.flatnonzero(y_train == y)
    idxs = np.random.choice(idxs, samples_per_class, replace=False)
    for i, idx in enumerate(idxs):
        plt_idx = i * num_classes + y + 1
        plt.subplot(samples_per_class, num_classes, plt_idx)
        plt.imshow(X_train[idx])
        plt.axis('off')
        if i == 0:
```

```
            plt.title(y)
plt.show()
```

[5]:
```
# Flatten the image data into rows
# we now have one 4096 dimensional featue vector for each example
X_train = np.reshape(X_train, (X_train.shape[0], -1))
X_test = np.reshape(X_test, (X_test.shape[0], -1))
print("Training data shape:", X_train.shape)
print("Test data shape:", X_test.shape)
```

```
Training data shape: (800, 4096)
Test data shape: (160, 4096)
```

1.2 1.1 k-Nearest Neighbor (kNN) (10 Marks)

We're now going to try to classify the test images using the k-nearest neighbors algorithm on the **raw features of the images** (i.e. the pixel values themselves). We will see later how we can use kNN on better features.

Here are the steps that we will follow:

1. We compute the L2 distances between every element of X_test and every element of X_train in `compute_distances`.
2. We split the dataset into 5 folds for cross-validation in `split_folds`.
3. For each fold, and for different values of `k`, we predict the labels and measure accuracy.
4. Using the best `k` found through cross-validation, we measure accuracy on the test set.

For your code implementation, follow these steps:

1. Using the Files tab on the left, browse to your lab5 folder and open it (right click then open).
2. You can now see `k_nearest_neighbor.py` file. Double click it and you can edit the codes inside.
3. Use what you did in lab4 to complete the main functions `compute_distances`, `predict_labels`, and `split_folds`.

[6]:
```
from k_nearest_neighbor import compute_distances

# Step 1: compute the distances between all features from X_train and from␣
 ↪X_test
dists = compute_distances(X_test, X_train)
assert dists.shape == (160, 800)
```

[7]:
```
from k_nearest_neighbor import predict_labels

# We use k = 1 (which corresponds to only taking the nearest neighbor to decide)
y_test_pred = predict_labels(dists, y_train, k=1)

# Compute and print the fraction of correctly predicted examples
num_test = y_test.shape[0]
num_correct = np.sum(y_test_pred == y_test)
accuracy = float(num_correct) / num_test
print('Got %d / %d correct => accuracy: %f' % (num_correct, num_test, accuracy))
```

```
Got 38 / 160 correct => accuracy: 0.237500
```

1.2.1 Cross-Validation

We don't know the best value for our parameter `k`.
There is no theory on how to choose an optimal `k`, and the way to choose it is through cross-validation.

We **cannot** compute any metric on the test set to choose the best `k`, because we want our final test accuracy to reflect a real use case. This real use case would be a setting where we have new examples come and we classify them on the go. There is no way to check the accuracy beforehand on that set of test examples to determine `k`.

Cross-validation will make use split the data into different fold (5 here).
For each fold, if we have a total of 5 folds we will have: - 80% of the data as training data - 20% of the data as validation data

We will compute the accuracy on the validation accuracy for each fold, and use the mean of these 5 accuracies to determine the best parameter `k`. Implement function `split_folds` in `k_nearest_neighbor.py`.

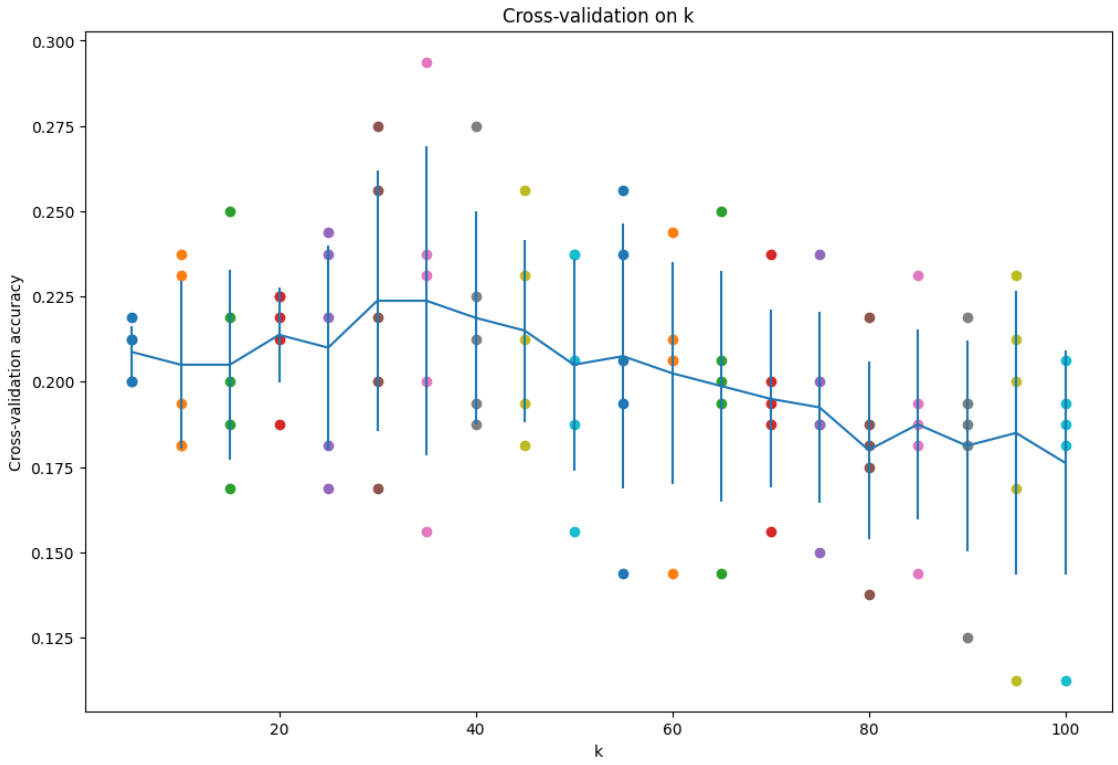
[9]:
```
from k_nearest_neighbor import split_folds

# Step 2: split the data into 5 folds to perform cross-validation.
num_folds = 5

X_trains, y_trains, X_vals, y_vals = split_folds(X_train, y_train, num_folds)

assert X_trains.shape == (5, 640, 4096)
assert y_trains.shape == (5, 640)
assert X_vals.shape == (5, 160, 4096)
assert y_vals.shape == (5, 160)
```

[10]:
```
# Step 3: Measure the mean accuracy for each value of `k`

# List of k to choose from
k_choices = list(range(5, 101, 5))

# Dictionnary mapping k values to accuracies
# For each k value, we will have `num_folds` accuracies to compute
# k_to_accuracies[1] will be for instance [0.22, 0.23, 0.19, 0.25, 0.20] for 5␣
 ↪folds
k_to_accuracies = {}

for k in k_choices:
    print("Running for k=%d" % k)
    accuracies = []
    for i in range(num_folds):
        # Make predictions
        fold_dists = compute_distances(X_vals[i], X_trains[i])
        y_pred = predict_labels(fold_dists, y_trains[i], k)

        # Compute and print the fraction of correctly predicted examples
        num_correct = np.sum(y_pred == y_vals[i])
        accuracy = float(num_correct) / len(y_vals[i])
        accuracies.append(accuracy)

    k_to_accuracies[k] = accuracies
```

```
Running for k=5
Running for k=10
Running for k=15
Running for k=20
Running for k=25
Running for k=30
```

```
Running for k=35
Running for k=40
Running for k=45
Running for k=50
Running for k=55
Running for k=60
Running for k=65
Running for k=70
Running for k=75
Running for k=80
Running for k=85
Running for k=90
Running for k=95
Running for k=100
```

[11]:
```python
# plot the raw observations
plt.figure(figsize=(12,8))
for k in k_choices:
    accuracies = k_to_accuracies[k]
    plt.scatter([k] * len(accuracies), accuracies)

# plot the trend line with error bars that correspond to standard deviation
accuracies_mean = np.array([np.mean(v) for k,v in sorted(k_to_accuracies.
 ↪items())])
accuracies_std = np.array([np.std(v) for k,v in sorted(k_to_accuracies.
 ↪items())])
plt.errorbar(k_choices, accuracies_mean, yerr=accuracies_std)
plt.title('Cross-validation on k')
plt.xlabel('k')
plt.ylabel('Cross-validation accuracy')
plt.show()
```



[12]:
```
# Based on the cross-validation results above, choose the best value for k,
# retrain the classifier using all the training data, and test it on the test
# data. You should be able to get above 26% accuracy on the test data.

# YOUR CODE HERE
# Choose the best k based on the cross validation above
# *****START OF YOUR CODE (DO NOT DELETE/MODIFY THIS LINE)*****
best_k = 30
pass
# *****END OF YOUR CODE (DO NOT DELETE/MODIFY THIS LINE)*****

y_test_pred = predict_labels(dists, y_train, k=best_k)

# Compute and display the accuracy
num_correct = np.sum(y_test_pred == y_test)
accuracy = float(num_correct) / num_test
print('For k = %d, got %d / %d correct => accuracy: %f' % (best_k, num_correct,␣
 ↪num_test, accuracy))
```

```
For k = 30, got 42 / 160 correct => accuracy: 0.262500
```

1.3 1.2: PCA (20 Marks)

Principal Component Analysis (PCA) is a simple yet popular and useful linear transformation technique that is used in numerous applications, such as stock market predictions, the analysis of gene expression data, and many more. In this tutorial, we will see that PCA is not just a "black box", and we are going to unravel its internals in 3 basic steps.

1.3.1 Introduction

The sheer size of data in the modern age is not only a challenge for computer hardware but also a main bottleneck for the performance of many machine learning algorithms. The main goal of a PCA analysis is to identify patterns in data; PCA aims to detect the correlation between variables. If a strong correlation between variables exists, the attempt to reduce the dimensionality only makes sense. In a nutshell, this is what PCA is all about: Finding the directions of maximum variance in high-dimensional data and project it onto a smaller dimensional subspace while retaining most of the information.

1.3.2 A Summary of the PCA Approach

- Standardize the data.
- Obtain the Eigenvectors and Eigenvalues from the covariance matrix or correlation matrix, or perform Singular Vector Decomposition.
- Sort eigenvalues in descending order and choose the k eigenvectors that correspond to the k largest eigenvalues where k is the number of dimensions of the new feature subspace ($k \leq d$).
- Construct the projection matrix $\mathbf{W}$ from the selected k eigenvectors.
- Transform the original dataset $\mathbf{X}$ via $\mathbf{W}$ to obtain a k-dimensional feature subspace Y.

[13]:
```
from features import PCA

pca = PCA()
```

1.3.3 1.2.1 - Eigendecomposition

The eigenvectors and eigenvalues of a covariance (or correlation) matrix represent the "core" of a PCA: The eigenvectors (principal components) determine the directions of the new feature space, and the eigenvalues determine their magnitude. In other words, the eigenvalues explain the variance of the data along the new feature axes.

Implement **`_eigen_decomp`** for class PCA in `features.py`.

[16]:
```
# Perform eigenvalue decomposition on the covariance matrix of training data.
e_vecs, e_vals = pca._eigen_decomp(X_train - X_train.mean(axis=0))

print(e_vals.shape)
print(e_vecs.shape)
```

```
(4096,)
(4096, 4096)
```

1.3.4 1.2.2 - Singular Value Decomposition

Doing an eigendecomposition of the covariance matrix is very expensive, especially when the number of features (`D = 4096` here) gets very high.

To obtain the same eigenvalues and eigenvectors in a more efficient way, we can use Singular Value Decomposition (SVD). If we perform SVD on matrix X, we obtain U, S and V such that:

$$X = USV^T$$

- the columns of U are the eigenvectors of XX^T
- the columns of V (or rows of V^T) are the eigenvectors of X^TX
- the values of S are the square roots of the eigenvalues of X^TX (or XX^T)

Therefore, we can find out the top `k` eigenvectors of the covariance matrix X^TX using SVD.

Implement **`_svd`** for class PCA in `features.py`.

[17]:
```
# Perform SVD on directly on the training data.
u, s = pca._svd(X_train - X_train.mean(axis=0))

print(s.shape)
print(u.shape)
```

```
(800,)
(4096, 4096)
```

[18]:
```
# Test whether the square of singular values and eigenvalues are the same.
# We also observe that `e_vecs` and `u` are the same (only the sign of each␣
 ↪column can differ).
N = X_train.shape[0]
assert np.allclose((s ** 2) / (N - 1), e_vals[:len(s)])

for i in range(len(s) - 1):
    assert np.allclose(e_vecs[:, i], u[:, i]) or np.allclose(e_vecs[:, i], -u[:
 ↪, i])
    # (the last eigenvector for i = len(s) - 1 is very noisy because the␣
 ↪eigenvalue is almost 0,
    #  so imprecisions in the computation build up)
```

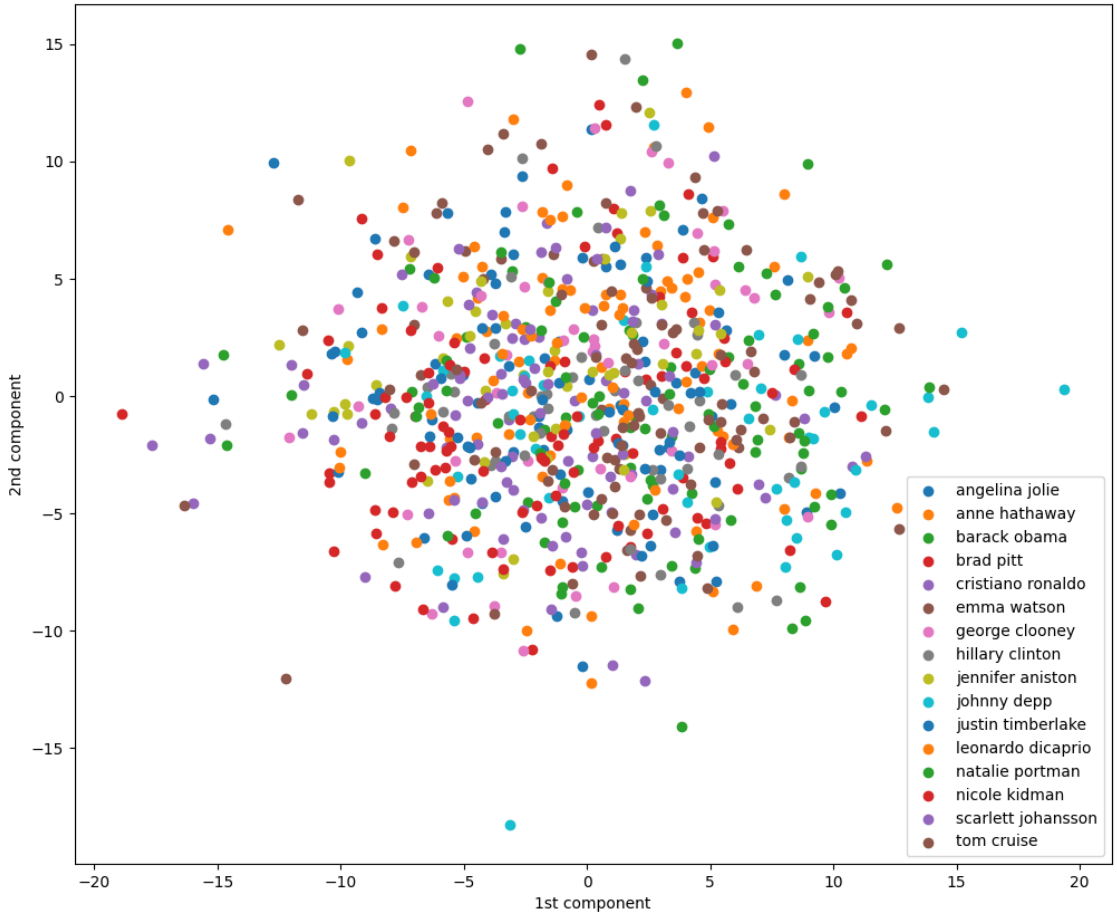
1.3.5 1.2.3 - Dimensionality Reduction

The top k principal components explain most of the variance of the underlying data.

By projecting our initial data (the images) onto the subspace spanned by the top k principal components, we can reduce the dimension of our inputs while keeping most of the information.

In the example below, we can see that **using the first two components in PCA is not enough** to allow us to see pattern in the data. All the classes seem placed at random in the 2D plane. Implement **`fit`** for class PCA in `features.py`.

[21]:
```
# Dimensionality reduction by projecting the data onto
# lower dimensional subspace spanned by k principal components

# To visualize, we will project in 2 dimensions
n_components = 2
pca.fit(X_train)
X_proj = pca.transform(X_train, n_components)

# Plot the top two principal components
for y in np.unique(y_train):
    plt.scatter(X_proj[y_train==y,0], X_proj[y_train==y,1], label=classes[y])

plt.xlabel('1st component')
plt.ylabel('2nd component')
plt.legend()
plt.show()
```



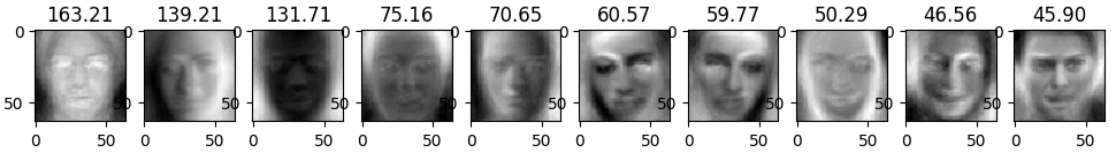
1.3.6 1.2.4 - Visualizing Eigenfaces

The columns of the PCA projection matrix `pca.W_pca` represent the eigenvectors of $X^T X$.

We can visualize the biggest singular values as well as the corresponding vectors to get a sense of what the PCA algorithm is extracting.

If we visualize the top 10 eigenfaces, we can see tht the algorithm focuses on the different shades of the faces. For instance, in face n°2 the light seems to come from the right when using SVD or left if using the eigen vectors due to the negative sign difference.

[22]:
```
for i in range(10):
    plt.subplot(1, 10, i+1)
    plt.imshow(pca.W_pca[:, i].reshape(64, 64))
    plt.title("%.2f" % s[i])
plt.show()
```



[24]:
```
# Reconstruct data with principal components
n_components = 100  # Experiment with different number of components.
X_proj = pca.transform(X_train, n_components)
X_rec = pca.reconstruct(X_proj)

print(X_rec.shape)
print(classes)

num_classes = len(classes)

# Visualize reconstructed faces
samples_per_class = 10
for y, cls in enumerate(classes):
    idxs = np.flatnonzero(y_train == y)
    idxs = np.random.choice(idxs, samples_per_class, replace=False)
    for i, idx in enumerate(idxs):
        plt_idx = i * num_classes + y + 1
        plt.subplot(samples_per_class, num_classes, plt_idx)
        plt.imshow((X_rec[idx]).reshape((64, 64)))
        plt.axis('off')
        if i == 0:
            plt.title(y)
plt.show()
```

```
(800, 4096)
```

```
['angelina jolie', 'anne hathaway', 'barack obama', 'brad pitt', 'cristiano
ronaldo', 'emma watson', 'george clooney', 'hillary clinton', 'jennifer
aniston', 'johnny depp', 'justin timberlake', 'leonardo dicaprio', 'natalie
portman', 'nicole kidman', 'scarlett johansson', 'tom cruise']
```

1.3.7 1.2.5 - Reconstruction error and captured variance

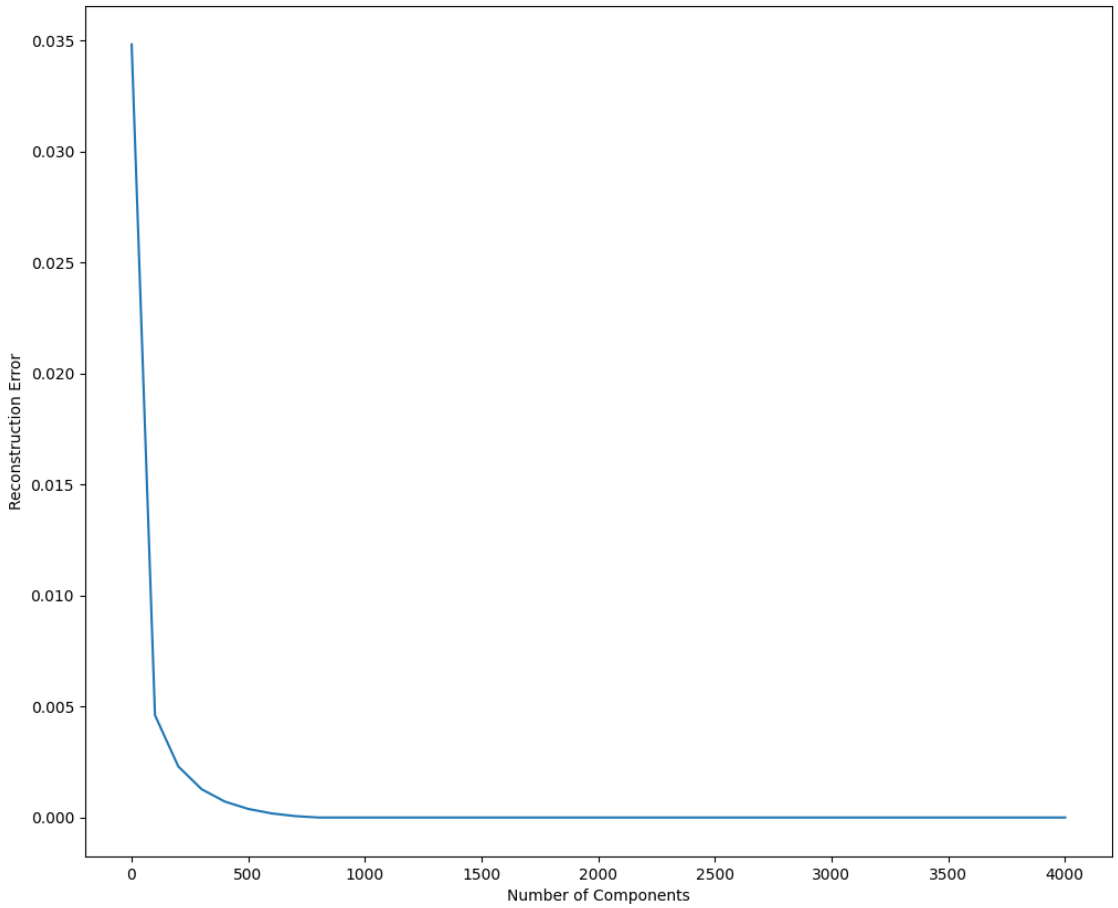
We can plot the reconstruction error with respect to the dimension of the projected space.

The reconstruction gets better with more components.

We can see in the plot that the inflexion point is around dimension 200 or 300. This means that using this number of components is a good compromise between good reconstruction and low dimension.

[25]:
```
# Plot reconstruction errors for different k
N = X_train.shape[0]
d = X_train.shape[1]

ns = range(1, d, 100)
```

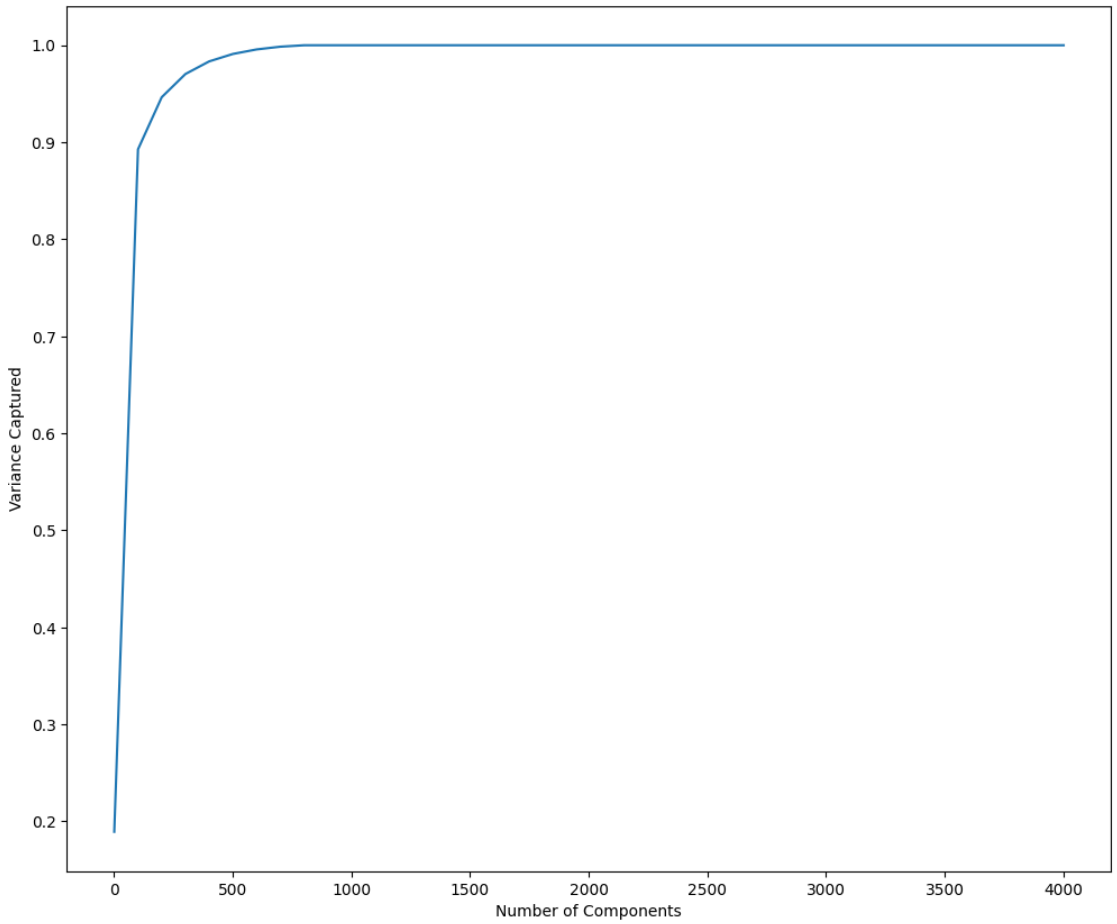
```
errors = []

for n in ns:
    X_proj = pca.transform(X_train, n)
    X_rec = pca.reconstruct(X_proj)

    # Compute reconstruction error
    error = np.mean((X_rec - X_train) ** 2)
    errors.append(error)

plt.plot(ns, errors)
plt.xlabel('Number of Components')
plt.ylabel('Reconstruction Error')
plt.show()
```



We can do the same process to see how much variance is captured by the projection.

Again, we see that the inflexion point is around 200 or 300 dimensions.

[26]:
```
# Plot captured variance
ns = range(1, d, 100)
var_cap = []

for n in ns:
    var_cap.append(np.sum(s[:n] ** 2)/np.sum(s ** 2))

plt.plot(ns, var_cap)
plt.xlabel('Number of Components')
plt.ylabel('Variance Captured')
plt.show()
```



1.3.8 1.2.6 - kNN with PCA

Performing kNN on raw features (the pixels of the image) does not yield very good results.
Computing the distance between images in the image space is not a very good metric for actual proximity of images.
For instance, an image of person A with a dark background will be close to an image of B with a

dark background, although these people are not the same.

Using a technique like PCA can help discover the real interesting features and perform kNN on them could give better accuracy.

However, we observe here that PCA doesn't really help to disentangle the features and obtain useful distance metrics between the different classes. We basically obtain the same performance as with raw features.

[27]:
```
num_test = X_test.shape[0]

# We computed the best k and n for you
best_k = 20
best_n = 500


# PCA
pca = PCA()
pca.fit(X_train)
X_proj = pca.transform(X_train, best_n)
X_test_proj = pca.transform(X_test, best_n)

# kNN
dists = compute_distances(X_test_proj, X_proj)
y_test_pred = predict_labels(dists, y_train, k=best_k)

# Compute and display the accuracy
num_correct = np.sum(y_test_pred == y_test)
accuracy = float(num_correct) / num_test
print('Got %d / %d correct => accuracy: %f' % (num_correct, num_test, accuracy))
```

```
Got 42 / 160 correct => accuracy: 0.262500
```

1.4 1.3 Fisherface: Linear Discriminant Analysis (20 Marks)

LDA is a linear transformation method like PCA, but with a different goal.
The main difference is that LDA takes information from the labels of the examples to maximize the separation of the different classes in the transformed space.

Therefore, LDA is not totally **unsupervised** since it requires labels. PCA is **fully unsupervised**.

In summary: - PCA perserves maximum variance in the projected space. - LDA preserves discrimination between classes in the project space. We want to maximize scatter between classes and minimize scatter intra class.

[28]:
```
from features import LDA

lda = LDA()
```

1.4.1 1.3.1 - Dimensionality Reduction via PCA

To apply LDA, we need $D < N$. Since in our dataset, $N = 800$ and $D = 4096$, we first need to reduce the number of dimensions of the images using PCA.
More information at: http://www.scholarpedia.org/article/Fisherfaces

[30]:
```
N = X_train.shape[0]
c = num_classes

pca = PCA()
pca.fit(X_train)
X_train_pca = pca.transform(X_train, N-c)
X_test_pca = pca.transform(X_test, N-c)
```

1.4.2 1.3.2 - Scatter matrices

We first need to compute the within-class scatter matrix:

$$S_W = \sum_{i=1}^{c} S_i$$

where $S_i = \sum_{x_k \in Y_i} (x_k - \mu_i)(x_k - \mu_i)^T$ is the scatter of class i.

We then need to compute the between-class scatter matrix:

$$S_B = \sum_{i=1}^{c} N_i (\mu_i - \mu)(\mu_i - \mu)^T$$

where N_i is the number of examples in class i. Implement **`_within_class_scatter`** and **`_between_class_scatter`** for class LDA in `features.py`.

[31]:
```
# Compute within-class scatter matrix
S_W = lda._within_class_scatter(X_train_pca, y_train)
print(S_W.shape)
```

```
(784, 784)
```

[32]:
```
# Compute between-class scatter matrix
S_B = lda._between_class_scatter(X_train_pca, y_train)
print(S_B.shape)
```

```
(784, 784)
```

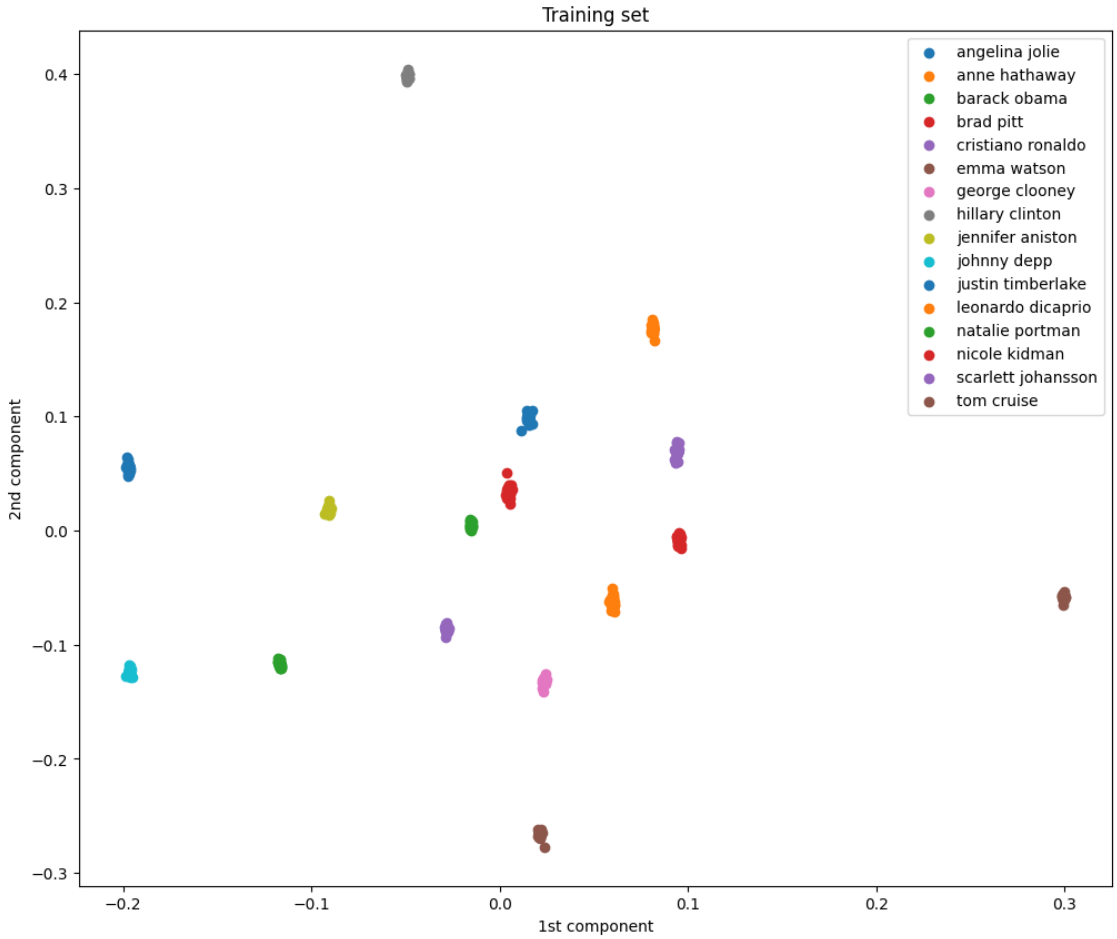
1.4.3 1.3.3 - Solving generalized Eigenvalue problem

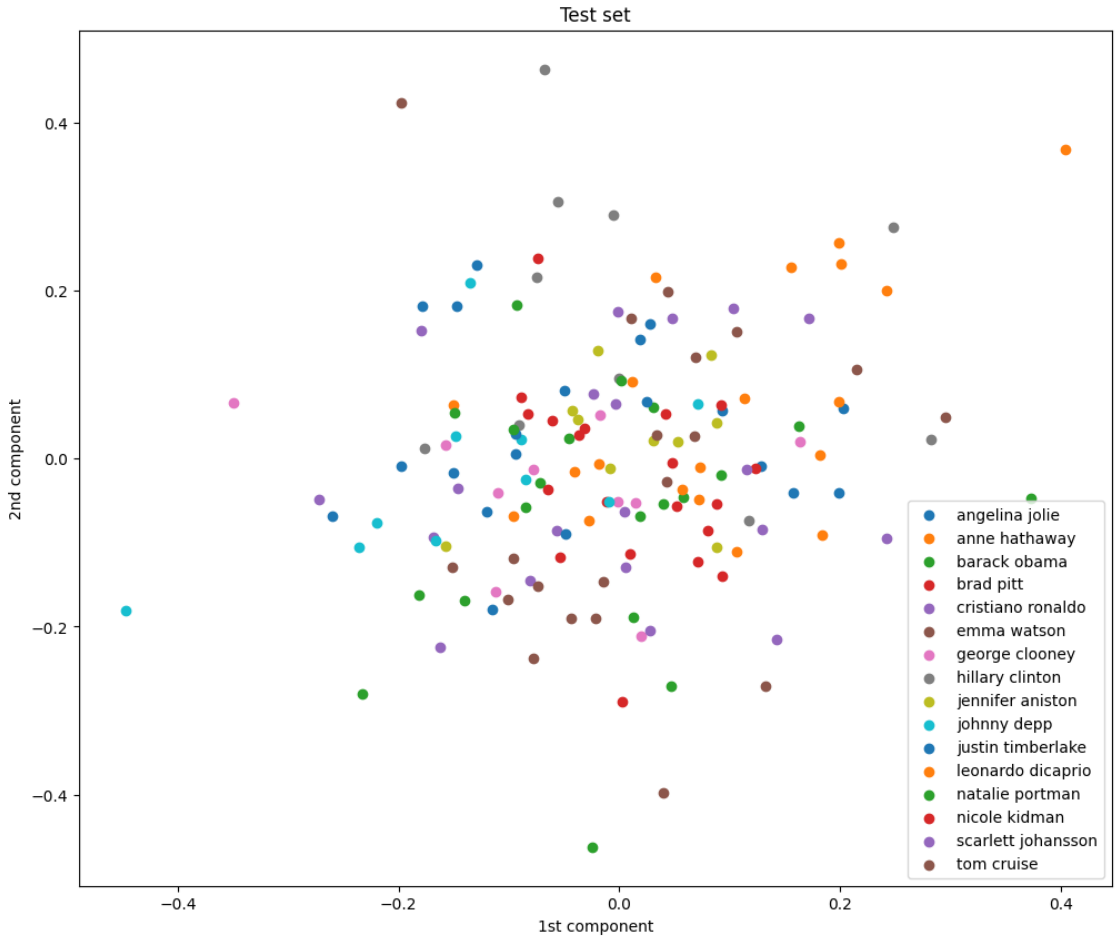
Implement methods `fit` and `transform` of the `LDA` class.

[37]:
```
lda.fit(X_train_pca, y_train)
print(lda.W_lda.shape)
```

```
(784, 784)
```

[38]:
```
# Dimensionality reduction by projecting the data onto
# lower dimensional subspace spanned by k principal components
n_components = 2
X_proj = lda.transform(X_train_pca, n_components)
X_test_proj = lda.transform(X_test_pca, n_components)

# Plot the top two principal components on the training set
for y in np.unique(y_train):
    plt.scatter(X_proj[y_train==y, 0], X_proj[y_train==y, 1], label=classes[y])

plt.xlabel('1st component')
plt.ylabel('2nd component')
plt.legend()
plt.title("Training set")
plt.show()

# Plot the top two principal components on the test set
for y in np.unique(y_test):
    plt.scatter(X_test_proj[y_test==y, 0], X_test_proj[y_test==y,1],␣
 ↪label=classes[y])

plt.xlabel('1st component')
plt.ylabel('2nd component')
plt.legend()
plt.title("Test set")
plt.show()
```


Training set
angelina jolie
anne hathaway
barack obama
brad pitt
cristiano ronaldo
emma watson
george clooney
hillary clinton
jennifer aniston
johnny depp
justin timberlake
leonardo dicaprio
natalie portman
nicole kidman
scarlett johansson
tom cruise
2nd component
1st component
0.4
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.2
−0.1
0.0
0.1
0.2
0.3



1.4.4 1.3.4 - kNN with LDA

Thanks to having the information from the labels, LDA gives a discriminant space where the classes are far apart from each other.
This should help kNN a lot, as the job should just be to find the obvious 10 clusters.

However, as we've seen in the previous plot (section 1.3.3), the training data gets clustered pretty well, but the test data isn't as nicely clustered as the training data (overfitting?).

Perform cross validation following the code below (you can change the values of `k_choices` and `n_choices` to search). Using the best result from cross validation, obtain the test accuracy.

[42]:
```
from collections import defaultdict
num_folds = 5

X_trains, y_trains, X_vals, y_vals = split_folds(X_train, y_train, num_folds)

k_choices = [1, 5, 10, 20]  # k for k-NN
n_choices = [5, 10, 20, 50, 100, 200, 500] # no. of LDA dimensions
```

```
# *****START OF YOUR CODE (DO NOT DELETE/MODIFY THIS LINE)*******
# You can here test new values of k_choices and n_choices
# *****END OF YOUR CODE (DO NOT DELETE/MODIFY THIS LINE)**********

# n_k_to_accuracies[(n, k)] should be a list of length num_folds giving the␣
 ↪different
# accuracy values that we found when using that value of n and k.
n_k_to_accuracies = defaultdict(list)

for i in range(num_folds):
    # Fit PCA
    pca = PCA()
    pca.fit(X_trains[i])

    N = len(X_trains[i])
    X_train_pca = pca.transform(X_trains[i], N-c)
    X_val_pca = pca.transform(X_vals[i], N-c)

    # Fit LDA
    lda = LDA()
    lda.fit(X_train_pca, y_trains[i])

    for n in n_choices:
        X_train_proj = lda.transform(X_train_pca, n)
        X_val_proj = lda.transform(X_val_pca, n)

        dists = compute_distances(X_val_proj, X_train_proj)

        for k in k_choices:
            y_pred = predict_labels(dists, y_trains[i], k=k)

            # Compute and print the fraction of correctly predicted examples
            num_correct = np.sum(y_pred == y_vals[i])
            accuracy = float(num_correct) / len(y_vals[i])
            n_k_to_accuracies[(n, k)].append(accuracy)


for n in n_choices:
    print()
    for k in k_choices:
        accuracies = n_k_to_accuracies[(n, k)]
        print("For n=%d, k=%d: average accuracy is %f" % (n, k, np.
 ↪mean(accuracies)))
```

```
For n=5, k=1: average accuracy is 0.192500
For n=5, k=5: average accuracy is 0.193750
```

```
For n=5, k=10: average accuracy is 0.192500
For n=5, k=20: average accuracy is 0.195000

For n=10, k=1: average accuracy is 0.278750
For n=10, k=5: average accuracy is 0.298750
For n=10, k=10: average accuracy is 0.297500
For n=10, k=20: average accuracy is 0.298750

For n=20, k=1: average accuracy is 0.355000
For n=20, k=5: average accuracy is 0.382500
For n=20, k=10: average accuracy is 0.383750
For n=20, k=20: average accuracy is 0.381250

For n=50, k=1: average accuracy is 0.311250
For n=50, k=5: average accuracy is 0.361250
For n=50, k=10: average accuracy is 0.363750
For n=50, k=20: average accuracy is 0.362500

For n=100, k=1: average accuracy is 0.226250
For n=100, k=5: average accuracy is 0.232500
For n=100, k=10: average accuracy is 0.248750
For n=100, k=20: average accuracy is 0.261250

For n=200, k=1: average accuracy is 0.148750
For n=200, k=5: average accuracy is 0.110000
For n=200, k=10: average accuracy is 0.118750
For n=200, k=20: average accuracy is 0.113750

For n=500, k=1: average accuracy is 0.140000
For n=500, k=5: average accuracy is 0.108750
For n=500, k=10: average accuracy is 0.102500
For n=500, k=20: average accuracy is 0.098750
```

[41]:
```python
# Based on the cross-validation results above, choose the best value for n, k,
# retrain the classifier using all the training data, and test it on the test
# data. You should be able to get above 40% accuracy on the test data.

best_k = None
best_n = None
# YOUR CODE HERE
# Choose the best k based on the cross validation above
# *****START OF YOUR CODE (DO NOT DELETE/MODIFY THIS LINE)*****

best_k = 5
best_n = 20

# *****END OF YOUR CODE (DO NOT DELETE/MODIFY THIS LINE)*****
```

```
# END YOUR CODE

N = len(X_train)

# Fit PCA
pca = PCA()
pca.fit(X_train)
X_train_pca = pca.transform(X_train, N-c)
X_test_pca = pca.transform(X_test, N-c)

# Fit LDA
lda = LDA()
lda.fit(X_train_pca, y_train)

# Project using LDA
X_train_proj = lda.transform(X_train_pca, best_n)
X_test_proj = lda.transform(X_test_pca, best_n)

dists = compute_distances(X_test_proj, X_train_proj)
y_test_pred = predict_labels(dists, y_train, k=best_k)

# Compute and display the accuracy
num_correct = np.sum(y_test_pred == y_test)
accuracy = float(num_correct) / num_test
print("For k=%d and n=%d" % (best_k, best_n))
print('Got %d / %d correct => accuracy: %f' % (num_correct, num_test, accuracy))
```

```
For k=5 and n=20
Got 69 / 160 correct => accuracy: 0.431250
```