

U23AI118

PCA-based Face Recognition (Eigenfaces)

Objective

The objective of this lab is to design and implement a basic facial recognition system using Principal Component Analysis (PCA). Learn how to project face images into a lower-dimensional feature space (“face space”) spanned by Eigenfaces and use this representation for image reconstruction and recognition.

Tasks Performed

1. Data Preprocessing
 - Load dataset images.
 - Flatten each image into a 1D vector.
 - Standardize (zero mean, unit variance).
 - Split dataset into training and testing sets.
2. Implement PCA (from scratch)
 - 1 • Compute covariance matrix of the dataset.
 - Compute eigenvalues and eigenvectors.
 - Sort eigenvectors by descending eigenvalues.
 - Select top k principal components (Eigenfaces).
3. Eigenfaces Visualization
 - Display the mean face.
 - Visualize first few Eigenfaces.
4. Image Reconstruction
 - Project images into PCA space with different values of k.
 - Reconstruct the original images.
 - Compare reconstruction quality vs. k.
5. Face Recognition
 - Train recognition system using projected features.
 - Implement nearest neighbor classifier in PCA space.
 - Test recognition accuracy for different values of k.
6. Performance Analysis
 - Plot recognition accuracy vs. number of principal components.
 - Discuss findings.
7. t-SNE Visualization (Bonus Task)
 - Use the PCA feature representations (e.g., top 50 components) as input to t-distributed Stochastic Neighbor Embedding (t-SNE).
 - Reduce to 2D or 3D for visualization.
 - Plot the resulting clusters with different subjects in different colors.
 - Comment on whether subjects form distinct groups in low-dimensional space.

```
import zipfile # for extracting the download
import numpy as np
import matplotlib.pyplot as plt
from pathlib import Path
from PIL import Image # python imaging library
```

1) Download the AT&T (ORL) dataset

We will download the AT & T dataset from https://git-disl.github.io/GTDLB/ench/datasets/att_face_dataset

```

# Dataset download and extraction
orig_data_dir = Path('att_faces')
zip_path = Path('att_faces.zip')
url = 'https://www.cl.cam.ac.uk/research/dtg/attarchive/pub/data/att_faces.zip'

# Try automatic download and extraction; if it fails, instruct the user to download manually
dataset_ready = False
if not orig_data_dir.exists():
    print('Dataset folder "att_faces" not found in the current working directory - attempting to download automatically')
    try:
        urllib.request.urlretrieve(url, zip_path)
        print('Download complete, extracting...')
        with zipfile.ZipFile(zip_path, 'r') as zf:
            zf.extractall('.')
        print('Extraction complete.')
        try:
            zip_path.unlink()
        except Exception:
            pass
    except Exception as e:
        print('Automatic download/extract failed:', e)
        print()
        print('Please download the AT&T dataset manually from:')
        print('  https://www.cl.cam.ac.uk/research/dtg/attarchive/pub/data/att_faces.zip')
        print("Then extract the archive so a folder named 'att_faces' is created in this notebook")
        print('After placing the dataset, re-run the cells.')
    else:
        print('Dataset already present at', orig_data_dir)

# Detect where the subject folders actually are (some extractions place s1..s40 at top-level)
# Strategy: prefer local './att_faces'; otherwise search recursively for any 'att_faces' folder;
# then look for a folder that contains many subject subdirectories with .pgm files;
# finally consider the case where subjects (s1..s40) are top-level directories.
candidate = None
# 1) prefer exact local folder
if orig_data_dir.exists():
    candidate = orig_data_dir
else:
    # 2) search recursively for a folder literally named 'att_faces'
    for p in Path('.').glob('**/att_faces'):
        if p.is_dir():
            candidate = p
            break
    # 3) if not found, look for any directory that looks like the dataset root
if candidate is None:
    for p in Path('.').iterdir():

```

```

if not p.is_dir():
    continue
# check if this directory contains many subject subdirectories
subdirs = [d for d in p.iterdir() if d.is_dir()]
if len(subdirs) >= 30:
    # quick check: do some subdirs contain .pgm files?
    has_pgm = any(len(list(d.glob('*.*pgm'))) > 0 for d in subdirs[:10])
    if has_pgm:
        candidate = p
        break
# 4) final fallback: if many top-level dirs start with 's' (s1..s40), treat '.' as dataset
if candidate is None:
    top_level_subjects = [d for d in Path('.').iterdir() if d.is_dir() and d.name.lower().startswith('s')]
    if len(top_level_subjects) >= 30:
        candidate = Path('.')

if candidate is not None:
    data_dir = candidate
    dataset_ready = True
    print('Using dataset directory:', data_dir)
else:
    data_dir = orig_data_dir
    dataset_ready = data_dir.exists()
    if not dataset_ready:
        print('\nDataset directory "att_faces" not found and no automatic candidate detected')
        print('If you have extracted files into a folder, either:')
        print(' - place a folder named "att_faces" next to this notebook (containing s1..s40)')
        print(' - or keep your existing folder structure but ensure the notebook working directory')
        print(' - or rerun the previous cell after manual download/extract')
        print('\nYou can also call the following helper to list likely candidate folders:')
        print(' [d for d in Path(".").iterdir() if d.is_dir()]')

# final status
if dataset_ready:
    print('Dataset ready at:', data_dir)
else:
    print('Dataset NOT ready. Please follow the printed instructions.')

Dataset already present at att_faces
Using dataset directory: att_faces
Dataset ready at: att_faces

```

2) Load images, flatten, and split into train/test

We will load all images (40 subjects x 10 images = 400). We'll create labels 0..39. Then flatten each 92x112 image into a 1D vector of length 10304. Finally we'll

split into training and testing sets (7 train / 3 test per subject).

```
# Load images
if not data_dir.exists():
    raise FileNotFoundError(
        "Dataset folder 'att_faces' not found."
)

img_h, img_w = 112, 92 # height, width ideally
images = []
labels = []
subject_dirs = sorted([p for p in data_dir.iterdir() if p.is_dir()])
print(f'Found {len(subject_dirs)} subject folders')
for subj_idx, subj in enumerate(subject_dirs):
    img_files = sorted(subj.glob('*.*pgm'))
    for imf in img_files:
        img = Image.open(imf).convert('L').resize((img_w, img_h)) #convert('L') used for gray
        arr = np.asarray(img, dtype=np.float64)
        images.append(arr.flatten())
        labels.append(subj_idx)
images = np.array(images) # shape will be (n_images, n_pixels)
labels = np.array(labels)
print('Loaded images shape:', images.shape)

# Stratified split per subject: 7 train / 3 test
X_train_list, y_train_list, X_test_list, y_test_list = [], [], [], []
rng = np.random.default_rng(seed=42)
for s in range(len(subject_dirs)):
    idxs = np.where(labels==s)[0]
    rng.shuffle(idxs)
    train_idx = idxs[:7]
    test_idx = idxs[7:]
    X_train_list.append(images[train_idx])
    y_train_list.append(labels[train_idx])
    X_test_list.append(images[test_idx])
    y_test_list.append(labels[test_idx])
X_train = np.vstack(X_train_list)
y_train = np.hstack(y_train_list)
X_test = np.vstack(X_test_list)
y_test = np.hstack(y_test_list)
print('Train shape:', X_train.shape, 'Test shape:', X_test.shape)

Found 40 subject folders
Loaded images shape: (400, 10304)
Train shape: (280, 10304) Test shape: (120, 10304)
```

3) Standardize data (zero mean, unit variance) and implement PCA from scratch

First we'll standardize data statistics. Then compute covariance matrix of the standardized training data, compute eigenvalues/eigenvectors, sort them, and keep top-k components (Eigenfaces).

```
class SimpleStandardScaler:
    def __init__(self, with_mean=True, with_std=True):
        self.with_mean = with_mean
        self.with_std = with_std
        self.mean_ = None
        self.scale_ = None

    def fit(self, X):
        if self.with_mean:
            self.mean_ = np.mean(X, axis=0)
        else:
            self.mean_ = np.zeros(X.shape[1], dtype=X.dtype)
        if self.with_std:
            # population std (ddof=0) to match sklearn's default
            self.scale_ = np.std(X, axis=0, ddof=0)
            # avoid division by zero
            zero_mask = (self.scale_ == 0)
            if np.any(zero_mask):
                self.scale_[zero_mask] = 1.0
        else:
            self.scale_ = np.ones(X.shape[1], dtype=X.dtype)
        return self

    def transform(self, X):
        return (X - self.mean_) / self.scale_

    def fit_transform(self, X):
        return self.fit(X).transform(X)

    def inverse_transform(self, X_std):
        return (X_std * self.scale_) + self.mean_

    # Standardize (fit only on training set)
scaler = SimpleStandardScaler(with_mean=True, with_std=True)
X_train_std = scaler.fit_transform(X_train)
X_test_std = scaler.transform(X_test)

# Compute covariance matrix of the standardized training data
print('Computing covariance matrix')
```

```

cov = np.cov(X_train_std, rowvar=False)
print('Covariance matrix shape:', cov.shape)

# Eigen decomposition (We can use eigh because cov is symmetric)
eigvals, eigvecs = np.linalg.eigh(cov)
# Sort eigen values in descending order
idx = np.argsort(eigvals)[::-1]
eigvals = eigvals[idx]
eigvecs = eigvecs[:, idx]
print('Top 10 eigenvalues:', eigvals[:10])

# get top-k eigenvectors
def top_k_components(k):
    return eigvecs[:, :k], eigvals[:k]

Computing covariance matrix
Covariance matrix shape: (10304, 10304)
Top 10 eigenvalues: [1629.8261863 1309.38728539 854.3120469 585.79531677 556.49705975
 323.08209339 260.4100063 237.87253637 208.75767421 195.30246445]

```

4) Visualize mean face and first eigenfaces

We'll show the mean face (computed on original pixel values) and the first few Eigenfaces (corresponding to largest eigenvalues). Eigenfaces are reshaped eigenvectors; they may contain negative values and appear as ghost-like faces.

```

plt.rcParams['figure.figsize'] = (10,6)

def show_images(images, titles=None, h=112, w=92, cmap='gray', ncols=5):
    n = len(images)
    ncols = ncols if 'ncols' in locals() else 5
    ncols = ncols
    nrows = (n + ncols - 1) // ncols
    fig, axes = plt.subplots(nrows, ncols, figsize=(1.8*ncols,2.2*nrows))
    axes = np.array(axes).reshape(-1)
    for i in range(nrows*ncols):
        axes[i].axis('off')
    for i, img in enumerate(images):
        axes[i].imshow(img.reshape((h,w)), cmap=cmap)
        if titles is not None:
            axes[i].set_title(titles[i], fontsize=8)
    plt.tight_layout()
    plt.show()

# Mean face (how original pixel scale from training set will look like)
mean_face = X_train.mean(axis=0)
plt.figure(figsize=(3,4))
plt.imshow(mean_face.reshape((img_h,img_w)), cmap='gray')

```

```

plt.title('Mean face (training set)')
plt.axis('off')
plt.show()

# Visualize first 10 Eigenfaces (from standardized covariance eigenvectors)
k_show = 10
evecs10, _ = top_k_components(k_show)
eigenface_images = []
for i in range(k_show):
    img = evecs10[:, i] # shape (n_pixels,)
    img = (img - img.min()) / (img.max() - img.min()) * 255.0 # Normalize the eigenvector to 0-255
    eigenface_images.append(img)
show_images(eigenface_images, h=img_h, w=img_w, ncols=5)

```

Mean face (training set)





5) Image reconstruction with different numbers of principal components

We'll project some sample test images into PCA space for different k , reconstruct them and display the results side-by-side to compare reconstruction quality.

```

def reconstruct(X_std, evecs_k, scaler):
    # X_std: standardized data (n_samples, n_features)
    # evecs_k: (n_features, k)
    # project and reconstruct in standardized space then inverse-transform to original pixel
    weights = X_std.dot(evecs_k)  # (n_samples, k)
    X_rec_std = weights.dot(evecs_k.T)  # (n_samples, n_features)
    X_rec = scaler.inverse_transform(X_rec_std)  # back to original pixel scale
    return X_rec

# picking 5 random test samples for showing reconstructions
rng = np.random.default_rng(1)
sample_idxs = rng.choice(len(X_test), size=5, replace=False)
originals = X_test[sample_idxs]
original_titles = [f'GT: {y_test[i]}' for i in sample_idxs]

ks = [5, 20, 50, 100, 200]  # different top components chosen counts to compare
recon_sets = []
for k in ks:
    evecs_k, _ = top_k_components(k)
    Xrec = reconstruct(X_test_std[sample_idxs], evecs_k, scaler)
    recon_sets.append(Xrec)

# display originals then each reconstruction row-by-row
print('Originals:')
show_images(originals, titles=original_titles, h=img_h, w=img_w)

```

```
for i, k in enumerate(ks):
    print(f'Reconstructions with k={k}')
    show_images(recon_sets[i], titles=[f'k={k}' for _ in range(len(sample_idxs))], h=img_h,
```

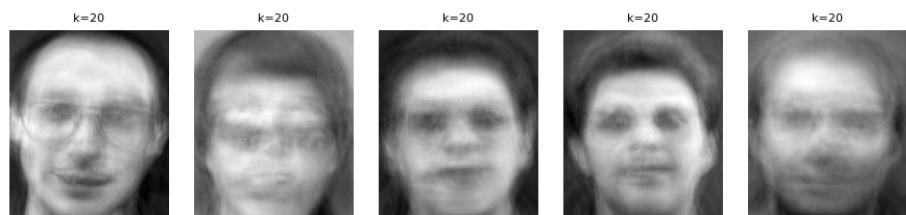
Originals:



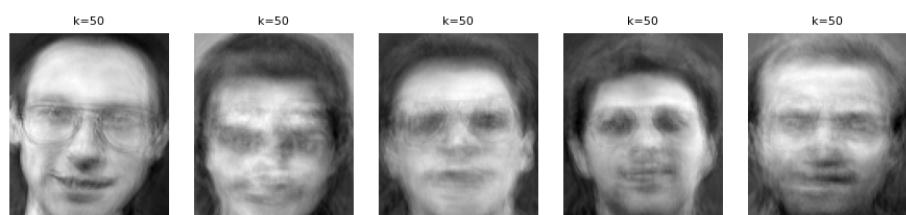
Reconstructions with k=5



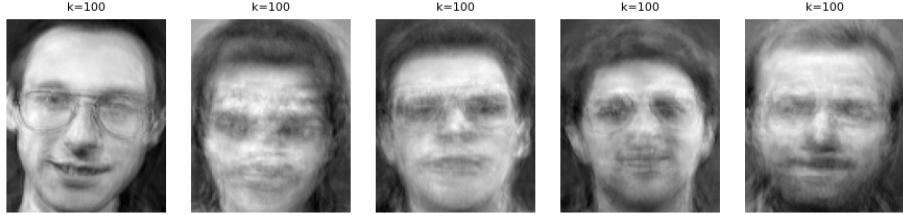
Reconstructions with k=20



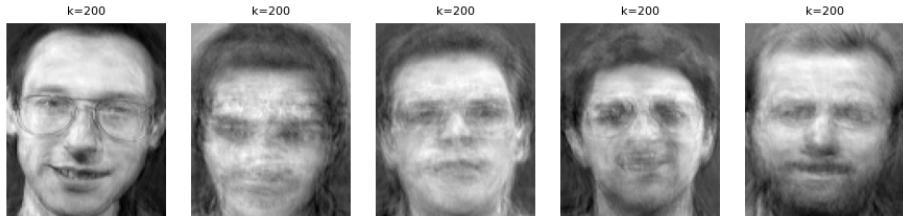
Reconstructions with k=50



Reconstructions with k=100



Reconstructions with $k=200$



6) Face recognition using 1-NN in PCA space

Implemented a simple 1-nearest-neighbor classifier in PCA space (Euclidean distance). We'll evaluate accuracy on the test set for different numbers of principal components k .

```

def knn_predict_1nn(X_train_proj, y_train, x_test_proj):
    x = np.atleast_2d(x_test_proj)
    # compute pairwise distances between x and X_train_proj
    dists = np.linalg.norm(x[:, None, :] - X_train_proj[None, :, :], axis=2) # (n_tests, n_
    idx = np.argmin(dists, axis=1)
    return y_train[idx]

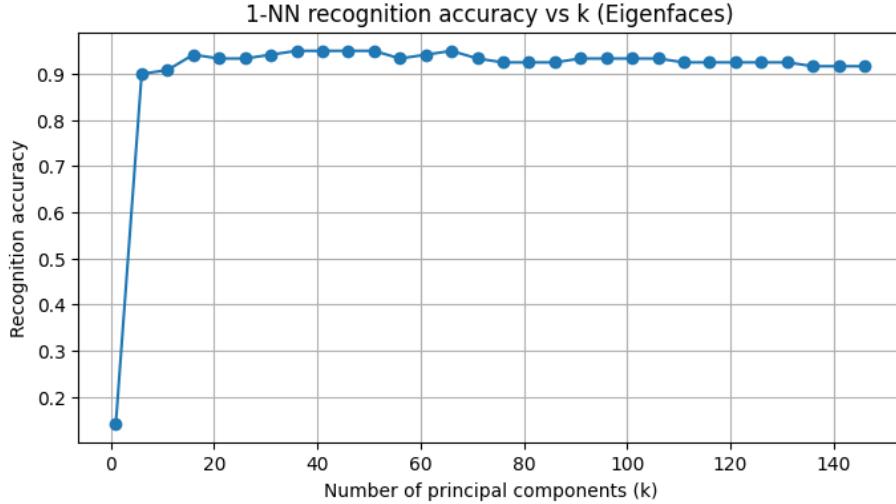
# Evaluate accuracy for a range of k values
k_values = list(range(1, 151, 5))
k_values = [k for k in k_values if k <= X_train.shape[1]]
accuracies = []
for k in k_values:
    evecs_k, _ = top_k_components(k)
    Xtr_proj = X_train_std.dot(evecs_k)
    Xte_proj = X_test_std.dot(evecs_k)
    y_pred = knn_predict_1nn(Xtr_proj, y_train, Xte_proj)
    acc = (y_pred == y_test).mean()
    accuracies.append(acc)
    print(f'k={k:3d} acc={acc:.3f}')

# Plot accuracy vs k
plt.figure(figsize=(8,4))
plt.plot(k_values, accuracies, marker='o')

```

```
plt.xlabel('Number of principal components (k)')
plt.ylabel('Recognition accuracy')
plt.title('1-NN recognition accuracy vs k (Eigenfaces)')
plt.grid(True)
plt.show()

k=  1  acc=0.142
k=  6  acc=0.900
k= 11  acc=0.908
k= 16  acc=0.942
k= 21  acc=0.933
k= 26  acc=0.933
k= 31  acc=0.942
k= 36  acc=0.950
k= 41  acc=0.950
k= 46  acc=0.950
k= 51  acc=0.950
k= 56  acc=0.933
k= 61  acc=0.942
k= 66  acc=0.950
k= 71  acc=0.933
k= 76  acc=0.925
k= 81  acc=0.925
k= 86  acc=0.925
k= 91  acc=0.933
k= 96  acc=0.933
k=101  acc=0.933
k=106  acc=0.933
k=111  acc=0.925
k=116  acc=0.925
k=121  acc=0.925
k=126  acc=0.925
k=131  acc=0.925
k=136  acc=0.917
k=141  acc=0.917
k=146  acc=0.917
```



7) Performance analysis and discussion

The plot shows recognition accuracy as a function of the number of principal components k . Generally, accuracy increases with more components up to a point then does not vary much. Lower k may discard discriminative features and very large k may include noise and overfit. With help of KNN we run a prediction on test set and map it with 1st nearest neighbour from the training set. When we are taking top 6 eigenvectors we are able to match 90% of images and by taking 36 top eigen vectors we predict 95% images.

8) Bonus: t-SNE on PCA features (visualization)

We'll use the top-50 PCA components to get compact features, then apply t-SNE to reduce to 2D for visualization. This helps see clustering by subject. t-SNE is computationally heavier; we use a random subset for speed.

```
from sklearn.manifold import TSNE #t-distributed Stochastic Neighbor Embedding
# Choosing top 50 PCA components to feed into t-SNE
k_tsne = 50
evecs_k, _ = top_k_components(k_tsne)
X_proj_all = np.vstack([X_train_std, X_test_std]) # standardized full set
y_all = np.hstack([y_train, y_test])
X_feat = X_proj_all.dot(evecs_k) # (400, k_tsne)

# subsample for faster t-SNE visualization
n_samples_tsne = 200
idxs = np.arange(X_feat.shape[0])
rng = np.random.default_rng(0)
sel = rng.choice(idxs, size=n_samples_tsne, replace=False) if X_feat.shape[0] > n_samples_tsne else idxs
```

```

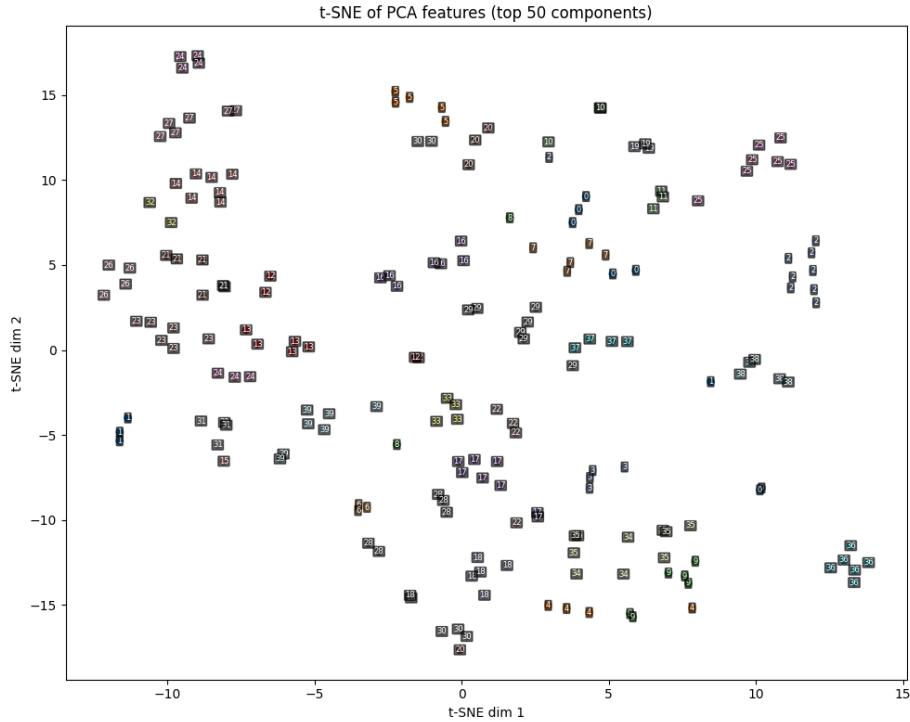
X_tsne_in = X_feat[sel]
y_tsne = y_all[sel]

print('Running t-SNE on', X_tsne_in.shape[0], 'samples')
tsne = TSNE(n_components=2, perplexity=30, max_iter=1000, random_state=42, init='pca')
Z = tsne.fit_transform(X_tsne_in)

# scatter plot colored by subject label (labels are drawn on the points for clarity)
plt.figure(figsize=(10,8))
# scatter all points with a categorical colormap
scatter = plt.scatter(Z[:,0], Z[:,1], c=y_tsne, s=30, cmap='tab20')
# annotate each point with its subject id (small readable labels)
for i, lbl in enumerate(y_tsne):
    plt.text(Z[i,0], Z[i,1], str(int(lbl)), fontsize=6, color='white',
             ha='center', va='center', bbox=dict(facecolor='black', alpha=0.6, boxstyle='round'))
plt.title('t-SNE of PCA features (top %d components)' % k_tsne)
plt.xlabel('t-SNE dim 1')
plt.ylabel('t-SNE dim 2')
plt.tight_layout()
plt.show()

```

Running t-SNE on 200 samples



The tsne generated provides which labels are closer to each other on a 2d plane.

Conclusion

We took 400 images with size 92x112. Took 7 images of each subject in train set. Computed PCA with this. Plotted mean eigenface. With help of top PCA components we tried plotting the original face. On the test set we used KNN to classify the image from one of the train set. Computed accuracy of different top PCA components. Finally we used tsne to plot a 2d plane where images are plotted based on their similarity. The nearer the image to each other the more they look same.