1

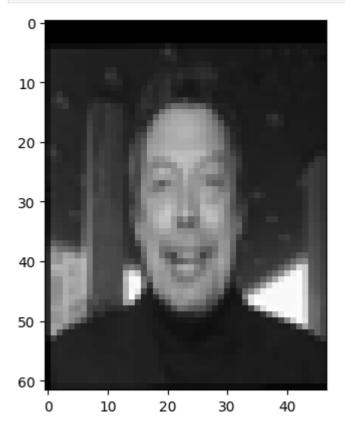
```
In []: from IPython.display import Latex

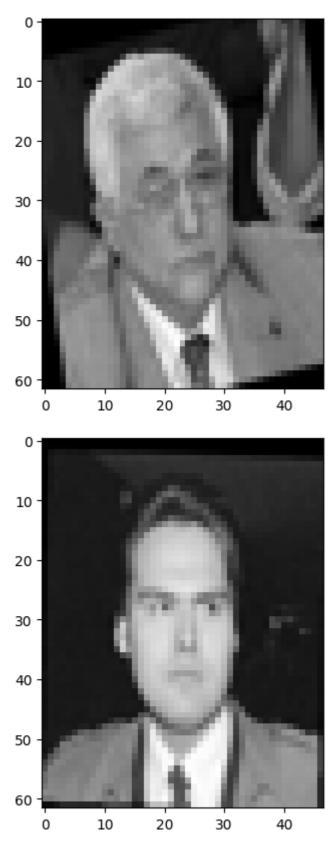
In []: #DownLoading dataset
    from sklearn import datasets
    dataset = datasets.fetch_lfw_people()
    X = dataset['data']
    #check data
    print(X.data.shape)

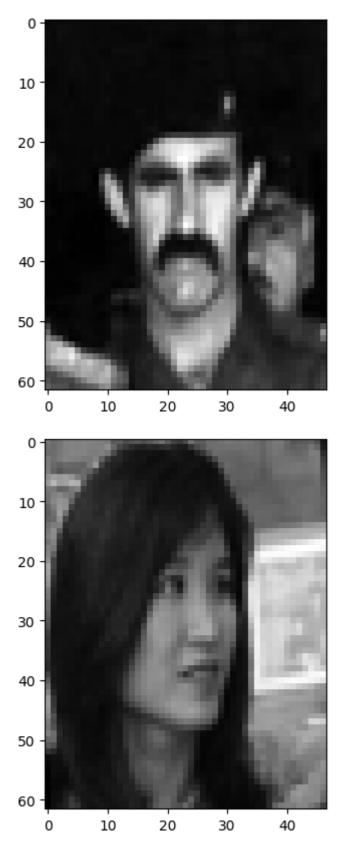
    (13233, 2914)

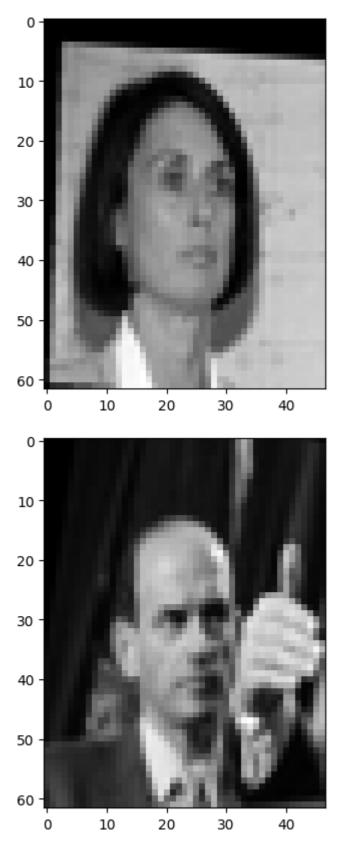
In []: #Relevant imports
    import matplotlib
    import numpy as np
    from matplotlib import pyplot
    from numpy import linalg
In []: #1.a
    for i in range(20):
```

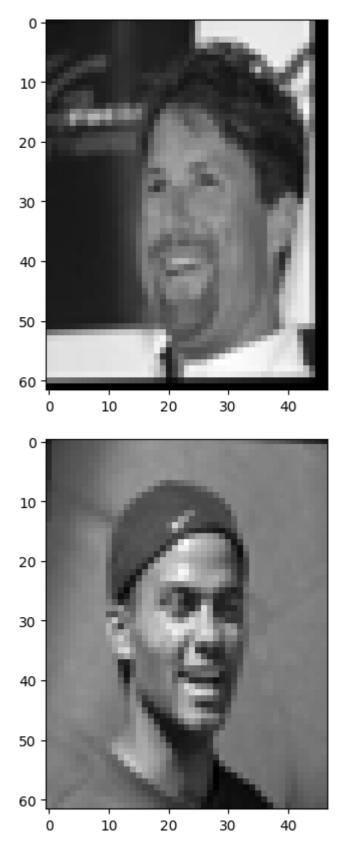


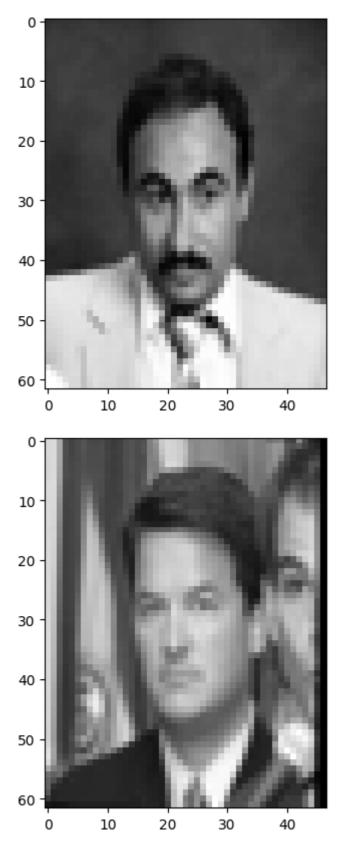


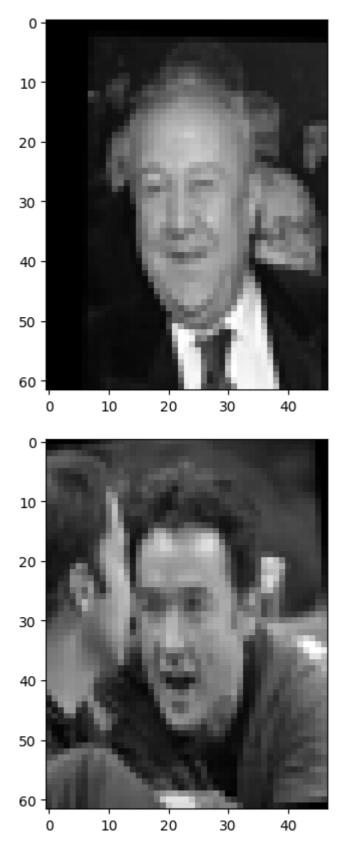


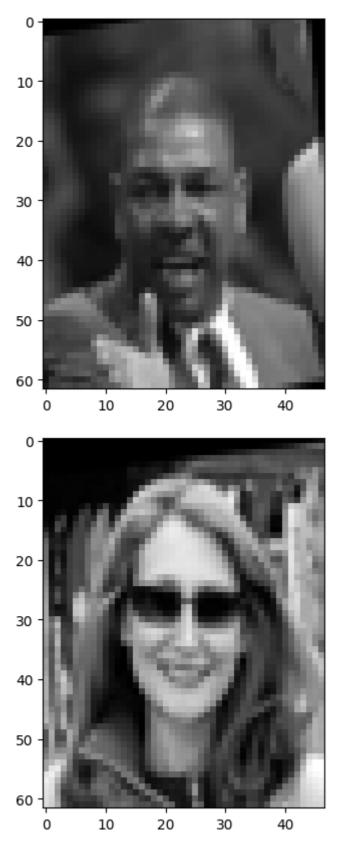


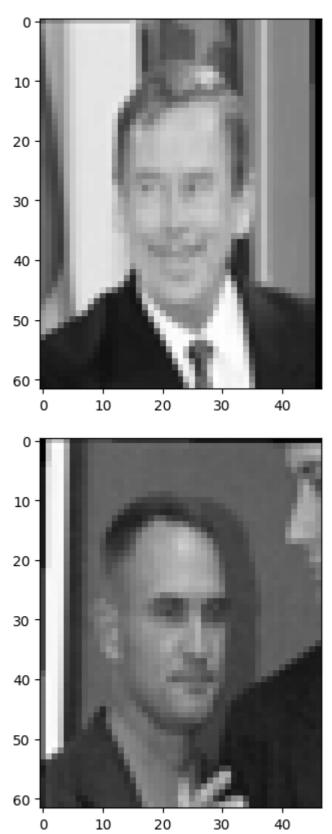


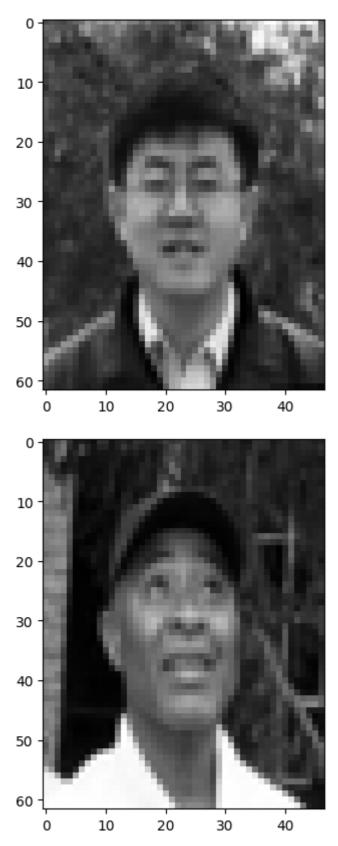


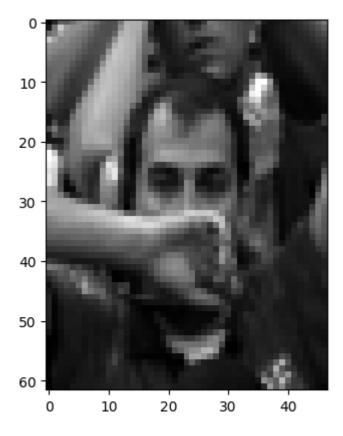










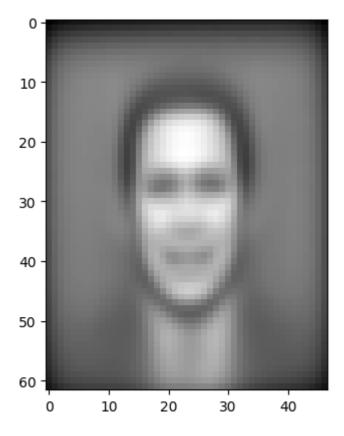


```
In [ ]: display(Latex(r"\newpage"))
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## \newpage

```
In []: #1.b
    average = X.mean(axis = 0)
    print(average)
    for i in range(X[0].size):
        X[i]-=average
    matplotlib.pyplot.imshow(average.reshape((62,47)), cmap=matplotlib.pyplot.cm.gray )
    matplotlib.pyplot.savefig(f'files/1_b=average.png')
    matplotlib.pyplot.show()
```

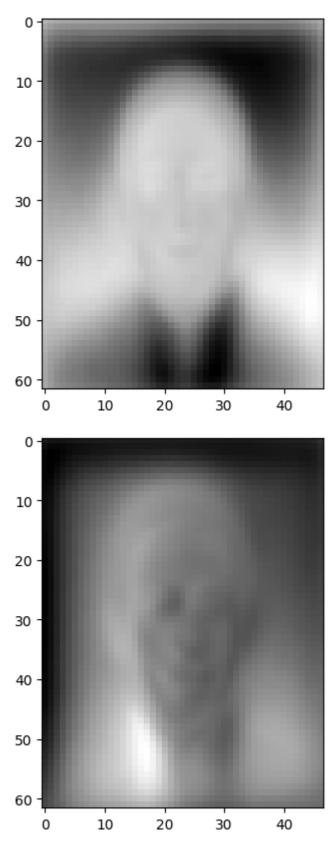
[0.13771963 0.15683803 0.17031944 ... 0.2221487 0.20515166 0.18089974]

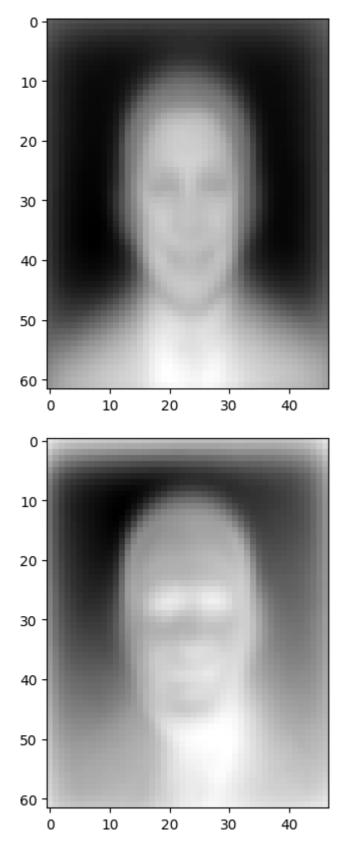


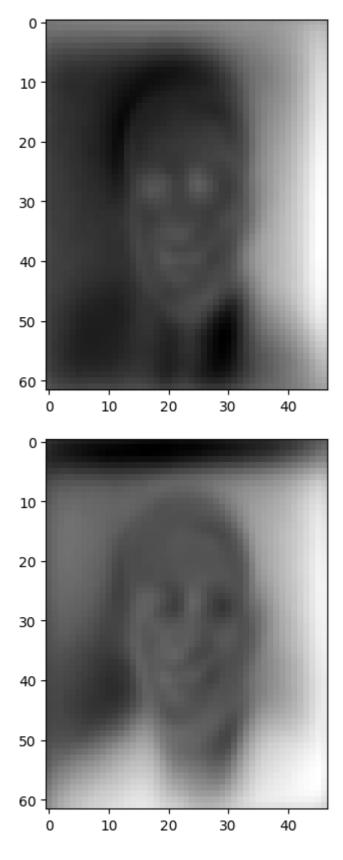
```
In [ ]: display(Latex(r"\newpage"))
```

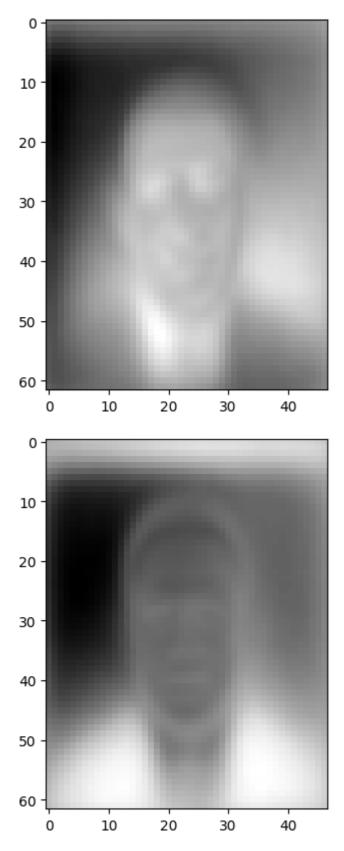
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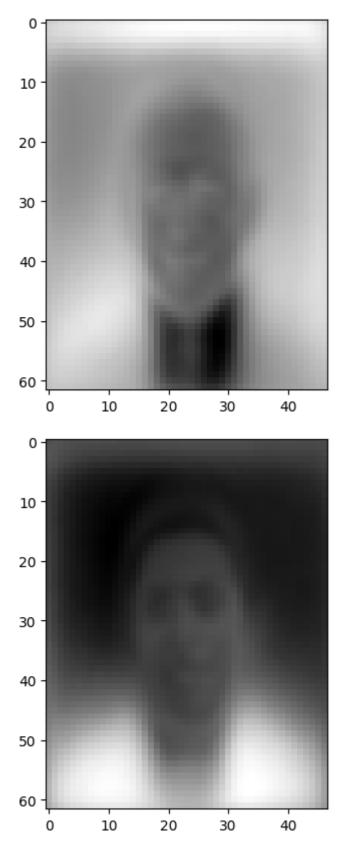
```
In [ ]: #1.c
        eig_vectors, eig_values,_ = np.linalg.svd(X.T@X)
In [ ]: #1.c
        def projectTopKEigenVectors(X, k, eig_values, eig_vectors):
            idx = eig_values.argsort()[::-1]
            eig_values = eig_values[idx]
            eig_vectors = eig_vectors[:,idx]
            k_eig_vectors = np.zeros(eig_vectors.shape)
            k_eig_vectors[:,:k] = eig_vectors[:,:k]
            X k = X @ k eig vectors
            X_recon = X_k @ k_eig_vectors.transpose()
            for i in range(20):
                matplotlib.pyplot.imshow(X_recon[i].reshape((62,47)), cmap=matplotlib.pyplot
                matplotlib.pyplot.savefig(f'files/1_c_top20_nr.{i+1}_k={k}.png')
                matplotlib.pyplot.show()
        projectTopKEigenVectors(X, 10, eig_values, eig_vectors)
        projectTopKEigenVectors(X, 100, eig_values, eig_vectors)
        projectTopKEigenVectors(X, 1000, eig_values, eig_vectors)
```

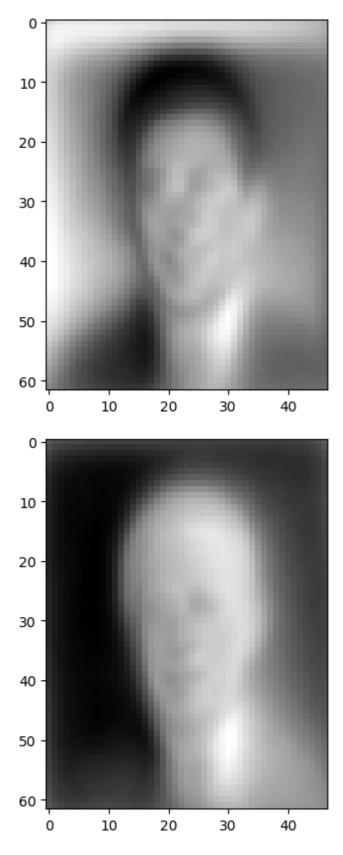


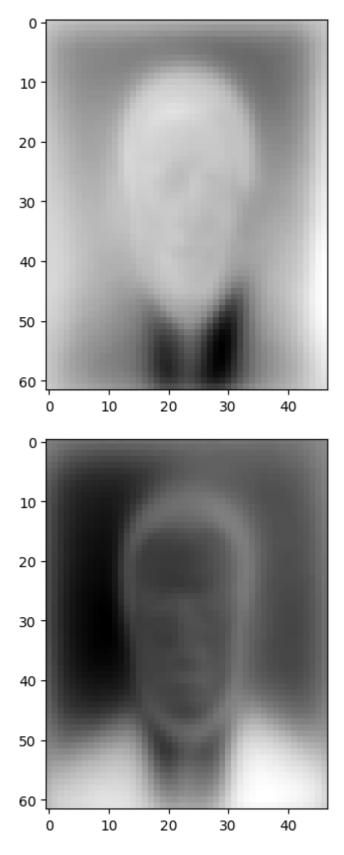


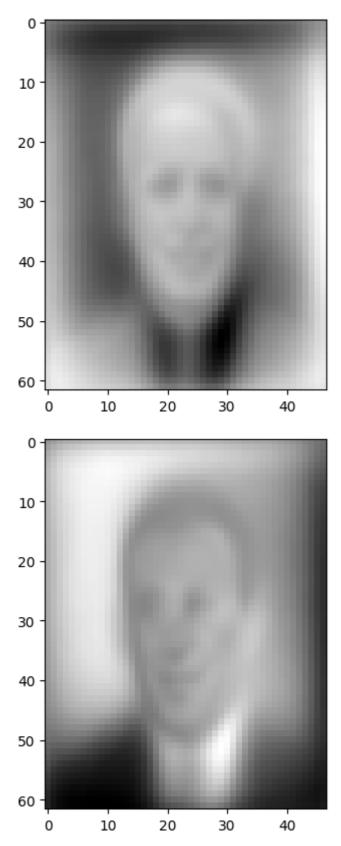


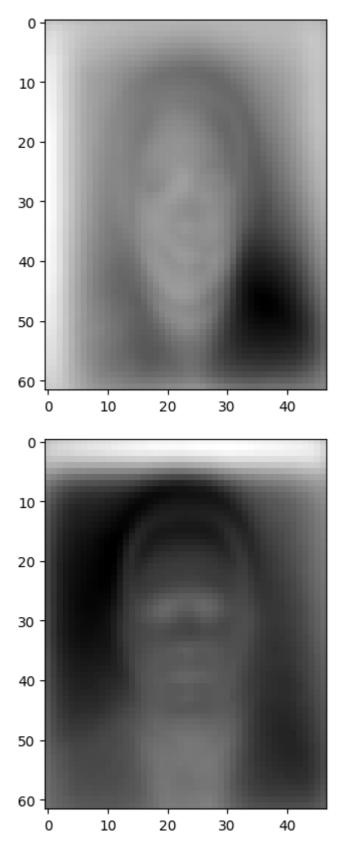


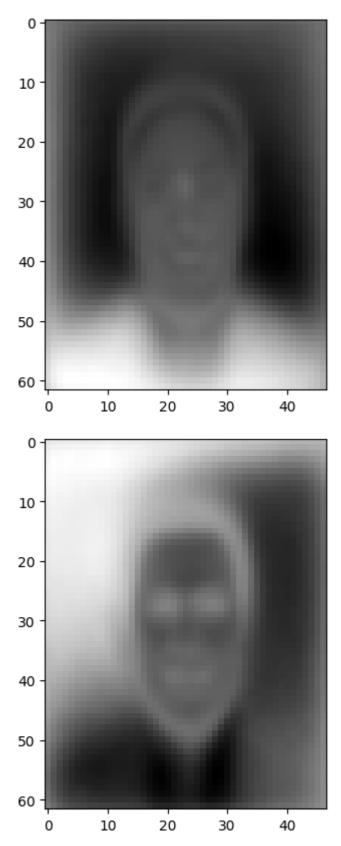


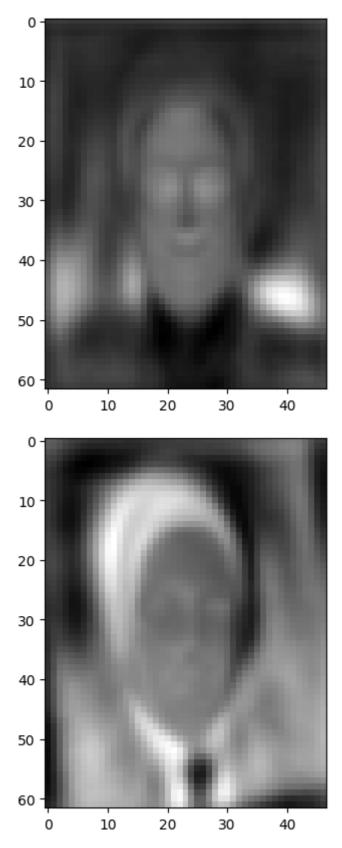


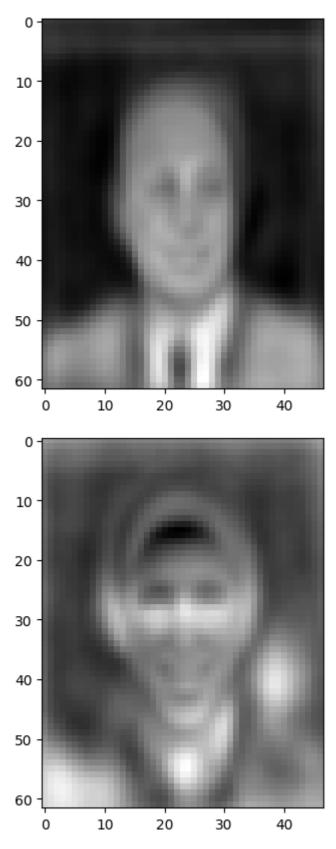


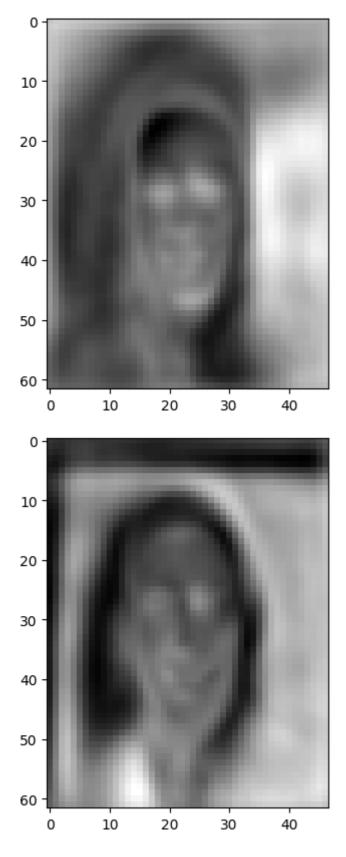


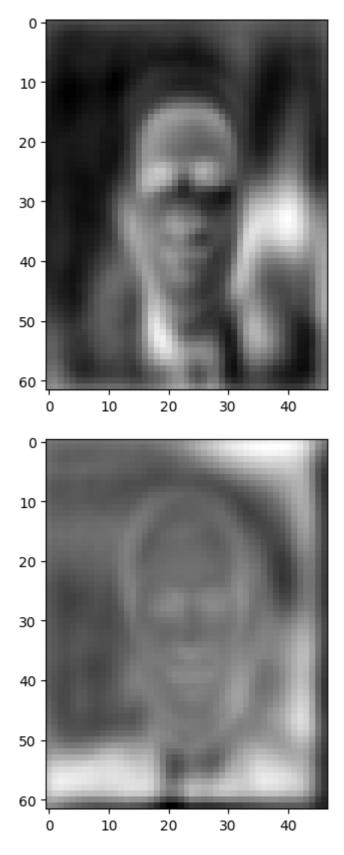


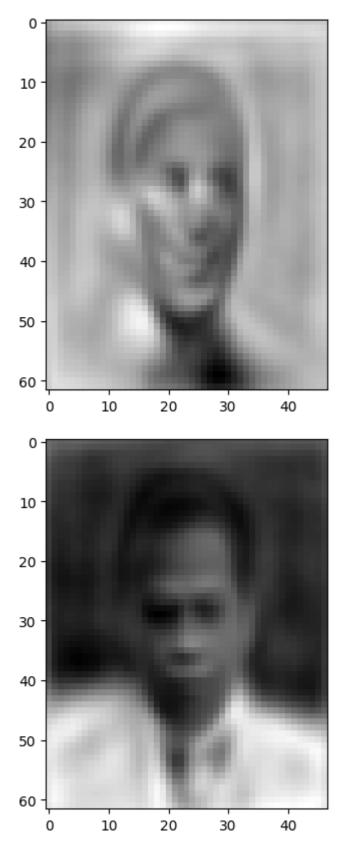


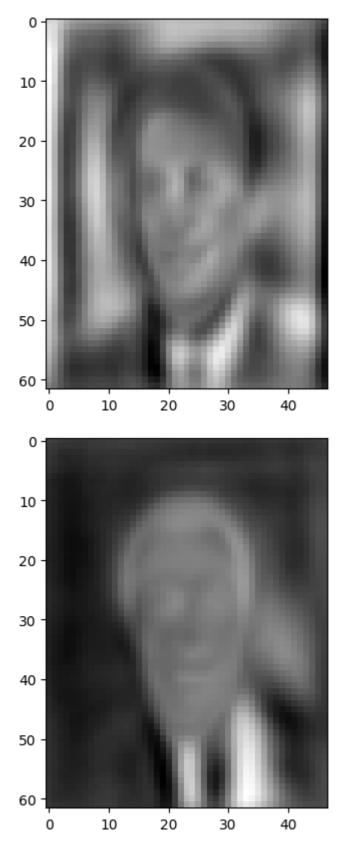


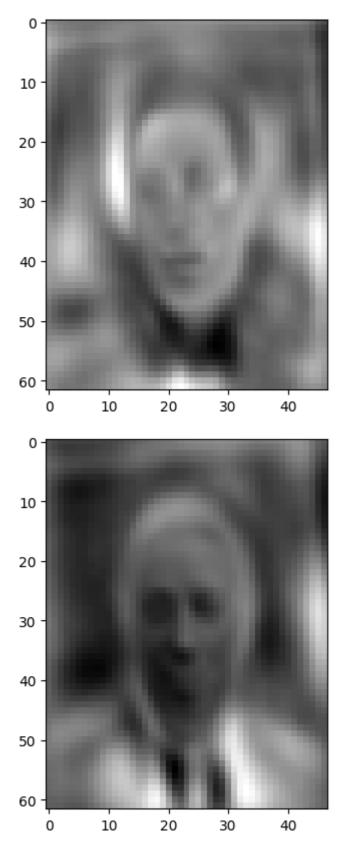


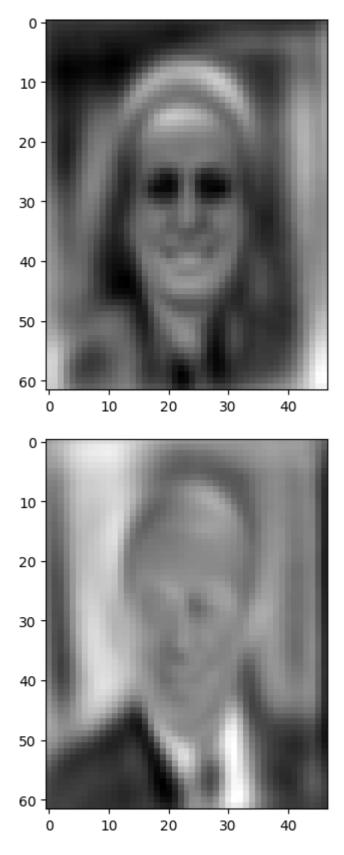


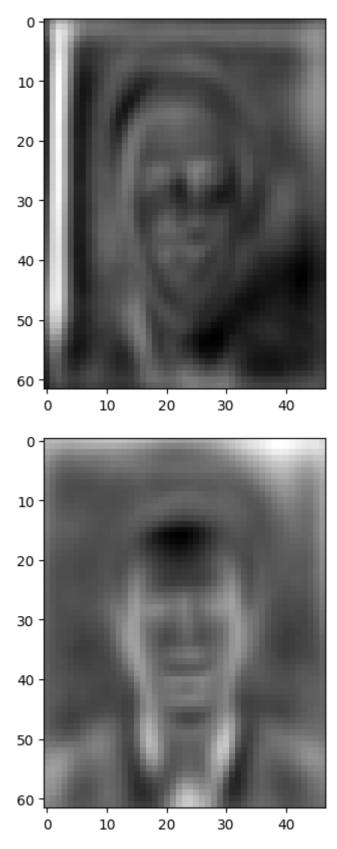


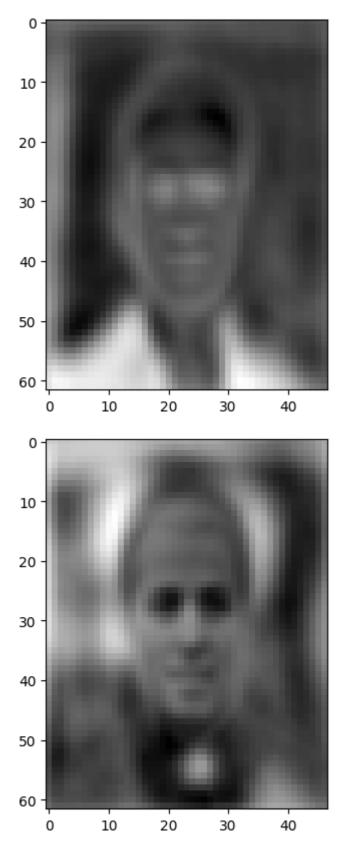


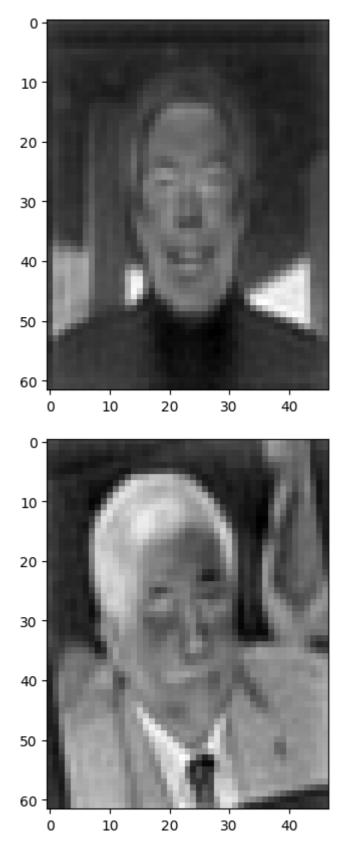


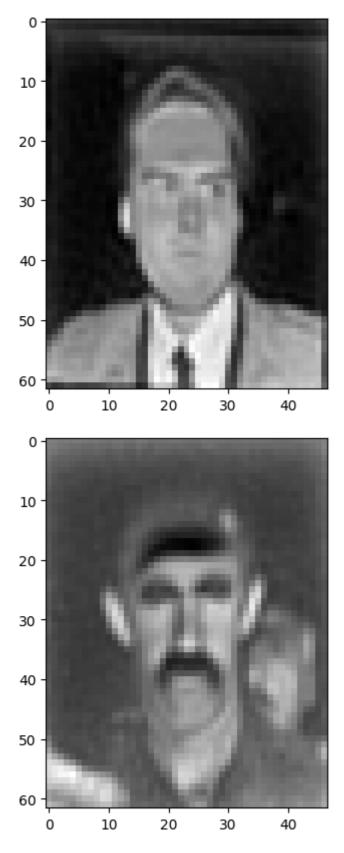


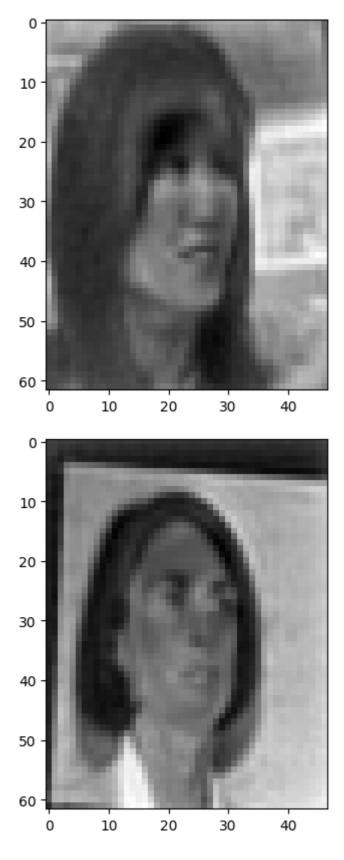


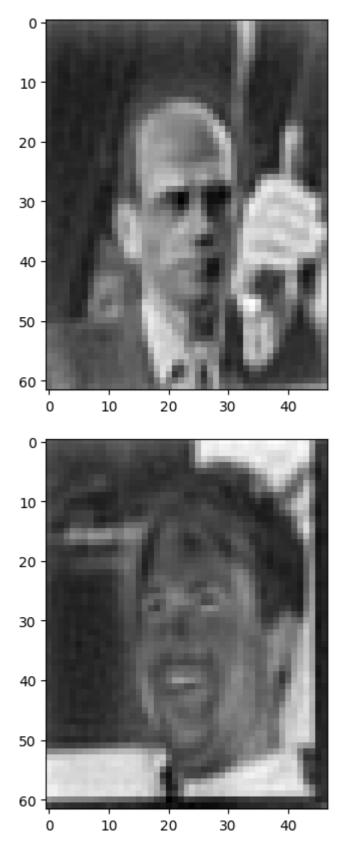


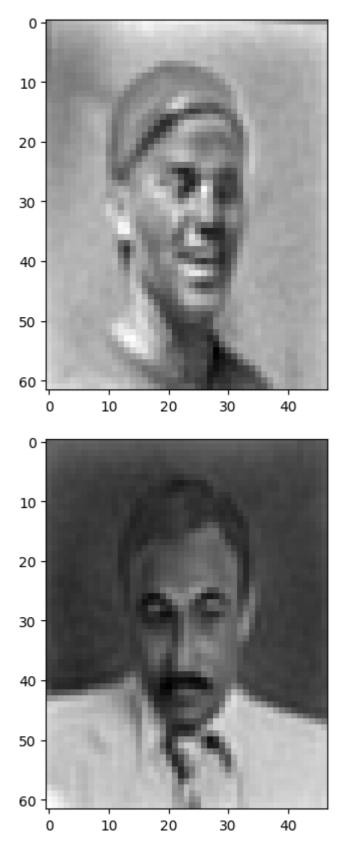


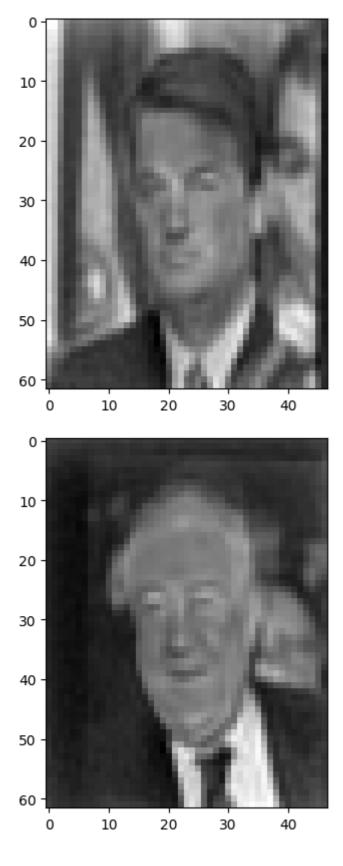


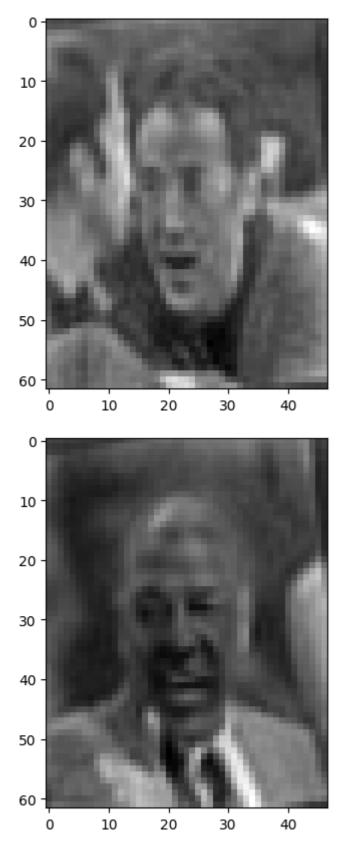


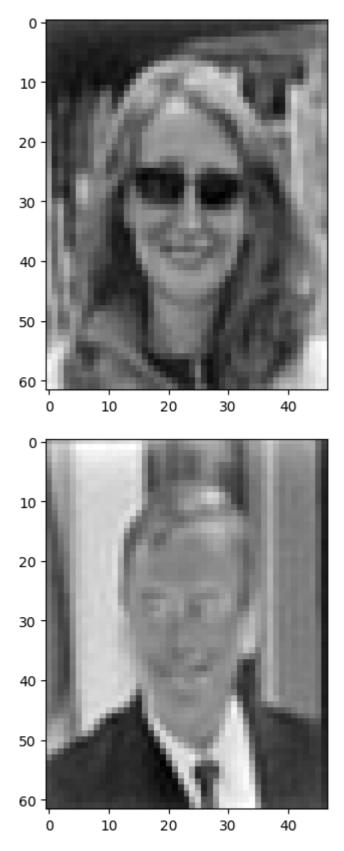


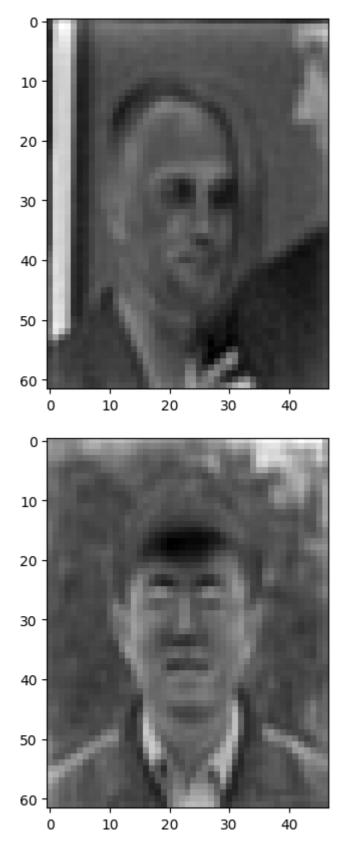


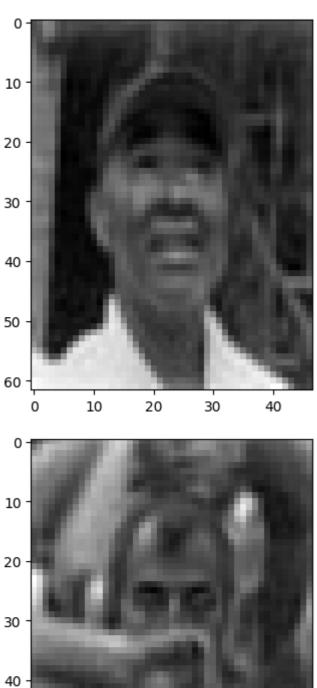












In [ ]: display(Latex(r"\newpage"))

30

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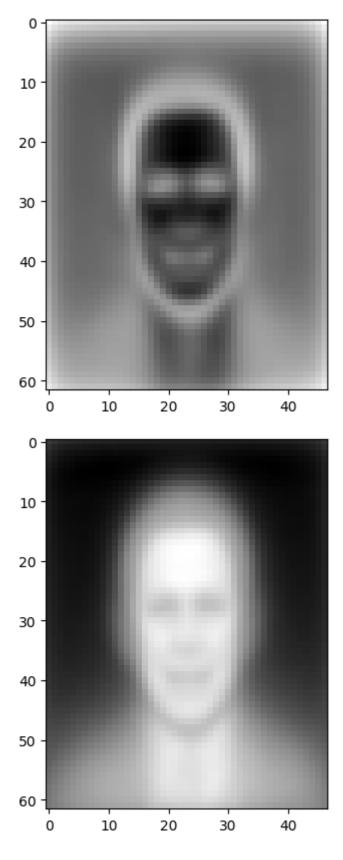
0

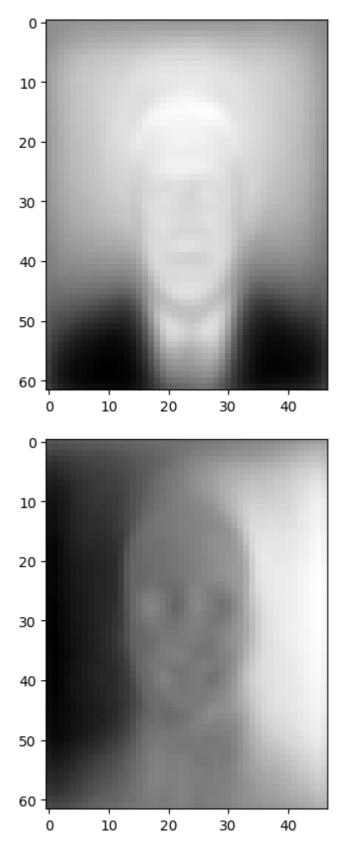
10

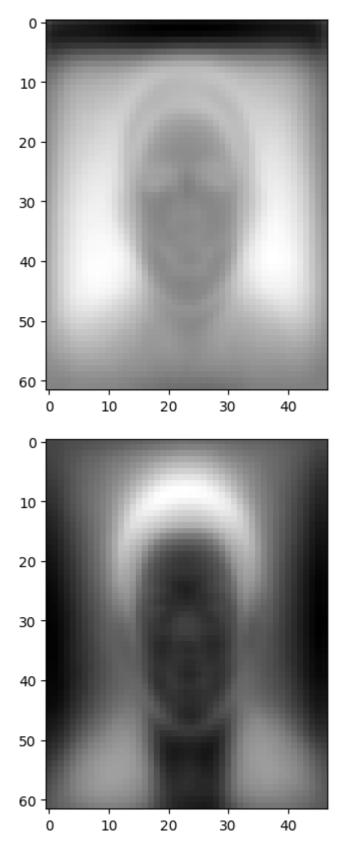
20

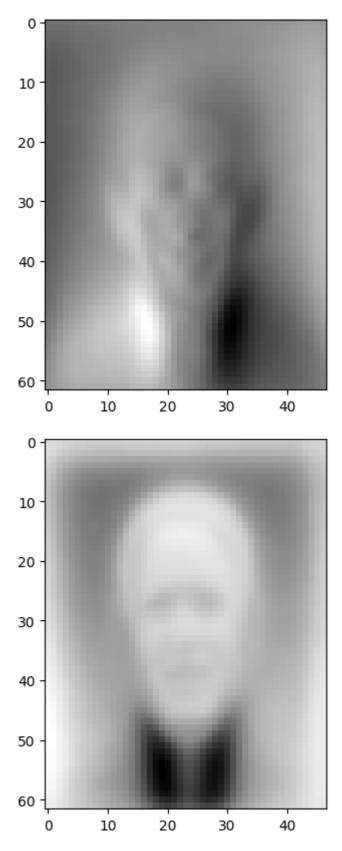
50

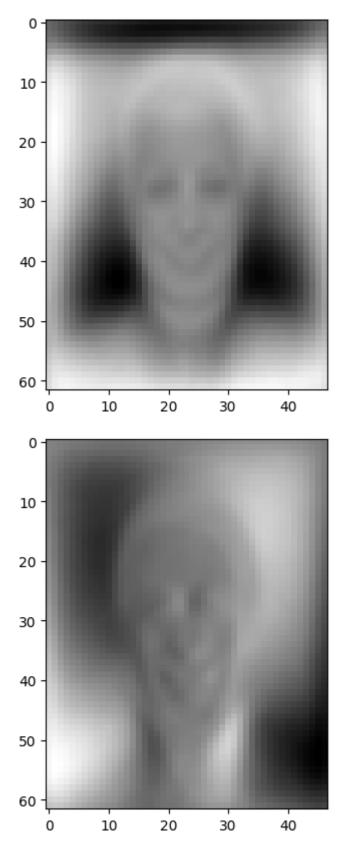
60

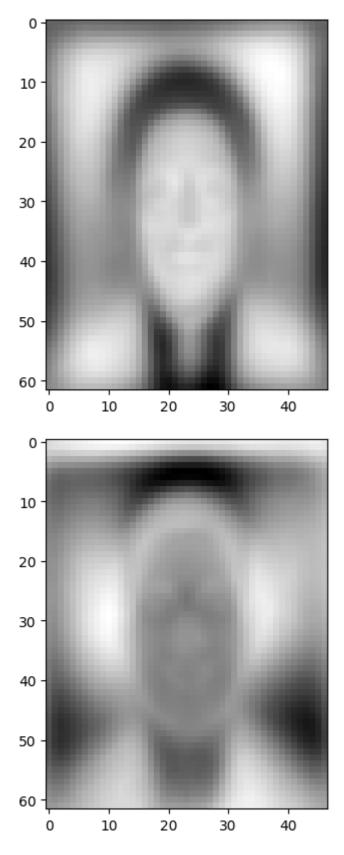


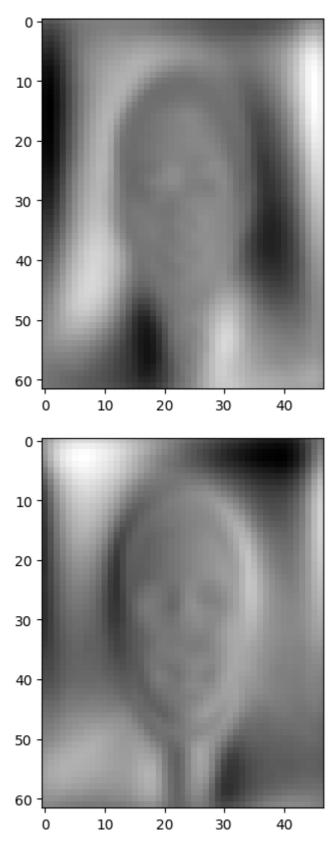


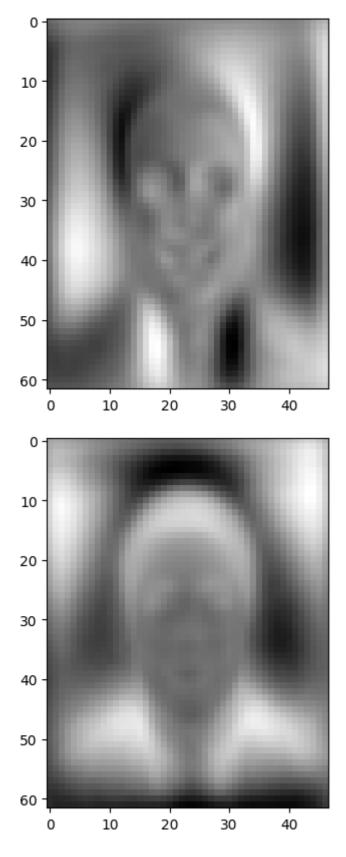


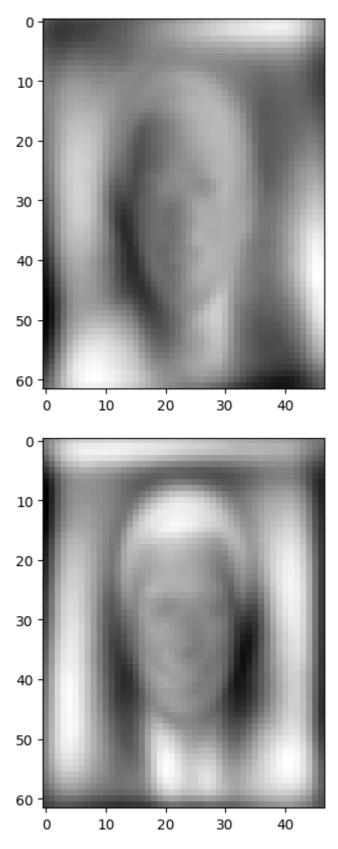


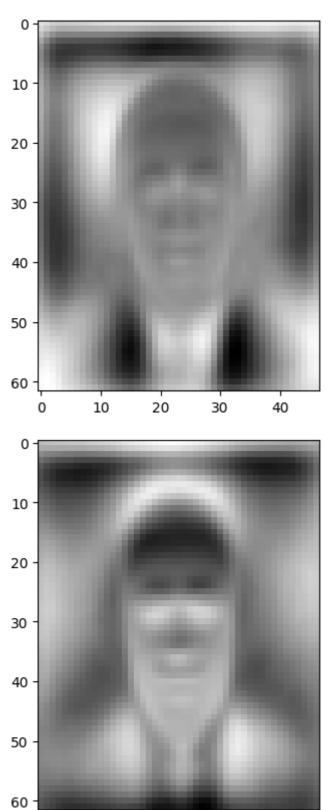












```
In [ ]: display(Latex(r"\newpage"))
```

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0

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20

```
In []: #1.e

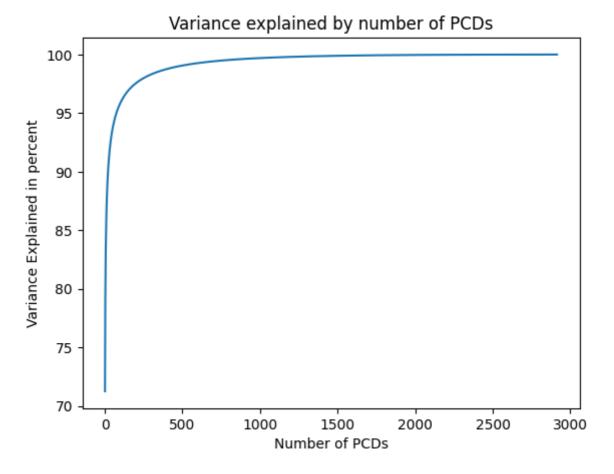
explained_variances = []
for i in range(len(eig_values)):
        explained_variances.append(eig_values[i] / np.sum(eig_values)*100)
        variance_explained_cum = np.cumsum(explained_variances)
```

```
k = 0
PCDs_needed=[]
for i in range(len(explained_variances)):
    k+=explained_variances[i]
    PCDs_needed.append(explained_variances[i])
    if k>95:
        break

print(f"One can see that we need {len(PCDs_needed)} PCDs to explain 95% of the varimatplotlib.pyplot.plot(np.arange(1, X.shape[1] + 1, 1), variance_explained_cum)
matplotlib.pyplot.ylabel('Variance Explained in percent')
matplotlib.pyplot.xlabel('Number of PCDs')
matplotlib.pyplot.title('Variance explained by number of PCDs')
```

One can see that we need 75 PCDs to explain 95% of the variance.

Out[]: Text(0.5, 1.0, 'Variance explained by number of PCDs')



```
In [ ]: display(Latex(r"\newpage"))
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```
In []: #1.f
    #Load X again since our previous X was centered
X = dataset['data']

X_train = X[:int(X.shape[0]*0.8)]
X_test = X[int(X.shape[0]*0.8):]

eig_vectors, eig_values, _ = np.linalg.svd(X_train.T@X_train)

idx = eig_values.argsort()[::-1]
eig_values = eig_values[idx]
eig_vectors = eig_vectors[:, idx]
```

```
training_loss = []
test_loss = []
number_of_PCDs = [10, 20, 50, 100, 500, 1000, 2914]

for k in number_of_PCDs:
    k_eig_vectors = np.zeros(eig_vectors.shape)
    k_eig_vectors[:,:k] = eig_vectors[:,:k]

X_train_reconstruction = X_train @ k_eig_vectors @k_eig_vectors.T
    training_loss.append(1/(X_train.shape[0]*X_train.shape[1])*np.linalg.norm(X_train.shape[0]*X_test_reconstruction = X_test @ k_eig_vectors @k_eig_vectors.T
    test_loss.append(1/(X_test.shape[0]*X_test.shape[1])*np.linalg.norm(X_test_reconstruction = X_test @ k_eig_vectors @k_eig_vectors.T
    test_loss.append(1/(X_test.shape[0]*X_test.shape[1])*np.linalg.norm(X_test_reconstruction = X_test @ k_eig_vectors @k_eig_vectors.T
```

For 10 number of PCDs, the training loss was: 0.024876154512220056, and the test 1 oss was 0.025062690624474873

For 20 number of PCDs, the training loss was: 0.01832719678080922, and the test loss was 0.018420726054348077

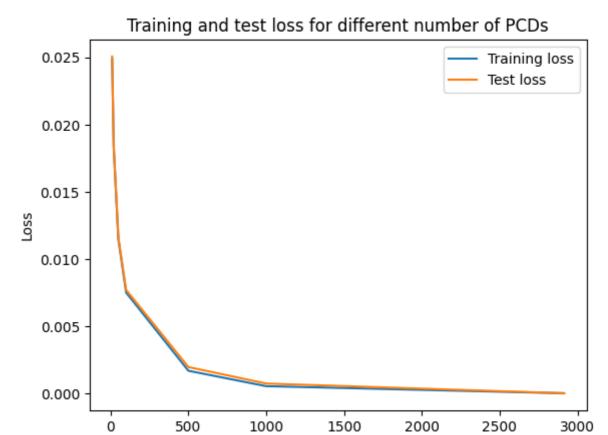
For 50 number of PCDs, the training loss was: 0.01145844974748309, and the test loss was 0.011592239534264808

For 100 number of PCDs, the training loss was: 0.00749010035300871, and the test 1 oss was 0.007688371896088376

For 500 number of PCDs, the training loss was: 0.0016752821280762095, and the test loss was 0.001950320561979342

For 1000 number of PCDs, the training loss was: 0.0005270785648694966, and the test loss was 0.0007230311720999202

For 2914 number of PCDs, the training loss was: 2.313802221591989e-16, and the test loss was 2.8704234588938264e-16



Number of PCDs

I worked with: · Jens Mristoffesen · Dherick Derahum an · Olan Nomeland · Sonhet Beheva entirely in my oun words and that I have not lacked at another student's solutions. 1 have given credit to all external sources I consulted

Building the heap: O(K) where k is the size of the heap. Remaining n-k points take O(losk) time. tinding the majority label of the h closest neigh bows take OCK) 1 me. Finding in earlidian distances take nO(d) time. TOTAL: O(h) + (n-h) O ((as h) + O(h) x n o(a) = o(nd) + o(h) + o(n loxh)

balls in botes, the number of monomials is (d+P) and this
to the dimension the point lives in. d is now (dtp). I clifp

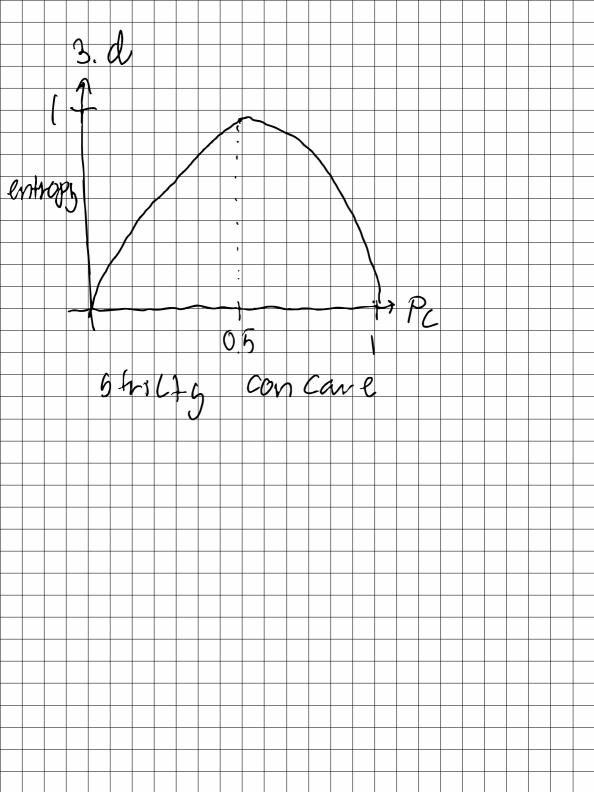
(dtp-p)!p! d!p Nen partime:

(D: left and right = 2 D: all sides and all corners Cells and 2 corners check each one of these cells so time complexity is O(2d+2d)

I will be a surprised since I then with 100% certainty what the outcome hould be.

Max suprised, my micr belief was that there was a 0% white ball.

when PB is either 0 or 15 when the entropy 15 minimized. Hy(0) = -01040 Maximized of PB=05 HB(0.5) = -0.5 las 0.5 - d. 5 los 0.5



P=P(Y=111X, v=1)P(X, v=1) \*P(Y=1) xj, v=0) P(xj, v=0) = (1) P(Xj,v=1) + 92 P(Xj,v=0) = 19, + (1-1) 92 where 2 is the probability that Show that H(4) - H(Y/X), v) is always positive if 9,792 > M(P(Y=1)) - Z P(X) = 1) H6(P(Y=1/3), (E)) -> +6() 9, +((-x)9) > ) - H5(9)+((-x)489)  $(\lambda q_1 + (1 + \lambda) q_2 (0) \lambda q_1 + (1 + \lambda) q_2)$ (1-20, +(1-1) 42) 105 (1-24, +(1-1)92)

1. (-9, 10, 9, - (1-9, ) 10, (1-9 + (1-x). (-42/03/92-01-9  $(a_1(1-q_1))$ -9 sees that as Hy is strictly concane, multiply in with lamda on the outside OF Hb function will read to a smaller value. t do not have abetter explanation;

-age: . 3 , M

not being piched. Lonest value of this function is at n=25 since it monatonically in Greating. M=25: (25-1)25 = 0.3604 + 125 limit: n-In n-in (1- n) = 1 im 0 / n(1-11es in 20.36

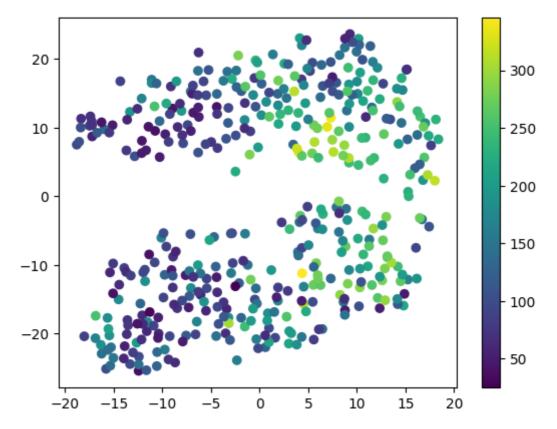
More 4ees - more comparation Plot the 1055 at different nr. OF Hees in an increasing manner and pich the number of frees when the loss levels sufficiently out towards its asymptote.

121 M3

4

```
In [ ]: from IPython.display import Latex
        import numpy as np
        import matplotlib.pyplot as plt
In [ ]: #Import dataset
        import sklearn
        from sklearn import datasets
        diabetes = sklearn.datasets.load_diabetes()
In [ ]: display(Latex(r"\newpage"))
        \newpage
In [ ]: #4.a
        from sklearn.manifold import TSNE
        x = diabetes["data"]
        y = diabetes["target"]
        d = 2
        tsne = TSNE(d)
        tsne_result = tsne.fit_transform(x)
        points = plt.scatter(tsne_result[:, 0], tsne_result[:,1], c = y, cmap = 'viridis')
        plt.colorbar(points)
        c:\Users\elias\AppData\Local\Programs\Python\Python310\lib\site-packages\sklearn\m
        anifold\_t_sne.py:800: FutureWarning: The default initialization in TSNE will chan
        ge from 'random' to 'pca' in 1.2.
          warnings.warn(
        c:\Users\elias\AppData\Local\Programs\Python\Python310\lib\site-packages\sklearn\m
        anifold\_t_sne.py:810: FutureWarning: The default learning rate in TSNE will chang
        e from 200.0 to 'auto' in 1.2.
          warnings.warn(
```

Out[ ]: <matplotlib.colorbar.Colorbar at 0x1cff409fca0>

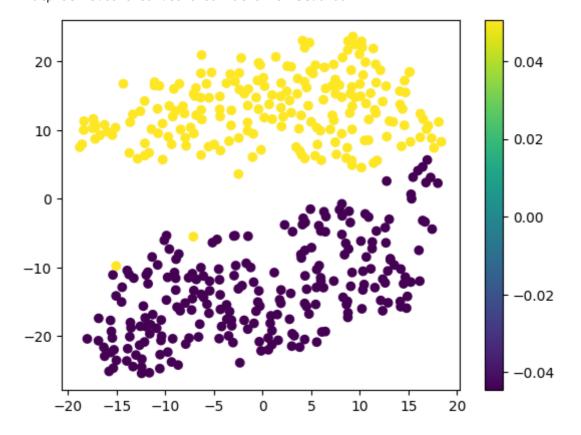


In [ ]: display(Latex(r"\newpage"))

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4.b The feature is sex.

Out[ ]: <matplotlib.colorbar.Colorbar at 0x1cff3ed0460>



```
In [ ]: display(Latex(r"\newpage"))
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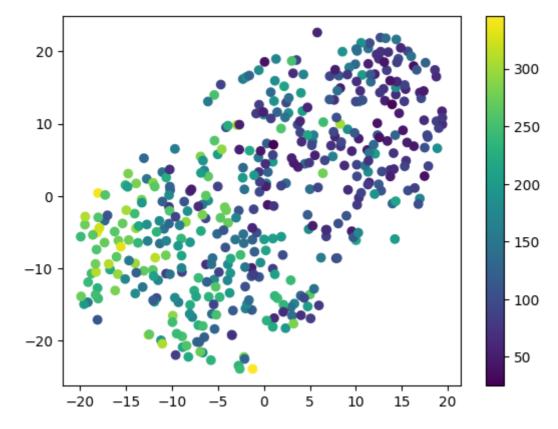
```
In []: #4.c
    new_x = np.delete(diabetes["data"], axis = 1, obj = 1)
    tsne = TSNE(d)

new_result = tsne.fit_transform(new_x)

points = plt.scatter(new_result[:, 0], new_result[:,1], c = y, cmap = 'viridis')
    plt.colorbar(points)

c:\Users\elias\AppData\Local\Programs\Python\Python310\lib\site-packages\sklearn\m
    anifold\_t_sne.py:800: FutureWarning: The default initialization in TSNE will chan
    ge from 'random' to 'pca' in 1.2.
    warnings.warn(
    c:\Users\elias\AppData\Local\Programs\Python\Python310\lib\site-packages\sklearn\m
    anifold\_t_sne.py:810: FutureWarning: The default learning rate in TSNE will chang
    e from 200.0 to 'auto' in 1.2.
    warnings.warn(
```

Out[ ]: <matplotlib.colorbar.Colorbar at 0x1cff3f6ffd0>



We do not see any two clear clusters anymore since tsne does not differentiate on sex. In other words, most of the data points got a lot of their variance from sex meaning females and males are quite similar besides being of different genders. The fact that sex was included ended up with "pulling" the data apart and forming two clusters.

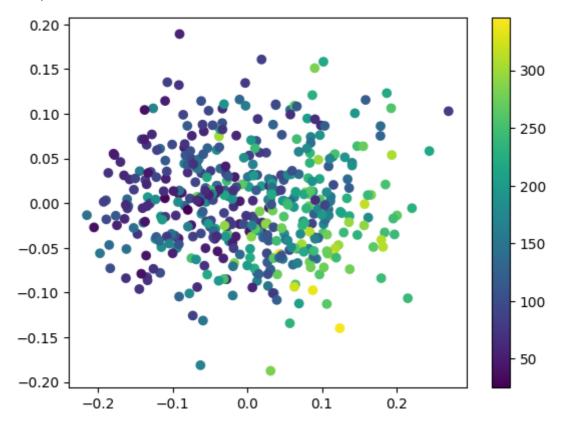
If the change did not occur and we did still see two clear clusters, it would mean that there would be another feature which was very binary in its distribution. If age was split in above 50 or below 50 this would also form two clusters.

```
In [ ]: display(Latex(r"\newpage"))
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```
In []: #4.d
    from sklearn.decomposition import PCA
    pca = PCA(d)
    pca_result = pca.fit_transform(x)
    points = plt.scatter(pca_result[:, 0], pca_result[:,1], c = y, cmap = "viridis")
    plt.colorbar(points)
```

Out[]: <matplotlib.colorbar.Colorbar at 0x1cff42b4220>



```
In [ ]: display(Latex(r"\newpage"))
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In [ ]: #4.e
        def MSE(y_hat, y_true):
             return (1/y_hat.shape[0])*np.sum((y_hat - y_true)**2)
        X_{train} = x[:100]
        y_{train} = y[:100]
        X_{\text{test}} = x[100:]
        y_{test} = y[100:]
        X_train_mtx = np.hstack([X_train, np.ones((100,1))])
        X_test_mtx = np.hstack([X_test, np.ones((342, 1))])
        w_ols = np.linalg.inv(X_train_mtx.T @ X_train_mtx) @ X_train_mtx.T @ y_train
        y_hat = X_test_mtx@w_ols
        test_mse = MSE(y_hat, y_test)
        print(f"The test MSE is: {test_mse}")
        def c_index(y_hat, y_test):
             nr conc = 0
             nr_disc = 0
```

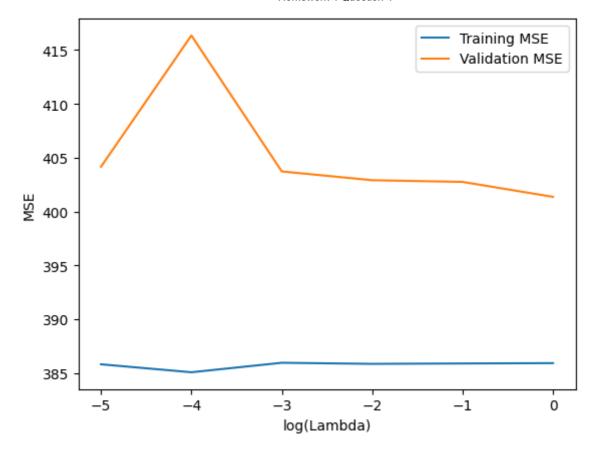
The test MSE is: 3430.9233826005243 The c index is: 0.7452930850514576

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In [ ]: #4.f
        from sklearn.linear_model import Ridge
        def cross_validation(X, y, k, model, loss_calculator):
            n = X.shape[0]
            idx = np.random.permutation(n)
            X_{shuffled} = X[idx]
            y_shuffled = y[idx]
            size = n // k
            validation_loss = np.zeros((n,))
            training_loss = np.zeros((n,))
            for i in range(k):
                start = i*size
                end = (i+1)*size
                X test = X shuffled[start:end]
                y_test = y_shuffled[start:end]
                X_train = np.vstack([X_shuffled[:start], X_shuffled[end:]])
                y_train = np.hstack([y_shuffled[:start], y_shuffled[end:]])
                model.fit(X_train, y_train)
                training_loss[i] = loss_calculator(model.predict(X_train), y_train)
                validation_loss[i] = loss_calculator(model.predict(X_test), y_test)
            return np.mean(validation_loss), np.mean(training_loss)
        lambdas = [10**-5, 10**-4, 10**-3, 10**-2, 10**-1, 1]
        validation MSE = []
        training_MSE = []
        for 1 in lambdas:
```

```
validation_MSE_current, training_MSE_current = cross_validation(X_train, y_trai
    validation_MSE.append(validation_MSE_current)
    training MSE.append(training MSE current)
    print(f"Lambda={1} has validation loss={validation_MSE_current} and training log
   print("")
plt.plot(np.log10(lambdas), training_MSE, label='Training MSE')
plt.plot(np.log10(lambdas), validation MSE, label='Validation MSE')
plt.legend()
plt.xlabel('log(Lambda)')
plt.ylabel('MSE')
best_lambda = lambdas[np.argmin(validation_MSE)]
ridge_best_lambda = Ridge(alpha=best_lambda).fit(X_train,y_train)
ridge y hat = ridge best lambda.predict(X test)
ridge_mse = MSE(ridge_y_hat, y_test)
print(f"The best lambda was {best_lambda}.\nThis lambda gave MSE with ridge = {ridg
Lambda=1e-05 has validation loss=404.15799243503966 and training loss=385.80102276
90261
Lambda=0.0001 has validation loss=416.3534904067575 and training loss=385.06213726
177435
Lambda=0.001 has validation loss=403.72113028383114 and training loss=385.94238469
552073
Lambda=0.01 has validation loss=402.9057175061709 and training loss=385.8414729654
401
Lambda=0.1 has validation loss=402.7489796064022 and training loss=385.87803508971
024
Lambda=1 has validation loss=401.3585709192019 and training loss=385.9097279767526
The best lambda was 1.
This lambda gave MSE with ridge = 5039.062537574326.
```



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