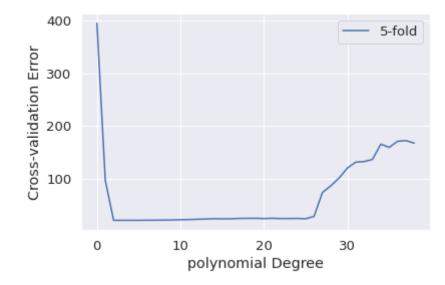
```
In [ ]: |data = np.array([[0,1],[1,1],[2,1],[2,3],[3,2],[3,3],[4,5]])
        # standardize the data
        from sklearn.preprocessing import StandardScaler
        from sklearn.decomposition import PCA
        scaler = StandardScaler()
        data = scaler.fit_transform(data)
        print('standardized data: \n',data)
        pca = PCA(n components=2)
        pca_data = pca.fit_transform(data)
        print('The two principal components in sorted order:\n', pca.components_)
        recon_data = scaler.inverse_transform(pca_data)
        print('the new transformed dataset using the first principal component\n',\
              recon data)
        standardized data:
         [[-1.720618
                       -0.92827912
         [-0.91766294 -0.92827912]
         [-0.11470787 - 0.92827912]
         [-0.11470787 \quad 0.51571062]
         [ 0.6882472 -0.20628425]
         [ 0.6882472
                       0.51571062]
         [ 1.49120227 1.95970037]]
        The two principal components in sorted order:
         [[ 0.70710678  0.70710678]
         [ 0.70710678 - 0.70710678]]
        the new transformed dataset using the first principal component
         [[-0.18984265 1.50971404]
         [ 0.51726413 2.29611156]
         [ 1.22437091  3.08250907]
         [ 2.49599243    1.66829551]
         [ 2.56728845  3.16179981]
         [ 3.20309921  2.45469303]
         [ 5.18182751    1.82687698]]
In [ ]: | data = np.array([[0,1],[1,1],[2,1],[2,3],[3,2],[3,3],[4,5]])
        print(' do not standardize the original data')
        pca = PCA(n components=2)
        pca_data = pca.fit_transform(data)
        print('The two principal components in sorted order:\n', pca.components )
        recon data = scaler.inverse transform(pca data)
        print('the new transformed dataset using the first principal component\n',\
              recon_data)
         do not standardize the original data
        The two principal components in sorted order:
         [[ 0.65908697  0.75206673]
         [ 0.75206673 -0.65908697]]
        the new transformed dataset using the first principal component
         [[-8.20287693e-01 1.22729401e+00]
         [ 5.39026785e-04 2.26894507e+00]
         [ 8.21365746e-01 3.31059613e+00]
         [ 2.69461309e+00 1.48485747e+00]
         [ 2.57881614e+00 3.43937786e+00]
         [ 3.51543981e+00 2.52650853e+00]
         [ 6.20951388e+00 1.74242094e+00]]
```

Principal Component Analysis is sensitive to standardizing, and usually we need to do mean centering before PCA. Because by doing Singular Value Decomposisiton, we try to find vectors in linear subspace that can minimize the distortion (which is calculated using L2 norm) and maximize the variance.

```
In [ ]: file path = '/content/gdrive/MyDrive/Colab Notebooks/542hw/poly data.csv'
         import pandas as pd
In [ ]: | df = pd.read_csv(file_path, header=None, sep=' ')
         df.head()
Out[17]:
                           1
          0 0.870951
                     8.125873
          1 0.838599
                     4.152377
          2 -0.044278 24.007025
          3 2.149839 -0.523928
          4 1.265048 -6.149399
In [ ]: from sklearn.model selection import KFold
         import copy
         from sklearn.linear model import LinearRegression
         def polynomial regression(k,p,x,y):
           new x = copy.deepcopy(x)
           for i in range(2, p+1):
             new x = np.hstack((new x, x**i))
           cv fold error = 0
           folds = fold.split(x)
           for t, v in folds:
             X train, Y train, X val, Y val = new x[t], y[t], new x[v], y[v]
             reg = LinearRegression()
             reg.fit(X train, Y train)
             y pred = reg.predict(X val)
             cv fold error += mean squared error(Y val, y pred)
           return cv fold error/5
         x = np.array([df[0]]).T
         y = np.array(df[1])
         cv error = []
         for p in range(1,40):
           cv error.append(polynomial regression(k,p,x,y))
```

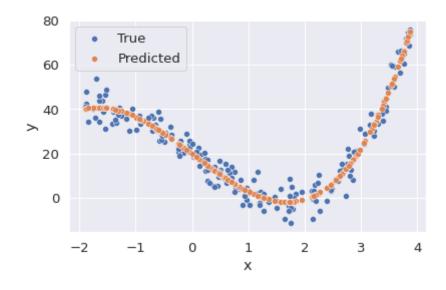
```
In [ ]: print('The value of k I use is 5')
    print('polynomial degree = %d fit the data the best' % (cv_error.index(min(
    x_axis = [i for i in range(len(cv_error))]
    sns.lineplot(x_axis, cv_error, label = '5-fold')
    plt.ylabel('Cross-validation Error')
    plt.xlabel("polynomial Degree")
    plt.legend()
    plt.tight_layout()
    plt.show()
```

The value of k I use is 5 polynomial degree = 3 fit the data the best



```
In [ ]: # best model, regress entire dataset
        x = np.array([df[0]]).T
        y = np.array(df[1])
        new_x = np.hstack((np.ones((x.shape[0], 1)), x))
        p = 3
        for i in range(2, p+1):
          new_x = np.hstack((new_x, x**i))
        beta = calculate beta(new x, y)
        y pred = new_x @ beta_
        print('Tthe polynomial coefficients are', beta_)
        print('Predicted y = %.2f + %.2f x + %.2f x^2 + %.2f x^3'%(beta [0], beta [
        sns.scatterplot(x.T[0], y, label = 'True')
        sns.scatterplot(x.T[0], y pred, label = 'Predicted')
        plt.ylabel('y')
        plt.xlabel("x")
        plt.legend()
        plt.tight layout()
        plt.show()
```

Tthe polynomial coefficients are [19.79510458 - 19.03450815 - 0.10790684 2.24897906] Predicted y = $19.80 + -19.03 \times + -0.11 \times ^2 + 2.25 \times ^3$



Problem 3

(a)

$$P(X = x | Y = +1) = \frac{1}{\sqrt{2\pi}} e^{-\frac{(x-5)^2}{2}} = \frac{1}{\sqrt{2\pi}} e^{-\frac{(x-5y)^2}{2}}$$

$$P(X = x | Y = -1) = \frac{1}{\sqrt{2\pi}} e^{-\frac{(x+5)^2}{2}} = \frac{1}{\sqrt{2\pi}} e^{-\frac{(x-5y)^2}{2}}$$

Thus

$$P(X = x, Y = y) = P(X = x, Y = y | Y = +1)P(Y = +1)$$

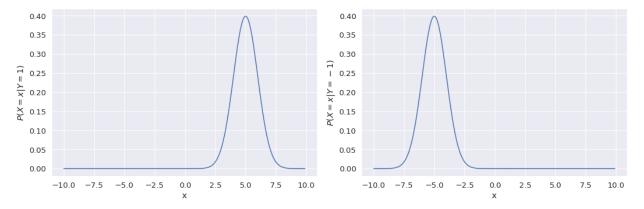
$$+ P(X = x, Y = y | Y = -1)P(Y = -1)$$

$$= \frac{1}{\sqrt{2\pi}} e^{-\frac{(x-5y)^2}{2}} \frac{1}{2} + \frac{1}{\sqrt{2\pi}} e^{-\frac{(x-5y)^2}{2}} \frac{1}{2}$$

$$= \frac{1}{2\sqrt{2\pi}} e^{-\frac{(x-5y)^2}{2}}$$

```
In [ ]:
    def prob3b(x,y):
        coef = 1/np.sqrt(2*np.pi)
        expo = - (x-5*y)**2/2
        res = coef * np.exp(expo)
        return res

        x_axis = np.arange(-10,10,0.1)
        y_pos = [prob3b(x,1) for x in x_axis]
        y_neg = [prob3b(x,-1) for x in x_axis]
        fig, ((ax1, ax2)) = plt.subplots(1,2,figsize = (15,5))
        sns.lineplot(x_axis, y_pos, ax = ax1)
        ax1.set_ylabel('${P(X=x | Y = 1)}$'); ax1.set_xlabel("x")
        sns.lineplot(x_axis, y_neg, ax = ax2)
        ax2.set_ylabel("${P(X=x | Y = -1)}$"); ax2.set_xlabel("x")
        plt.tight_layout()
        plt.show()
```



(c)

$$h^*(x) = \begin{cases} 1, & x \ge 0 \\ -1, & x < 0 \end{cases}$$

$$P(X = x | Y = +1) = \frac{1}{\sqrt{2\pi}} e^{-\frac{(x-5)^2}{2}} \to \mathcal{N}(5, 1)$$

$$P(X = x | Y = -1) = \frac{1}{\sqrt{2\pi}} e^{-\frac{(x+5)^2}{2}} \to \mathcal{N}(-5, 1)$$

$$\begin{split} Pr(h^*(x) \neq y) &= \mathbb{E}[\mathbb{1}_{h^*(x) \neq y}] \\ &= \frac{1}{2} (Pr(x \geq 0, y = -1) + Pr(x < 0, y = 1)) \\ &= \frac{1}{2} ((1 - Pr(x + 5 < 5 | y = -1)) + Pr(x - 5 < -5 | y = 1)) \\ &= \frac{1}{2} (1 - \Phi(5) + \Phi(-5)) \\ &= 1 - \Phi(5) \end{split}$$

(e) $P(X = x | Y = +1) = \frac{1}{\sqrt{2\pi}} e^{-\frac{(x-5)^2}{2}}$ $P(X = x | Y = -1) = \frac{1}{\sqrt{2\pi}} e^{-\frac{(x+5)^2}{2}}$ $P(X = x, Y = y) = \frac{1}{2\sqrt{2\pi}} e^{-\frac{(x-5y)^2}{2}}$

Thus

$$P(X = x) = P(X = x | Y = +1)P(Y = +1) + P(X = x | Y = -1)P(Y = -1)$$

$$= \frac{1}{\sqrt{2\pi}} e^{-\frac{(x-5)^2}{2}} \frac{1}{2} + \frac{1}{\sqrt{2\pi}} e^{-\frac{(x+5)^2}{2}} \frac{1}{2}$$

$$= \frac{1}{2\sqrt{2\pi}} (e^{-\frac{(x-5)^2}{2}} + e^{-\frac{(x+5)^2}{2}})$$

Thus

$$P(Y = +1|X = x) = \frac{P(Y = +1, X = x)}{P(X = x)}$$

$$= \frac{\frac{1}{2\sqrt{2\pi}}e^{-\frac{(x-5)^2}{2}}}{\frac{1}{2\sqrt{2\pi}}(e^{-\frac{(x-5)^2}{2}} + e^{-\frac{(x+5)^2}{2}})}$$

$$= \frac{e^{-\frac{(x-5)^2}{2}}}{e^{-\frac{(x-5)^2}{2}} + e^{-\frac{(x+5)^2}{2}}} = \frac{1}{1 + e^{-\frac{(x+5)^2}{2}}} = \frac{1}{1 + e^{(-\frac{(x+5)^2}{2} + \frac{(x-5)^2}{2})}}$$

$$= \frac{1}{1 + e^{-10x}}$$

Therefore the distribution satisfies this assumption:

$$P(Y = +1|X = x) = \frac{1}{1 + e^{-\beta_0 - \beta_1 x}}$$

where

$$\beta_0 = 0, \beta_1 = 10$$

Example of 4 points in a 2D plane: if there are two clusters in total, and

cluster 0 consists of (\sqrt{t}, a) and $(\sqrt{t}, -a)$,

cluster 1 consists of $(-\sqrt{t}, a)$ and $(-\sqrt{t}, -a)$,

then the two centroids are $(\sqrt{t}, 0)$ and $(-\sqrt{t}, 0)$.

Thus OPT = $min_{c_1,\dots,c_k} \sum i = 1^n ||x_i - c(x_i)||_2^2 = \text{t*OPT for any t>1, any } a \in \mathcal{R}$

For n data points, p dimensions and k clusters,

consider data points
$$(\sqrt{t}, a, 0, \dots 0_p), (-\sqrt{t}, a, 0, \dots 0_p), (\sqrt{t}, 2a, 0, \dots 0_p), (-\sqrt{t}, 2a, 0, \dots 0_p)...$$

If k is 2n, then the centroids can be $(0, a, 0, \dots 0_p)$, $(0, 2a, 0, \dots 0_p)$... if k is smaller or larger then the clusters for above centroids merges or splits. Thus OPT = $min_{c_1,\dots,c_k}\sum i=1^n||x_i-c(x_i)||_2^2=t^*$ OPT for any t>1 still stands

```
In [ ]: from sklearn.datasets import fetch_lfw_people
faces = fetch_lfw_people(min_faces_per_person=60)
```

```
In [ ]: | # sklearn version issue, bypass import error of RandomizedPCA
        # according to https://stackoverflow.com/questions/54494785/sklearn-0-20-2-
        from sklearn.decomposition import PCA as RandomizedPCA
        def random pca(data, n pc):
          pca = RandomizedPCA(n components=n pc, svd solver='randomized')
          pca.fit(data)
          return pca.components_
        def plot_portraits(images, titles, h, w, n_row, n_col):
            plt.figure(figsize=(2.2 * n_col, 2.2 * n_row))
            plt.subplots adjust(bottom=0, left=.01, right=.99, top=.90, hspace=.20)
            for i in range(n_row * n_col):
                plt.subplot(n_row, n_col, i + 1)
                plt.imshow(images[i].reshape((h, w)), cmap=plt.cm.gray)
                plt.title(titles[i])
                plt.xticks(()); plt.yticks(())
        n_samples, h, w = faces.images.shape
        X_images = faces.data
        y names = faces.target
        n_features = X_images.shape[1]
        print("Total dataset size:")
        print("n_samples: %d" % n_samples)
        print("n_features: %d" % n_features)
        n pc = 150
        C 150 = random pca(X images, n pc)
        C 25 = C 150[:25,:]
        eigenfaces = C 25.reshape((25, h, w))
        eigenface titles = ["eigenface %d" % (i+1) for i in range(eigenfaces.shape[
        plot portraits(eigenfaces, eigenface titles, h, w, 5, 5)
```

Total dataset size: n_samples: 1348 n features: 2914



```
In []: def reconstruction(data, components):
    subspace = data @ components.T # reconstruct with the first 150 principal
    recon_data = (subspace @ components)
    return recon_data
    selected_img = X_images[:8]
    # print('original')
    plot_portraits(selected_img, ['original'+str(i) for i in range(8)], h, w, n
# print('reconstructed')
    recon_data = reconstruction(selected_img,C_150)
    plot_portraits(recon_data, ['recon'+str(i) for i in range(8)], h, w, n_row=
```

