q3

November 25, 2018

1 Question 3

1.1 * Important information

1.1.1 -Use self organizing maps as a substitute for K-means.

1.1.2 -Sample the data to include only images of '1' and '5' using sk-learn to load the data.

1.1.3 -Document the dimension of the SOM computed and the learning parameters used to generate it

1.1.4 -Provide 2D plot of the regions for '1' and '5' for both SOM and K-means solutions.

1.2 * Import Libraries

```
In [1]: import numpy as np # Library for scientific computations, we are mainly using it for c
        import matplotlib.pyplot as plt # Allows us to plot diagrams
        import matplotlib.patches as patches # Extra plotting functionality
        from minisom import MiniSom # Library has an implementation of a minimilistic SOM algo
        from random import shuffle # Used to shuffle the dataset as two list ones and fives.
        import pandas as pd
        from sklearn.decomposition import PCA
        from sklearn.preprocessing import scale
        from sklearn.cluster import KMeans
```

1.2.1 -Sample the data to include only images of '1' and '5' using sk-learn to load the data.

Iris is the well-known Fisher's Iris data set. He measured the length and width of the sepal and petal (two parts of the flower) of three species of Iris. Each row contains the measurements from one flower and there are measurements for 50 flowers of each type, hence the dimensions of iris.data. The actual type of the flower is coded as 0, 1, or 2 in iris.target; you can recover the actual species names (as strings) from iris.target_name.

Fisher showed that his then-new discriminant method could separate the three species based on their sepal and petal measurements and it's been a standard classification data set ever since.

```
In [2]: from sklearn.datasets import fetch_mldata
        mnist = fetch_mldata('MNIST original', data_home='.cache')
        list_of_types = mnist.target.tolist() ## refer the paragpraph above the target allows
                                  ## We need as a list to partition it
        def partition_the_list(label):
            return [(x, label) for x in mnist.data[list_of_types.index(label) : list_of_types.


        #Getting a dataset of ones and fives as a tuple
        ones = partition_the_list(1)
        fives = partition_the_list(5)

        dataset = ones + fives
        shuffle(dataset)
        df = pd.DataFrame(dataset)
        df.head()
```

```
Out[2]:                                                         0  1
        0  [0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...  1
        1  [0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...  1
        2  [0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...  5
        3  [0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...  1
        4  [0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...  1
```

1.2.2 -Document the dimension of the SOM computed and the learning parameters used to generate it

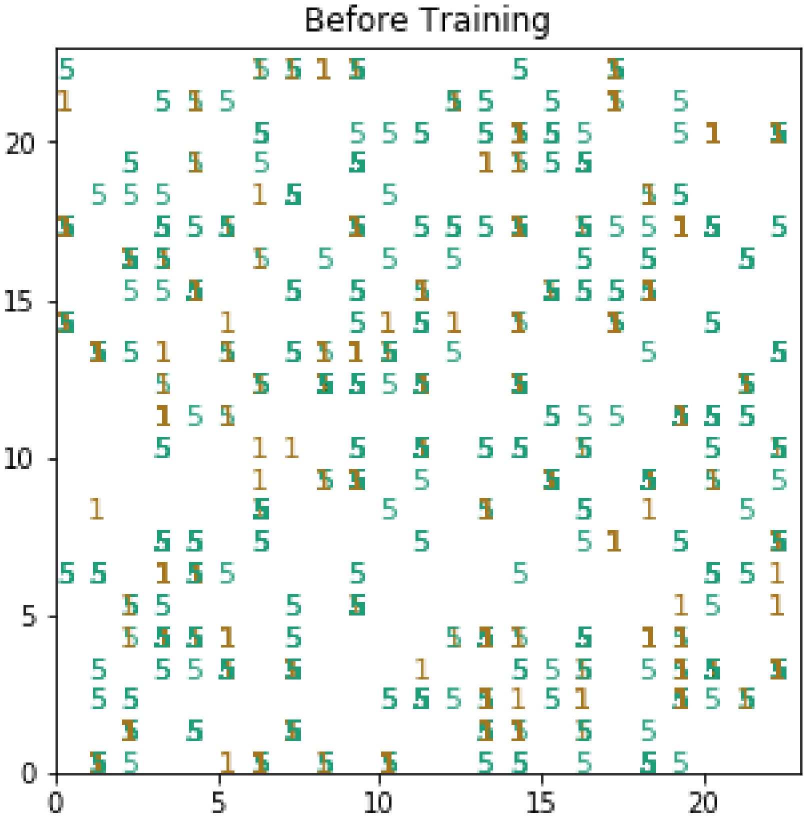
```
dim: A rule of thumb to set the size of the grid for a dimensionality
     reduction task is that it should contain 5*sqrt(N) neurons
     where N is the number of samples in the dataset to analyze.

sigma : float, optional (default=1.0)
     Spread of the neighborhood function, needs to be adequate
     to the dimensions of the map.
```

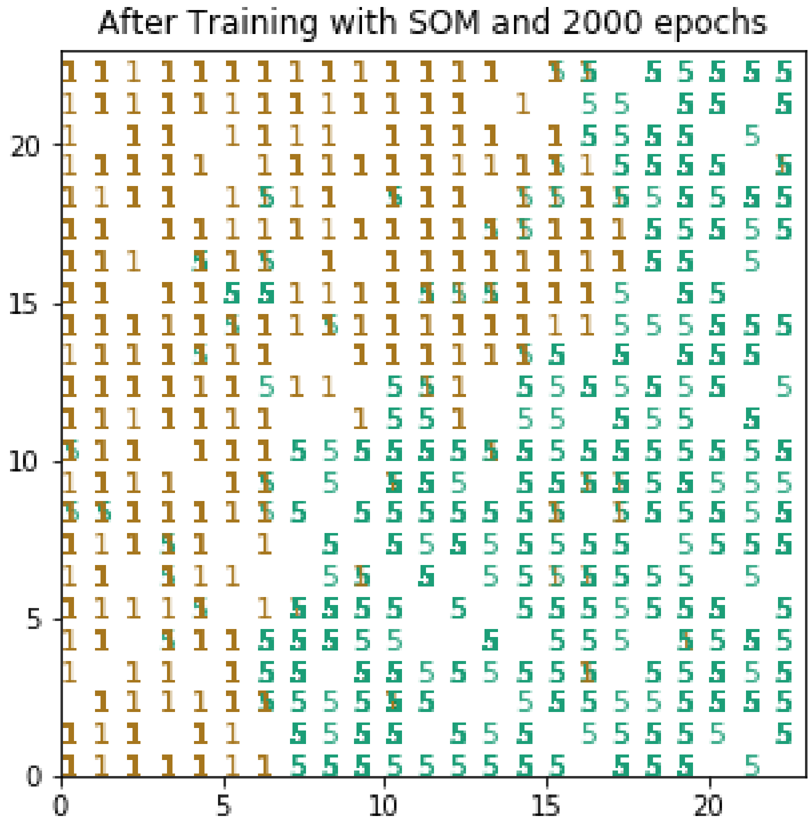
```
In [3]: dim = int(np.sqrt(5*np.sqrt(len(dataset))))
        x_dim = dim
        y_dim = dim
        input_len = 784
        sigma = 0.9
        learning_rate = .20

        som = MiniSom(x_dim, y_dim, input_len, sigma=sigma, learning_rate=learning_rate)
```

1.2.3 -Provide 2D plot of the regions for '1' and '5' for SOM.

```
In [4]: def som_plot(title):
            plt.figure(figsize=(5, 5))

            for index, item in enumerate(dataset):
                image, label = item
                i, j = som.winner(image)
                plt.text(i, j, str(label), color=plt.cm.Dark2_r(label / 5.), fontdict={'size':
            plt.axis([0, x_dim, 0, y_dim])
            plt.title(title)
            plt.show()
```

```
In [5]: som_plot('Before Training')
        epochs = 2000
        som.train_random([i[0] for i in dataset[:1024]], epochs)
        som_plot('After Training with SOM and %s epochs' % epochs)
```





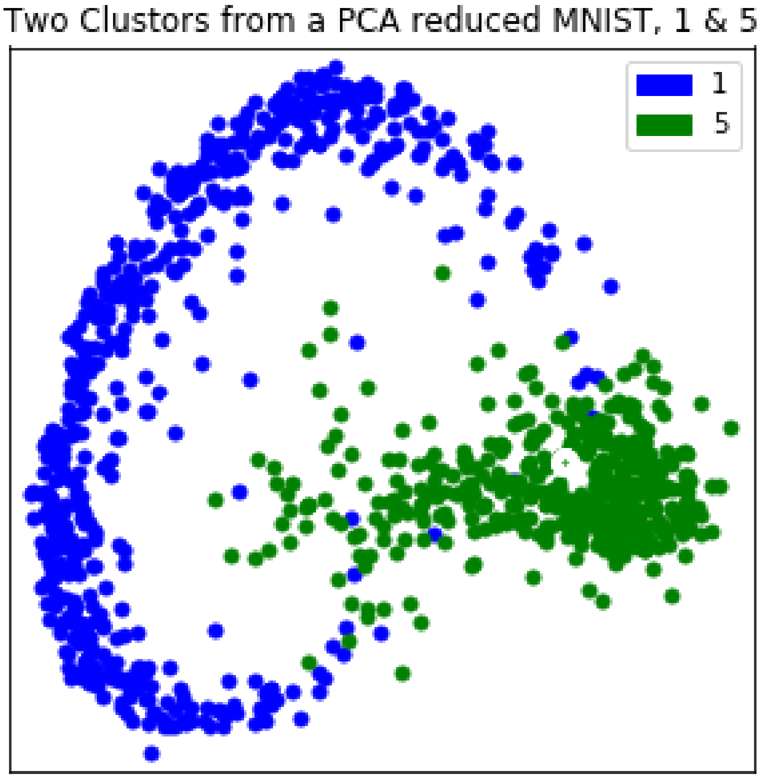
1.2.4 -Provide 2D plot of the regions for '1' and '5' for K-means solutions.

```
In [6]: def min_max(np_arr):
            return [np_arr.min() - 1, np_arr.max() + 1]

        rd = PCA(n_components=2).fit_transform([scale(x[0].astype(float)) for x in dataset[:10
        kmeans = KMeans(n_clusters=2)
        kmeans.fit(rd)
```

```
Out[6]: KMeans(algorithm='auto', copy_x=True, init='k-means++', max_iter=300,
            n_clusters=2, n_init=10, n_jobs=1, precompute_distances='auto',
            random_state=None, tol=0.0001, verbose=0)
```

```
In [7]: plt.figure(figsize=(5, 5))

        x_min, x_max = min_max(rd[:,0])
        y_min, y_max = min_max(rd[:,1])


        legend = []
        for label, color in [(1, 'blue'), (5, 'green')]:
```

```
        _ = np.array([rd[i] for i in range(1024) if dataset[i][1] is label])
        plt.plot(_[:, 0], _[:, 1], 'k.', markersize=10, color=color)
        legend.append(patches.Patch(color=color, label=str(label)))

    centroids = kmeans.cluster_centers_
    plt.scatter(centroids[:, 0], centroids[:, 1], s=1, color='w', zorder=10, marker='*', li
    plt.title('Two Clustors from a PCA reduced MNIST, 1 & 5')
    plt.legend(handles=legend)
    plt.xticks([])
    plt.yticks([])
    plt.xlim(x_min, x_max)
    plt.ylim(y_min, y_max)
    plt.show()
```



```
In [ ]:
```