CSEN 1099 – Introduction to Biomedical Engineering

Assignment #3

(Due on: June 9, 2022 at mid-night)
(This assignment can be done in teams of maximum 2 students – Please include a text file with your names and IDs in the submission)
Submit the Assignment to: bmemet2022@gmail.com

Implement the spike sorting algorithm explained in Lecture 10.pdf. Your function should take as inputs the raw extracellular activity of multiple electrodes. The function should return a vector that contains the timestamps of the peaks of the detected spikes for each neuron and a vector for the mean spike of each neuron. Apply your function to the data provided in the file "Data.txt".

Each column in the data file corresponds to one electrode. The sampling rate of this data is 24414 Hz. To detect spikes, compute the threshold as either 3.5 times the standard deviation of the first 500 samples of each electrode, or 5 times the standard deviation of the first 500 samples of each electrode. Spikes should be aligned based on their peak value. Extracted spikes should be of duration 2 msec, where the peak is at the center of the extracted spike window.

Deliverables:

- Your code

- The feature space obtained for each electrode after applying Principal Component Analysis (PCA) to the aligned extracted spikes of each electrode. Use two principal components. Name the figures "FeatureSpace_1_3_5.jpg" for electrode 1 and "FeatureSpace_2_3_5.jpg" for electrode 2 for threshold of 3.5 times the standard deviation, and "FeatureSpace_1_5.jpg" for electrode 1 and "FeatureSpace_2_5.jpg" for electrode 2 for threshold of 5 times the standard deviation.

- A text file stating the number of clusters that you identified by visual inspection of the feature space of each electrode. Name the file "Number of Neurons_3_5.txt" for threshold of 3.5 times the standard deviation and "Number of Neurons_5.txt" for threshold of 5 times the standard deviation.

- A figure showing the first 20,000 samples of the raw data of each channel with an "*" marking the detected spikes colored with different colors depending on the neuron each spike belongs to. Name the figures "DetectedSpikes_1_3_5.jpg" for electrode 1 and "DetectedSpikes_2_3_5.jpg" for electrode 2 for threshold of 3.5 times the standard deviation, and "DetectedSpikes_1_5.jpg" for electrode 1 and "DetectedSpikes_2_5.jpg" for electrode 2 for threshold of 5 times the standard deviation.

- A figure showing the average spike of each neuron colored with different colors. Name the figure "Templates_3_5.jpg" for threshold of 3.5 times the standard deviation, and "Templates_5.jpg" for threshold of 5 times the standard deviation.

Note: You can use the PCA function available in Python. No need to re-implement it.