Assigment 2 Biomedical Eng.
**Nourhan mohamed saleh** (section 3)
**python version** 3 .7
Bench number : 43913

Followed steps:
1- rectify data
2- calculate the threshold using the raw data (first 500 samples)
3-for each threshold on each electrode
→ extract all indices above the threshold (using rectified data to extract the peaks)
→ search for each spike's peak (using rectified data to extract the peaks)
→ for each peak , extract the whole spike values and its time stamp (using raw data)
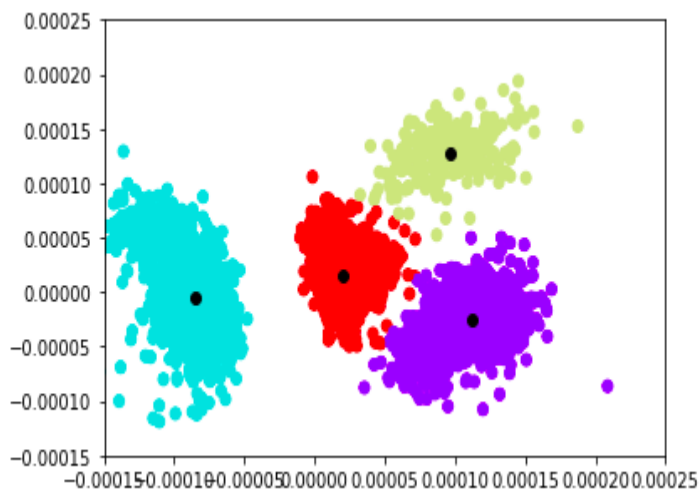5-apply PCA to fit spikes on 2D
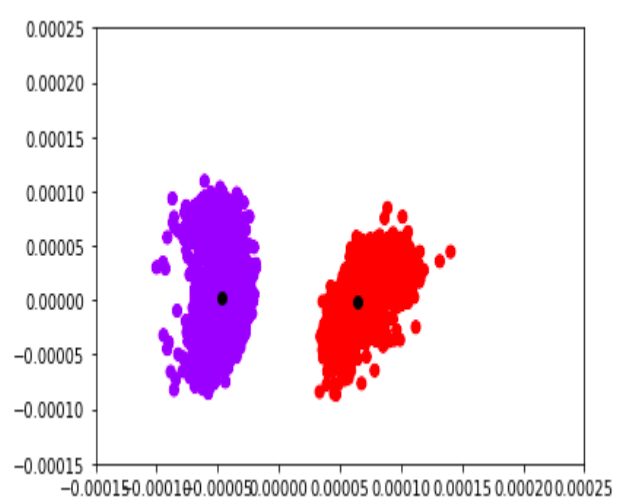6-use k-means clustering

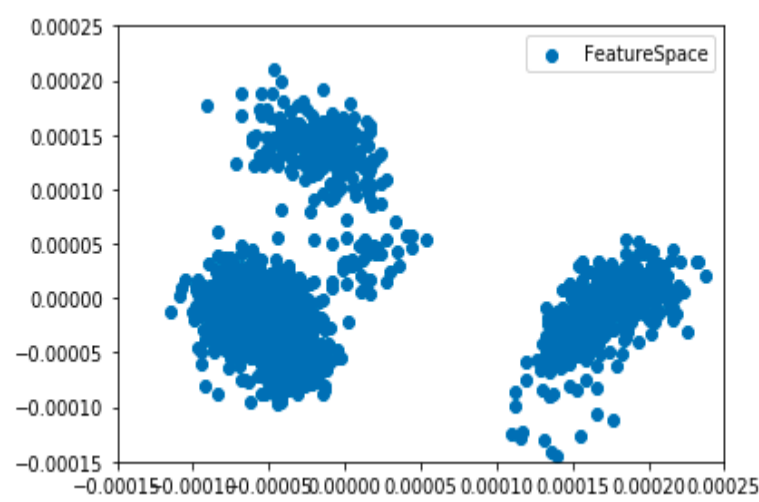**at threshold=3.5*std**
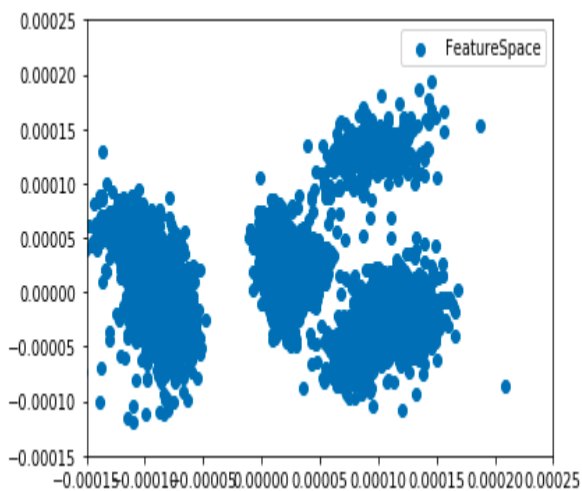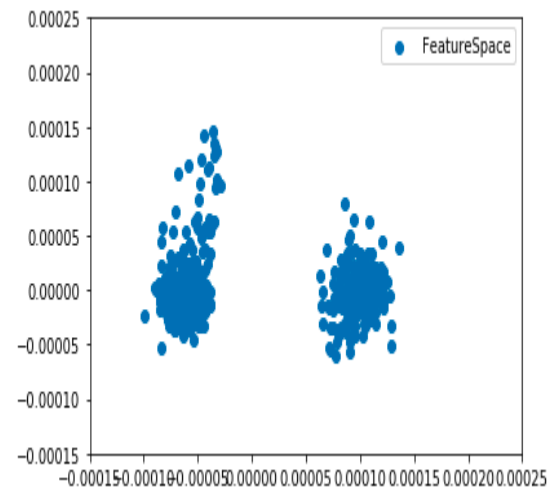

electrode 1
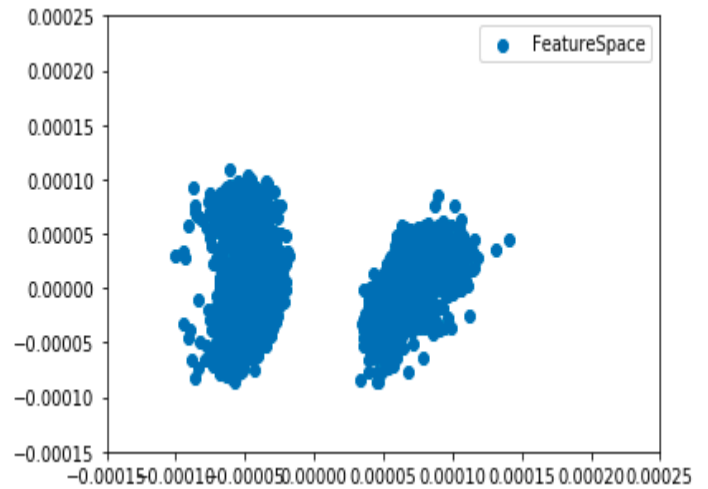
electrode 2

k = 4

k=2

at threshold= 5*std

electrode 1

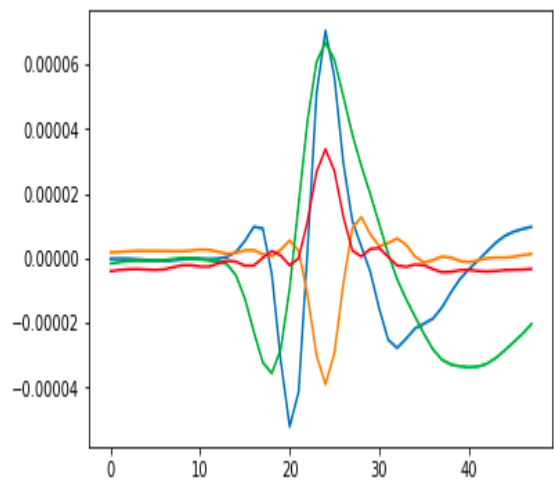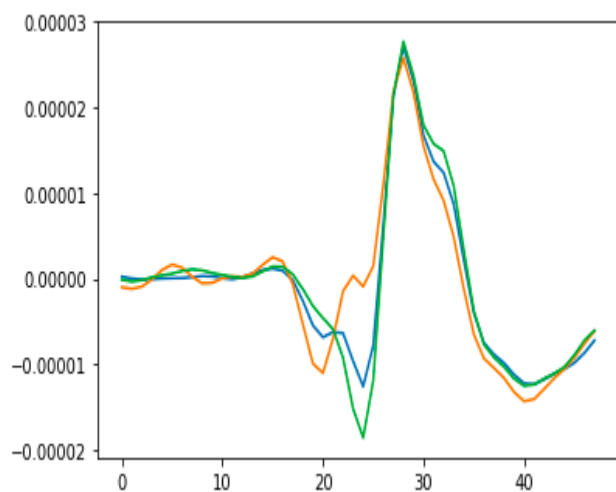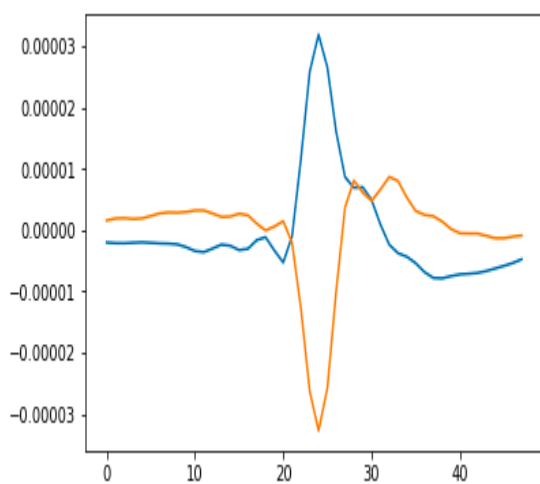**electrode 2**
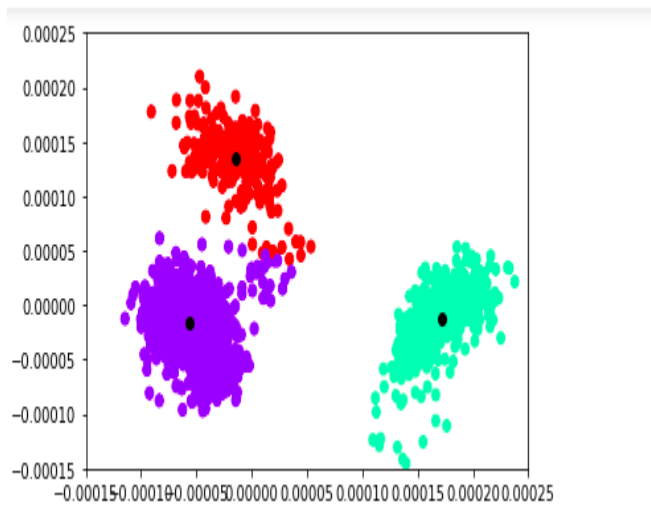
k=3
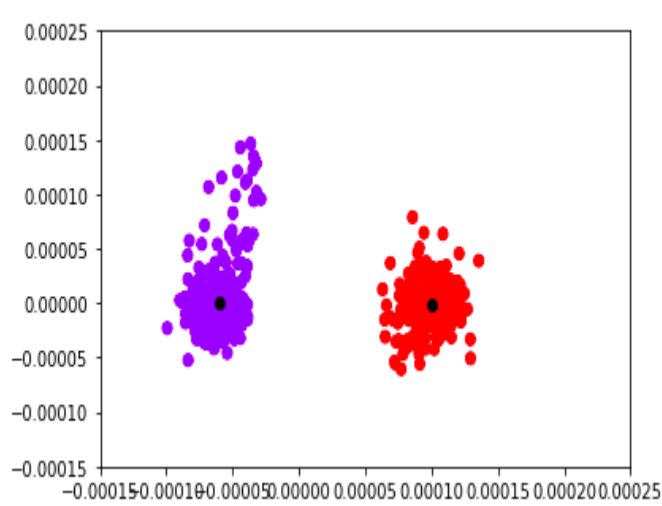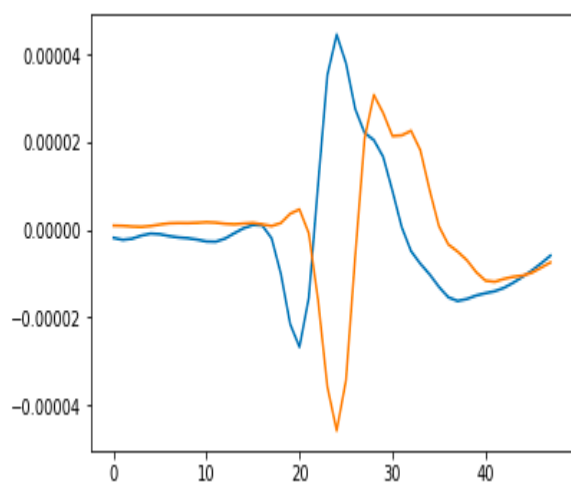

k=2

Templates:

electrode1 threshold=3.5*std

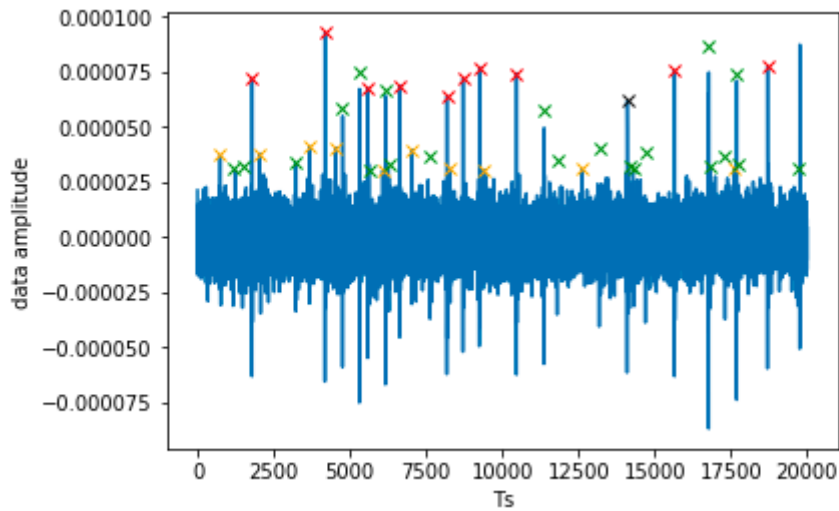**electrode 1 threshold= 5*st**

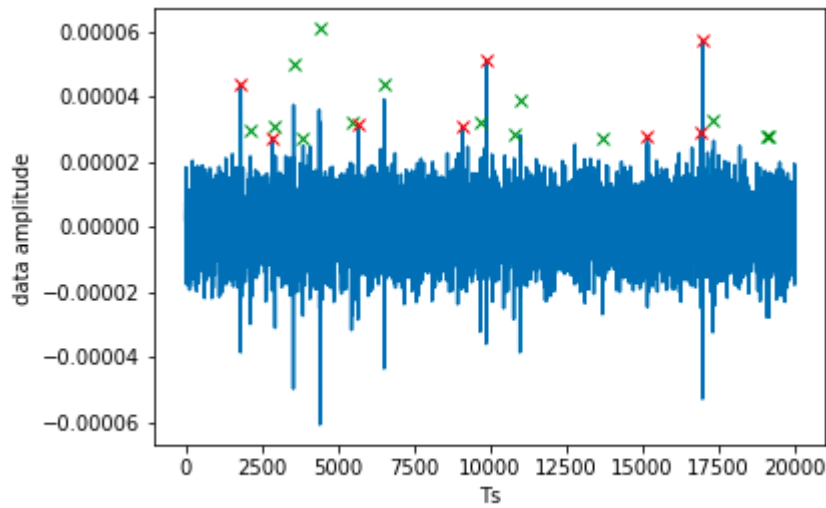**electrode 2 threshold=3.5*st**

electrode 2 threshold= 5*st

first 20,000 samples of the smoothed data of each channel with an "*" marking the detected spikes colored with different colors depending on the neuron each spike belongs to
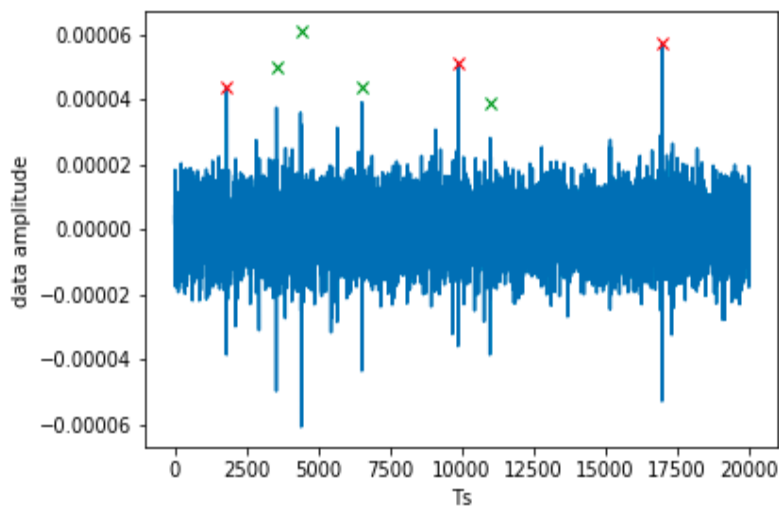
electrode1 threshold=3.5*std

electrode2 threshold=3.5*std

electrode2 threshold= 5*std

electrode 1 threshold= 5*std