

Project Phase 2: EMG Decomposition

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Introduction

A discussion on the EMG signal and motor unit action potentials (MUAPs) was presented in *Project Phase 1: EMG Report*. The main points to be taken from the discussion are that EMG decomposition is necessary to understand the complete science of muscles and useful for applications. This report now shows a pipeline created for EMG decomposition. The main steps are translating the data into a usable format, filtering, detecting spikes, aligning spikes, extracting features, clustering spikes, classifying spikes as different MUs, and analyzing the MUAP data that becomes available. The results of each stage are presented for 3 datasets in the corresponding section.

1 Input File

The base structure for importing the data into MATLAB was provided by Professor Liu. The data comes from a .csv file which gets extracted into MATLAB. The first column represents time while the others represent channel data in mV. The time, sampling rate, and channel data are stored in variables. The data from each channel is then plotted. One specific channel is then selected to be analyzed by the pipeline. Dataset 1 is from 'EMG_example_2_fs_2k' channel 3, Dataset 2 is from 'EMG_example_20s_2000Hz-2016', and Dataset 3 is from '32171_P06_100618_PLATE_LG_EMG'

Dataset 1

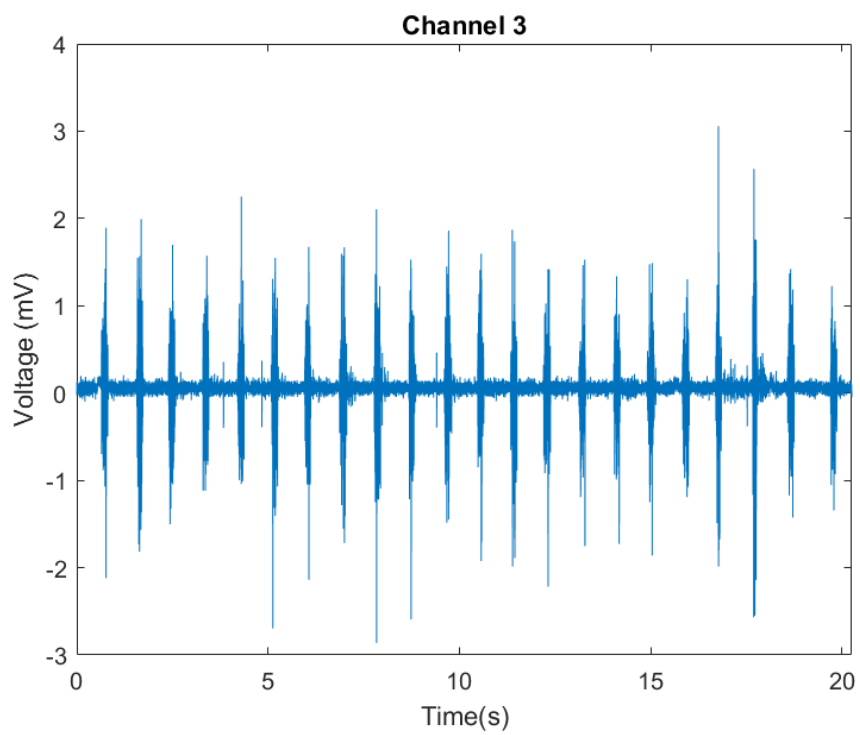


Figure 1: Raw EMG data

Dataset 2

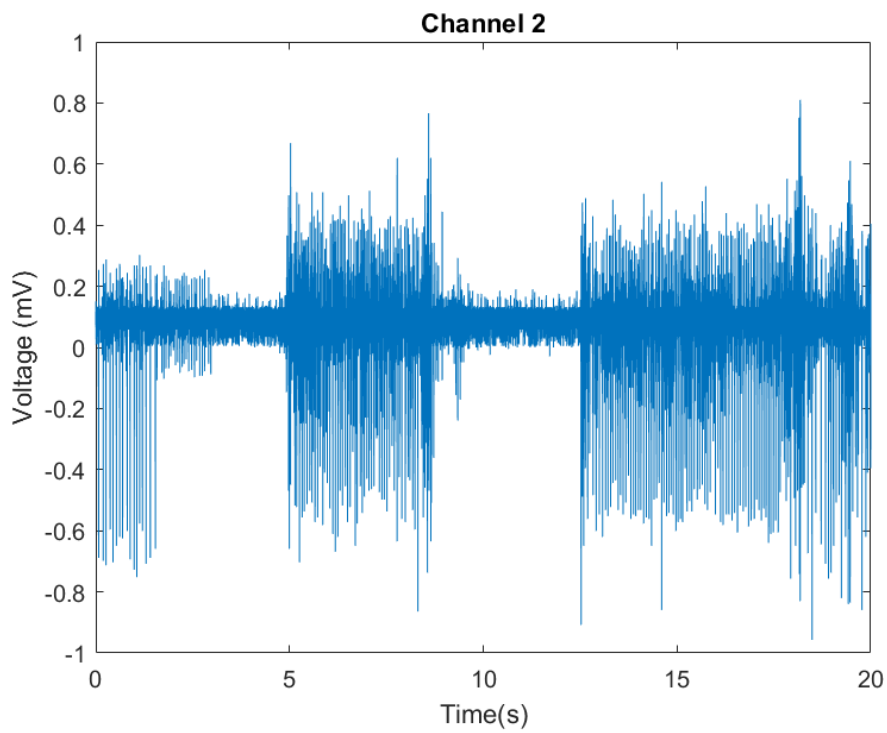


Figure 2: Raw EMG data

Dataset 3

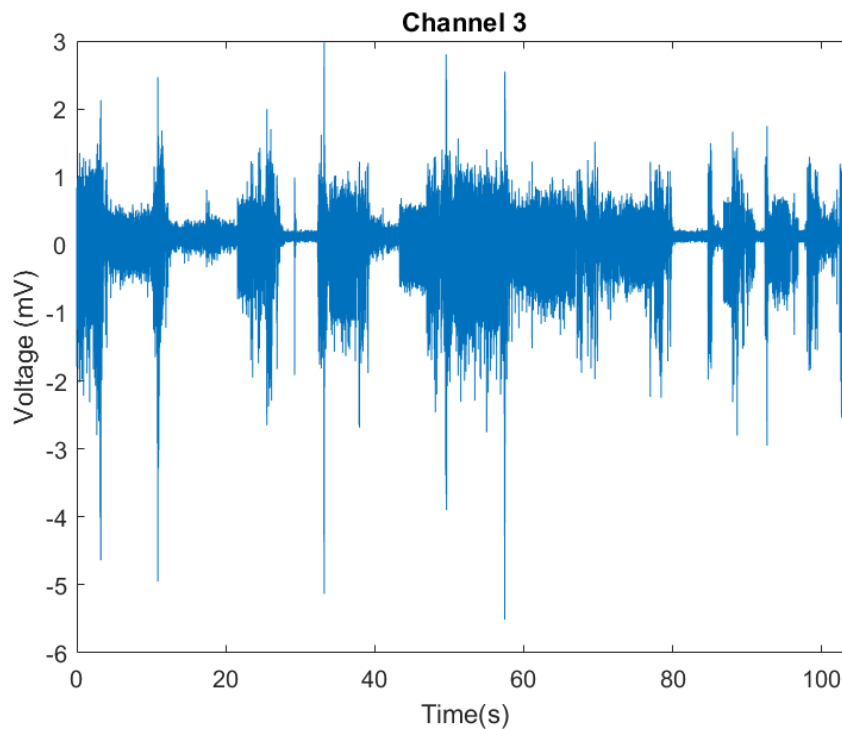


Figure 3: Raw EMG data

These channel recordings are fairly diverse so altogether they provide a good test of the pipeline.

2 Filter Signal

The signal now has to be filtered with the goal of improving the signal-to-noise ratio and improving spike detection. An EMG signal has a bandwidth of around 1Hz to 500Hz. The Fourier Transform of the raw EMG signal showed a very large spike around 0Hz suggesting that low frequencies are noisy and should be filtered out. Since the majority of EMG power is in the range of 50 Hz to 150 Hz, the low cutoff frequency was chosen to be 50 Hz. High frequency data is important for detecting spikes, so the high frequency cutoff was chosen to be at the upper limit of EMG bandwidth, 500 Hz. The built-in bandpass function in MATLAB was used.

Dataset 1

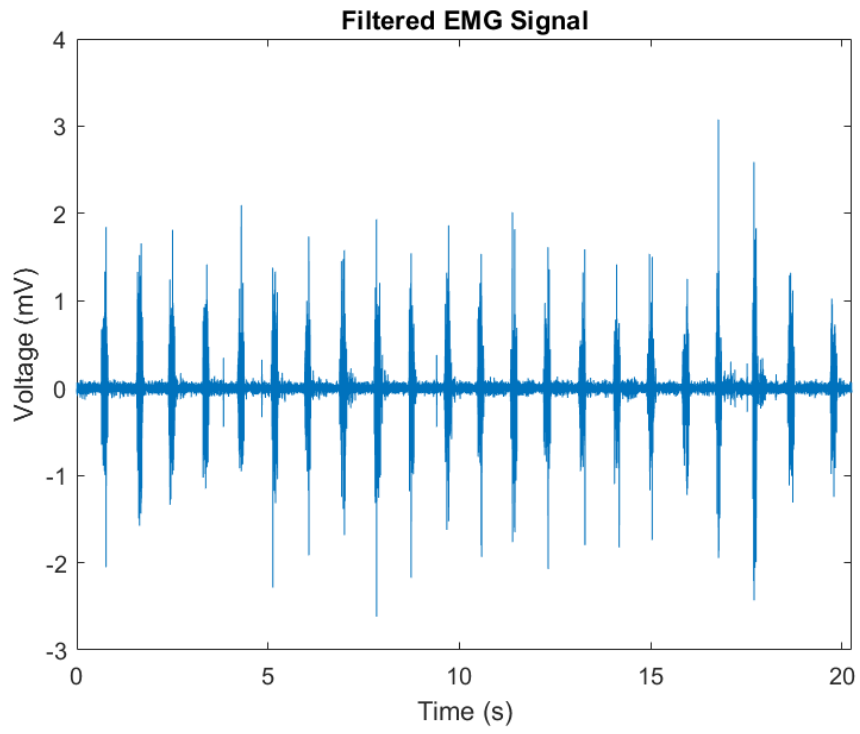


Figure 4: Filtered EMG Data

Dataset 2

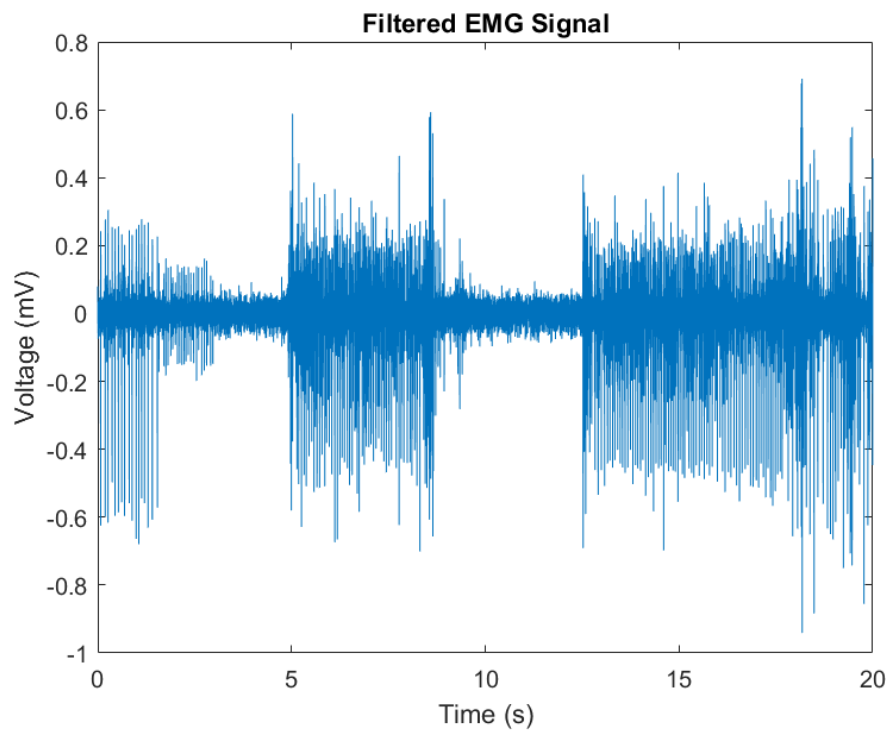


Figure 5: Filtered EMG Data

Dataset 3

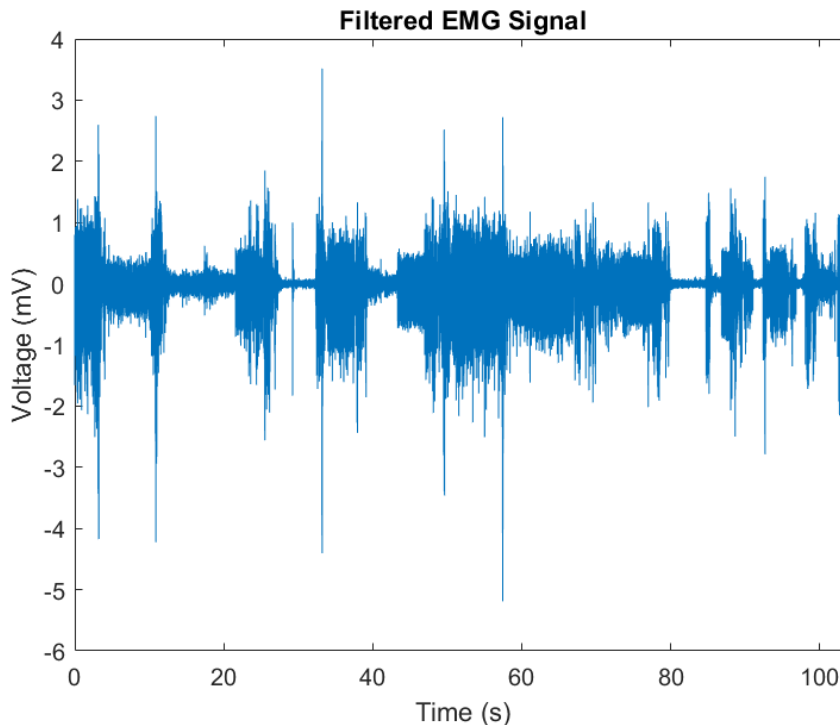


Figure 6: Filtered EMG Data

Though the effect of filtering is not clear from the zoomed out view in these figures, filtering does affect classification performance.

3 Detect Spikes

Now the the signal has been filtered, the spikes can be detected. The method being used is a threshold detector with the threshold chosen at 2 times the *rms* value of the signal. Though $3 * rms$ is generally the standard, this threshold was chosen for the datasets shown in this report since it captured visible spikes that a $3 * rms$ threshold did not and did not add a significant number of false positives. Finding peaks using the non-linear energy operator (NEO) with a constant threshold of 2 to 3 times rms was also attempted but was found to detect significantly less spikes and thus lowered the clustering performance.

The peaks were found using the `findpeaks` built-in function of MATLAB, inputting the absolute value of the signal. The minimum distance between peaks was set to be equal to the number of samples. This avoids multiple peaks in the same window region to improve the alignment stage. However, if the number of samples is too high, spikes may be missed which is why the window size was chosen to be 16 samples giving 8 ms of data with sampling rate of 2000. This enough to capture either the most significant portion of a MUAP or all of it as the Extract Features section discusses further.

Dataset 1

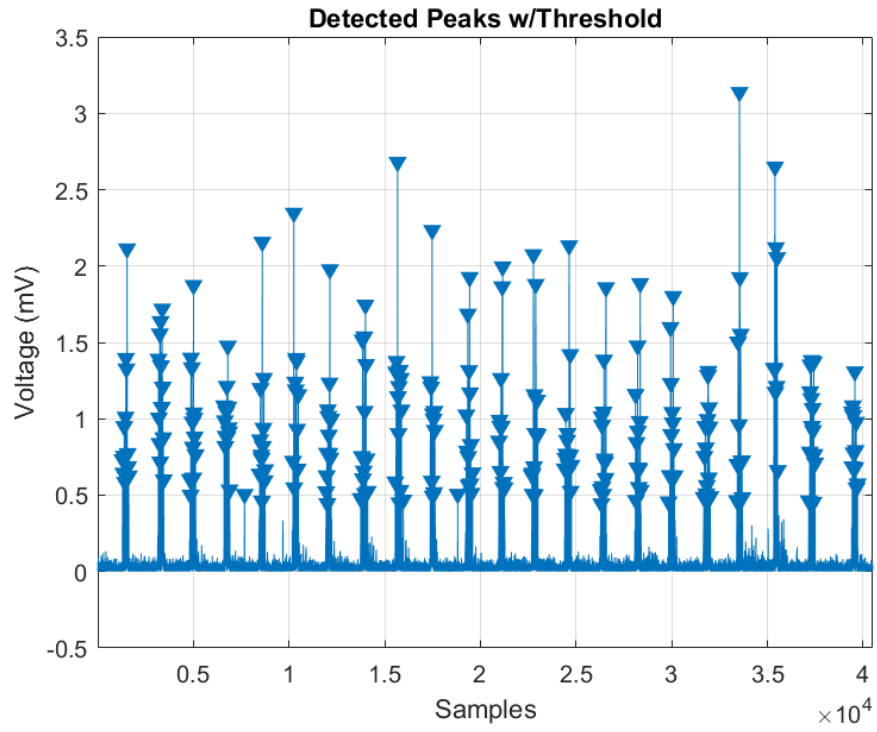


Figure 7: Spikes detected over the full course of recording shown by triangles

Dataset 2

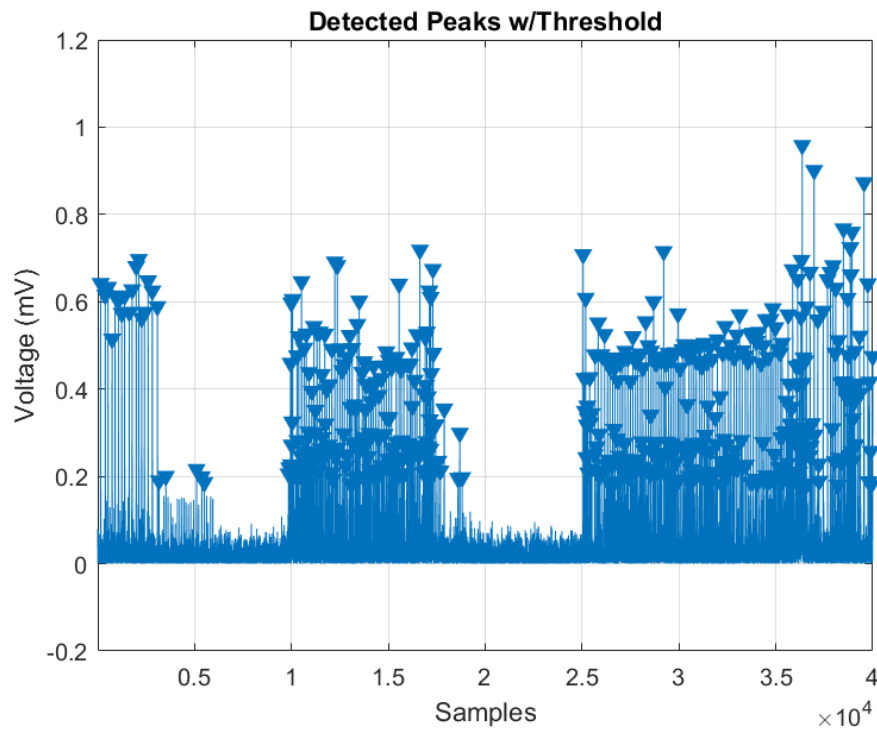


Figure 8: Spikes detected over the full course of recording shown by triangles

Dataset 3

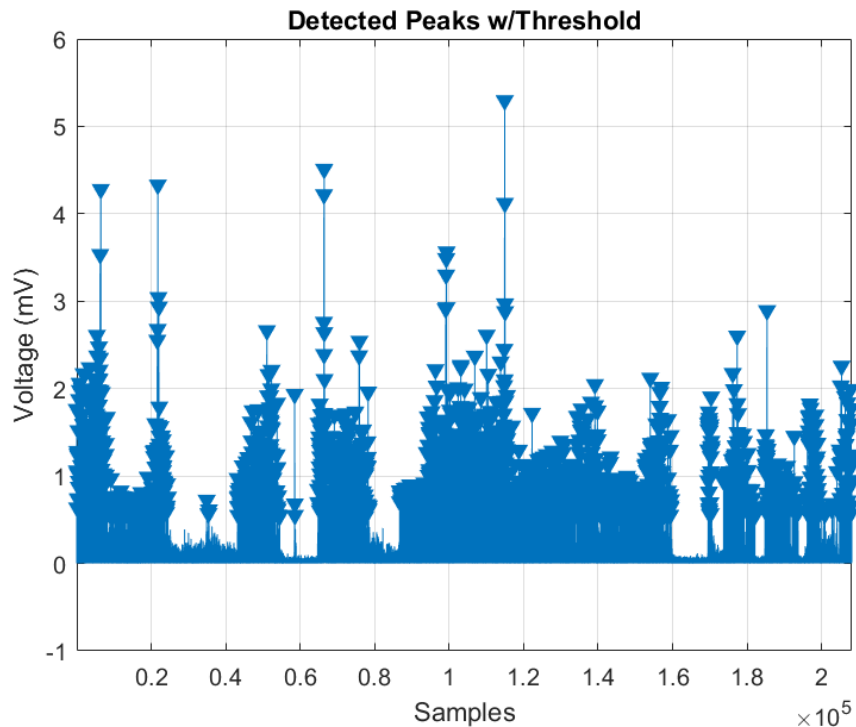


Figure 9: Spikes detected over the full course of recording shown by triangles

The disadvantage of constant threshold detection is that it may miss lower amplitude spikes. Some of these spikes can be seen in Dataset 2 from about 0.4s to 1s. A threshold that varies in time could help solve this, though calculating this adds significant complexity.

4 Align Spikes

The spikes have to be aligned before analysis. A window around the spike maximum is made using an adjustable number of samples. 16 samples were taken with 7 taken from before the spike and 8 from after. Significant improvements were not found for a higher number of samples. The spikes are loaded into an array of dimension (number of spikes detected X number of samples) with values in the matrix representing voltages.

Dataset 1

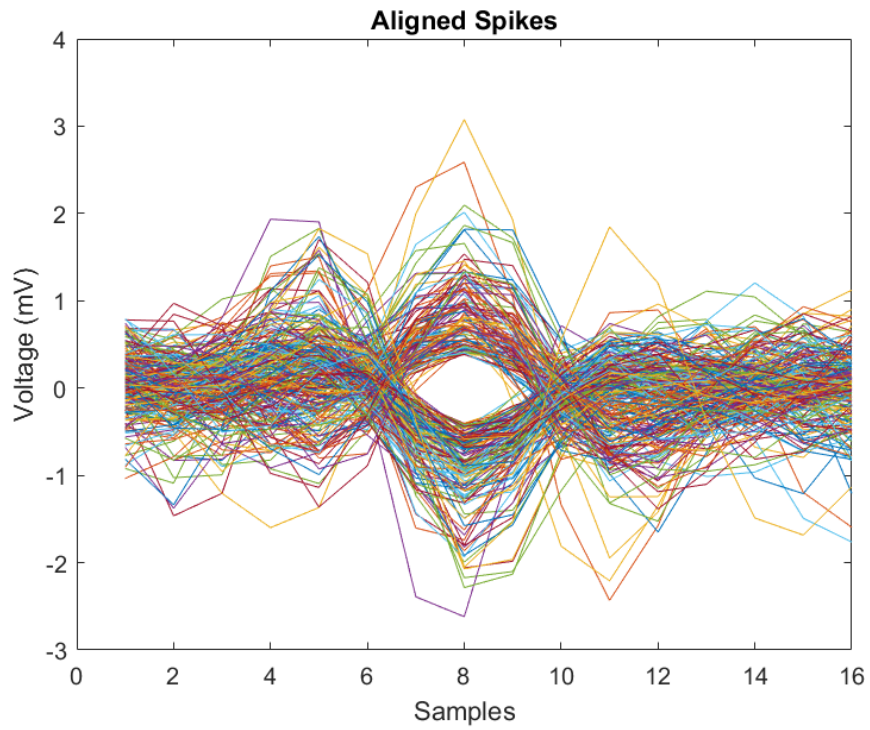


Figure 10: Aligned Spikes with 16 sample window

Dataset 2

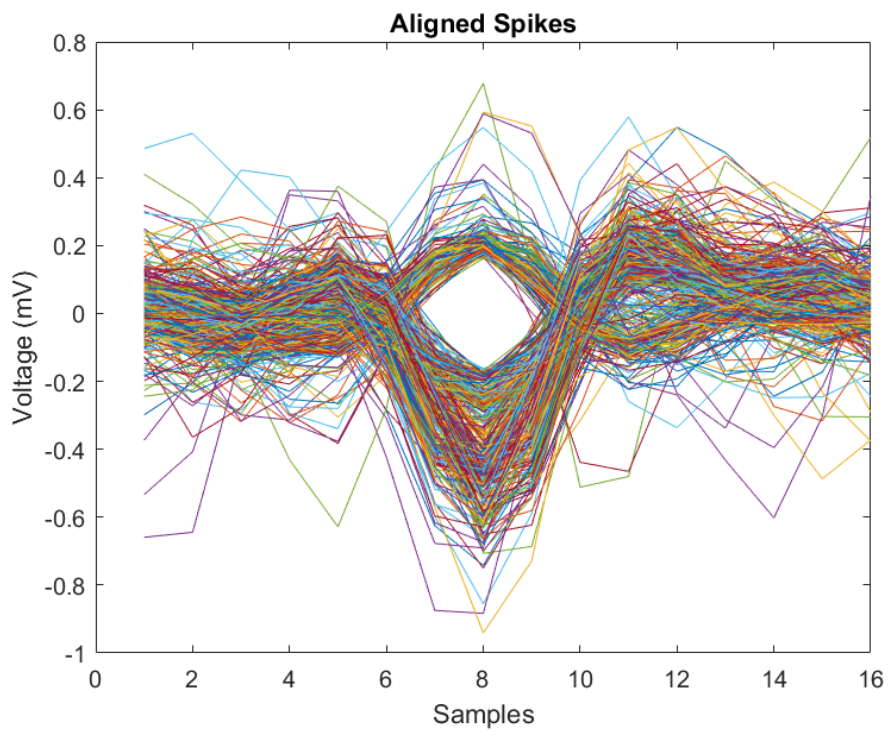


Figure 11: Aligned Spikes with 16 sample window

Dataset 3

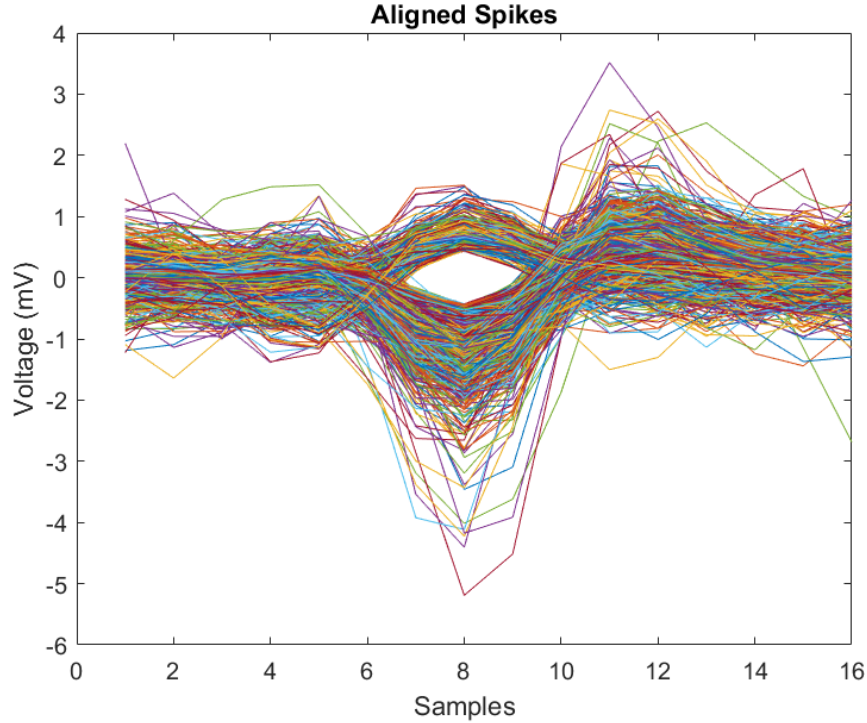


Figure 12: Aligned Spikes with 16 sample window

A variable length window could capture shorter spikes more effectively but makes analysis in the rest of the stages more difficult. The alignment step was found to generally take the most time out of all the stages.

5 Extract Features

The samples can be used to extract features from each windowed spike. Principal Component Analysis (PCA) is used to transform the dimensions of data such that most of the variation is along the first PC. The second PC must be orthogonal to the first and contains the maximum variation possible under this constraint. The same goes for the rest of the PCs. The total number of PCs is equal to the total number of features inputted which is 16 in this case.

PCA allows for dimensionality reduction, viewing feature importance, and visualizing the data. PCA was not used to reduce data dimensionality for clustering since doing so did not improve performance. PCA was used for visualization and determining which features have the most variability and so are more likely to convey relevant information. A higher absolute value for the weight of a sample in the first principal component implies that sample is more informative. The visualization was used to estimate the initial number of clusters used in the next stage.

Dataset 1

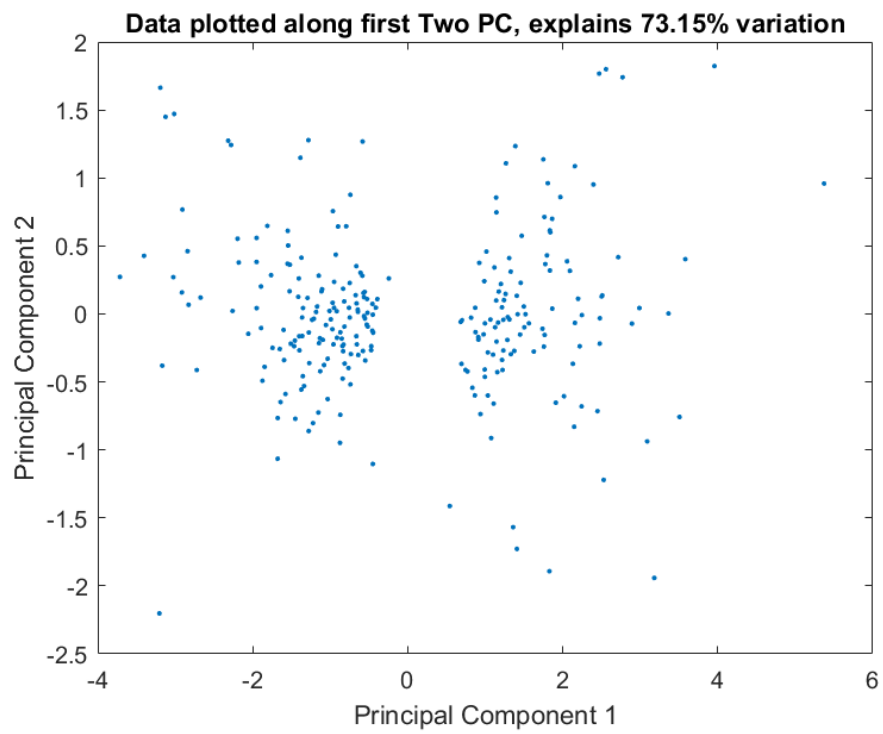


Figure 13: Plot of data in PC space

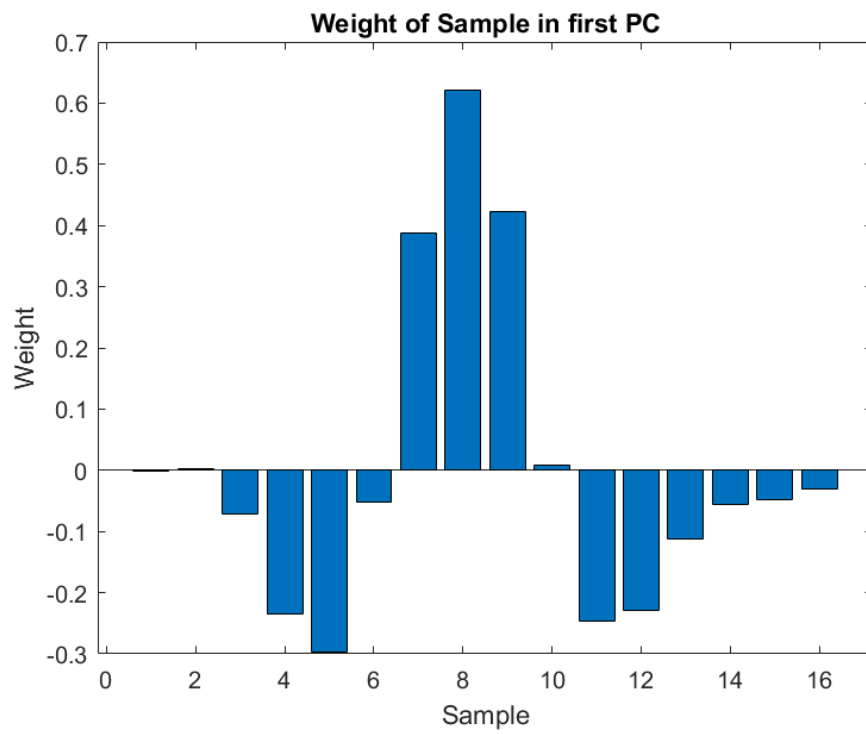


Figure 14: Weight of all samples towards determining first PC

Dataset 2

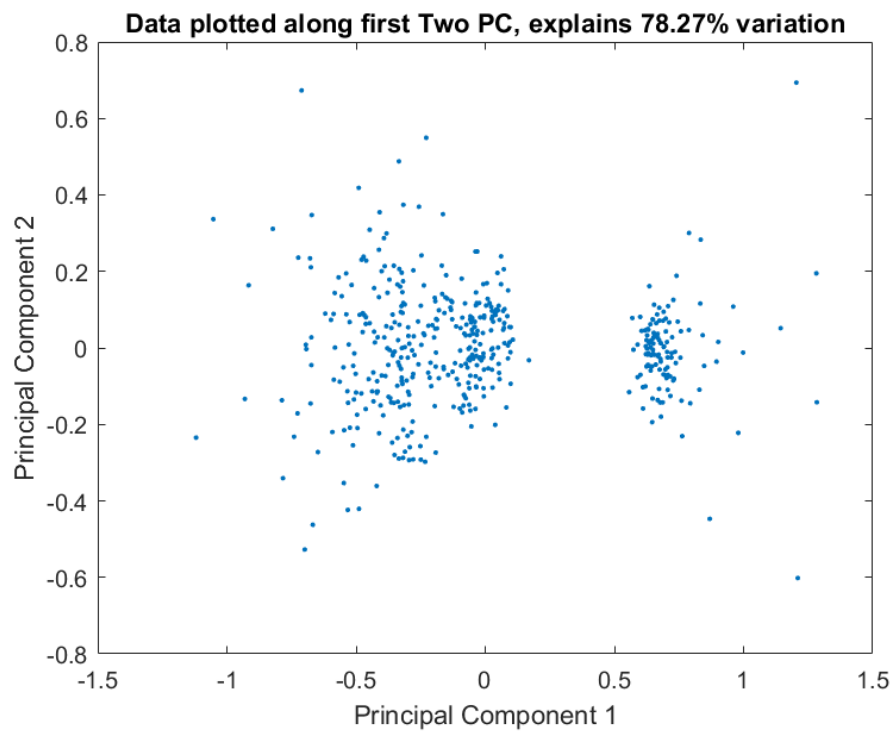


Figure 15: Plot of data in PC space

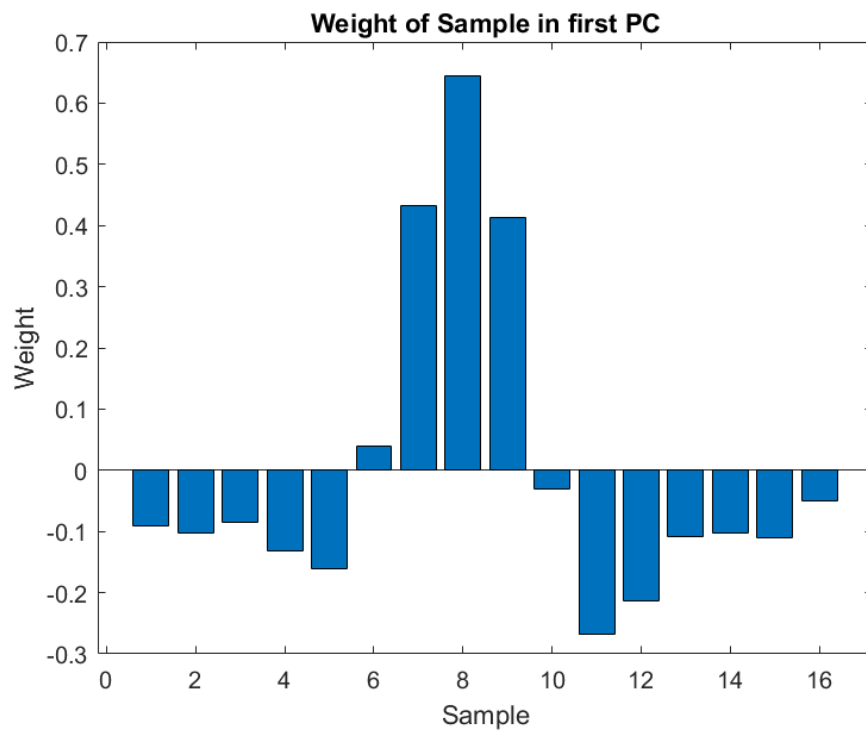


Figure 16: Weight of all samples towards determining first PC

Dataset 3

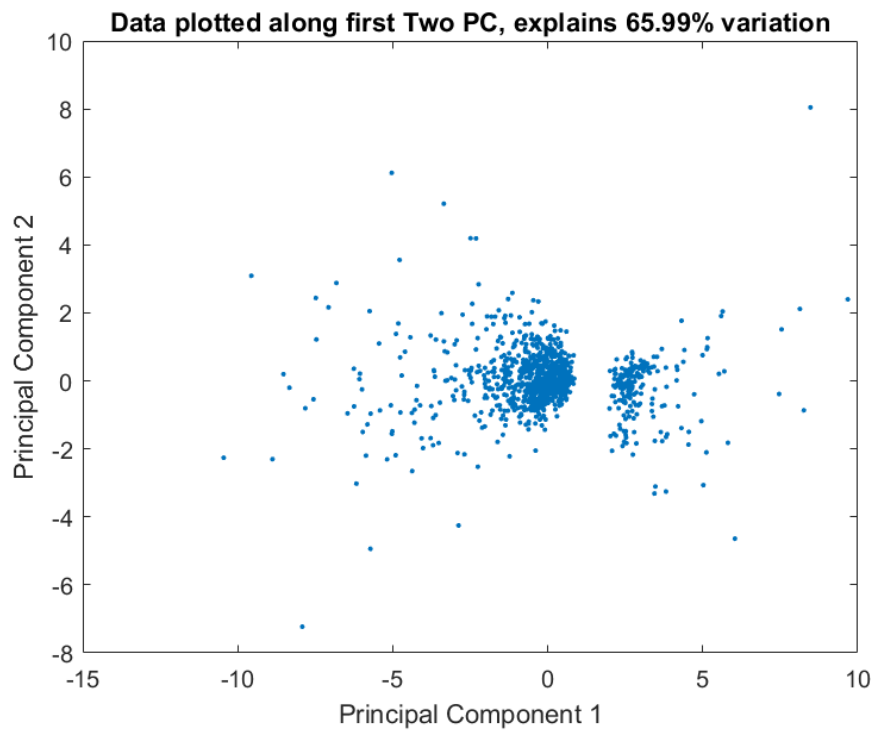


Figure 17: Plot of data in PC space

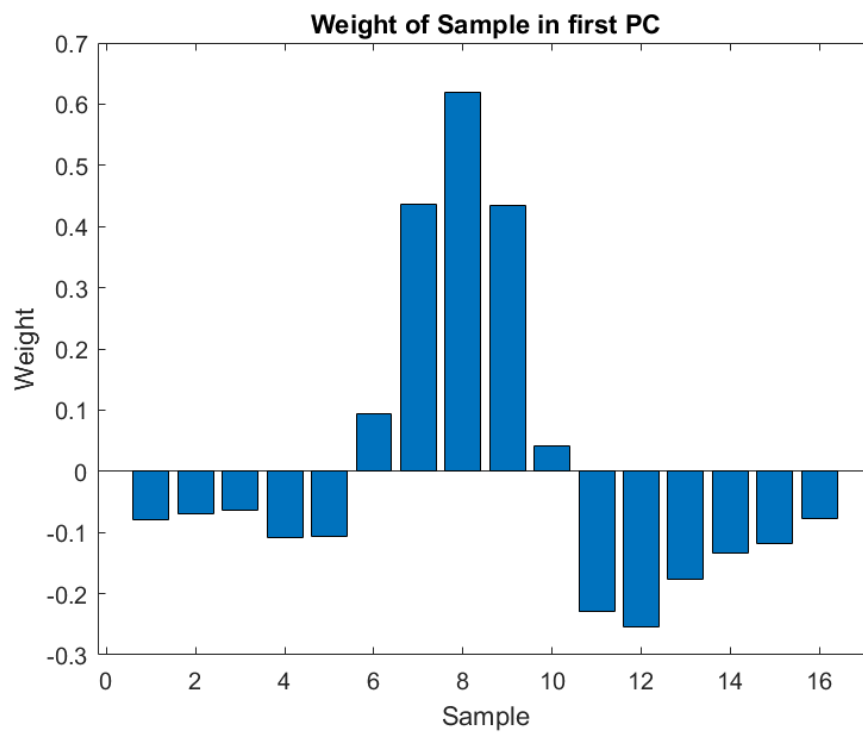


Figure 18: Weight of all samples towards determining first PC

The spikes in the PCA space show at least 2 clear clusters for every dataset. There are often points far away from a cluster which suggests these spikes are significantly different from that group type but have not had enough occurrences to form a cluster themselves. The sample weights for the first principal component are centered and highest around the maximum where the spike occurs for all datasets. This is expected since those are the samples that vary the most between observations. The weights drop off strongly towards the edge which suggests that 16 samples are enough to characterize a MUAP since more samples would likely not add much more informative data.

6 Cluster Spikes

Spike clustering relies on the assumption that MUAPs from the same motor unit will be similarly shaped. Clustering finds groups that are similar which are then each classified as a motor unit. The algorithm used is k-means clustering through its built-in implementation in MATLAB. The number of clusters can be adjusted if the initial estimate does not give good results. Viewing the results of the following stages can also help with adjusting the number of clusters. The algorithm initializes cluster centers randomly which can sometimes lead to inaccurate results so the random seed can be changed to potentially improve results. After clustering, the data is plotted in the PC space and colored by group.

Dataset 1

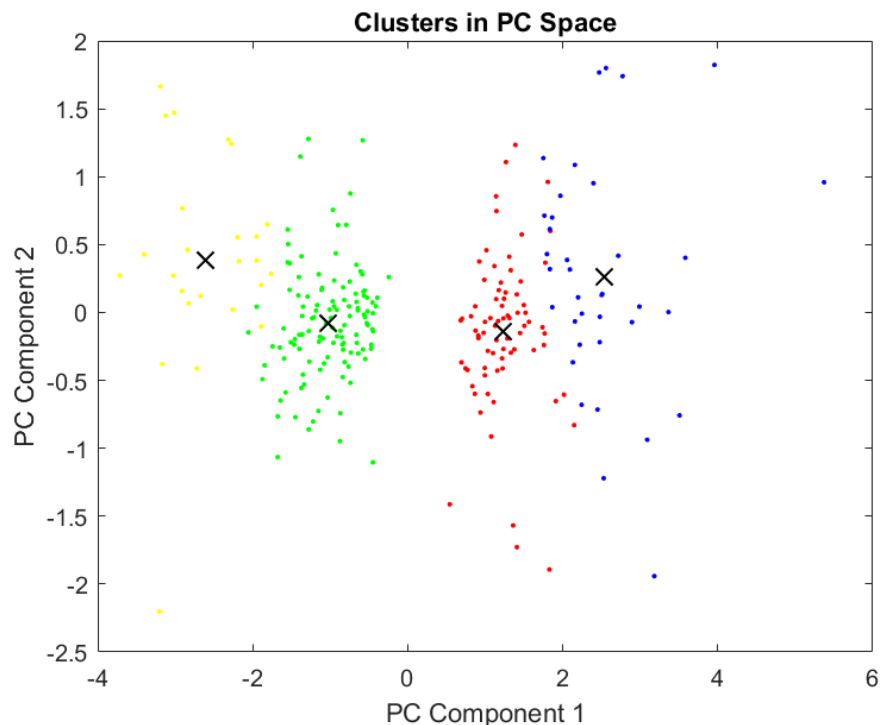


Figure 19: Spikes plotted in PC space, colored by cluster. Black X marks the centroid

Dataset 2

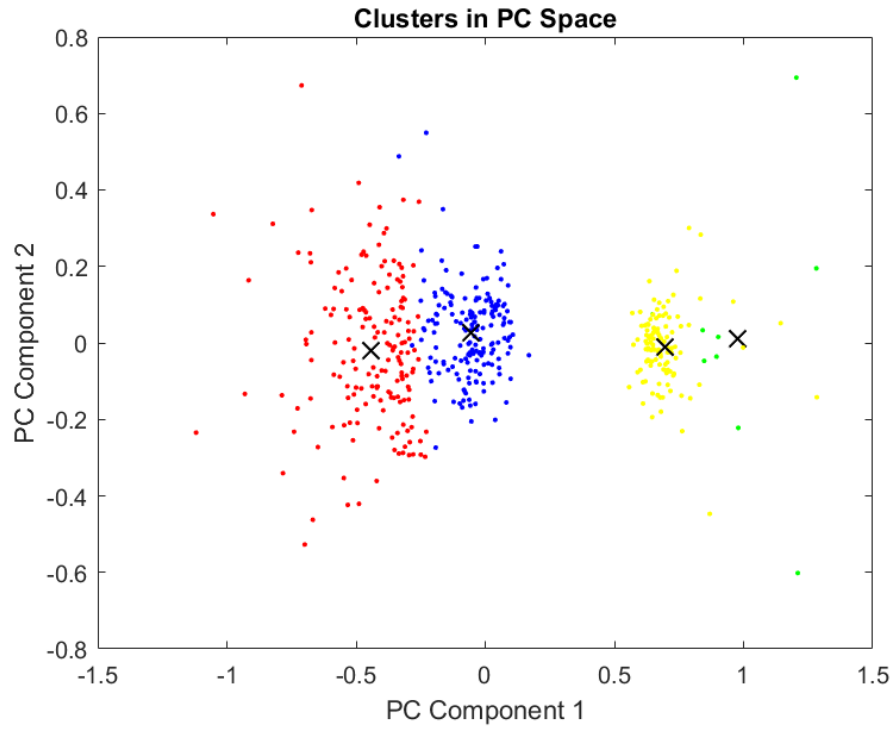


Figure 20: Spikes plotted in PC space, colored by cluster. Black X marks the centroid

Dataset 3

Though some classified groups don't show a clear cluster in the PC space, the next section will show that there is a noticeable difference in spike shapes.

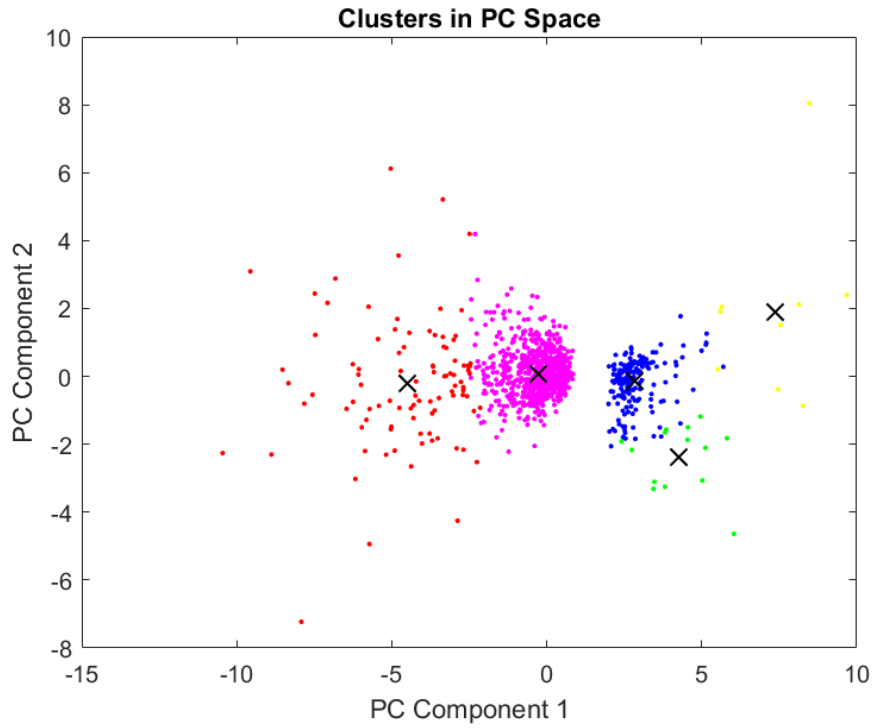


Figure 21: Spikes plotted in PC space, colored by cluster. Black X marks the centroid

7 Classify Spikes

Now that the spikes have been clustered, a template of the action potential for each motor unit is made using the centroid from k-means clustering. The spikes are also displayed again, now classified and colored according to estimated motor unit.

Dataset 1

This dataset show approximately four different spikes. The blue, red, and green spikes are triphasic spikes with different amplitudes while the yellow spike is a biphasic spike.

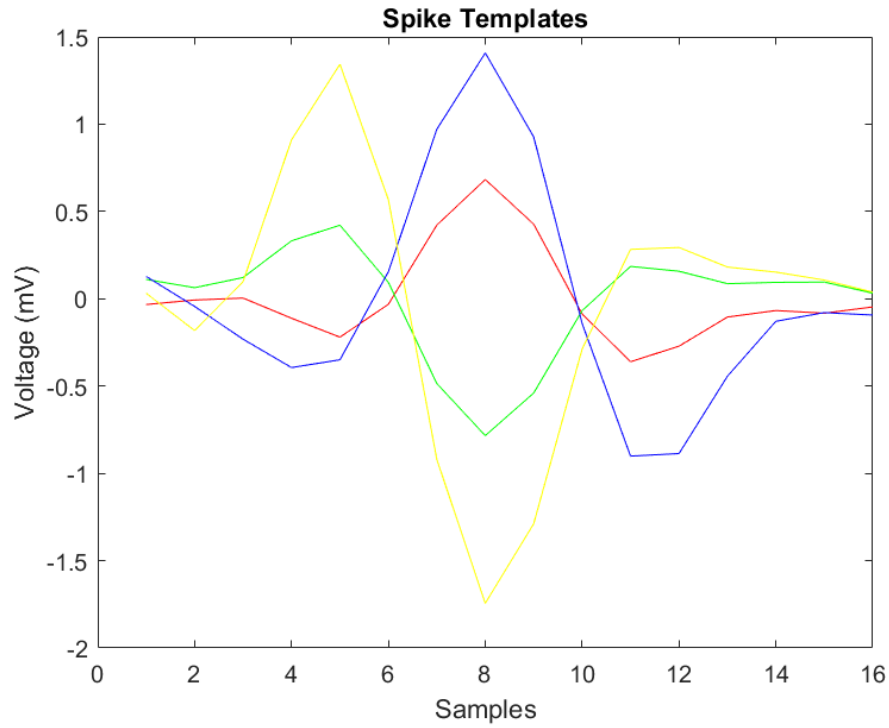


Figure 22: Spike templates. Found using centroid results of k-means clustering

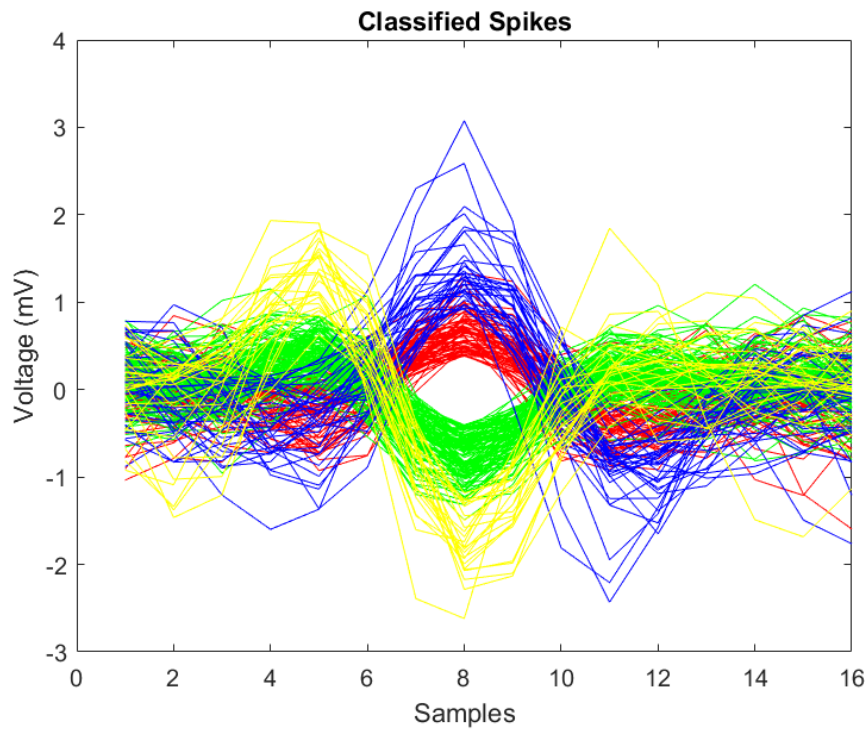


Figure 23: All detected spikes colored by class

Dataset 2

This dataset also shows about 4 spikes. The blue, red, and yellow spikes are triphasic while the green appears more biphasic.

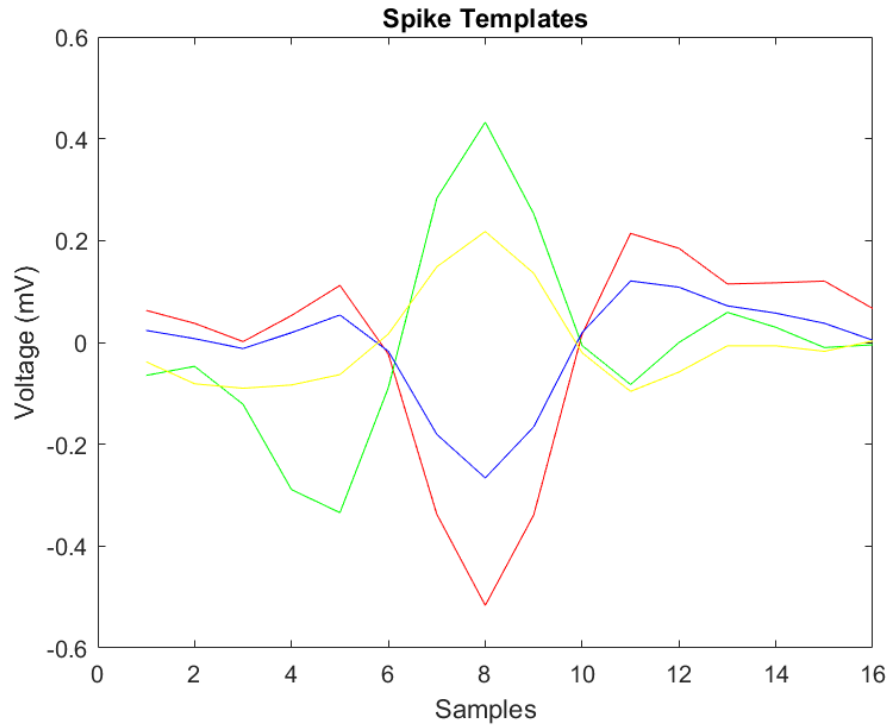


Figure 24: Spike templates. Found using centroid results of k-means clustering

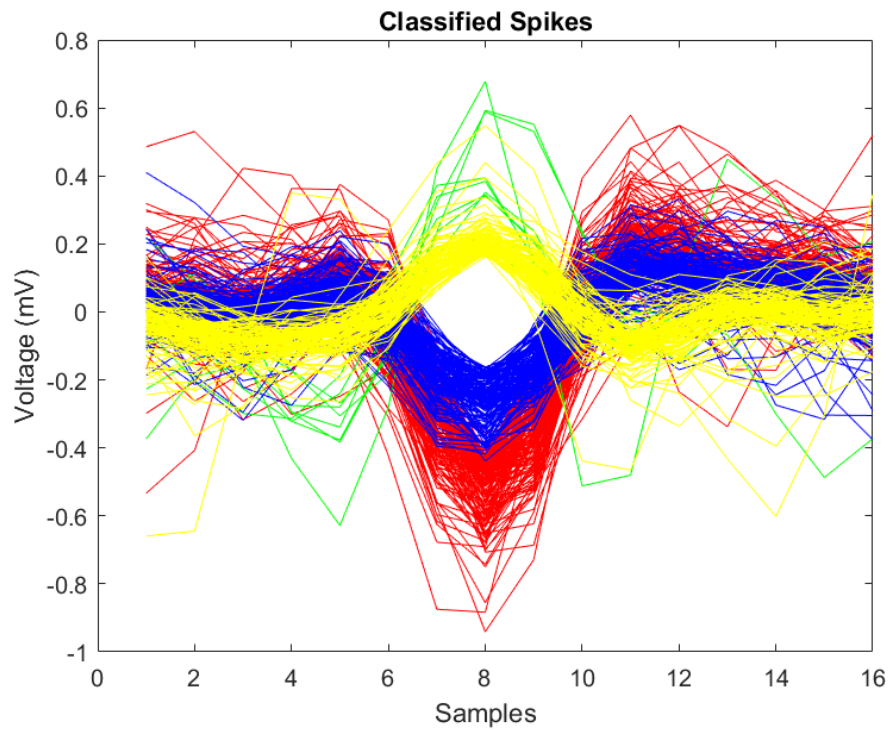


Figure 25: All detected spikes colored by class

Dataset 3

This dataset is about 5 times longer than the others at 100s long and is estimated to have 5 motor units. The blue, purple, and red spikes are triphasic with different amplitudes.

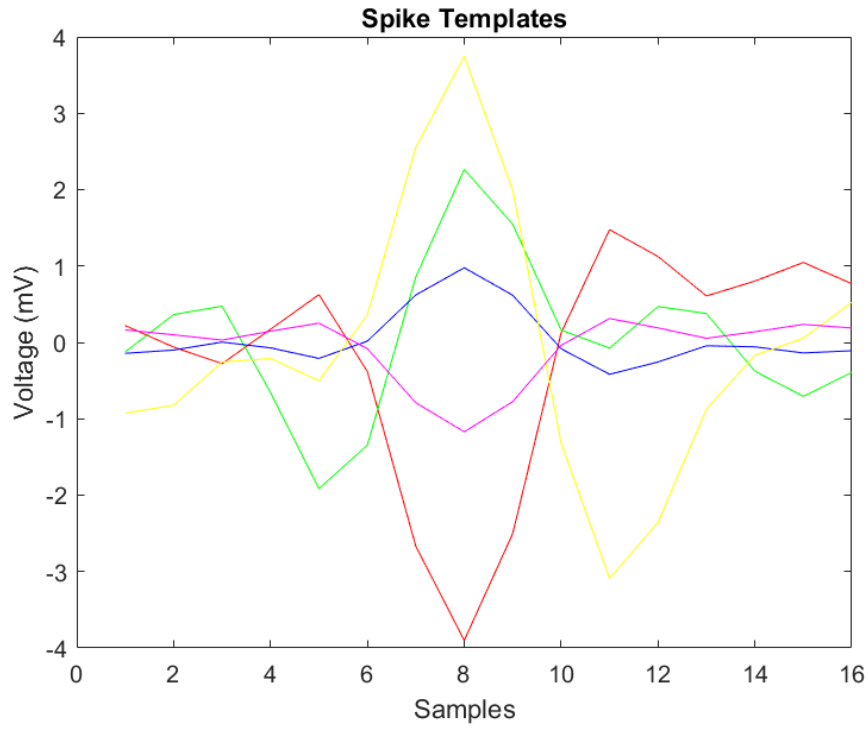


Figure 26: Spike templates. Found using centroid results of k-means clustering

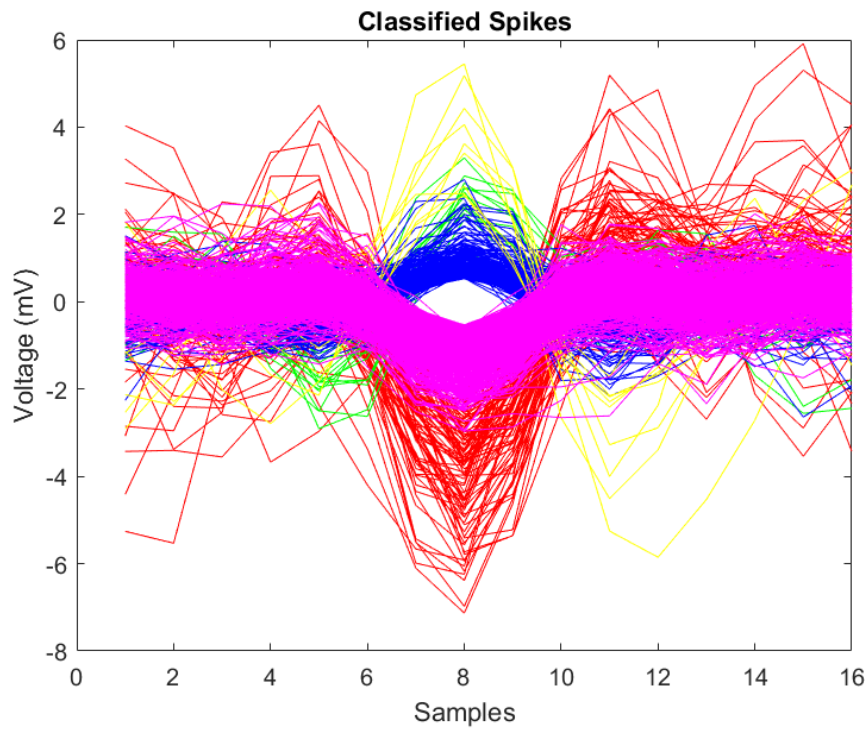


Figure 27: All detected spikes colored by class

The green and yellow spikes are biphasic with different shapes and amplitudes.

8 Analysis

With every spike now assigned to a particular motor unit, spike patterns can be analyzed. The spikes from each motor unit were plotted over time. Firing rates were found by counting the number of spikes in 100 bins over the whole interval. Additionally, a distribution of the inter-spike interval times (ISIs) is shown.

Dataset 1

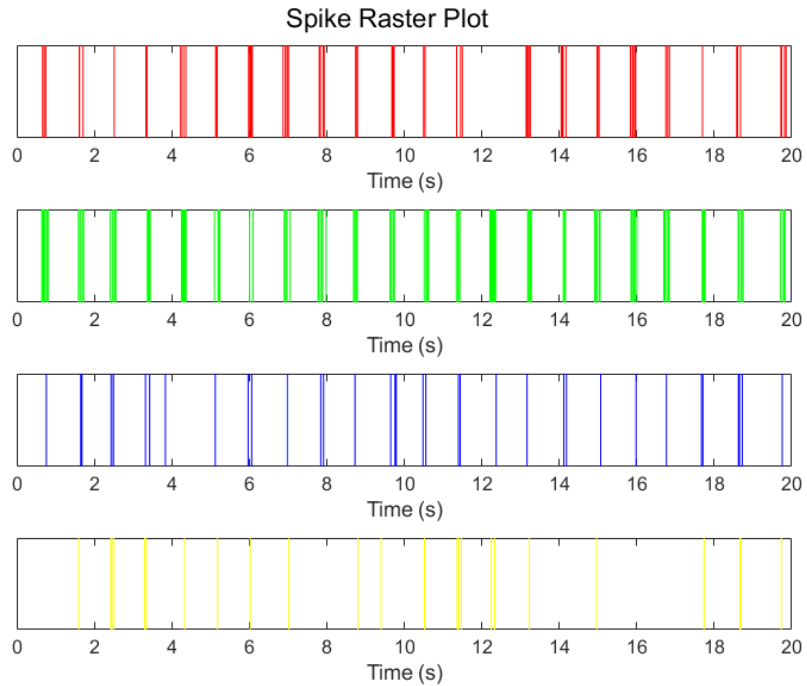


Figure 28: Spike rasters. Each line represents a spike at that particular time

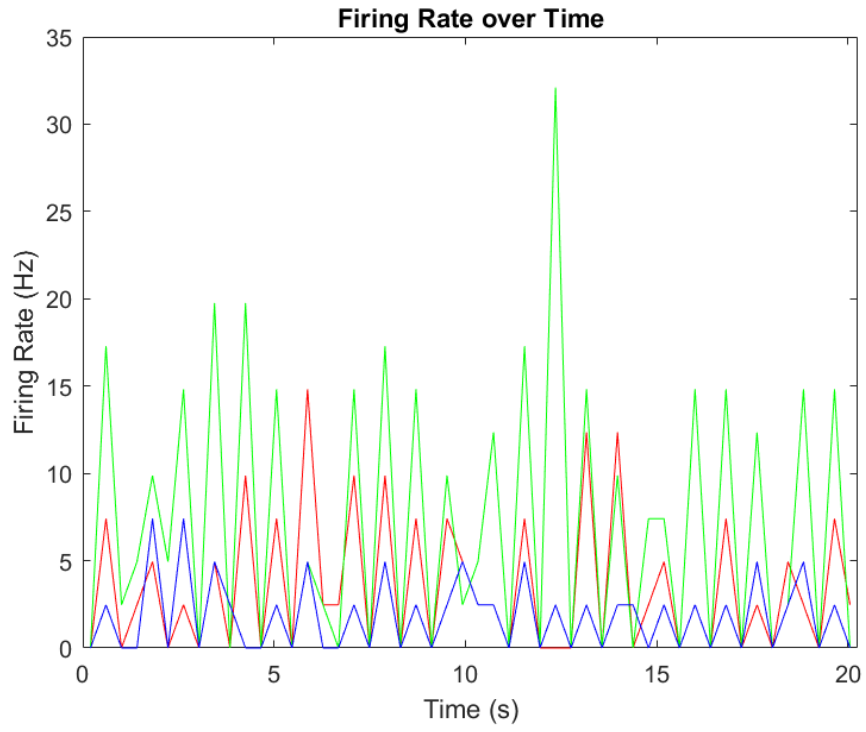


Figure 29: Firing rates calculated using bins

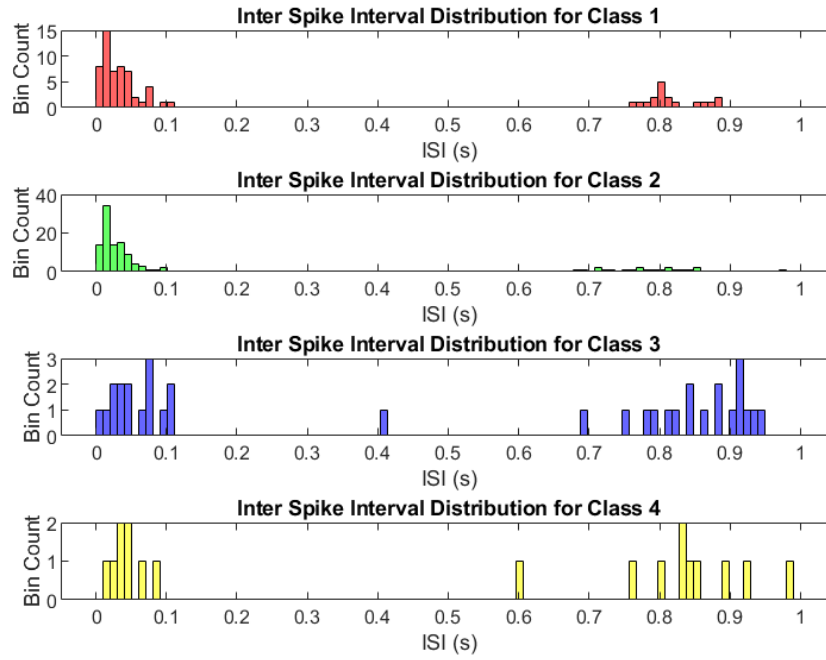


Figure 30: Distribution of times between spikes (ISIs)

Dataset 2

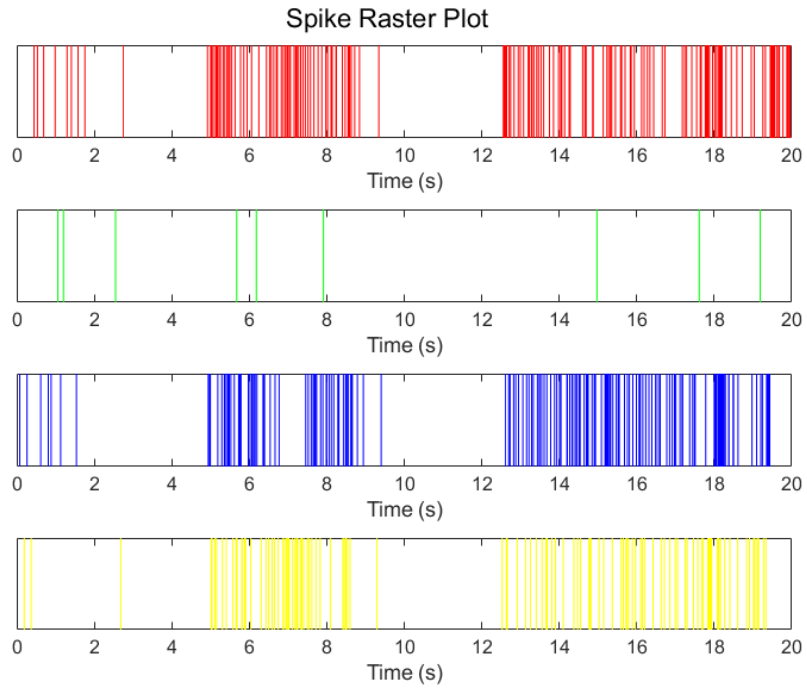


Figure 31: Spike rasters. Each line represents a spike at that particular time

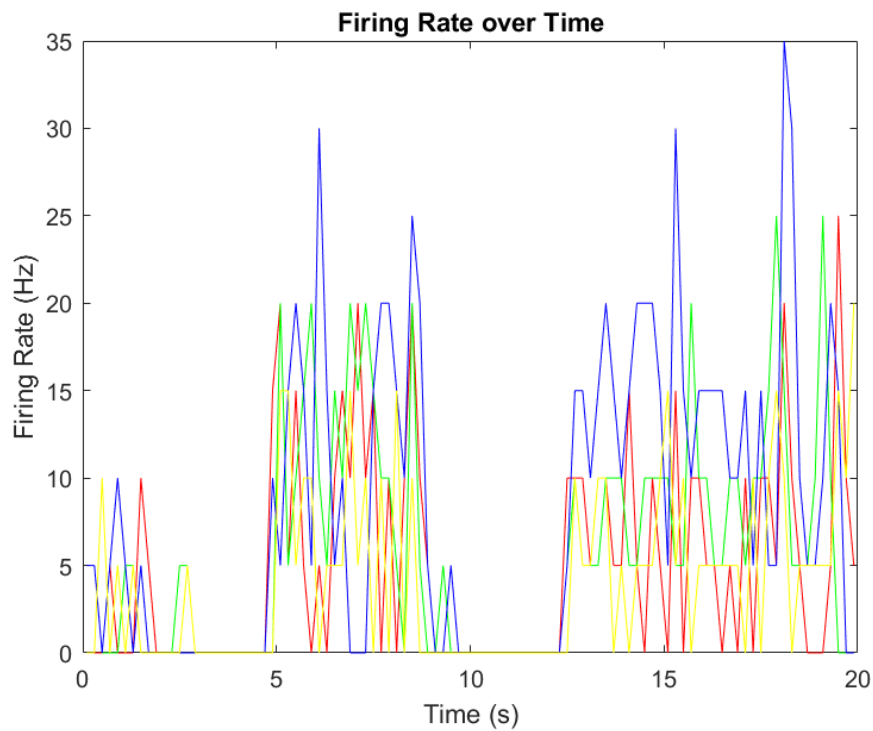


Figure 32: Firing rates calculated using bins

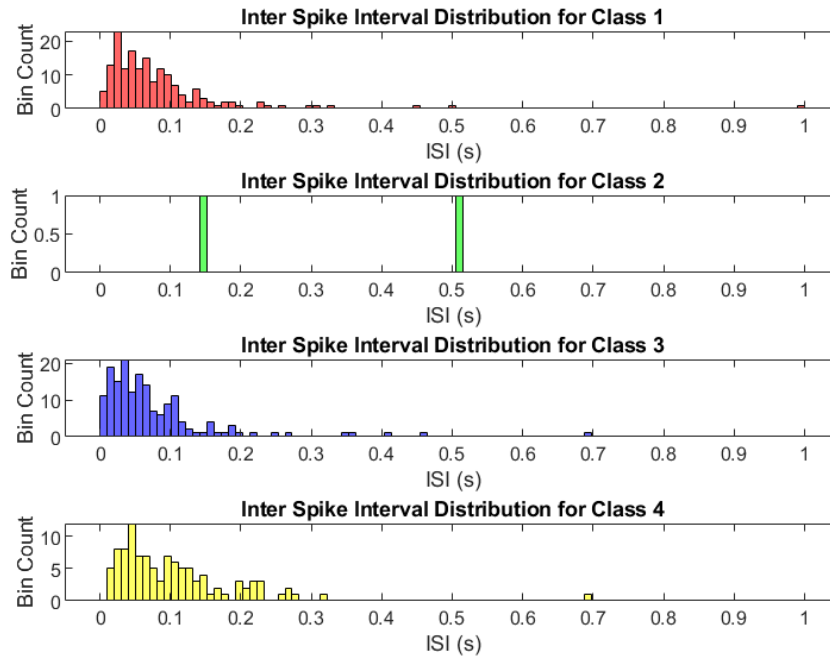


Figure 33: Distribution of times between spikes (ISIs)

Dataset 3

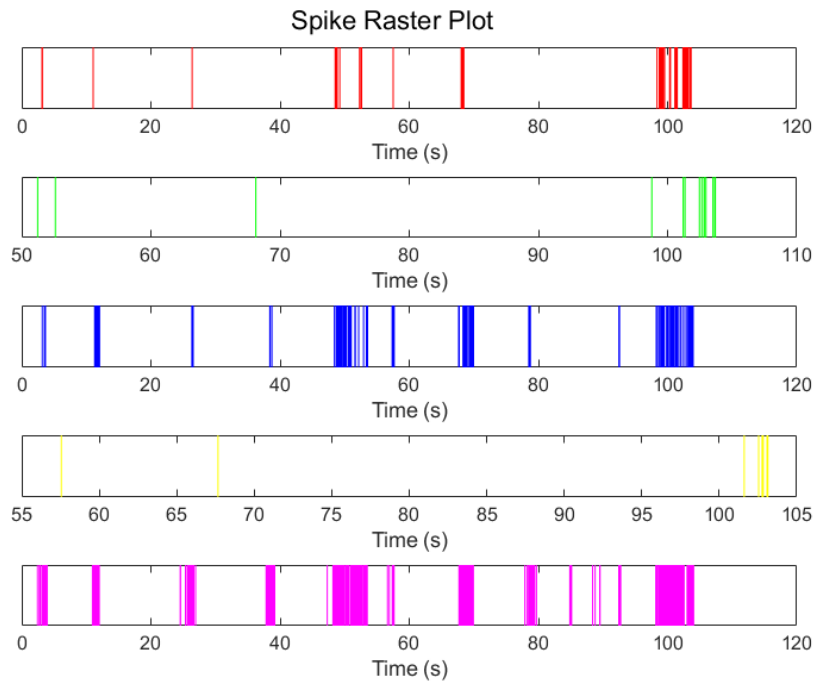


Figure 34: Spike rasters. Each line represents a spike at that particular time

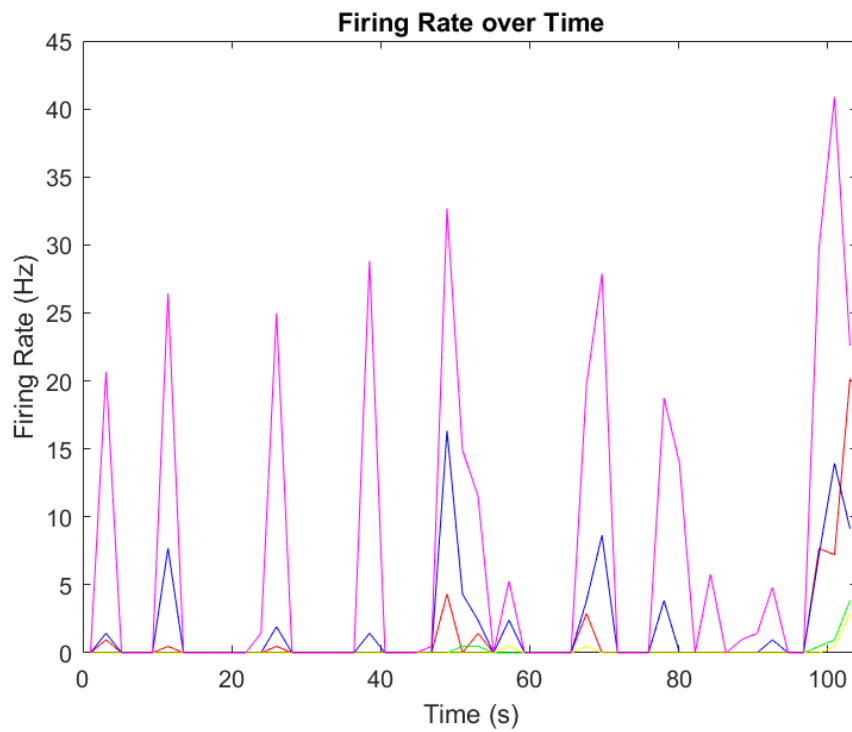


Figure 35: Firing rates calculated using bins

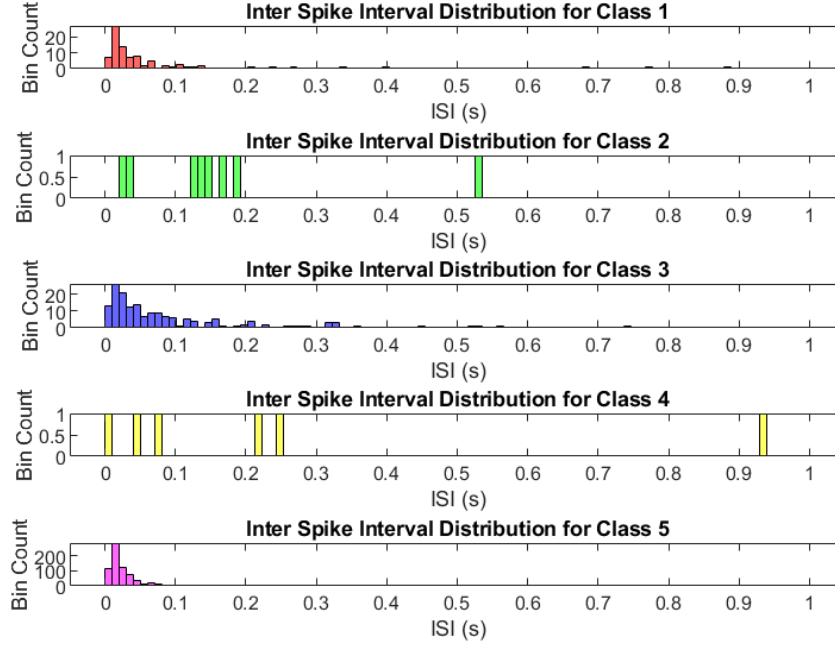


Figure 36: Distribution of times between spikes (ISIs)

The firing rates are generally under 20 Hz though some motor units spike at higher rates, especially the purple colored unit in Dataset 3. The spike raster plot and firing rate plots show that the units tend to fire in bursts. Michael Asmussen provides a potential explanation for this in a paper "...bursts of activity likely occur because motor units are constrained to fire temporally close to one another and thus the impulses are "clustered" with short delays to elicit bursts of muscle activity." [1] This data supports that theory.

A slow motor unit fires around 1 Hz, accordingly the ISIs in this dataset are only shown from 0s to 1s to make the count distribution visible. The ISI distribution can help give information about spike classification accuracy since motor units generally fire around the same frequency so if the ISIs are very spread it out (high variance), it suggests the spikes may not all be from the same unit. The ISIs in this data are generally distributed around a mean, though motor units with less spikes detected have more spread out ISIs. However, since a significant number of observations are necessary to determine the mean and variance of a variable accurately, it is difficult to gain information about whether these low count spikes are accurately classified from this. With more time, to improve accuracy I would have further investigated the ISIs that were larger or more spread out to determine whether the corresponding spikes were valid and classified correctly.

Conclusion

The lack of ground truth data makes quantitatively evaluating the efficacy of EMG decomposition difficult. Qualitatively, this pipeline appears to be fairly successful at dis-

tinguishing spikes with significantly different amplitudes and biphasic vs triphasic spikes. It cannot distinguish between spike pairs that occur very close together, since one of those spikes will be ignored during detection. It does not work well if there is a very large difference between the spike amplitude of different motor units. This is because the threshold is constant and so can be biased higher and thus miss lower amplitude spikes. An algorithm that adjusts the threshold depending on signal properties, like the EC-PC spike detection discussed by Professor Liu, could help address this issue. Using a filter that adapts to varying signal-to-noise ratios over the course of a recording could also improve results. Additionally, data with a significant number of artifacts can strongly impact results since artifact removal was not directly addressed in the pipeline. ICA could be used to help solve this.

Overall, this pipeline presents a straightforward implementation of EMG decomposition that is successful at detecting motor units with significantly different action potentials, provides informative visualizations, and creates a framework that can be built upon for improvement.

References

- [1] M. J. Asmussen, V. V. Tschärner, and B. M. Nigg, “Motor unit action potential clustering—theoretical consideration for muscle activation during a motor task,” *Frontiers in Human Neuroscience*, vol. 12, 2018.