

Sparse Representation and Possible Application for Neural Data from a Utah Array

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Abstract

In this paper, L_1 -minimization was used to reconstruct an accurate representation of the dataset of neuronal action potentials, using sample points from this dataset, with the peaks of the values in both the original data, and the reconstructed data being relatively equal. We found that with a higher percentage of sampling, we managed to get lower error rates. This can be extended to different applications such as determining which neurons fired a certain set of action potentials, using the interspike intervals (ISI) through K-means clustering.

1 Introduction

Analyzing neuronal data is a fundamental problem today. Not only are we limited in knowledge about the brain and its functions, actually collecting data and making reasonable conclusions can be difficult. There are so many processes occurring at any one time that it can be complicated to sample specific data without much noise. And even if noise could be eradicated, the data can vary. For example, in just a few seconds of sampling many action potentials from different neurons are recorded. Inherently, analysis of neuronal data is dependent on computer science to collect, measure and organize.

This paper develops three parts involved in neuronal data analysis: the formulation of a mathematical constraint problem derived from the collected data, proving and implementing the theoretical background that makes this constraint problem solvable, and discussing the results of the approach.

Formulation of the problem stems from making certain assumptions and observations about the data so that it mirrors the l_1 -minimization problem. Transforming neuronal data into this minimization allows sampling of a small percentage of this data. By reducing the problem size, performing operations on and distribution of data becomes simpler. Not only is sampling percentage reduced, but also analysis of the approach is discussed with respect to clustering action potentials to identify which neuron fired the action potentials in each cluster.

2 Neuroscience Background

The goal of this project is to build a system that will take a compressive sensing approach to sampling neuronal data collected from a single probe of a micro-electrode array (Utah Array), recreate it with enough accuracy to identify action potentials and inter-spike intervals (ISIs), and cluster the resulting ISIs. Utah arrays are compact 10x10 matrices of electrical recording spikes

that can be surgically implanted in the brain. The property of the signal that allows a compressive sensing approach is the scarcity of the occurrence of an action potential in the time domain. Since the recorded neuron is more likely not firing than firing at any given instance, the data can be considered sparse.

The probes on the Utah array work by determining the electrical potential created by neurons. Since the arrays cover an area of cortex larger than a single neuron, the resulting data collected can be assumed to cover multiple neurons. The benefit of this is that it allows for analysis of the firing in regions of the brain, instead of just along a single neuron. Neuronal data is transmitted by the frequency at which neurons spike, therefore the important component of the data is the ISI. A potential source of a problem with these probes is that they will record from all neurons that they touch. It has recently been shown though that it is the firing frequency in a small, localized region that is important, not the individual neuron.

Signals are transported along the lengths of the dendrites and the axon of a neuron in discrete signals known as action potentials. These signals are caused by the neuron actively pumping sodium, potassium, and calcium ions in and out of the cell membrane. These signals all follow a general pattern of an initial depolarization of the membrane, followed by a sharp hyperpolarization, and then depolarizing back to the initial starting potential. Because of this regularity of spiking patterns, the firing of different neurons can be analyzed together. This inflow/outflow of ions can be modeled by the Hodgkin-Huxley equation; an extension of the Nerst equation.

3 Mathematical and Computational Approach

Given this neuronal dataset, the goal is to fit it into the *l_1 -minimization problem*. This section explains firstly what the *l_1 -minimization problem* is and how it is solved algorithmically; then it shows how the data is transformed into a minimization problem; and lastly, it reviews the computational approach that was used to arrive at our results.

First, it is important to note that l_1 -minimization has a subset of problems. That is, there are different types of l_1 -minimizations; for example, there is one subset of l_1 -minimization with equality constraints while there is another with quadratic constraints[1]. The neuronal problem that is being solved is simply a matter of equality constraints. The *l_1 -minimization problem*, which can be modeled using the following program,

$$\min \|x\|_1 \text{ subject to } Ax = b \quad (1),$$

finds the vector with the smallest l_1 -norm,

$$\|x\|_1 := \sum_i |x_i| \quad (2),$$

that satisfies the results in b, where A is a $m \times n$ matrix, $x \in \mathbb{R}^n$ and $b \in \mathbb{R}^m$. Given that x is sufficiently sparse and that all values in A are mutually perpendicular and unit vectors, there exists a solution x_0 that satisfies the conditions[5]. There are a few possible algorithms used to solve this problem, including the *Primal-Dual Interior Point method*, which is the method used in this paper[2].

To even begin this method, equation (1) should be cast as a linear program as follows:

$$\text{minimize } c^T x \text{ subject to } Ax + s = b, s \geq 0 \quad (3)$$

$$\text{maximize } -b^T z \text{ subject to } A^T z + c = 0, z \geq 0 \quad (4).$$

Equations (3) and (4) are the inputs for the *Primal-Dual Interior Point method*, equation (3) being the primal minimization while equation (4) refers to the dual[2]. Using this linear program, we can apply the algorithm as follows[4]:

1. Initialize s, x and z , where s and $z > 0$
2. Compute residuals and evaluate stopping criteria (algorithm will end here)
3. Compute the scaling direction
4. Select the barrier parameter
5. Compute the search direction
6. Update iteration variables and return to step 1

The basic idea lies in the residuals, which can be defined as follows:

$$r_p = Ax + s - b, r_d = A^T z + c, r_g = s^T z \quad (5)$$

Once these residuals are calculated in step 2, steps 3-5 define the linearization of the three residuals within the predefined equations in (3) and (4)[4]. That is, the solutions for the equations are found. At each iteration a new solution is found until satisfy the stopping criteria. The stopping criteria for the algorithm is defined below:

$$\|r_p\| \leq \epsilon_{feas} \max\{1, \|b\|\} \text{ and } \|r_d\| \leq \epsilon_{feas} \max\{1, \|c\|\} \quad (6)$$

If both of these are satisfied then we must assure that the duality gap is at the proper level:

$$c^T x < 0 \text{ and } \frac{s^T z}{-c^T x} \text{ or } -b^T z > 0 \text{ and } \frac{s^T z}{-b^T z} \quad (7)$$

So at each step s, x and c must satisfy conditions (6) and (7); if this is not the case, then the algorithms terminates and we have found the vector x_0 which represents the value of the minimization[4]. This is the *Primal-Dual Interior Point method* used to calculate the minimized vector for the l_1 -minimization problem.

Since it is shown previously that the neuronal dataset is sparse, it can be used with the l_1 -minimization problem. In equation (1), x can be defined as a vector of n samples from the dataset, A is a $m \times n$ orthonormal matrix with unit vectors and b is a vector of m points from the original neuronal dataset[1][3][5]. To apply the compressive sensing technique of data recovery, the algorithm described above can be applied to this same data. The matrix A is computed, n samples are taken from dataset and then the equation and algorithm is applied. The result should be extremely similar to the original dataset.

Having the mathematical background and values necessary for this problem, the algorithm can now be applied. This was done using the *l1-magic* Matlab package, which makes it quite simple to perform these type of minimization[1]. More on the implementation of this

136 algorithm can be seen in the code provided.

137

138 **4 Results and Discussion**

139 The results of the project indicate several trends about the reconstructed data. First, the more
140 sampling that is used – in the case above, 40% of the original data was sampled – the higher the
141 accuracy of the reconstructed data when compared to the original data. The reconstructed data was
142 calculated to be 8.2616% different from the original data that was used, which indicates that while
143 there are a few deviant points which are drastically different from the original data, most of the
144 reconstructed data was relatively accurate to the original. In another experiment, the sampling
145 percentage was set to 0.15, so that 15% of the values from the original data set were used to
146 develop the reconstructed data. When this value was used, the percent error changed to -
147 14.3735%. The negative percentage indicates that on average, the reconstructed values were
148 smaller than the original values, and as it can be noted, the percentage magnitude is greater than
149 that of the data sampled at 40%.

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151 As a final experiment, the sampling amount was set to 65% of the original data. The result was
152 that the average error was -3.494%. The magnitude of this error is less than both of the previous
153 experiments, which demonstrates the understanding that more sampling means higher accuracy,
154 simply because more of the original data is being used in the reconstruction process. For these
155 calculations, the following percentage difference formula was used:

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$$\Delta x(\text{percentage}) = \frac{x - x_0}{x_0}$$

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159 for x being the reconstructed data and x_0 being the original data value.

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161 The second major observation taken from this experiment is that the time values of the peaks are
162 exactly the same. Several experiments were run, and the peaks of each signal – where peak is
163 defined to be the maximum positive value of a signal – from the original data set were in the exact
164 same location as in the original data set. This implies that the sampling method that was used,
165 which was the primal-dual interior point method, was able to accurately reconstruct the locations
166 of peaks. This was assumed to be due to the extreme values the peaks take with regards to the
167 other values in the data set. The max value of the peaks in the original data was over 238.7 times
168 higher than the average value of the data; for the reconstructed data, the max value was over 315.8
169 times higher per neuron spike. Because of this nature, the algorithm that was reconstructed could
170 readily identify and reconstruct this outlier value.

171

172 **5 Conclusion**

173 While our goal of producing an algorithm that identifies which neuron fired a given action
174 potential was not met, we are satisfied with our results. Dealing with data of such size can be
175 complicated. We made the correct analysis on our data, applied the mathematical
176 foundations that went with our analysis, and our results indicate that it worked. We were
177 able to sample at a rate of 15% and still have a solid recovery, as indicated by our error
178 results.

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180 The most important result, though, is always reproducing the action potentials in the data.
181 Plenty of noise is observed, but the action potentials were always recovered, and that is the
182 most important aspect of this project. A very important next step would be to deliver on our
183 goal. This could be done by calculating the interspike intervals (ISIs) of the action
184 potentials, applying the k-means algorithm to this set of ISIs, and use the result, a set of
185 clusters, to map a neuron to each cluster. This approach seems as it would work because
186 neurons fire at different frequencies. By applying k-means to the ISIs, we have clustered
187 with respect to firing frequency. This surely would result in positive identification.

Figure 1

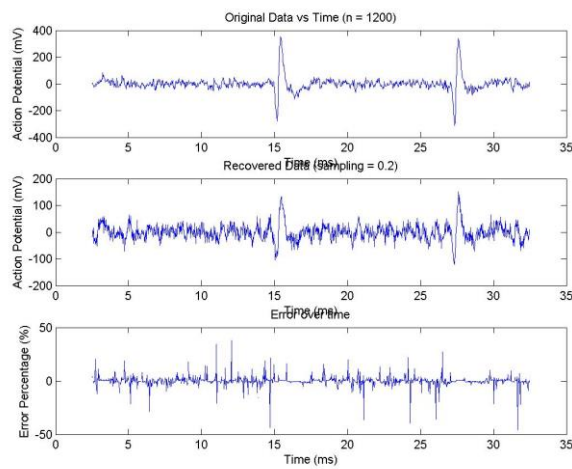


Figure 3

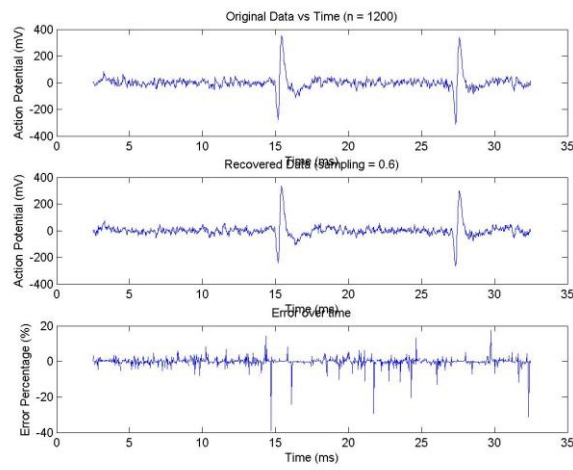


Figure 2

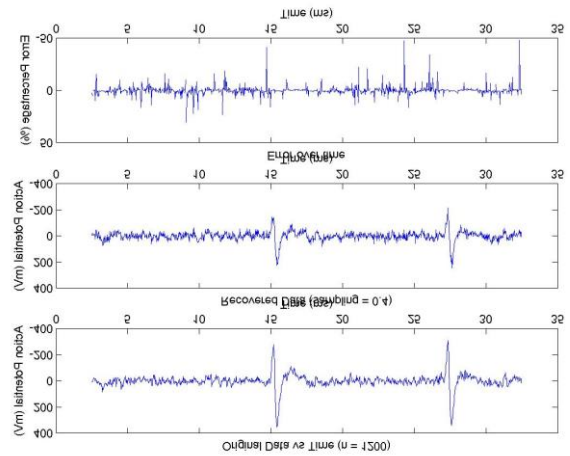


Figure 4

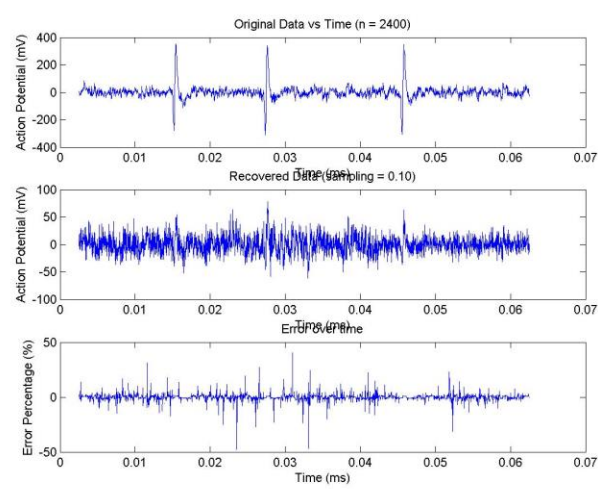


Figure 5

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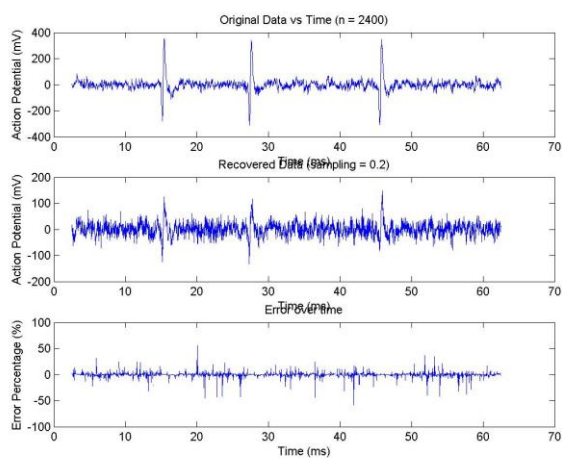


Figure 6

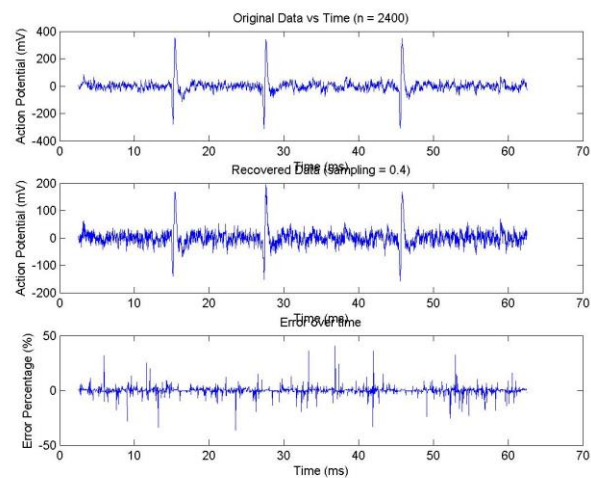


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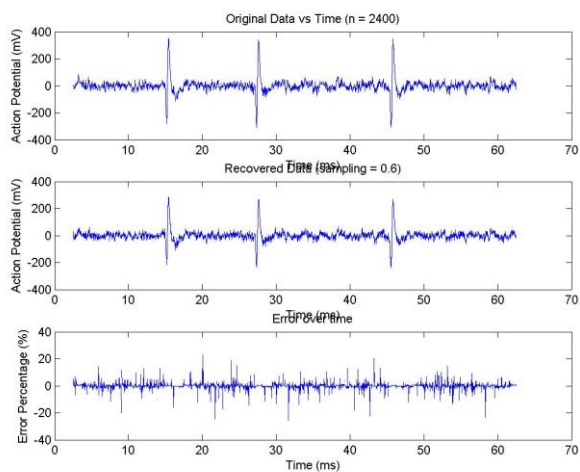
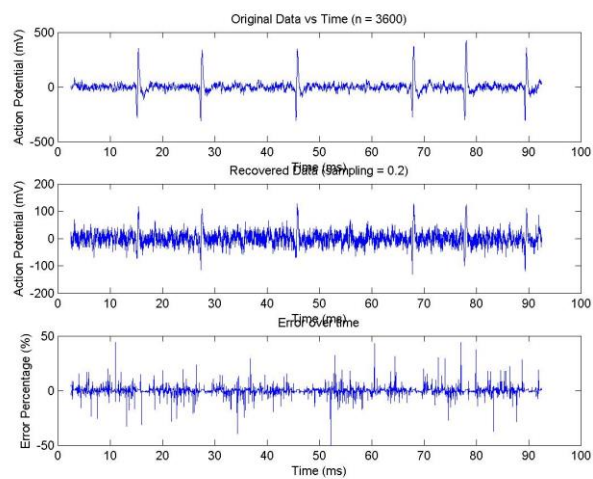


Figure 8



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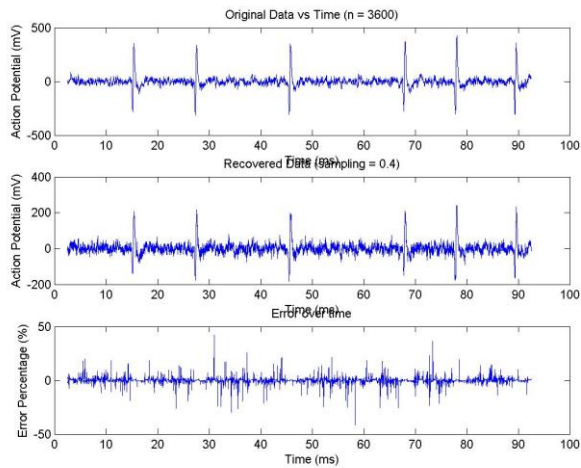
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Figure 9

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205 References

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