Honors Thesis Project Proposal for 2018-2019
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This project merges the mathematical field of algebraic topology with the analytic study of biological neural networks. My approach to this will consist of investigating the algebraic structure of neural networks found in biology and comparing them to different possible networks that do not occur in nature in an effort to discover why biology has favored one and not the other. Using the c. elegans connectome model and with the computational techniques of persistent homology, we are able to find out what features of a biological network are crucial to the dynamics that the network performs. Once we have sufficient knowledge of the dynamic structure of biological neural networks, we will develop an algorithm that will generate a neural network similar to those found in nature that will help computational neuroscience research in the future.

Double majoring in mathematics and neuroscience, the research I've been doing since sophomore year with my two advisors tries to apply both disciplines in the study of these biological systems. Although the mathematics I am the most interested in is rather pure, seemingly impossible to apply to the real world, there are a multitude of ways abstract mathematics can uncover hidden information in complicated biological systems. Participating in the EXTREEMS-QED undergraduate research program the summer of 2017 gave me valuable research experience in this interdisciplinary project. The combination of computer science, mathematics, and neuroscience used to tackle this problem have shown great success in learning more about the mathematical structure of these biological neural networks.

This project aims to gain insight into biological systems with relatively pure mathematics. So far, we have constructed a Hindmarsh-Rose neuron model using Python that exhibits dynamic behavior sufficient enough to simulate complicated multi-neuron coupled systems. Now that we can construct our own neural networks *in silico,* we will use software packages written specifically for computational topology to determine the algebraic properties of these networks. We can then compare different network structure with the c. elegans connectome, a complete map of the brain of a nematode, the only connectome to be mapped so far. Using previous research from Riemann et al., there is a distinct difference between the structure of the c. elegans brain architecture and randomly generated networks which implies that there are benefits to how these networks that occur in nature are constructed. We will then use this classification of neural networks to create an algorithm that generates neural networks similar in structure to the c. elegans connectome. Since most computational neuroscience research is dependent on neural network simulation, it will be extremely helpful to the field to be able to run simulations on networks that are consistent with the ones that actually exist in nature. A large portion of this project will be computational and so the simulations we run might grow in complexity as we approach larger and larger networks so the need to use the high-performance computing cluster might arise.

Only recently have biological neural networks begun to be studied in this way. The relatively young field of applied algebraic topology is currently exploding with research and my project is an attempt to contribute to the rapidly growing area of study. I have always been interested in combining different disciplines and I believe that

knowledge from one can often help uncover secrets in another. Pursuing a project in this interdisciplinary field will prepare me for my future as a researcher as I move on to graduate school to get my PhD in mathematics. This project takes seemingly incompatible ideas and merges them together which I believe is the direction that research is going. More interdisciplinary strategies to investigate complex problems are being taken to bring in new ideas and methods and my project aims to do exactly that.