I have long been interested in studying neuroscience. During high school, after losing three grandparents to Parkinson's and dementia and giving piano lessons to an adult with Downs Syndrome, my interests evolved to focus on neuropathology, in particular in the molecular and genetic mechanisms of the diseases that shaped the lives of my friends and family. Studying neuropathology is much like debugging code. You have an amazing, complex system, and something breaks. In a program, you would pour over thousands of lines of code running unit tests to in a sandboxed environment to uncover what variable or function call went awry. In the brain, you would examine millions of neurons by running molecular screens in a petri dish or animal models to uncover what gene or protein interaction went awry. But, in both cases, you have an incredible number of things happening behind the scenes, so you have to develop some sort of algorithm to identify potential problem areas before you start testing every possibility. That's where my interest in bioinformatics comes in. I like looking at big problems, be it a disease with hundreds of candidate genes or a graph with nodes of huge cardinality, and finding ways to isolate the signal from the noise to spot the missing link that is the bug in your code or the misbehaving protein in your cell. Furthermore, I want to do research in computational biology because I think it holds the key to solving a lot of biomedical problems whose solutions the entire community has been trying to unearth for decades.

In freshman year, I began research in neuropathology, joining a 3-year team research project in the Gemstone Honors Program under Dr. Matthew Roesch in the Neuroscience and Cognitive Science program. My team of eleven undergraduate students has so far independently applied for and won a grant from HHMI, applied for and received IACUC approval for our experiments, and presented once at a research colloquium, twice at campus-wide poster sessions, and once at the 2013 Society for Neuroscience Annual Meeting. We will be submitting our manuscript, "Impact of prenatal nicotine exposure on impulsivity and neural activity", for publication this winter, and will be publishing and defending our 150-page thesis before a committee in April. Our project measures signal-neuron activity in the medial prefrontal cortex (mPFC) in prenatal nicotine-exposed (PNE) rats performing the stop-signal task to correlate firing (or lack thereof) to behavioral measures. PNE is linked to several psychiatric disorders, including ADHD. Behavioral, neurochemical, and neuroanatomical disturbances following PNE and the benefits observed from methylphenidate treatment have pinpointed PNE rats as a potential model of ADHD. We used the stop-signal task, which measures inhibition of an already-initiated action, and performed single-unit recordings from cells in the mPFC. Consistent with our hypothesis, we found that PNE rats were faster and more impulsive, and that mPFC activity was modulated by trial direction and type. PNE mPFC neurons were overall hypoactive as compared to controls, but the directional encoding was not affected. This suggests that reduced firing in the mPFC may promote impulsive behavior and that general increases in mPFC activity might rescue the deficits observed following PNE. Thus, our research is the first connection between the cause, the behavior, and the underlying neural firing patterns.

For this research, I personally contributed to literature review, experimental design, data collection, designing and presenting all three posters, data analysis, and writing the results section. To supplement my research, I have taken courses in neural systems, diseases of the nervous system, and mammalian physiology, including a complementary lab emphasizing rat surgical techniques as a method for modeling human physiology.

Recently, I became interested in taking a computational approach to my research. After taking an algorithms course as part of my computer science major, I was eager to see how graph theory could be applied to finding disease targets in signaling and gene interaction networks, and

so I joined the lab of Dr. Sridhar Hannenhalli at the Center for Bioinformatics and Computational Biology. Here, I work on two projects, each with one other undergraduate student.

First, I research how the location of enhancers relative to the promoter affects the regulation in which that enhancer participates. Previous studies have found that there are many enhancers in introns and that first introns in particular tend to be highly conserved. We predict that intronic enhancers closer to the promoter will be involved in downregulation. We mapped p300-bound regions to either upstream of a gene or inside the introns of a gene, then calculated the Spearmann correlation coefficient between the DHS score for that site and the RNAseq score for that gene across 15 tissue types. We have found that in introns, more negatively-correlated, or downregulating, enhancers are found closer to the promoter, while the opposite trend is true in upstream promoters. Later, we will be looking at biological data, including ChipSeq to see if strong negative intronic enhancers are associated with strong TF binding sites, RNAseq for antisense RNA to determine if intronic enhancers are enhancing RNA polymerase action in the opposite direction, conservation scores to see if negative intronic enhancers are highly conserved, histone methylation to determine if intronic enhancers carry enhancer or promoter methylation marks, and motif enrichment to determine if particular motifs are involved in downregulation in intronic enhancers as compared to downregulation elsewhere. We intend to publish our manuscript, "Intronic enhancer function determined by distance from promoter", in spring. By uncovering the characteristics of intronic enhancers, we can better understand how the human genetic regulatory landscape really works.

Second, I am developing a pipeline to determine whether the intrinsic disorder characteristic of proteins is preserved via purifying selection. My work so far on this project, and an expansion I propose as a potential PhD thesis topic, are discussed in depth in my research proposal. I have presented my research so far once as a departmental talk and once at a campus-wide poster session and intend to submit our manuscript, "Natural selection of intrinsic disorder characteristic in proteins", for publication this winter. For both projects, I personally contributed to the experimental design, writing code, and data collection and analysis. For the second project, I also conducted the literature review and designed and presented both an oral presentation and a poster of our preliminary results. To supplement my research, I have taken courses in algorithms and bioinformatics.

Outside of my research and class, I tutor and teach, support the efforts of the Association for Women in Computing, and run the undergraduate research journal.

I was an organic chemistry volunteer tutor for two years and have been a teaching assistant (TA) for an algorithms course. Last year, I taught a 2-hour seminar on human evolution to high school students. This semester, I am a TA for a bioinformatics course, help answer student questions for a physiology course, and was invited to and gave a guest lecture in a senior-level physiology course. Next semester, I will be a teaching assistant for a physiology course, leading a discussion section for adults continuing their education. I have taken positions both to solidify previous coursework relevant to my research and to learn knew material. I have been able to give original lectures, run review sessions, help design homework, grade homework and exams, and work with students of all ages and backgrounds. Each teaching position has been an opportunity to challenge myself to learn how to better communicate material. I hope to continue my teaching in graduate school and throughout my career.

Since freshman year, I have been the webmaster for the Association for Women in Computing (AWC). In AWC, we reach out to incoming and freshmen students, who are most

likely to drop out of the major due to challenging beginning coursework and lack of peers in the major. We build a social structure for them, hosting weekly study sessions and meetings with faculty to help them discover their own potential. We also celebrate female professionals in the field by hosting professors and corporate leaders to speak in the hopes of inspiring our students further. Beyond the campus, we host camps and training days for middle and high school girls. Iin the future, I hope to bring my science to local grade schools whenever possible, especially in programs that are hands-on and aimed at ending the gender gap in the hard sciences.

I have also helped advance the spread of research by working for the undergraduate research journal. Our mission is to help undergraduate students at the University of Maryland communicate their research by accepting manuscripts, helping authors edit their papers so that they better express their work, and publishing news about science in and around campus alongside these manuscripts. For years, I was the webmaster and graphics chair, so I designed the layouts for both the print and online editions to encourage more students to read each volume in order to learn about current research on campus and encourage them to contribute to research themselves. In my junior year, I was also the editor-in-chief; I solicited submissions by meeting with deans of departments and honors programs, worked with section editors to ensure that all manuscripts were well-written, and coordinated deadlines across our five staffs. I hope to one day review manuscripts for an international journal to continue the dissemination of research.

I intend to earn a PhD in Biomedical Informatics, for which I am a unique candidate for 4 reasons: (1) I will be graduating with a Computer Science degree, which means I have a background in algorithms and coding that I will use to solve problems with a computational or informatics approach; (2) I have spent years giving presentations to audiences ranging from expert physiologists to elementary school students, so I have honed my communication skills; (3) I have developed decision making and team management skills from running the undergraduate research journal and working on a 3-year 11-person research team; and (4) I will have already completed a project similar to a group PhD by the time I graduate through the Gemstone honors program, including proposals, grant writing, thesis writing, and thesis defense.

I think that graduate school will help prepare me for a career in interdisciplinary research. First, the labs I am looking to work in have both wet lab and computer science lab aspects. In my ideal lab, I would start running a gel in the morning and write a script to analyze the data from that gel in the afternoon. Second, graduate school will give me additional training in how to design research projects, propose them to a non-scientific audience, and communicate your results effectively. Finally, graduate school will allow me to conduct an independently-directed research project uninterrupted by a heavy course load or extracurriculars, an opportunity I have only had during summer breaks in the past. I chose Stanford to help me reach these goals because their interdisciplinary Biosciences PhD program and Bio-X program would allow me to collaborate both with computational and clinical faculty. Finally, receiving the NSF fellowship will help me achieve these goals by allowing me to conduct research without needing to take teaching assistanceships to fund my education. It would also give me access to computational resources that I would need to run time-intensive algorithms.

I would like to make a career out of using a molecular systems approach to studying genetic regulation and protein interaction in neural diseases. I hope to work either for a nonprofit research group or a university where I can both conduct research and teach. I want to do research that is translational and not purely theoretical; I want my research to unveil new drug targets and pathological mechanisms and to create new software that others can use for medical research. Most of all, I want to bridge the gap between computational biology and biomedical sciences.