**Personal/motivation:**

It is August 2008, and there is a little blue house on an empty street speckled with houses and surrounded by forest. Just down the road farmers break the soil and their backs every year to turn sunlight into food for their families and the community, but this little blue house does not contain farmers, but rather a UPS driver, a stay-at-home-mom and their three boys, of which I was the middle child, then preparing to leave the countryside for Michigan State University, one of the largest universities in the United States.

Nobody in my family expected me to pursue higher education when I was growing up. Neither of my parents has completed a four-year degree and my parents were merely hoping I could graduate high school and stay out of correctional institutions. Early in adolescence I was socially awkward, angry at the world and convinced I was stupid. In school I was attacked nearly every week. Kids threw bricks at my head, jumped me in groups and slammed my face into lockers. I responded by fighting back, and became a short-fused explosive who would start brawls over any snide remark.

At the same time, I was bored with my classes and rarely tried. Everyone around me soon accepted my ineptitude, but after years of inadequate grades and low self-esteem, I finally decided I would put all my efforts into school to see if I could prove everyone wrong. Before long I was getting along with my peers and insisting on leaving my remedial classes, and later my generalized classes, and was placed on the advanced track. I had found something I was good at, and it fueled me. Furthermore, in tenth grade I met a biology teacher that exposed me to concepts in biology for the first time since I started paying attention. I was so fascinated by his lectures that I consistently stayed after class with additional questions and stayed after school for his Microbiology Club.

Therefore, after high school I decided to pursue my newfound thirst for biological inquiry at MSU, and in my first year I had the opportunity to get involved in a genetics lab under the guidance of Dr. Cornelius Barry. In his lab, I worked with other lab members towards answering questions regarding what genetic factors cause certain fruit ripening and terpene production phenotypes in both tomato (*Solanum lycopersicum*) and its cousins. Our research on terpene production was published in *The Plant Journal* in 2012. The paper attributed the unusually high intra-specific variation in terpene synthesis in the glandular trichomes of *Solanum habrochaites,* at least in part, to sequence variation in the *TPS20* locus. While I enjoyed doing wet-lab genetics work with Dr. Barry, I was also interested in exploring computational biology, so I took some computer programming classes and one introductory bioinformatics class.

In addition to taking these classes I wanted to do computational research to explore my interest. I therefore earned a position in Dr. Shin-Han Shiu’s lab where I had the opportunity to play a significant role in a project studying how whole genome duplication has affected gene evolution in the family Brassicaceae. As part of this project, we assembled the *Raphanus raphanistrum* (wild radish) genome and transcriptome from next-gen sequencing data. This data was used, along with genomic data from Arabidopsis thaliana, A. lyrata and Brassica rapa, to answer questions regarding the evolution of genome structure, duplicate genes and pseudogenes in plants. Our research for this project was published in 2014 in The Plant Cell. Moreover, I had the opportunity to play an active role in the writing process. I was exclusively responsible for several parts of the methods and results sections. This research helps us understand plant evolution better, and specifically what happens to genes after they are duplicated as the evolutionary forces acting on them are changed instantly. [pseudogenes project] The independence I received in the Shiu lab as well as my experiences designing my own computational algorithms, asking compelling biological questions and collaborating with other lab members significantly increased my affinity towards science and confirmed my suspicion that computational biology was the right field of research for me.

[other experiences that prepared me for PhD:

I am now a second year PhD student in Iowa State University’s Bioinformatics and Computational Biology (BCB) Program….[research] [TA]

Post-Doc and career in industry

Now, while I still enjoy my time with family and friends, I spend much of my time, both in and out of the lab, thinking about how to solve biological problems, and often stay late at the lab just because that is where I want to be. Doing research is what makes me happy and therefore, when it came time to decide whether to pursue a Ph.D. and continue research, I knew instantly that graduate school was precisely where I wanted to be.

I have questions about how the world works that keep coming back to me: How did so much diversity and complexity evolve in so little time? What secrets do intergenic sequences hold regarding the conversion of genotype to phenotype? Are the assumptions computational biologists use with their algorithms really the best we can do? These are the sorts of problems that buttress my interest in the more humble questions of my research, but to answer even those questions I needed the academic background to do the research that intrigues me.

**Background/Resume**:

In order to acquire the knowledge necessary to answer biological questions, I took several courses that were not required for my degree. I took 3 computer-programming courses and Introduction to Bioinformatics (PLB400). The programming courses were Introduction to Programming I and II and Software Design (CSE231, CSE232 and CSE335 respectively). In these courses, I familiarized myself with Python and C++ programming, the first of which I have used regularly for my research with Shin-Han Shiu. Furthermore, PLB400 provided me a general understanding of the kinds of problems that bioinformaticians solve, and helped me ultimately make the decision to join the Shiu lab.

Before joining the Shiu lab, I did undergraduate research for Cornelius Barry. In his lab, I worked with other lab members towards answering questions regarding what genetic factors cause certain fruit ripening and terpene production phenotypes in both tomato (*Solanum lycopersicum*) and its cousins. Our research for this paper successfully attributed the unusually high intra-specific variation in terpene synthesis in the glandular trichomes of *Solanum habrochaites,* at least in part, to sequence variation in the *TPS20* locus.

After realizing what really interested me was computational science, I joined Dr. Shiu’s lab where I had the opportunity to play a significant role in a project studying how whole genome duplication has affected gene evolution in the family Brassicaceae. As part of this project, we assembled the *Raphanus raphanistrum* (wild radish) genome and transcriptome from next-gen sequencing data. This data is being used, along with genomic data from *Arabidopsis thaliana*, *A. lyrata* and *Brassica rapa* to answer questions about the evolution of genome structure, duplicate genes and pseudogenes. This research will help us understand eukaryotic evolution better, and specifically what happens to genes after they are duplicated and their selective pressures are changed instantly.

In Dr. Barry’s lab, I worked with other students and scientists towards answering questions regarding what genetic factors cause certain fruit ripening and terpene production phenotypes in both tomato (Solanum lycopersicum) and its cousins. Our work on terpene synthesis was published in *The Plant Journal* in June 2012. Our research for this paper successfully attributed the unusually high intra-specific variation in terpene synthesis in the glandular trichomes of Solanum habrochaites, at least in part, to sequence variation in the TPS20 locus.

In the Shiu lab, I had the opportunity to play a significant role in a project studying how whole genome duplication has affected gene evolution in the family Brassicaceae. As part of this project, we assembled the Raphanus raphanistrum (wild radish) genome and transcriptome from next-gen sequencing data. This data is being used, along with genomic data from Arabidopsis thaliana, A. lyrata and Brassica rapa, to answer questions regarding the evolution of genome structure, duplicate genes and pseudogenes in plants. The project is nearing completion, and we have therefore begun the process of preparing a manuscript. Moreover, I have had the opportunity to play an active role in the writing process. This research helps us understand plant evolution better, and specifically what happens to genes after they are duplicated and the evolutionary forces acting on them are changed instantly.

**Future:**

I have enjoyed doing evolution and genomics research using computational methods, and therefore desire to continue doing this sort of research in graduate school. After earning my Ph.D., I plan on seeking a post-doctorate and then starting my own evolutionary genomics research lab either as a professor at a university or a private research institute.

**Conclusions:**

In conclusion, my academic and research background has inspired me to pursue a Ph.D. in computational biology, and MSU would be a suitable university for my graduate studies. MSU is a fitting school for me because of its BMS and QB programs and the vastness and variety of research and faculty that interests me. Earning my Ph.D. at MSU would allow me to acquire the training necessary to obtain a post-doctorate degree and ultimately start my own evolutionary genomics research lab while simultaneously catalyzing my growth as a computational biologist.

In conclusion, my academic and research backgrounds have inspired me to pursue a Ph.D. in evolutionary genomics and computational biology. Furthermore, the joint CMU-Pitt Computational Biology Program is fitting for my graduate studies because of the vastness and variety of faculty and classes that interest me. Biological inquiry in general is becoming increasingly dependent on computational work, and I believe many of the most important questions in medicine, neurobiology, ecology, evolution will be answered using computational methods. This is why it is important to train computational biologists who are prepared to solve these problems. I believe because of my drive and my academic and research backgrounds, this program would allow me to develop as a computational biologist and acquire the training necessary to independently conduct my own research and join the effort to explain our world.