Tyler Shimko
Statement of Purpose

I first came to appreciate the power of biological research in my high school biology class. Through the instruction of my incredibly devoted teacher, I recognized that genomic research had the power to make predictions about and alter the traits of living creatures. Upon graduating from high school, I chose to attend the University of Utah, where, with the help of the school's Office of Undergraduate Research, I had an immediate opportunity to become deeply involved in research and pursue my interests to the fullest. Since beginning my undergraduate studies, I have been fortunate to take part in research at three universities and participate in projects ranging from molecular biology to neurobiology to quantitative genetics. Through these experiences my appetite for discovery has only grown. I now seek to undertake the next step in my scientific education, the pursuit of a PhD, to prepare myself for a career in research.

Over the course of my undergraduate career, I have sought every opportunity to delve further into the process of research. As a freshman, I began attending the genetics research seminar series held at the University of Utah's Eccles Institute of Human Genetics. During my sophomore year, while conducting research in Dr. Erik Jorgensen's lab, I initiated a weekly undergraduate lab meeting, an informal gathering where the undergrads in the lab could share their work and experiences. I have found scientific communication and outreach to be a fascinating component of the research process. Consequently, I participated in extracurricular activities that have opened the door for others to become aware of or involved in research.

I was fortunate to gain access to academic research early at the University of Utah through the university's Office of Undergraduate Research. To provide my fellow students with similar opportunities, I joined the office as an Undergraduate Research Ambassador and Advisor. In this position, I was able to talk with students and prospective students about the unique opportunities that research had afforded me and direct them to laboratories and research groups pertinent to their interests. I also helped to set up and oversee the university's annual Undergraduate Research Symposium, which allowed me the chance to get to know the projects of my fellow students. While attending the Undergraduate Research Symposium, I recognized that the most interesting and effective presenters were those who could most accurately and succinctly describe their research to a non-expert. To improve my own communication skills, I applied for a position on the Public Library of Science's Student Blog. I realized that the Student Blog would be an excellent platform for me to experiment with different communication styles and to have an audience outside of my area of expertise, an opportunity not necessarily available through traditional academic publishing channels.

In my writing for the Student Blog, I have focused on developing, broadly applicable topics within the biological sciences. For instance, my most recent post discussed the implications of increased experimental automation within biology, especially as it relates to molecular biology and the phenotyping of model organisms. I have learned a great deal about effective communication in my experience writing for the blog. I hope to one day apply these communication skills alongside my wide array of research-related skills as a professor and researcher at a major research university.

In addition to my outreach efforts, I have also had fantastic opportunities to make substantial contributions to the scientific community. In the lab of Dr. Erik Andersen, I was given freedom and guidance that few other undergraduates get to experience in their research. Over the course of a summer, I developed a complete suite of software to read, clean, and analyze data from the lab's high-throughput screening experiments. I recognized the importance of my work as a time-saving device for many other labs using similar screening hardware. Accordingly, with Dr. Andersen's permission, I taught myself the basics of R package

development so that I could assemble the functions that I had created into accessible tools for the broader research community. I generalized all of the code that I had developed to be applicable to a wide array of potential research questions and built them into a package complete with documentation and examples. This package was then submitted to the Comprehensive R Archive Network. To share this work with the greater community, Dr. Andersen suggested that I submit a paper covering my package to an academic journal. Over the course of the next several weeks I drafted, refined, and submitted a paper detailing my package to the journal *PLOS ONE*, where it was subsequently published. This experience of being heavily involved in the development and writing processes of science allowed me to truly grow as a researcher and prepared me well for the increase in responsibility that will come with my transition to graduate education. Throughout this work, I have been unwavering in my commitment to the open dissemination of scientific knowledge.

Throughout my research career, I have attempted to maintain a commitment to openness and transparency in both my academic and professional development. I have made a great effort to ensure that all software that I write is publicly accessible and licensed in such a way that allows for free reuse and modification. I have made use of available tools, including GitHub, to make outside contributions to my work easy to integrate. Additionally, I have chosen to publish my work in an open-access journal to ensure its widespread distribution. As I move forward in my academic career, I plan to continue this commitment to open, accessible, and reproducible research. I believe that by lowering barriers to research through the way in which results are published and made accessible growth within the sciences can be fostered.

Most recently, I have become deeply interested in the large-scale analysis of genomic data. I want to refine the methods used to connect phenotypic traits back to specific genomic variants, especially with respect to human disease. This problem is interesting from both a biological and a computational perspective. In order to accurately and efficiently connect physiological traits to genetic differences, a massive amount of phenotypic and genotypic data must be collected and analyzed. This problem is pertinent to many facets of modern human health. Genomic information utilized in the diagnosis and treatment of certain diseases has proven to be a paradigm-shifting development in medicine. During my tenure in a PhD program and through my career as a researcher, I will work to confront the theoretical, logistical, and scientific challenges related to problems in quantitative and population genetics.

I have selected UCSF because of the extraordinary faculty working within my areas of interest. Specifically, I am interested in the work of Drs. Noah Zaitlen and John Witte, who have both closely examined the role of genetics in human disease. Dr. Zaitlen's research group has contributed a wide array of computational tools to the study of gene-environment interactions. Likewise, Dr. Witte's group has contributed significantly to the analysis of genome-wide association data. I am also interested in the work of Dr. Sergio Baranzini, who has combined the computational and statistical methods of quantitative genetics with classical genetics techniques in a model organism to elucidate the molecular mechanisms disease. Additionally, the work of Drs. Mark Seielstad and Ryan Hernandez provides an interesting perspective from which to address issues of genetics and human disease. Both Dr. Seielstad and Dr. Hernandez have studied elements of population genetics and begun to apply this information to the interplay between disease and genome evolution. The mentorship that I will receive from faculty at UCSF will prepare me exceptionally well to begin a career in research.