

Kenyon College applicant majoring in Molecular Biology who applied to the UCSF SRTP

High-throughput DNA sequencing has forever changed molecular biology. We can now study genetic interactions at unprecedented resolution. The ever-increasing volume of genomic and transcriptomic data this technology produces has been accompanied by new tools and methods for studying living systems. I want to explore the emerging field of systems biology and use high-throughput sequencing methods to study how transcription networks evolve to create new traits.

After completing my undergraduate degree, I intend to pursue a PhD in systems biology, and later, as a professor at a research university, start a research program studying the evolution of transcription networks. I am fascinated by the coordination of cellular processes, and how the structure of regulatory networks can produce functions beyond the effects of gene products themselves. While reductionist methods in molecular biology and biochemistry have been successful at determining the mechanisms behind many processes, there are even more open questions regarding the interactions between genetic circuits. I want to study how living systems perform computations using signals from the environment and networks of transcription factors.

Over the past five semesters, I have been involved with molecular biology and microbial genetics research. During this time, I have learned both computational and wet-lab skills that I will continue to develop in graduate school. As a molecular biologist, I have focused on understanding living systems in the context of chemical interactions. For example, using thermodynamics and chemical kinetics to understand metabolic pathways and enzyme mechanisms. Additionally, my curriculum puts great emphasis on developing computational and statistical skills in both lecture and lab courses. To further develop these skills, I have taken a course in computational genomics, where I used the statistical programming language R and unix shell scripting to study population genetics, transcriptomics, and co-expression networks. I have also written computational workflows to automate analysis of flow cytometry and growth curve data for the lab I research in at Kenyon.

The UCSF program is especially interesting to me because of the wide variety of bioengineering projects available, and the amazing research resources available at the institution. In particular, I am interested by projects like those in Dr. Marshall Wallace's lab. His group uses imaging, genetics, and computational methods to study how cells solve geometrical problems. I want to learn how to combine such methods for my own research, so I would value an experience with Dr. Wallace or similar groups at UCSF.