

STATEMENT OF PURPOSE: UNIVERSITY OF OREGON BIOLOGY PH.D.

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Quantitative biology research has opened new horizons for human health and understanding of the forces driving evolution. With recent advances in technology, genetics research, and access to large datasets, the field has become more equipped to solve complex problems that will play a large role in current and future generations to come. I am applying to graduate school because I believe it is a necessary challenge to nourish my biological skill set and interest in quantitative problem-solving. This training will present an opportunity for me to leverage my computational background and to help find creative solutions to problems facing the field at an exciting time for biology. Moving forward, I would like to help progress the field and participate in the discussions that define our understanding of complex systems. My professional goals are to build tools (software) that biologists can use to help solve a wide variety of problems in genetics research.

My undergraduate degree in Computer and Information Science has provided a background in algorithms and data structures best suited for particular styles of problems, as well as the programming skills needed to implement them. The research I have participated in has brought to light the wide variety of problems in genomics for which a computational approach is necessary. These problems include things like inferring genealogical ancestry given a set of sample haplotypes, or training neural networks to make predictions on causal loci. As sequencing becomes more efficient, and the number of samples grows larger, we stand to gain an immense amount of insight using modern computing methods. The current advances produced by biology experts, along with the flood of data we anticipate, has shaped an exciting future for genetics that I am eager to be a part of.

A large portion of the results I have produced thus far, have relied heavily on the software which has been released to the public. My latest research project has involved using deep learning to infer recombination rates. For this and many other related projects, my lab is dependent on a range of tools: Tensor Flow for efficient machine learning, SLiM and msprime for simulating large and complex datasets, and a broad spectrum of software for analyzing results. Using these tools, our trained neural nets are currently outcompeting with industry standards such as LD Hat. Software engineering has proven to be an extremely effective method at abstracting complex scientific concepts into convenient building blocks such that researchers can tailor them to their specific needs. Working on the implementation of *Tree Sequence Recording* in SLiM (see CV for details), has sparked my interest in providing, maintaining, and improving the tools that other researchers may use to make progress in the field.

Through graduate training in biology, I aspire to be truly interdisciplinary. Lying at the intersection of computer science and biology, I strive to effectively communicate with experts on both sides, so as to bridge the fields. As discussions surrounding things such as gene therapy, precision medicine, and genomic security become closer in proximity to our reality, I hope that my research will contribute to the progression of quantitative biology. The Institute of Ecology and Evolution at the University of Oregon has proven to maintain close ties with other departments such that we may see the full benefit of working with other fields. I believe working in labs such as the Ralph and Kern lab will present an opportunity for me launch my career.