## Chris Talbot – Statement of Purpose, UC-SC Ecology & Evolutionary Biology PhD

**Research Interests**

Driven by my experience and long-standing interests in environmentalism and programming, my research interests focus on developing computational and statistical methods to study evolutionary adaptation. Understanding the mechanisms underlying adaptation is crucial for predicting how species can respond to future change, enabling conservationists to allocate resources effectively by targeting populations at greater risk of extinction or with higher chances of long-term survival. To this end, using spatiotemporal population genomic data, I aim to infer the relative strength, importance, and timing of evolutionary processes such as selection, drift, and gene flow in natural populations. These data encode information about evolutionary patterns and processes over contemporary timescales and across landscapes. Inferring evolutionary processes using these data will provide unique insights into the tempo and mode of evolution and the potential of species to adapt to future climate and other human-induced changes.

**I would be excited to develop a research program at the University of California-Santa Cruz that centers around the following questions:**

1. How do spatial and temporal patterns of genetic variation inform our understanding of population demography and local adaptation?

2. In what ways can computational and statistical methods be enhanced to better infer evolutionary processes from complex genomic data?

3. How can insights into the evolutionary mechanisms of adaptation help predict species resilience under future global change?

I am particularly eager to work with Dr. Malin Pinsky. His interests in temporal genomic methods for analyzing cod adaptation to change align closely with my interests. I also appreciate his emphasis on open and collaborative approaches to science. Our discussions have helped shape my research interests, including my NSF GRFP proposal, which discussed novel machine learning approaches to inferring fisheries-induced evolution from temporal and spatial cod genomic data.

**Relevant Experience**

At age 11, I programmed my first Minecraft mod, setting forth my interests in programming and problem-solving and defining my career trajectory. The first in my family to attend college, I studied computer science during my Associate's degree before transferring to the University of Michigan. Seeking ways to align my skills and environmental interests, I declared a major in Ecology & Evolution, seeking to use my quantitative skills to solve environmental crises. I built computational skills in discrete mathematics, algorithms, proof-based real analysis, and linear algebra while engaging in rigorous biological coursework, including macroevolution and genetics.

In Dr. Roberto Márquez's lab at Michigan, I gained hands-on experience developing CRISPR techniques in poison-dart frogs to study the evolutionary and genetic mechanisms

generating aposematism. A Biomedical & Life Sciences Fellowship allowed me to research full-time for a summer. After completing that project, I began independent research on spatiotemporal floral community dynamics, asking whether flowers of a color bloom together with Dr. Marjorie Weber. I developed a Python program to extract floral color from thousands of iNaturalist images and used mixed models to analyze relationships among floral color, distributions, and phylogeny across 1,000+ species. I discovered that close relatives that overlap in time and space tend to display more disparate floral colors than expected by chance, receiving Highest Honors for this work. I have an associated first-author manuscript in preparation.

Now, as a computational technician in Dr. Gideon Bradburd's lab at Michigan, I directly engage with population genetics by testing and documenting *gaia*, a statistical method implemented as an *R* package that leverages Ancestral Recombination Graphs to infer the spatial locations of a population's ancestors. Using *SLiM* simulations, I am examining the impact of temporal sampling schemes on inference accuracy. I am also developing an interactive map dashboard to visualize *gaia* inference. This experience has solidified my passion for population biology and provided expertise in modern techniques, setting me up for success in designing new, robust models of evolutionary processes at the University of California-Santa Cruz. Additionally, I've honed my programming skills in the context of large projects, preparing me to develop complex new programs and software to contribute to the computational biology ecosystem at UC-SC and at large.

**Looking Forward**

Ultimately, I aim to pursue academic careers to leverage my computational skills to understand further how biodiversity will respond to global change. The Ecology & Evolutionary Biology PhD program is the best place to leverage my strengths to contribute to biodiversity research. My proposed advisors and other potential collaborators across the department and school provide the optimal network to advance my research program and gain a well-rounded perspective on approaching complex problems in evolutionary biology. Further, UC-SC stands out as one of the leaders in computational biology. Though my research interests prioritize evolutionary biology and global change, my interest in computational approaches would benefit from access to some of the leading computational biologists in academia, both as instructors and collaborators. I hope to contribute to Santa Cruz's diverse, rigorous, and forward-thinking academic environment soon.