

Chris Talbot – Academic Statement of Purpose, Cornell Computational Biology PhD

I began developing computational skills at age 11, when I learned to program Minecraft mods from Codecademy and YouTube. I continued learning throughout middle and high school, designing custom websites, phone apps, and command line programs. As a first-generation student, pursuing a college degree hadn't crossed my mind; but, I realized I could apply my computational skills to solve problems I cared about, particularly biodiversity loss and global change. To pursue this goal, I enrolled at Grand Rapids Community College, completing courses ranging from environmental science to C++ programming.

Transferring to the University of Michigan, I completed courses in discrete mathematics, data structures, algorithms, and the rigorous *Honors Mathematics I*, where we went from learning to write proofs to proving theorems in real analysis, abstract algebra, and topology over a single semester. In parallel, I discovered research through Michigan's undergraduate research program for transfer students. My first experience was in Dr. Roberto Márquez's lab, where I gained hands-on experience developing CRISPR techniques in non-model organisms (poison-dart frogs). A UROP Biomedical & Life Sciences Summer Fellowship allowed me to continue this work full-time for one summer and deepened my interests. Deciding to pursue biological research as a career, I switched majors to Ecology & Evolutionary Biology and transferred labs to gain diverse perspectives.

Later, with Dr. Marjorie Weber, at the University of Michigan, I conducted independent research on spatiotemporal floral color community dynamics. I developed a Python program with a Graphical User Interface to extract mean floral color from thousands of iNaturalist images and used generalized linear mixed models to analyze relationships among floral color, distributions, and phylogeny across 1,000+ species. This work culminated in an honors thesis for which I received Highest Honors in Ecology & Evolutionary Biology. I also presented my work at multiple international conferences, including Botany and Evolution, and I am currently preparing a manuscript for publication as first author.

Currently, as a computational technician in Dr. Gideon Bradburd's lab at Michigan, I am directly engaging with spatial population genetics and method development. I help develop and test *gaia*, a method that leverages Ancestral Recombination Graphs to infer the spatial locations of ancestors given georeferenced genomic samples. In addition to identifying potential optimizations, I am using *SLiM* simulations and the *tskit* Python API to test the impact of various spatial and temporal sampling schemes on *gaia*'s inference accuracy. This experience has solidified my passion for evolutionary inference, provided expertise in modern techniques in population genetics, and has set me up for success designing new, robust models of evolutionary processes.

Driven by my experience and long-standing interests in environmentalism and programming, my research interests have come to 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, I aim to infer the relative strength, importance, and timing of evolutionary processes such as selection, drift, and gene flow in natural populations using spatiotemporal population genomic data. 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 not only

into the tempo and mode of evolution but also into the potential of species to adapt to future climate and other human-induced changes.

I would be excited to develop a research program in my graduate studies that centers around the following major 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 aim to emphasize purposeful discovery throughout my career. Collaborating with researchers across fields, bridging theory, experimentation, and application, my research will explore innovative methodologies while directly addressing real-world problems. Cornell offers the ideal set of interdisciplinary collaborators (across Computational Biology and other departments) and computational resources for me to pursue my academic goals.

I have already had extensive conversations with three faculty at Cornell who I would be excited to work with. Dr. Philipp Messer's experience studying rapid evolution and developing methods for evolutionary inference align closely with my goals. Our conversations regarding potential projects in his lab have helped me refine and solidify my research interests.

Another faculty member at Cornell who I have discussed potential collaboration with is Dr. Daniel Anstett. We have discussed sequencing DNA from herbarium specimens to generate land plant spatiotemporal genomic datasets. These data could then be used to investigate how plants adapt to changing climate, particularly drought conditions. This work would contribute significantly to our understanding of how global change will impact biodiversity from a unique evolutionary standpoint, furthering the goals of the Biodiversity Initiative at Cornell.

I have also been in contact with Dr. Nina Therkildsen, whose interest in using time series genomic data to understand human-induced evolution suits my proposed research program well. With Drs. Messer and Therkildsen, I developed a GRFP proposal using deep learning on ancient DNA time series to infer fisheries-induced selection, which is currently being reviewed by NSF.

Ultimately, I aim to leverage my computational skills to further our understanding of how biodiversity will respond to global change. I admire Cornell's dedication to biodiversity research as highlighted by the Biodiversity Initiative, and I believe the Computational Biology PhD program is the best place for me to leverage my strengths to contribute to biodiversity research. My proposed advisors at Cornell provide the optimal network to advance my research program, and through collaboration or co-advising arrangements with these and other theoretical and empirical-focused faculty at Cornell, I can gain a well-rounded perspective on how to approach complex problems in evolutionary biology. I hope to soon begin contributing to Cornell's diverse, rigorous, and forward-thinking academic environment.