The Impacts of Global Change on Community Stability and Community Assembly

Given the field of ecology's pervasive interest in community stability and community assembly, the impact of global change on these processes requires deeper understanding. From decreased seed viability from changing temperatures[1] to increased death rates among aquatic vertebrates from habitat toxification[2], changing environmental factors can increase species' mortality rates. Increased mortality rate can have substantial impacts on a population and its community, such as extinction or community collapse, respectively. Previous theoretical work on understanding the impacts of environmental change on community composition assumed species are lost instantaneously[3]; however, in reality, environmental changes occur more gradually, decreasing population density continuously due to increasing mortality rates. Neglecting to explicitly model this phenomenon results in the loss of pertinent biological information such as the extinction of a non-perturbed species prior to the perturbed species due to mutualistic or predator-prey interactions. These earlier studies also failed to account for the process of community assembly. Notably, environmental changes may lead to conditions that allow for other species to invade and alter the community composition[4]. **I propose to develop a theoretical framework to understand how changes in species' mortality rates impact community stability and community assembly.**

Methods: To model the dynamics of the ecological community, I will use general Lotka Volterra (gLV) equations. The gLV equations model species' densities within a community over time using two sets of parameters: a matrix of pairwise species' interaction strengths and a vector of species' low density growth rates. The gLV model is a commonly used model of species interactions, has a well-developed mathematical theory, and has been empirically parametrized for a diverse set of ecological systems.

New mathematical theory for the gLV equations identifies what subsets of species can coexist and possible transitions between these communities due to species invasions[5]. This theory is based on invasion growth rates, defined as the average per-capita growth rate of a species when rare, from modern coexistence theory. By harnessing these approaches, mathematical structures, known as invasion graphs, explore the interplay of species coexistence and community assembly[5]. In this adapted approach, I will restrict the model to exclusively single-species invasions and communities accessible through a series of single-species invasions from an empty community; this Community Assembly Graph (CAG) (Figure 1) has nodes (states) represent possible coexisting communities and the directed edges represent transitions between states due to species invasion.

Community assembly either terminates at an end state (a community resistant to invasion attempts from the remaining species) or may cycle indefinitely between different communities due to continuous species invasion. Following a change to a species' mortality rate, an end state may change due to loss of a species or due to a species being able to invade that was previously unable to. To understand this process, I will identify if an end state exists by detecting if there exist any nodes with no outgoing edges. Then, I will change the mortality rate corresponding to the species of interest (the focal species)

Figure 1: Example of a CAG with species 1-6. End states depicted in yellow.

and study the corresponding end state. This will allow me to understand how the community assembly process changes with the mortality rate of a population.

Aim 1: As the mortality rate of the focal species increases, there will be a change in community composition at a critical threshold. To assess the stability of the end state, **I will identify how much of an increase to a species' mortality rate is required to alter the end state's community composition**. Conducting this analysis for each species within the end state's community, I can address if communities are more resistant to perturbations of some species than others.

Aim 2: Once I have determined when the composition changes following perturbation to the focal species, I will explore **how the community changes and if there exist larger shifts following increasing mortality rates of some species than others.** There exist two possible changes to the end state: a species
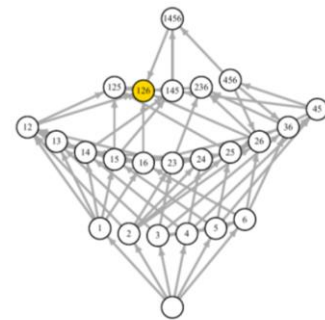
can invade or species go extinct. If the species richness of the end state increases, a species from the species pool invaded without displacing any resident populations. If the species richness stays the same but the community composition changes, an invading species displaced a resident population. If the species richness decreases, multiple species were lost following an invasion. Doing this for each species in the initial end state's community, I can identify if perturbation of certain species leads to larger initial changes to an end state's community than others.

Aim 3: After studying the first change to the community composition, **I will continue to increase the mortality rate, tracking how the end state changes over time, until the focal species is lost.** I can then investigate how attributes of the end state such as species richness change over time as a function of the mortality rate of the focal species. Comparing these findings across all species of an initial end state, I will determine which species lead to the most change in the end state as their mortality rate continues to change over time.

Aim 4: I will perform all of these aims across empirically-parametrized datasets. With over 30 gLV datasets identified[6], I will gain a deep understanding of how changing mortality rates can impact real-world systems. However, while the empirically based models are at a single trophic level, most ecological communities are multitrophic. **How do multitrophic level communities respond differently to increasing mortality rates than single trophic level communities?** To supplement the single trophic level datasets, I will employ random matrix generation of the interaction matrix and intrinsic growth vector[7]. I will constrain the parameters of the randomly generated matrices and vectors such that they hold properties of consumer-resource models[7,8]. I expect more shifts in end states of multitrophic level communities than single trophic level communities due to higher trophic level species relying on lower trophic level species. Additionally, I predict that generalist species are more likely to persist as a non-focal species since they are less likely to lose their only resource. Conversely, I predict the specialist species are likely to reach extinction quickly following perturbation to their specialized species.

Intellectual Merit: By integrating the processes of community assembly and global change ecology into studies of community viability, this method provides a novel, theoretical framework to better understand shifts in community composition due to global change[9]. By studying community viability through shifting mortality rates as opposed to instantaneous extinction, I address how perturbation can affect communities during and after species decline, filling an important research gap. Furthermore, CAGs provide a mathematically rigorous framework for understanding community assembly with gLV equations. By making the code to generate CAGs from gLV equations publicly available, scientists can implement this method on their own datasets. By anchoring this research in empirical datasets, I ensure that generalizations drawn from the models represent real ecological systems.

Broader Impacts: Recognizing the broader relevance of this research to professionals in non-academic sectors, I will establish connections with professionals from the US Fish & Wildlife Service. This collaboration will facilitate dialogue about how to use this method to address biologically relevant questions while closing the gap between academic and non-academic professionals. For example, numerous species reintroduction efforts have failed due to environmental factors not facilitating successful species invasion[10]. However, using CAGs, one can mathematically test if species reintroduction will be successful given the parameters to the gLV equations. I will mentor an undergraduate student who will help develop the code for random matrix generation and conduct statistical analyses. Given the increasing demands for quantitative and computational skills in biology, this opportunity will provide the student with skills that are not gained in typical biology coursework. I will apply for funding through the Center for Population Biology at UC Davis to provide financial support to the student, enhancing accessibility to low-income students.

References: [1] Klupczyńska & Pawłowski. (2021) *International journal of mol. sci.* [2] Da Silva, et al. (2023) *Enviro. Pollution.* [3] Ebenman & Jonsson. (2005) *Trends in Eco. & Evo.* [4] Stachowicz, et al. (2002) *PNAS* [5] Spaak & Schreiber. (2023) *Ecology Letters* [6] Spaak, et al. (2021) *Ecology Letters* [7] Gellner et al. (2023) *PNAS.* [8] Chesson. (1990) *Theoretical Pop. Bio.* [9] Eichenwald & Reed. (2021) *Bioscience* [10] Jourdan, et al. (2019) *Biological Reviews.*

I attain my focus amidst the steady mechanical whirring and banging. I attempt to read my chemistry notes through the thin layer of all-purpose flour on my glasses, obscuring my vision. As I glance at the clock on the wall that requires resetting every other day to maintain its accuracy, the hand strikes 1:00 AM–only two hours left of my shift and eight more hours until my chemistry midterm. My friends come in at the end of my shift, just like many before. While I shared laughs with them and handed over leftover slices of lukewarm cheese pizza, I could not help but silently envy their freedom to choose how they spent their nights–sleeping, studying, partying. All the while, I had to work three to four night shifts a week to cover housing and tuition costs. Although many nights at the pizza shop were filled with cherished memories, many of those nights were marred by fatigue and a lingering feeling of jealousy. Why can't I just be like all my other friends and classmates?

Broader Impacts: Many first-generation college students, like myself, often find ourselves facing challenges that extend beyond academics; we often have to juggle our course load, financially support ourselves and our education, and learn generational academic knowledge by ourselves. Unlike some of our peers who may be financially capable of working without pay, we often cannot partake in unpaid internships or volunteer opportunities to enhance our resumes. To counteract these barriers, I dedicated myself in my later years of college to supporting these students. I became an active member of the diversity board of the College of Charleston's Honors College, working specifically with low income and first-generation college students to educate them on available resources to gain the knowledge needed to succeed in college. Furthermore, as the Diversity, Equity, and Inclusion coordinator of my college's tour guide association, I reworked our tour script to be more inclusive to first generation and low-income college students as well as for LGBTQ+ and BIPOC prospective students. As a PhD student in Population Biology at the University of California, Davis (UC Davis), I will continue to support first-generation college students through my role as Recruitment Coordinator in my graduate program's diversity committee. By advocating for holistic review of applications that acknowledges the barriers first-generation, low-income, and other applicants from disadvantaged communities face, we can ensure a more equitable and accessible admissions process.

Though being a first-generation college student had its fair share of challenges during my academic journey, growing up as a gay kid in the deep South is an experience that has shaped me throughout my whole life. From being ridiculed by people who I trusted to strangers walking down the street, being openly LGBTQ+ can be emotionally taxing. Moreover, **I have never had a queer role model in my life.** Growing up as the odd-one-out in society in itself is challenging, but doing so without anyone in my life who had faced similar challenges made these experiences truly isolating. Openly queer people were a rarity, reinforcing my feelings of loneliness within not only society, but within the scientific and academic communities. **I didn't meet my first queer scientist until graduate school in 2023**. It took me over 22 years to meet someone who could act as a queer role model in my life.

I am dedicated to ensuring other students do not have to endure the same profound sense of isolation that I experienced throughout my academic journey. In my first year of graduate school, I joined Out in STEM, a club committed to increasing the retention of LGBTQ+ individuals in STEM fields. I have had the pleasure to take part in a mentoring program where I offer guidance to an undergraduate biology student on how to navigate academia not only as an aspiring scientist but as a LGBTQ+ individual. Additionally, I am currently in the process of initiating a science communication project: a podcast aimed at increasing LGBTQ+ visibility within STEM. The podcast will interview a diverse group of queer STEM professionals, delving into their research interests, career path, and advice for aspiring scientists. By providing aspiring queer scientists a resource to learn about successful queer scientists in their fields of interest, we can work to increase the recruitment and retention rate of LGBTQ+ individuals in STEM fields. Throughout my academic career, my unwavering dedication stands firmly in making science accessible and inclusive. **I am and will continue to be the queer role model that I never had.**

In addition to mentoring undergraduate students, I have actively engaged in teaching and mentoring high school students. Through a summer program at UC Davis called "COSMOS", I aided in instructing over 20 students on methods of developing, analyzing, and simulating mathematical models inspired by biological systems. By studying the interplay of biology and mathematics, students gained proficiency in addressing biological questions through computational and mathematical techniques. To apply this

knowledge, students were tasked with tackling a biological research problem of interest using quantitative tools. Subsequently, students presented their findings in two distinct ways: an oral presentation to the class and a poster presentation to an audience with no presumed knowledge of biology and math. This approach taught students not only how to "do science" but also how to communicate their findings to both scientific and non-scientific audiences. I will continue to participate in COSMOS throughout the duration of my PhD to foster scientific curiosity among high school students.

Intellectual Merit: During my undergraduate education at the College of Charleston, I double majored in biology and mathematics out of interest in both fields independently. Initially, I perceived these majors as disconnected until I took a course on biodiversity and ecology the same semester I was taking differential equations. To my shock, a harmonious connection existed between these fields in the context of population biology. It became clear that I can answer the myriad of biological questions I had from my biology coursework by using the mathematical and computational skills from my mathematics major. This realization ignited my desire to pursue research in biology through the use of mathematical and computational models.

In the summer of 2021, **I received a competitive undergraduate research grant from the National Institutes of Health: the IDeA Networks of Biomedical Research Excellence grant in Computational Biology (NIH INBRE)**. With this grant, I studied how to use a phylogenetic tree of a host and one of a parasite to infer the shared history of these groups, known as coevolution. By developing an algorithm and mathematical basis to combine these phylogenetic trees into one mathematical structure, biologists can unravel the nuances of coevolutionary relationships. This project taught me a variety of skills such as the art of constructing models, algorithm development, and the translation of biological reality into mathematical abstractions. This research led to **an oral presentation of my research** as well as **two separate poster sessions: one for the College of Charleston Research Symposium and one for the NIH INBRE Research Symposium**. Furthermore, this research accumulated into my senior thesis, **which was published through the College of Charleston's Honors College**. Outside of my research, I had the opportunity to take highly relevant graduate level courses during my undergraduate education in biology and mathematics such as Biometry and Numerical Analysis respectively. At the end of my undergraduate education, I received an array of academic honors such as graduating with summa cum laude and being awarded the Outstanding Student Award by both the Department of Biology and the Department of Mathematics, standing as a testament to my ability to meld theories from both disciplines.

During the first year of graduate school, in addition to rigorous coursework in the Population Biology PhD program, I began two research projects. The first project, a collaborative effort with my advisor Sebastian Schreiber, revolved around the development of a model of community assembly–the process of species arrivals to a landscape and its consequences on the ecological community's dynamics. This model, known as Community Assembly Graphs (CAGs), takes a system of ordinary differential equations representing the population dynamics of an ecological community and creates a network modeling the assembly process: nodes (possible states of the system) representing possible community compositions and edges (how the states interact) representing transitions from successfully colonizing species introduced at low density. The novelty of this approach is that it requires no simulations, making this a computationally effective way of understanding the community assembly process of a community. We then applied datasets from the literature on the CAGs to distill general information and trends about the community assembly process. This project has led to **co-authorship of an oral presentation at the Ecological Society of America** and the ongoing **development of a manuscript**. Throughout this project, I learned how to further translate biological concepts into mathematical models, write efficient and succinct code, and how to motivate theoretical ecology research using both studies from theoretical and empirical biology. Moving forward, I will continue using CAGs as a research method, but addressing how the community assembly process changes as perturbations are introduced such as increased mortality rates.

The second research project, in collaboration with UC Davis professor Elizabeth Crone, aims to understand the prevalence of chaotic dynamics in mast seeding populations. Mast seeding, characterized by highly variable and synchronous production of seeds across a population, has been studied extensively for decades. Theoretical work on mast seeding has found that these populations can exhibit chaotic

population dynamics, wherein small changes in seed production lead to drastically different seed production in the future. Motivated by this theoretical work and its biological implications, this project analyzes over 400 time series of mast seeding populations. We employ a chaos detection algorithm to identify which mast seeding populations exhibit chaotic dynamics. We then can see if certain species/populations are more likely to exhibit chaotic dynamics based on ecological traits such as their method of pollination, method of seed dispersal, and latitude. As it is my first research project that uses a large amount of data, I have learned pertinent skills for preparing and organizing data. Given my goal to continue motivating my theoretical work through empirical data, this research project has given me a solid foundation in how to wrangle data in an effective manner, preparing me for future research projects.

Both of these research projects share a common thread: the integration of theoretical and empirical biological insights. Given the gap between theory and empiricism, I have made intentional efforts in ensuring that my theoretical research problems are motivated and deeply rooted in empirical research and hypotheses. To further remedy this disconnect, I am dedicated to ensuring that I connect with a wide-ranging community of scientists to develop interdisciplinary research goals. During the first year of the fellowship, I will network with a diverse group of empirical and theoretical scientists at UC Davis through the Department of Evolution and Ecology and the Department of Environmental Science and Policy, as well as professionals in other universities and non-academic sectors such as conservation managers. In subsequent years, I will nurture and maintain these connections by holding meetings with these professionals. These discussions will go over not only the questions that I am addressing through mathematical models, but, crucially, the assumptions underpinning them. Theoretical scientists will have valuable insights on the methodological aspects of the research while empirical scientists will be able to gauge the validity of assumptions in the models when applied to real-world systems. By taking this unique approach to developing models in population biology, I will create and collaborate on research that takes a holistic approach to the diverse field of biology. By sharing this approach with my peers in the Theoretical Population Biology (TPB) group at UC Davis, we can collectively help close the gap between theory and empiricism. With TPB members spanning many programs such as Population Biology, Mathematics, and Physics, we can work together to facilitate collaboration between our fields to achieve our common goal of understanding biological phenomena through mathematical and computational methods.

Future Goals: Throughout the rest of my career, I aspire to continue tackling problems in population biology through a mathematical and computational lens. To achieve this dream, I will become a professor, where I will have the ability to mentor students while also teaching courses. To kickstart my career in mentorship, I will mentor at least two undergraduate biology students by helping them develop and perform an independent research project during the duration of the fellowship. To ensure that this opportunity is accessible to low-income and first-generation college students, I will apply for funding through the Center for Population Biology at UC Davis to pay the interns for the hours that they work. As I continue my academic journey, I am dedicated to solving biologically relevant problems facing society, especially in the face of anthropogenic change. By integrating concepts from community ecology and conservation biology with methods from theoretical ecology and mathematical biology, I will develop models that can extract pertinent biological information while maintaining the mathematical rigor and computational efficiency required to make these models generalizable.

On top of academic work, I will continue participating in science communication such as the interview podcast on LGBTQ+ scientists. Additionally, at UC Davis, Biodiversity Museum Day is an annual community engagement day where many departments at the university will open their collections to the public. Despite the thousands of participants learning about the wonderful diversity of life, there is currently no presenter at the event discussing the rapid loss of biodiversity and ways we can act to sustain said biodiversity. I will incorporate this into Biodiversity Museum Day to educate the public on not only biodiversity but also on ways that scientists, managers, and members of the public take steps to conserve the planet. I will work in conjunction with the Population Biology Graduate Group and the Department of Evolution and Ecology. By continuing to bring my diverse perspectives to my research and advocacy, I will continue pushing the boundaries of science, both in the novelty of my research and the inclusivity of all scientists and members of the public.