

Research Statement *Tad Dallas*

My research attempts to apply quantitative tools to develop and test theory in population, community, and macroecology, with a focus on ecological forecasting. Much of my research has examined the complex interactions between host and parasite communities, though I often utilize field data from zooplankton communities, data from published research studies, and data gathered by federal agencies (e.g., USDA FIA data). While my interests are diverse, they are linked by the goal of understanding and actively predicting ecological processes and interactions. To this end, my research can be broken into three main classes; 1) population ecology of infectious disease, 2) forecasting ecological phenomena, and 3) testing macroecological theory.

Population ecology of infectious disease

Host-parasite interactions have fascinated me, successfully derailing my proposed physics major early in my undergraduate education. Instead, I began fieldwork examining small mammal host species and their ectoparasite communities. A desire to thoroughly test ecological theory lead me to microcosm research, where I paired phenomenological models with experimental populations of zooplankton infected by a fungal pathogen to examine how environmental contaminants, competition, host density, and temperature variability influenced pathogen emergence and epidemic dynamics (see CV for relevant publications). A final portion of this work examined the cost of pathogen exposure and infection across a number of host species, finding that pathogen exposure reduced host fitness in the absence of infection, and demonstrated that different species paid different costs, even for host species which do not become infected in natural populations. Together, this work aimed to address how biotic and abiotic interactions could influence the host-pathogen relationship.

My current work as a postdoctoral researcher with Alan Hastings examines dynamical systems theory to populations and communities of flour beetles (*Tribolium* sp.) to test how species interactions and environmental fluctuations can influence dispersal, metapopulation stability, and set geographic range limits. My decision to temporarily abandon host-pathogen interactions was tactical, as I believe the techniques and theory learned during my population research will be applicable to pathogen populations within host individuals and species.

Ecological forecasting

A second branch of my research focuses on the predictability of complex ecological interactions. Forecasting ecological interactions and resulting dynamics is an important area for future research, as climatic and distributional changes are likely to strongly influence species geographic distributions, interactions, and extinction risk. Utilizing approaches from machine learning and niche modeling, I determined the predictability of helminth parasite communities of fish species (Dallas, Park, Drake 2016), the role of host species extinction on host-pathogen network structure (Dallas and Cornelius 2015), and estimated parasite extinction risk given estimated host range dynamics in response to climate change (Carlson *et al.* 2017).

Further, I have contributed to and utilized existing host-pathogen databases and machine learning approaches to rank host species importance to parasite sharing (Dallas *et al.*, submitted to *Royal Society Interface*),

determine phylogenetic patterns of host specificity (Presley *et al.* 2015, Park *et al.* in review), and identify likely, but unobserved, host-parasite associations given host and parasite trait profiles (Dallas *et al.*, 2017). Together, this body of work relates functional trait information of host and parasite species to both their roles in host-parasite networks, and the likelihood of their interactions. Predicting interactions in networks is a long-standing and core problem in network theory, and could help the prediction and mitigation of infectious disease through forecasting potential spillover events in host-pathogen networks. To this end, as part of an ongoing collaboration with vector biologists at University of Georgia and the Cary Institute of Ecosystem Ecology, we are applying these methods to mosquito vector-virus associations in order to predict the likely, though presently unknown, mosquito carrier of Zika virus, a current emerging infectious disease (Evans *et al.* 2017).

This work bridges community and disease ecology, combining existing knowledge of host-parasite interactions with advanced computational approaches. This allows for the estimation of the bounds of prediction in ecology, and addresses questions of both conservation (host/parasite extinction risk) and public health (vector distributions and potential host-vector associations) importance.

Testing macroecological theory

The emergence of macroecology—coupled with the availability of large ecological datasets—has allowed for the testing and forecasting of ecological interactions at global scales. This is the most recent of my research foci, promoted by my involvement with the NSF-funded Macroecology of Infectious Disease Research Coordination Network. The RCN consists of an international team of scientists specializing in disease ecology, phylogenetic comparative methods, network science, machine learning, and macroecology (Stephens *et al.* 2016). In collaboration with these scientists, I have spearheaded efforts to understand and predict parasite sharing in ecological networks (Dallas *et al.* in review), latitudinal gradients in host and parasite body size (Bergmann’s rule; Dallas *et al.* in prep), and the compositional and structural dissimilarity of host-pathogen interaction networks with increasing spatial distance (Dallas and Poisot, in review).

Apart from applications to host-pathogen interactions, I have utilized existing data sources to test macroecological theory. By example, I have thoroughly examined empirical support for the hypothesized relationship between population abundance and distance from a species geographic range or climatic niche center (i.e. *distance-abundance* relationships). The longstanding assumption that population abundance should be greatest within the range or niche interior has surprisingly little empirical support, despite serving as a foundational assumption to many other ecological hypotheses.

Currently, this work aims at weighing support for proposed macroecological relationships. Eventually, I aim to utilize modeling approaches and machine learning to address the predictability of macroecological relationships, especially under changing environments. That is, how sensitive are macroecological relationships to a changing environmental landscape and species introductions or extinctions, and how does this sensitivity influence forecasting of ecological relationships based on macroecological hypotheses.

Open science

I am a strong advocate of open science, open data, and open source software. I have been involved in efforts to promote open science through my involvement in radio interviews (Georgia Public Radio) and conferences (SEC Academic Collaboration Conference). Further, I maintain an open lab notebook (<https://taddallas.github.io/LabNotebook>) with information on on-going projects, many of which are freely accessible on Github. As a proponent of open data, I have released data and analytical code to reproduce all analyses and re-create figures from a majority of my published articles, either alongside the published article or on a digital resource repository (e.g., Dryad or Figshare). Further, I have contributed to data cleaning and quality control of the US National Parasite Collection, and the Global Mammal Parasite Database, and have been involved in efforts to publish these data in order to make them widely available. I currently maintain two open source software *R* packages; one for the analysis of metacommunities (*metacom*; Dallas 2014) and the other to query the London Natural History Museum’s extensive host-parasite database (*helminthR*; Dallas 2016). Lastly, I actively contribute to other packages allowing open and programmatic access of ecological data through my involvement with ROpenSci, a diverse group of ecologists and programmers promoting open science and reproducible research.

Future research

Broadly, my future research plan is to continue developing and testing ecological theory using experimental microcosms and published data sources. The increasing availability of ecological data has created a need for the development of computational methods, and the possibility to address large scale ecological questions. I plan to build on my previous experience contributing to **distributed R**—which enables **R** to handle big data by distributing data (or models) among numerous machines—by both utilizing distributed and parallel computing to address big data in ecology and developing software tools to enable users to programmatically access data stores. By example, a current project (Dallas and Drake, in review at *Nature*) uses a distributed feature reduction algorithm to reduce the global climatic landscape to an order of magnitude fewer features. I believe this paper will be the first of many, as this reduced climatic manifold makes it possible to address species niches, geographic range shifts, and the distribution of climates over time in a much more feasible way. Lastly, I aim to continue using the flour beetle laboratory system to investigate ecological and evolutionary theory relating to species interactions, spatial spread, and metacommunity dynamics. More efficient dispersers are often genetically dissimilar from populations closer to the range center. However, experimental layers such as competitor abundance or habitat quality may influence selection gradients. Lastly, while a large body of theory has developed for metapopulations, and a similarly large body of theory is currently being developed for metacommunities, empirical tests are fairly rare. My future research will address this obtrusive gap by providing experimental demonstrations of metapopulation and metacommunity theory, offering both empirical validation and continued refinement of existing theory.