

# MICHIGAN STATE UNIVERSITY

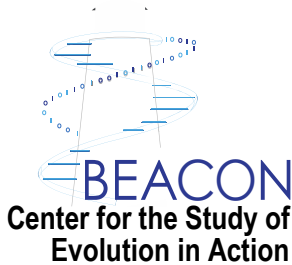
September 30, 2019

Dear Search Committee Members,

Thank you for considering my application for the position of Assistant Professor of Evolutionary Biology at Adelphi University. I completed my Ph.D. with Dr. Richard Lenski at Michigan State University, where I used both a long-term bacterial evolution experiment and digital organisms to ask fundamental questions about how predictable and repeatable the evolutionary process is, and how general are the patterns observed across different systems. I would be a good fit for this position due to my strong background in microbial and digital evolution, my proven track record in publication and grant writing, and my demonstrated interest and ability in teaching, including experience teaching introductory biology in both lab and lecture format, and both graduate and undergraduate evolution courses.

My basic science research addresses question of the repeatability and predictability of the evolutionary process. In terms of predictability, I look at whether data from early on in an evolution experiment can predict future data within that same experiment. In terms of repeatability, I ask whether these predictions are only valid for the aggregate set of many independent evolutionary trajectories. Or, alternately, whether individual trajectories are similar enough that predictions can be made about individual trajectories. One of the chapters from my dissertation – published in *Science* – showed that even after 50,000 generations of adaptation to a consistent laboratory environment, *E. coli* populations exhibit improvements in fitness that are best fit by functions without an upper boundary, implying they are so far from a fitness peak that even if a peak exists, it isn't playing a meaningful role in their adaption. I've since measured similar dynamics over even larger number of generations in a variety of computational environments, finding similar patterns with a lack of an upper limit to fitness. I've further explored whether it's possible to set up environments in these systems that might give an artificial impression of an upper boundary being reached. By working across multiple systems, both laboratory and computational, I seek to determine whether the patterns I find are specific to a given system, or part of evolutionary systems writ large. Additional experiments in these computational systems which I've undertaken or am currently engaged in seek to address questions of evolutionary genetics – for example, how genomes change over long time scales both in the presence and absence of widespread horizontal gene transfer – in ways that are not feasible in physical organisms.

This combination of research interests would integrate nicely with the department's strengths in evolution, ecology, and microbiology. Microbial experiments allow us to reach meaningful levels of replication in a manageable space and budget. Computational experiments leverage these advantages even



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further, and allow us to see how general our patterns are. Both systems provide rich opportunities for student experimentation beyond my already planned research directions. Both of these systems are highly amenable to working with undergraduate and masters students, due to the rapid nature of data generation.

Throughout my scientific training, I have sought out opportunities to teach, to improve my instructional skills and knowledge, and to learn how one can assess student learning gains. As a graduate student, I took course work in science and math education, and completed my university's certification program in teaching college science. I sought out opportunities to teach even while supported by fellowships or research assistantships, resulting in the chance to be either co- or lead instructor for several courses at Michigan State University, and winning the department's graduate student teaching award at Stanford, given to one student per year. For several years, I have been the lead instructor in a graduate course on evolution, and I am now in my second semester teaching in the introductory sequence at my current university.

I have paid particular attention to issues of inclusion in both my teaching and research. In the classroom, this has been most relevant when discussing issues of population differentiation among human groups; I have worked with my center's diversity director to ensure that my approach to this topic and my language choices do not exacerbate existing biases or activate stereotype threat. In my research, I have acted as a research mentor to several women in computer science, and have trained both a student with different physical capabilities and several racial minority biology students in laboratory protocols, ensuring that all were able to participate in a large group project I coordinated in the lab. As a member of the LGBT community, I recognize the importance of making clear that an individual's identity has many components, and none of them need interfere with the roles of student or scientist.

I am well situated for teaching courses in introductory biology, evolution, genetics, population biology, and biostatistics immediately. With some preparation, I could also teach courses in microbiology, or behavior. With a PhD in Evolutionary Biology, and BS degrees in Biochemistry and Psychobiology, I have a broad base of knowledge and training in biology. I am particularly excited about the possibility of incorporating authentic research in experimental evolution, either in the core undergraduate laboratory courses, or through student research projects. Alternately, I could develop a course as an evolution lab focused on microbial evolution.

Please find included my application my curriculum vitae, teaching statement, research statement, and contact information for my references. I would be happy to provide further materials, such as teaching evaluations, a diversity statement, or representative publications or syllabi upon request, but thought it best to only include what was specifically asked for in the job posting. Thank you again for your consideration of my application.

Sincerely,

Michael Wiser

Instructor – Biological Sciences Program  
Michigan State University

**Professional Positions:**

Current           Instructor, Biological Sciences Program, Michigan State University  
2016 - 2019      Postdoctoral Research Associate, BEACON Center, Michigan State University

**Education:**

2015           PhD, Zoology Department, Michigan State University, Lab of Dr. Richard Lenski  
Dual PhD Degree Program: Ecology, Evolutionary Biology, & Behavior  
2006           MS Biological Sciences, Stanford University, Lab of Dr. Brendan Bohannan  
2003           BS Biochemistry, University of Southern California, summa cum laude  
Lab of Dr. Steven Finkel (Biology)  
Minor: History  
2003           BS Psychobiology, University of Southern California, summa cum laude  
Lab of Dr. Laura Baker (Psychology)

**Publications:**

2019+           Wiser MJ, R Canino-Koning, C Ofria. Horizontal Gene Transfer Leads to Increased Task Acquisition and Genomic Modularity in Digital Organisms. The 2019 Conference on Artificial Life. p 243-244  
2019           Canino-Koning, R, MJ Wiser, C Ofria. Fluctuating environments select for short-term phenotypic variation leading to long-term exploration. PLOS Comp Bio 15(4) e1006445  
2018           Dolson, EL, AE Vostinar, MJ Wiser, C Ofria. The MODES toolbox: Measurements of Open-ended Dynamics in Evolving Systems. Artificial Life 25 (1), p 50-73.  
2018           Kohn, C. et al. A Digital Technology-based Introductory Biology Course for Non Life-Science STEM Majors. *Computer Applications in Engineering Education* 2018;1-12  
2017+           Wiser, MJ, L Zaman, BD Connelly, and C Ofria. Threshold for Cooperation on Irregular Spatial Networks. Proceedings of ECAL 2017 the 14th European Conference on Artificial Life  
2017+           Lalejini, AM, MJ Wiser, and C Ofria. Gene duplications drive the evolution of complex traits and regulation. Proceedings of ECAL 2017 the 14th European Conference on Artificial Life.  
2016           Taylor, T et al. *Open-ended evolution: perspectives from the OEE workshop in York*. Artificial Life 22(3), 408-423  
2016           Smith, JJ et al. *An Avida-ED digital evolution curriculum for undergraduate biology*. Evolution: Education and Outreach 9(1)  
2016+           Wiser, MJ, LS Mead, JJ Smith, and RT Pennock. *Comparing Human and Automated Evaluation of Open-Ended Student Responses to Question of Evolution*. ALife XV  
2016+           Dolson EM, MJ Wiser, and C Ofria. *The Effects of Evolution and Spatial Structure on Diversity in Biological Reserves*. ALife XV  
2016+           Canino-Koning R, MJ Wiser, and C Ofria. *The Evolution of Evolvability: Changing Environments Promote Rapid Adaptation in Digital Organisms*. ALife XV  
2015           Lenski RE\*, MJ Wiser\*, et al. *Sustained fitness gains and variability in fitness trajectories in the long-term evolution experiment with Escherichia coli*. Proc Royal Soc B. 282:20152292  
\* joint first authors  
2015           Wiser MJ and RE Lenski. *A comparison of methods to measure fitness in Escherichia coli*. PLOS ONE 10:e0126210  
2013           Wiser, MJ, N Ribeck, RE Lenski. *Long-Term Dynamics of Adaptation in Asexual Populations*. Science, 342(6164), 1364-1367  
2013           Wielgoss, S, et al. *Mutation rate dynamics in an Escherichia coli population reflect tension between adaptation and genetic load* PNAS 110(1) 222-227

+ denotes a conference paper in the Artificial Life conference. These are peer-reviewed papers with ~40% acceptance rates

**Non-Peer-Reviewed Scholarly Work:**

2018           Wiser, MJ. Soonish: *Ten Emerging Technologies That'll Improve and/or Ruin Everything* by Zach and Kelly Weinersmith. Book Review. Artificial Life Vol. 24 No 3., pp. 224-226.

- 2017 Wiser, MJ and RE Lenski. Evolutionary Theory and Experiments with Microorganisms. In *Reference Modules in Life Sciences*. Elsevier, Oxford, UK.
- 2009 Lenski, RE, and MJ Wiser. Evolution, theory and experiments with microorganisms. pp. 550-564 in M. Schaechter, ed. *Encyclopedia of Microbiology*, 3rd edition. Elsevier, Oxford, UK.

Submitted Journal Articles:

- 2018 Wiser, MJ, EL Dolson, A Vostinar, RE Lenski, C Ofria. The Boundedness Illusion: Asymptotic projections from early evolution underestimate evolutionary potential. doi: <https://doi.org/10.7287/peerj.preprints.27246v1>

**Recent Funded Research Grants:** (Total value: \$348,762)

- 2019 Enhancing BEACON's educational legacy with a set of curricular materials derived from our center's research, BEACON Center  
M. J. Wiser, M. Kjellvik, E. Schultheis, L. S. Mead  
\$63,947  
My role: Project concept, lead author on the grant. I obtained agreement from a set of researchers to work with them to generate outreach materials from their research (in the form of Data Nuggets), and am in the process of doing that. My coauthors on the grant will be working to make sure the materials end up in the correct final format, and so that the material is presented appropriately for the targeted age and mathematical reasoning levels.
- 2018 Synthesizing Concepts Within Evolution in Action, BEACON Center  
M. J. Wiser, C. Ofria  
\$39,052  
My role: Project concept, lead writing a synthesis paper on how fitness is conceptualized in evolutionary biology and evolutionary computation, contribute to writing a synthesis paper on how diversity is generated and maintained in both of these disciplines; work with a graduate student on how these synthesis papers will be organized to facilitate future ones. Lead author on the grant.
- 2017 Harnessing Eco-Evolutionary Dynamics for Open-Ended Evolution of Intelligence, BEACON Center  
E. Dolson, S. Jorgensen, M. J. Wiser, W. Banzhaf, C. Ofria,  
\$63,567  
My role: Help the MS student leading the project with experimental design, ground the manuscript in the biology literature, perform statistical analysis on the data.
- 2016 How Do Evolutionary Forces Shape Local Fitness Landscapes, BEACON Center  
C. Ofria, W. Banzhaf, R. E. Lenski, M. J. Wiser  
\$87,057  
My role: Contribute data to the project, assist with experimental design, place the project appropriately within the biological literature, perform statistical analysis on both my data and the data contributed by others.
- 2016 Writing Through STE(A)M: Engaging Evolution in Creative Spaces, BEACON Center  
C. Rohbacher, E. Weigel, C. Baskett, M. Kjellvik, M. J. Wiser, A. Warwick, R. Hayes  
\$26,191  
My role: Provide feedback to students about how their writing about science and science fiction relates to what we currently understand about the underlying science, answer student questions about scientific phenomena.
- 2016 Personal Genomics in the Classroom, BEACON Center  
M. J. Wiser, L. S. Mead, A. Hintze  
\$6,140  
My role: Project concept, develop instructional exercises using personal genomics data. Lead author on the grant.
- 2014 Investigating the Impact of Horizontal Gene Transfer with Digital Organisms, BEACON Center  
M. J. Wiser, B. Kerr, C. Ofria  
\$62,808  
My role: Project concept, experimental design, data analysis, ground the project in the biological literature. Lead author on the grant.

**Teaching Experience:**

Fall 2019 Instructor, Cell and Molecular Biology, Michigan State University (undergrad)  
Instructor in 1 section of ~250 students, active learning classroom design

2019 Instructor, Cell and Molecular Biology Lab, Michigan State University (undergrad)  
Lab and recitation, 28 students / section, 2 sections each Spring and Fall

Fall 2016-19 Lead instructor, Evolution for Non Life Scientists, Michigan State University (grad)  
Significant redesign of ~ 40% of course material  
Lecture/discussion, ~ 4 - 10 students per term

Fall 2015 Co-Instructor, Evolution for Non Life Scientists, Michigan State University (grad)  
Redesigned ~15% of course material  
Lecture/discussion, ~ 6 students

Summer 2011 Instructor, Evolution in Action, Michigan State University (high school)  
Developed course from scratch with one other graduate student  
Lecture/field, ~ 25 students

Spring 2009 Co-Instructor, Digital Evolution, Michigan State University (grad)  
Lecture/discussion, ~ 15 students

Spring 2009 Teaching Assistant, Evolution, Michigan State University (undergrad)  
Ran two recitation sections, ~ 25 students each

Winter 2005 Teaching Assistant, Microbial Ecology, Stanford University (grad and undergrad)  
Lecture/discussion, ~ 30 students

Fall 2004 Teaching Assistant Genetics, Biochemistry, and Molecular Biology, Stanford University (undergrad)  
Ran two recitation sections, ~ 30 students each out of ~ 350 in the class as a whole

Winter 2004 Teaching Assistant, Molecular Evolution, Stanford University (grad and undergrad)  
Ran recitation section, ~ 20 students out of ~ 60 in the class as a whole

2002-2003 Supplemental Instructor, University of Southern California (undergrad) (4 semesters)  
Mechanical Physics, Introductory Chemistry, Honors Introductory Chemistry  
Ran four weekly discussion section for ~ 5-25 students each.

Summer 2001 Teaching Assistant, Upward Bound program, SUNY at Buffalo  
Biology, Chemistry, and Earth Science (high school)  
Lecture and lab demonstration, 3 courses of ~ 20 students each

**Courses in which I have given guest lessons:**

International Baccalaureate Biology (Spring 2018) ~30 students  
Activity exploring what is random about mutations

Exploring Genomes and Personal Genetic Data (Spring 2018, Spring 2017) ~25 students / term  
Discussion of human genetics inferred from 23andMe; activity calculating allelic associations w/ traits

Statistical Methods in Ecology and Evolution (Fall 2016, Fall 2017) ~30 students / term  
Discussion and activity comparing non-nested models and calculating posterior odds ratios

Evolution (Fall 2016) ~50 students  
Activity exploring genetic drift

**Invited Talks:**

2019 Machina ex Machina workshop, University of Arizona

2019 CELFI workshop, Buenos Aires (Argentina)

2019 Seminar speaker, Biology Department, University of South Alabama

2018 Natural Science Colloquium, University of Michigan Dearborn

2017 Origins lecture series, Hastings College (Nebraska)

2015 Rising stars session, BEACON Congress

2015 Seminar speaker, Biology Department, University of Memphis

**Conferences in which I have presented research:**

Evolution (2012-)

Society for the Advancement of Biology Education Research (2017)

Artificial Life / European Conference on Artificial Life (2016-)

Gordon Research Conference in Microbial Population Biology (2005-, every 2<sup>nd</sup> year)

BEACON Congress (2010-)

**Professional Development:**

2009 Certificate in Teaching College Science, Michigan State University

**Outreach Activities:**

2018 Darwin Day Road Show (4 schools throughout Michigan)  
2014, 16, 18 USA Science and Engineering Festival, Washington DC  
2014, 17, 19 Science Festival, Michigan State University  
2012-19 Elementary Science Nights (~45, assorted schools), Lansing area, MI.  
2012-14 BEACON Summer High School Institute Inquiry Day, Kellogg Biological Station  
2012-19 Darwin Day, MSU Museum  
2011 Children's Science Day, Potter Park Zoo, Lansing

**Scholarships/Fellowships:**

2013-14 Dissertation Completion Fellowship, Michigan State University  
2008 Supplemental Graduate Fellowship, Michigan State University  
2006 University Distinguished Fellowship, Michigan State University  
2003 **National Science Foundation Graduate Research Fellowship**  
2003 Stanford Graduate Research Fellowship  
2003 Renaissance Scholar, University of Southern California

**Travel Awards**

2015 Society for the Study of Evolution  
2013-15 Department of Zoology, Michigan State University  
2011, 13-15 Graduate School, Michigan State University  
2011, 13-15 College of Natural Science, Michigan State University  
2012-19 BEACON center, Michigan State University  
2011-19 Ecology, Evolutionary Biology, and Behavior Program, Michigan State University

**Academic Awards:**

2005 **Norman K Wessels Teaching Award**, Department of Biological Sciences, Stanford University  
2003 Undergraduate Research Symposium, Life Sciences Honorable Mention, Univ. of Southern Cal.  
2002 Undergraduate Research Symposium, Social Sciences First Place, Univ. Southern Cal.

**Journals and Conferences for which I've been a reviewer (number of reviews):**

American Biology Teacher (1)  
BioScience (1)  
Environmental Microbiology (1)  
Genetics (1)  
Heredity (1)  
Scientific Reports (8)  
Artificial Life Conference (5)

**Scientific Agencies that have asked me to review grants:**

National Science Foundation

We live in a world of information. The vast majority of students these days have access to the internet, and thus more information than they could ever process. Increasingly, this has been true not just in their most recent years, but for as long as they can remember. The roles played by teachers have adjusted accordingly. Instructors can help students in a variety of ways. We can help assemble seemingly disparate information into a cohesive framework, and call out the connections between the material. We can pick out the key concepts to focus on, learning more by covering a smaller number of topics in greater depth. We can show students how to determine how reliable an information source is, a skill that is essential whether they remain in science or not. And we can serve as a local domain expert, able to answer questions about the content and relate it to the large context of the field as a whole. I've taken steps to incorporate all of these aspects in my teaching. **Within the context of your program, I would be most interested in teaching existing courses in evolution (such as 220, 625, or 438), introductory biology (such as 111 or 112), biostatistics (such as 620), or genetics (such as 222, 209, or 640). I am also interested in developing new courses in experimental or computational evolution, particularly with a laboratory component.**

While I have taught a variety of courses, the one I've taught most often – and had the most control over the course structure within – has been Evolutionary Biology for Non-Life Scientists; it is from this course that most of my examples are drawn. As it is a somewhat unusual course, a small amount of background is relevant. Students in this course – most often graduate students – are overwhelmingly computer scientists, engineers, with backgrounds in physics or mathematics, but not biology. BEACON, the multidisciplinary center where I work, is dedicated to the study of evolution in action. While most of the faculty are biologists, a substantial number are computer scientists or engineers who use evolutionary or genetic algorithms to solve complex engineering problems. This course prepares students to take other graduate biology courses, and provides the necessary background to understand the evolutionary forces at play in their programming.

*Scaffolding information.* Students are frequently taught a large list of facts in relative isolation from each other, with the assumption that they will see the connections among them. Reality, however, shows that even very bright students often do not make connections that seem obvious to experts in the field. This was demonstrated very clearly to me in a course I took about teaching college level biology, where we watched a video clip of science and engineering students at an elite institution on graduation day confidently telling us that the dry mass of a tree branch came from nutrients absorbed from the soil by the tree, and then – in the next question – being able to provide the formula for photosynthesis without ever making the connection that the majority of the mass of that sugar came from carbon dioxide in the air.

Because of the need to make these connections more explicit, in my teaching practice nearly every piece of information either refers back to a related topic from a previous class session, or is pointed out as being tied into something coming up later in the course. For example, the fact that genetic information is stored in physical molecules means that mutation is unavoidable. Machinery exists to check for and correct errors, but organisms pay a cost in time and energy for doing this, which foreshadows the mutation-selection balance that we discuss later in population genetics. The gene flow discussed in the population genetics section ties directly into both species concepts and how we interpret phylogenetic trees. Etc. After only a handful of times modeling this, I'm able to then pose the question to the students about how a particular

concept we just discussed ties back to previous material, and watch as **they** make the connections, and thus cement both the facts and their implications within this scaffold.

*Picking out key concepts.* Reform practices in introductory science courses are moving away from the previous model of extreme breadth with little depth, toward a focus on a few major topics that are covered repeatedly, in different contexts. In my teaching practice, this has meant building a course that is modular. Students in my Evolution for Non-Life Scientists course encounter three modules throughout the term. One focuses on the chemical basis of life; one focuses on population genetics; and one focuses on personal genomics. These modules allow us to address related concepts in a familiar context. For example, we discuss how a single base pair change can result in a substantial phenotype with the example of sickle cell disease. We return to this in population genetics as a classic example of heterozygote advantage, and how the fitness consequences are highly dependent on the environment. And then when we get to the unit on personal genomics, we discuss this as a case where the exact causal mutation is known, and why a company may or may not test directly for the known mutation rather than a genetically linked marker.

In each of these modules, students address the evidence behind the claims, what experiments were run to provide evidence for one explanation vs. another, and what it is we still don't know for certain. For example, in the chemical basis of life unit, we discuss experiments involving using radioactively labeled viral particles, with the radiolabeled elements confined to either just the protein coat or just the DNA, and using that to trace whether it is the protein or the DNA that carries the genetic information. While this takes more time than merely providing the facts, it results in a deeper understanding of the material, and greater retention among the students. As such, it is crucial to pick out the most important concepts to focus on.

As alluded to in the scaffolding section, information has more value when it is not held in isolation. This is true not only within a course, but across courses. Because I am invested in my course having value to my students' progression through their program, I've actively sought out meetings with the curriculum committee and the instructors in the course for which mine is a prerequisite, to determine what material is essential for the students to come out of my class knowing. For example, the personal genomics module has largely taken the place of a previous set of lessons around various species concepts; after discussion with other instructors, we realized it was best to reduce, not eliminate the species concepts to free up time for the personal genomics unit. This coordination is not obvious to the students, but it is essential to make sure that students are not short-changed by one instructor unilaterally choosing what they will cover.

*Critical assessment of information sources.* Many students enter university studies – and, all too often, even graduate studies – ready to accept nearly anything an instructor says just because that person is an instructor, or the information is in Wikipedia, or a book if previous teachers have made them wary of internet sources. Yet one of the great benefits of a university education is the ability to think for oneself. In my course, I expect my students to become fluent with the evidence for the facts they learn and how they are presented in different media. Within the personal genomics unit, each student picks a trait of low medical sensitivity – examples include the difference between wet and dry earwax, or the ability to detect the odors of asparagus metabolites in urine – to research in depth. They start with the information presented by a personal genomics company, then find and read the referenced journal articles in the primary literature, and further search the internet for popular news stories about their trait of interest. The students eventually have to present on the trait, describing the phenotype and its genetic basis, what experiments were conducted to determine that. From there they critique



how it's presented to the general public, including what a newspaper or magazine article about the trait shows, and how the information changes (or doesn't) across the different sources. This is an eye-opening experience for many of these students, and one that moves beyond the cursory guidelines many had drilled into them in earlier years.

*Serving as a domain expert.* There is a lot to be gained, pedagogically, by having students construct knowledge together. This sort of student-focused classroom practice can give students a greater sense of participation in the process, and make them more active in their learning throughout their careers. But that needs to be balanced with the fact that sometimes the students don't yet know enough information to be able to construct the knowledge. Further, if students perceive an instructor as rarely providing information, a substantial percentage will question what the point of having an instructor present is. This negative affective response can cause them to shut down entirely, backfiring and ultimately reducing student learning gains.

In my practice, these competing interests of wanting the students to construct knowledge but knowing that they often lack the some of the necessary foundational knowledge mean that I frequently give presentations – either of me speaking, or from quality educational videos, such as from the HHMI – of no more than 15 minutes, followed by group discussions of the topic, and what else we would need to know and how we could go about gathering that information. As such, students are largely responsible for making the connections between material, and use that as a large component of constructing knowledge, but the individual pieces are often supplied to them. Further, I ask students at the beginning of most class sessions what is still unclear from previous ones, and they are encouraged at any time to ask questions when something doesn't make sense. Something I've found particularly helpful is to directly tell students “I don't know” when they ask something I'm unsure of, and then brainstorm with them what knowledge or experiments we would need to find the answer.

Further, the presence of a domain expert in the class means that we can tailor it to some extent to the students. In my smaller, discussion-based courses, this has meant some adjustment of topics based on student interests. For example, one year I had a relatively large percentage of students whose research involved evaluating and improving phylogenetic algorithms, so I spent additional time that semester on phylogenetics and the uses of such trees. A different year, I had a large fraction of students with interest in mathematics, so we spent a class session on evolutionary game theory and how it differed from classical game theory. In larger courses I've TAed, this has instead meant adjusting the examples of phenomena to student interest. When TAing an introductory biology course predominantly taken by pre-health students, I chose examples primarily from traits within humans instead of other organisms; when TAing an upper division course taken predominantly by zoology majors, I shifted a larger percentage of the examples to be about non-human animals.

Taken as a whole, these approaches have allowed me to run a largely student-centered classroom, while still providing enough structure and direction to ensure we cover essential topics. Further, they allow us to ensure we don't stall out due to the fact that the students are, fundamentally, students, and thus not expected to know the material without instruction. Some of these practices, like coordination with other instructors in terms of curriculum, largely take place out of view of the students. Some are explicitly modeled, such as discussing the evidence for assertions, and asking how concepts relate. Others are simply built into the way the course is structured, such as frequent discussions after short periods of providing information. Together, they allow me to act more in the role of a guide to information they need, rather than only as the direct source of information.

**My research focuses on the evolutionary process itself.** *How predictable is evolution?* Can we use data from the early stages of evolution to predict trajectories over much longer time scales? *How repeatable is evolutionary change?* If we start from identical starting conditions many times, would we get similar patterns across the different replicates? Is any predictability we find restricted to the average outcome, or are the evolutionary trajectories of individual instances also predictable? *How general are the observed patterns?* Do the findings from one system apply to others? Or are the patterns we find specific to just the system in which they are uncovered? **I use experimental evolution in both a wet lab bacterial system and a computational system to address these fundamental questions about evolution.**

**Past research:**

**Bacterial:** As a graduate student, I worked with Dr. Richard Lenski as part of the Long-Term Evolution Experiment (LTEE), an ongoing experiment in which 12 populations of *E. coli* have been evolving independently from each other for more than 60,000 generations over the past 30 years (1). A key feature of this system is that bacteria can be frozen, stored indefinitely, and then revived later, allowing us to measure populations from different time points in a common environment in the present. As such, I was able to compete populations from tens of thousands of generations directly against their ancestors. By mapping out fitness within each of the populations, I showed that not only are the patterns of fitness change highly repeatable across populations – and therefore evolutionary replicates – but that **we can use early fitness data to accurately predict changes over much longer time scales (Fig. 1A)**. Strikingly, the model that both best fits the current data, and best predicts future data, is one where fitness does not have an asymptote, but grows in an unbounded fashion (2), confirmed in a follow-up study that looked in more depth at changes between 40,000 and 60,000 generations (1). This means that even after 50,000 generations in a relatively constant environment, populations are so far from reaching a fitness peak that we can't detect evidence that such a peak exists, so perhaps we should reconsider ecological models that assume populations are at fitness peaks unless the environment has been recently disturbed.

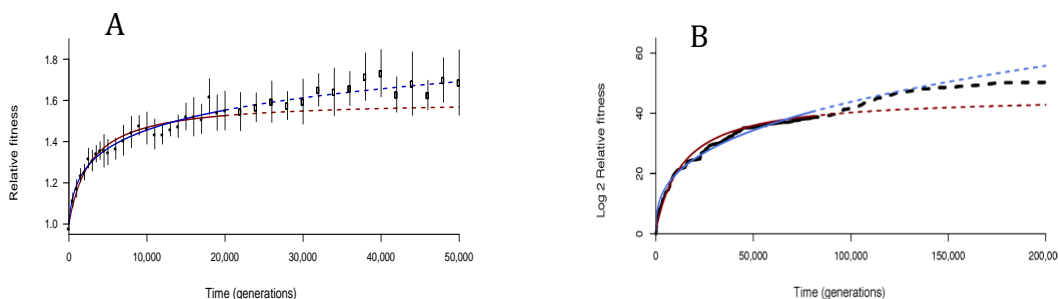


Fig. 1 Comparison of a bounded (dark red) and an unbounded (medium blue) model of fitness change. Filled circles (A) / solid black line (B) show the data used to fit the models, which are solid red or blue lines through this data. Dashed lines show model predictions for data not used in the model fit; open circles (A) / dashed black line (B) show empirical data from these generations. A) Figure based on (2), (bacterial). B) Figure based on (3) (computational)

**Computational:** To address whether these patterns of fitness change were specific to the LTEE, I turned to a fundamentally different system in collaboration with Dr. Charles Ofria. Avida is a digital evolution software platform in which self-replicating computer programs compete for digital resources (4). This self-replication is not perfect; the user defines mutation rates for the digital organisms, which provides a source of

variation for the population. Because this system has variation (from the mutations), heredity (from replication), and selection (from competition over digital resources), evolution by natural selection is an inevitable outcome; it is an instance of evolution, rather than a simulation of it. **Although many of the details of this system are different than the bacterial system** – smaller population size, a growth model more similar to continuous culture than serial batch transfer, greatly simplified metabolism and replication, etc – **the same basic pattern emerges (Fig 1B)**, suggesting that power law models of fitness change may be inherent to evolving systems (3).

#### Ongoing and future research:

To make quantitative predictions about future evolution, we need to use time as part of our prediction. How do we best measure time? Is it based on absolute time of days, month, years? Or is it more meaningful to measure time in terms of generations? Populations can experience more absolute time in one environment, such as low-nutrient stationary phase, while having most of their generations in another, such as high-resource exponential growth, as they do in batch culture experiments. **My research will quantify the relative importance of these two approaches to time.**

*Bacterial:* We hypothesize that populations within the LTEE are subject primarily to selection for growth during exponential phase. This is because most of their generations occur here, even though most of their absolute time is spent in stationary phase. I have been investigating whether repeated exposure to short-term stationary phase in the LTEE has primed evolved populations for long-term starvation (Fig. 2). I've found that evolved populations – which have evolved lower population sizes with consequently larger cells – initially die more slowly than their ancestors. As the ancestral populations die, the evolved populations scavenge for released nutrients and exhibit net growth late in these competitions.

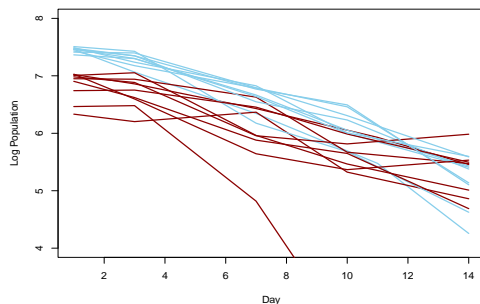


Fig 2. Population sizes within long-term starvation competitions between evolved populations (dark red) and their ancestors (light blue). Unpublished preliminary data.

How are the evolved populations growing late in these competitions? My hypothesis is that the larger cell size of the evolved populations (5), thought to be a direct result of selection for rapid growth as soon as resources are available upon transfer, underlies this increased tolerance for long term starvation. **I am working with a current graduate student to assay cell size across the populations of the LTEE over time**, and test if this correlates with a) fitness changes within the environment of the LTEE, and b) increased competitive ability in long-term starvation. **My lab will systematically measure long-term starvation competitive ability for populations from the LTEE.** This will allow us to **assess whether cell size, fitness during a typical transfer cycle, or both are useful predictors of fitness during long-term starvation.**

Further, all of these populations are ones evolved under a particular transfer cycle: fresh nutrients every 24 hours. Previous work has shown, though, that there is very little death during this cycle length for the ancestral populations (5). It is therefore difficult to tease apart how much of the improved ability in long term starvation competitions is due to improved tolerance of stationary phase, and how much is due to a correlated response to selection for larger cell size.

To address these questions, **my lab will experimentally evolve populations in three different transfer cycle lengths: 24, 48, and 72 hours**. We will additionally assay populations from the LTEE at time points corresponding to those from our new evolution experiments. I predict that different cycle lengths will lead to different levels of death from stationary phase, and therefore to an increasing role of selection for lower stationary phase death as the cycle length increases. Selection for rapid growth upon transfer – thought to be the primary driver of increased cell size evolved in the LTEE – will remain high, but the relative importance of these two selective pressures will differ across treatments. Further, this will allow an additional comparison of time, as these different transfer cycles will differ substantially in the amount of absolute time spent in low-nutrient stationary phase, but will be relatively consistent in the number of generations spent in high-nutrient exponential growth.

**Can we use deviation from predictions to uncover ecological interactions?**

My research has provided a large number of precisely measured fitness values of independent populations in the same species. From these fitness values, I've been able to make quantitative predictions of which populations should be able to invade other populations, and how more than two populations would fare in a joint competition. I have then conducted the invasion experiments and the multi-population competitions. The invasion experiments have yielded direct evidence of negative frequency dependence in fitness for certain invader-host pairings. These pairings include one where the equilibrium frequency is so low that it wouldn't have been detectable by mixed population sequencing. With a collaborator, I am currently sequencing the communities at specific time points to compare the actual competitions to the mathematical model I built of expected dynamics based on their individual fitness values relative to the ancestor; deviations from expectation here would also be indicative of ecological interactions across these populations, which have been isolated from each other for 50,000 generations. Once we have identified which population pairings exhibit ecological interactions, we can use the genetic differences among populations to screen for underlying causal mutations.

*Computational:* A common finding of many genetic and evolutionary algorithms is that any trait of interest – fitness, complexity, etc. – improves for some period of time, then appears to stagnate (6). This is contrary to biology, where evolution appears much more open-ended. To address this disconnect, I am working with computer scientists to both a) **identify and quantify the barriers to open-ended evolution** (7), and b) demonstrate that **the appearance of stagnation can be an illusion**, such that systems which are still evolving may temporarily and artificially appear to stopped. **I am further investigating the relationship between time in generations and time in CPU cycles for predicting fitness change.**

Computational systems also allow us to control parameters that are impractical in organic systems. For example, we can precisely control both the rate of mutation and distribution of fitness effects of mutation in a computational system, in a way we simply cannot in biology. **My lab will examine the impact of different distributions of fitness effect of mutation on the resulting fitness trajectories**. I predict that distributions with more small effect mutations will better support an unbounded model of fitness increase, while ones with rare but large effect mutations will better support bounded models; this is the basis of what I've called the boundedness illusion.

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