

## Statement of Research, Teaching and Service

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Department of Biological Sciences

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As a faculty member of the Department of Biological Sciences at The University of Alabama (UA), 40% of my workload is research, 40% teaching, and 20% service. In order to be eligible for tenure and promotion, tenure-track faculty must demonstrate the following:

- 1) A strong record of research productivity, evidenced by consistent publications (*average of one per year*) and persistent efforts to obtain extramural funding
- 2) Effective instructional performance, assessed, in part, by student opinion of instruction (SOI) surveys and peer evaluations
- 3) A continuing commitment to academic citizenship, as evidenced by relevant service and outreach activities.

I have included the UA Department of Biological Sciences Tenure and Promotion Policies and Procedures document for more details on these requirements. I have also included my current CV and two research publications at the end of this document.

### Research

The overarching goal of my research is to discover the rules of genome evolution. One of the main drivers of genome evolution is sexual reproduction, or the lack of it through the evolution of self-fertility and asexuality. Sex increases genetic variation through recombination and results in a broad array of consequences at genetic and phenotypic levels. Evolutionary theory predicts that populations and genomes should evolve differently depending on reproductive strategy, but until recently the field lacked the technologies required to generate data and test theoretical predictions. As a result, there are still many gaps in our understanding of the influence of sex, self-fertility and asexuality on genome evolution.

My research program takes an innovative approach to integrating evolutionary theory and modern molecular data. Evolutionary theory has a rich conceptual and mathematical history, but until recently we could not generate the necessary data to test theoretical predictions and produce informed, biologically grounded theory. Biological technology is rapidly advancing on all fronts and recent progress in computing, high-throughput sequencing, and molecular biology means that we are now poised to test many theoretical predictions regarding genetic evolution. For example, biologists have long known that the phenotypic effect of a mutation is determined by a complex, interconnected network of molecular interactions but most evolutionary theory was formulated by examining one or two genes at a time. A major goal of my research is also to understand system-level evolution by inferring network structure from biological data and studying computational network models.

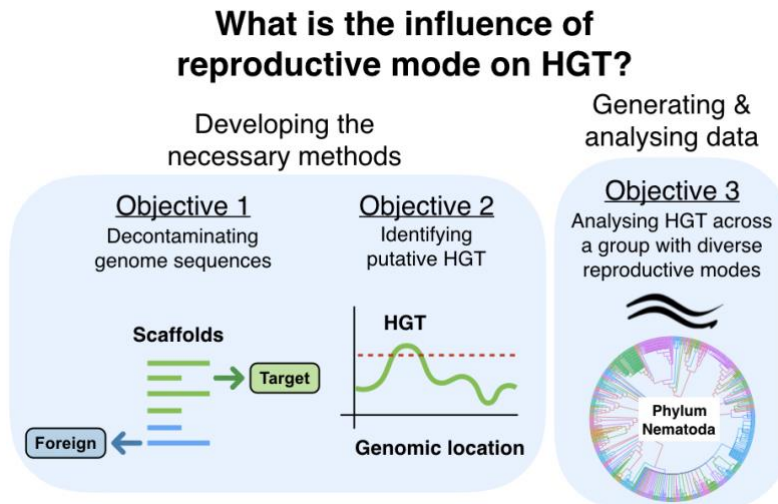
My research program addresses fundamental questions in evolutionary genetics through concept-driven theoretical modeling, comparative genomic analyses and bioinformatic methods development. The bioinformatic and computational aspects of my research transfer across

organismal systems and I enjoy collaborating with other researchers. My recent work focuses around both theoretical and empirical investigations and developing the tools and techniques necessary to pursue my research questions. Below, I describe my core research foci, relevant publications and funding.

## Reproductive mode and genome evolution

Nematode worms display variation in reproductive ‘modes’ including closely related dioecious outcrossing species, androdioecious species with males and self-fertile hermaphrodites, trioecious species with males, females and self-fertile hermaphrodites and both mitotic and meiotic parthenogenetic (i.e., asexual) species. These tiny worms have a fascinating array of reproductive variation and are the perfect system in which to study how reproductive mode influences genome evolution.

For example, self-fertile *Caenorhabditis*, including the model organism *C. elegans*, have genomes 20-30% smaller than related outcrossing male-female species. My lab group is quantifying the genomic changes that accompany reproductive modes of outcrossing and self-fertility. We are sequencing and assembling nematode genomes, performing fine-scale comparative genomic analyses and quantifying molecular variation across genomic features including untranslated regions (UTRs), exons, introns, repeats and intergenic regions. We are using phylogenetic comparative methods to test adaptive hypotheses linking variation in genome features with reproductive mode. We are also interested in the impact of reproductive mode on genetic architecture and the potential for adaptive evolution (Adams et al. *in revision*; O’Connor et al. *in revision*). Funded by an NSF CAREER award (DEB-1941854) my lab is investigating the frequency and significance of horizontal gene transfer across the nematode phylogeny.



**Figure 1.** In order to analyze the influence of reproductive mode on horizontal gene transfer my group is developing bioinformatic methods, sequencing and assembling nematode genomes and analyzing genomic patterns with rigorous phylogenetic comparative methods.

In pursuing our research questions my lab group works on problems regarding the nature of identity in genomic data. Empirical biologists joke that molecular biology is moving minute amounts of clear fluid from one tube to another. Practically, this means that sequenced DNA extracts often contain mixtures of organismal DNA and my group is developing bioinformatic decontamination methods (Fierst and Murdock 2017; Fierst et al. 2017). Technology limits the

amount of DNA we can obtain from samples with few cells but we know that causal genomic variation occurs at this scale. My group is working on experimental design for these problems (Sutton and Fierst *in review*; Fierst 2015).

### **Publications**

- In revision* Adams, P.E., A.L. Crist, E.P. Young, J.H. Willis, P.C. Phillips and **J.L. Fierst**. Slow recovery from inbreeding depression generated by the complex genetic architecture of segregating deleterious mutations. *In revision*, Molecular Biology and Evolution.
- In revision* O'Connor, C. H., K.L. Sikkink, T.C. Nelson, **J.L. Fierst**, W.A. Cresko, and P.C. Phillips. Complex pleiotropic genetic architecture of evolved heat stress and oxidative stress resistance in the nematode *Caenorhabditis remanei*. *In revision*, G3.
- In review* Sutton, J.M. and **J.L. Fierst**. Optimizing experimental design for genome sequencing and assembly with Oxford Nanopore Technologies. *In review*, iScience.
- 2017 **Fierst, J.L.**, and D.A. Murdock. Decontaminating eukaryotic genome assemblies with machine learning. BMC Bioinformatics 18(1): 533.
- 2017 **Fierst, J.L.**, D.A. Murdock, C. Thanthiriwatte, J.H. Willis, and P.C. Phillips. Metagenome-assembled draft genome sequence of a novel microbial *Stenotrophomonas maltophilia* strain isolated from *Caenorhabditis remanei* tissue. Genome Announcements 5(7): e01646-16.
- 2015 **Fierst, J.L.** Using linkage maps to correct and scaffold *de novo* genome assemblies: methods, challenges and computational tools. Frontiers in Genetics 6: 220.

### **Funding**

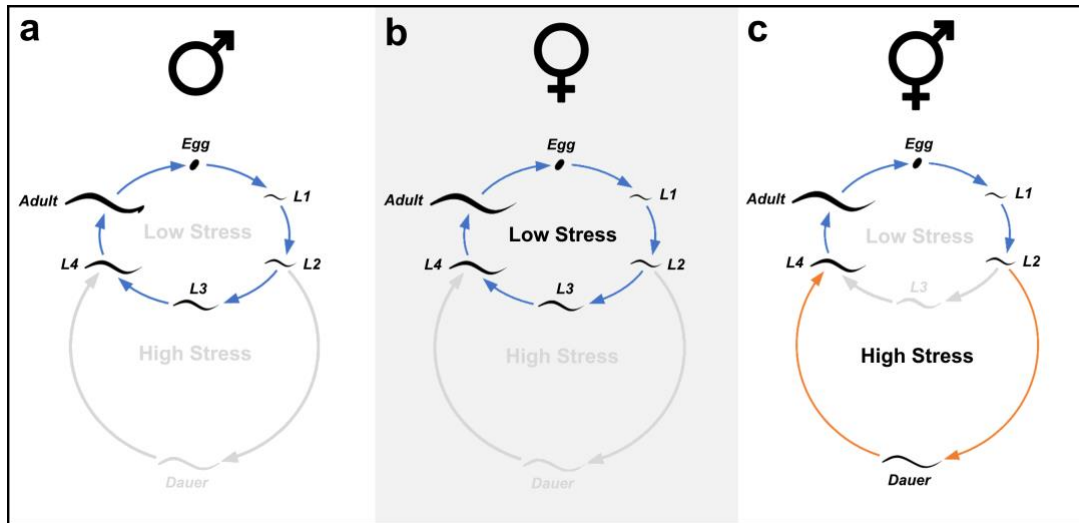
National Science Foundation \$1,135,944 8/2020 - 8/2025  
CAREER: Reproductive mode and horizontal gene transfer in nematode worms: Training early career researchers in computational evolutionary biology

### **Resilience, robustness and evolvability in biological systems**

Complex systems approaches utilize advances in computational science to provide tools for resolving complex interrelationships across levels of biological organization. Network analysis is a powerful conceptual tool for distilling complex systems into essential components and interactions. On the data side, network inference extracts relationships and emergent patterns from high-dimensional, large-scale datasets; on the theory side, network models can reveal the evolution of genotype-phenotype relationships.

Biological systems must be robust in order to function despite mutations and environmental change but at the same time evolvable, or able to change. A fundamental question is how a system produces both a robust phenotype and the variance necessary for evolutionary change. Theoretical studies have demonstrated that selection for plasticity can result in the evolution of genetic robustness, but such predictions have not been extensively tested in empirical systems. Funded by a collaborative grant from the National Science Foundation (EF-1921585), my lab group is combining statistical inference of network structure from genomic, epigenomic,

transcriptomic, and metabolomic data from bumblebees (Heraghty et al. *in review*) with network modeling to explore if phenotypic variance is due to parallel genetic changes or plasticity mediated through epigenetic changes driving transcriptomic and metabolic differentiation. We are analyzing if evolvability, resilience and robustness are achieved through changes at a single level of biological organization or if environmental signals propagate through levels.



**Figure 2.** Under low-stress conditions eggs develop into male and female nematodes depending on chromosomal content (males are X0 and females are XX). Under stressful or resource-limited conditions XX individuals enter the dormant dauer life stage and develop into hermaphrodites.

We are also interested in how an organism's life history can produce population-level resilience. Nematode worms have a dormant dauer stage that they enter under conditions of stress or resource limitation. The nematode *Auanema freiburgensis* also uses the dauer stage for sex determination. Female and male worms are produced in stress-free conditions and stress induces female worms to enter the dormant dauer stage and develop into hermaphrodites. We studied a theoretical model to investigate how this unique environment-dependent sex determination can produce population-level resilience (Anderson et al. 2020). We are studying the conditions that determine dauer exit, a biological process that is currently poorly understood (Bubrig et al. *in revision*).

## Publications

- 2020\* Anderson, A.G., L.T. Bubrig and J.L. Fierst. Environmental stress maintains trioecy in nematode worms. *Evolution* 74-3: 518-527.
- In revision* Bubrig, L.T., J.M. Sutton, and **J.L. Fierst**. *Caenorhabditis elegans* dauer recovery varies with worm-bacteria interactions. *In revision*, *Ecology and Evolution*.
- In review* Heraghty, S.D., J.M. Sutton, M.L. Pimsler, **J.L. Fierst**, J.P. Strange, and J.D. Lozier. *De novo* genome assemblies for three North American bumble bee species: *Bombus bifarius*, *Bombus vancouverensis*, and *Bombus vosnesenskii*. *In review*, G3.

## **Funding**

National Science Foundation

\$2,589,602 5/2020 - 10/2023

Understanding the Rules of Life Epigenetics: Bumble bee cold tolerance across elevations—  
From epigenotype to phenotype across space, time, and levels of biological organization

## **The evolution of novelty in microbial metabolism**

Metabolic interactions form complex, delicately balanced networks. How do new metabolisms evolve and how do new interactions impact the cellular network? To answer these questions we are examining acetylene metabolism in microbes. Acetylene is a trace constituent of Earth's atmosphere resulting from anthropogenic combustion of fuels, biomass burning, and natural microbial production (Akob et al. 2018; Fig. 3). It is an intermediate in biotic and abiotic degradation of chlorinated solvents and acetylene build up can stop the degradation process and result in the accumulation of toxic daughter products. Only 3 known microbes encode an acetylene hydratase enzyme (Akob et al. 2017; Baeman et al. *in revision*; Sutton et al. 2017; Sutton et al. 2017) yet up to 30% of metagenomic cultures can break down acetylene. We are sequencing and assembling microbial genomes and analyzing metagenomic cultures in a search for new acetylenotrophs and new enzymes capable of bioremediating chlorine contamination. We are using phylogenetic reconstruction to study the evolution of acetylenotrophy and its relationship to other tungsten-molybdenum containing nitrate reductases. We have also studied the impact of engineered microbial metabolism on cellular physiology (Ma et al. 2016).

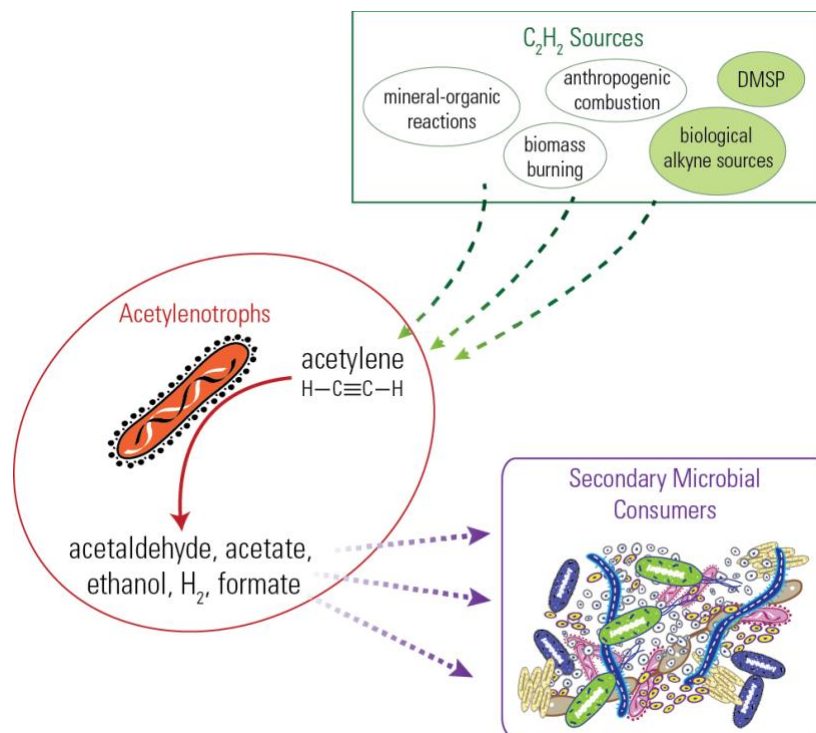


Figure 3. Acetylene degrading bacteria play a critical role in remediation.

## **Publications**

*In revision* Baesman, S.M., J.M. Sutton, **J.L. Fierst**, D.M. Akob, and R.S. Oremland.

- 2018\* *Pelobacter acetylenovorans*, strain SFB93, sp. nov., a diazotrophic, acetylene-fermenting anaerobe isolated from San Francisco Bay intertidal sediments. *In revision*, International Journal of Systematic and Evolutionary Microbiology.
- 2017\* Akob, D.M., J.M. Sutton, **J.L. Fierst**, K.B. Haase, G.W. Luther III, and R.S. Oremland. Acetylenotrophy: a hidden but ubiquitous microbial metabolism? FEMS Microbiology Ecology 94(8): fiy103.
- 2017\* Akob, D.M., S.M. Baesman, J.M. Sutton, **J.L. Fierst**, A.C. Mumford, Y. Shrestha, A.T. Poret-Peterson, S. Bennett, D.S. Dunlap, K.B. Haase, and R.S. Oremland. Detection of diazotrophy in the acetylene-fermenting anaerobe, *Pelobacter* strain SFB93. Applied and Environmental Microbiology. 83: e01198 - 17.
- 2017\* Sutton, J.M., S.M. Baesman, **J.L. Fierst**, A.T. Poret-Peterson, R.S. Oremland, D.S. Dunlap, D.M. Akob. Complete genome sequences of two acetylene-fermenting *Pelobacter acetylenicus* strains. Genome Announcements 5(6): e01572-16.
- 2017\* Sutton, J.M., S.M. Baesman, **J.L. Fierst**, A.T. Poret-Peterson, R.S. Oremland, D.S. Dunlap, and D.M. Akob. Complete genome sequence of the acetylene-fermenting *Pelobacter* strain SFB93." Genome Announcements 5(6): e01573-16.
- 2016 Ma, C., J. Ou, N. Xu, **J.L. Fierst**, S-T Yang and X. Liu. Rebalancing redox to improve biobutanol production by *Clostridium tyrobutyricum*. Bioengineering 3(1): 2.

## **Funding**

University of Alabama Research Grants Committee	\$82,446	6/2015 - 2/2017
Genome-scale model guided metabolic engineering of <i>C. tyrobutyricum</i>		

## Education and Mentoring

### **Overview**

I believe the objective of university teaching is to aid in each student's intellectual and personal development. We achieve this through lectures, assignments and tests, as vehicles for teaching students to organize and process information, develop critical thinking and analysis, communicate effectively, balance work and other pressures, and operate as community members. One of the reasons I enjoy teaching is because it requires me to develop my own skills in these areas. I started my teaching career at the high school level after I had finished my undergraduate degree. I had no plans for graduate school but teaching forced me to learn the material in a way I never had as a student. I developed an appreciation for science and research, and that led me to graduate school. Integrating teaching and research keeps me motivated in both areas and broadens my perspective on scientific research.

### **Teaching Experience**

I have taught for 9 semesters at UA (Spring 2015 course release; Spring 2017 maternity leave) including 6 semesters of Introduction to Bioinformatics (BSC 473/573) and 3 semesters of



Computational Biology Lab (BSC 426/526). Both classes involve learning computational skills and applying these to biological questions. Introduction to Bioinformatics focuses primarily on genetic questions and analyzing high throughput sequencing data while Computational Biology focuses on Python programming, network analysis and process-based modeling.

When I began my appointment in 2015 there were no textbooks appropriate for my upper division undergraduate and early graduate students. I worked hard to develop materials and ensure they are accessible to biology students with no computational background but also interesting for those with more experience. My classes consistently fill with undergraduate and graduate students from Biological Sciences, Chemistry, Engineering, Mathematics, Computer Science and Psychology. I find students are really interested in the material but it is challenging to keep this diverse population engaged. I achieve this by highlighting the differences between the fields and using the strengths of each in class exercises.

Biology requires complex concepts, abstract material and ‘big picture thinking.’ Students with mathematics, computer science and engineering backgrounds often have developed quantitative skills but less experience with abstract thinking and creative self-determination. Throughout the class I highlight the importance of developing both a conceptual framework and practical skills and communicate how valuable these are for education and work.

At UA, as at many other colleges and universities in the US, a large proportion of our students are unprepared for college because their early education did not provide them with the skills they need to succeed. I firmly believe we can help students develop skills through effective, innovative research-based teaching practices. For example, discipline-based education research has found that best practices for effectively teaching biology include a focus on broad conceptual foundations and inquiry-based, discovery-led approaches. In contrast, computing education researchers have found that many students fail to make progress in computing, algorithm development and problem-solving with minimally guided instruction. Specific instructional approaches that help students make progress in computing include collaborative learning activities like pair programming and guided instruction including collaborative in-class problem solving. These activities are effective in increasing overall student retention and academic engagement and have been proven to significantly increase the retention of women and students of color. I incorporate these research-based practices throughout my classes. In our technology-enabled world computing and computational skills are social justice issues. Increasing participation and understanding is central to equity in higher education.

### **Course Descriptions and Student Evaluations**

Every semester graduate and undergraduate students evaluate course and instructor on a 1-5 point scale where 5 is the highest through anonymous digital surveys administered by UA. Below I have included a description, learning outcomes, student evaluations and Faculty Peer Evaluations for each course. There is no teaching assistant (TA) support for my courses.

#### **Introduction to Bioinformatics (BSC 473/573)**

##### **Course Description**

Bioinformatics BSC 473/573 is a lecture course that covers the tools and approaches necessary to perform computational analysis of large datasets. We will focus on analyzing high-throughput sequencing data although the tools we will learn are applicable to a wide range of modern biological questions. Specific topics include operating in a UNIX/bash shell environment,

scripting, genome assembly, alignment, and algorithms. BSC 473/573 is a writing course and writing proficiency within this discipline is required for a passing grade in this course.

### **Student Learning Outcomes**

- Navigate in a Unix/bash shell environment
- Understand genomic alignment algorithms
- Understand genome assembly algorithms
- Work with public databases and bioinformatics tools
- Present completed research findings to the class
- Work both collaboratively and independently

Average Course Evaluation: 4.59/5

Average Instructor Evaluation: 4.61/5

Faculty Peer Evaluation: 4.5/5

### **Computational Biology Lab (BSC 426/526)**

#### **Course Description**

Computational Biology Lab introduces the programming skills, statistical methods and conceptual foundations necessary to pursue computational analysis and modeling of biological systems. This course is designed for biology students, and it is not expected that students will have prior with experience with computing or programming.

#### **Course Objectives**

- Write short Python programs
- Analyze datasets in Python including visualization and summary statistics

### **Student Learning Outcomes**

- Demonstrate understanding of the fundamentals of computer programming
- Implement programmatic solutions to computational problems
- Implement computational solutions to biological data analysis
- Demonstrate understanding of biological networks metrics

Average Course Evaluation: 4.07/5

Average Instructor Evaluation: 4.36/5

Faculty Peer Evaluation: 5/5

### **Student Comments on Instructional Quality**

*“She is a great instructor and truly appears to care about the class, and where it is going.”*

*“Dr. Fierst is super nice and approachable. She cares that you try your best and is very good at recognizing when you do so.”*

*“It is very apparent any time Dr. Fierst speaks in class that she has an immensely thorough understanding of the material. Due to the material being quite dense, it was often difficult to immediately understand the material, and Dr. Fierst seems to always be aware of this and structures her lectures accordingly.”*



*“Respectful.”*

*“This class is a really fun biology elective because it is so different than any other biology class. I think it is important for bio majors to take because it teaches you a different set of skills that you can't really get elsewhere. I'm excited to take bioinformatics with Dr. Fierst next semester.”*

*“Dr. Fierst made a good course that taught a lot to the beginner in bioinformatics. Due to the nature of the material, she was very flexible in working with her students questions and mistakes. This made the course a good learning experience and I would recommend it to anyone in the biology department.”*

*“The course material can feel a bit foreign to anyone who is used to typical biology courses like Ecology or Cell Biology, but if you take the time to understand the assignments given it becomes apparent the uses of these materials in biology.”*

*“She did a great job teaching a topic that is difficult for beginners.”*

*“Dr. Fierst is a great teacher. She is extremely helpful and was always understanding and available for assistance if needed.”*

*“She is a great teacher and she knows her subject really well.”*

*“Dr. Fierst was very kind and clearly cares about her students. She made class enjoyable and was always willing to answer questions.”*

### **Undergraduate and Graduate Research Mentorship**

One of the highlights of my job is mentoring students. My goal is to produce high-quality research, excellent training and intellectual development for early career researchers in an interactive, supportive intellectual community. I have found the best approach to mentoring is a combination of structure through weekly meetings, readings and specific goals, and flexibility with projects designed and altered according to students needs and interests. This combination provides students with positive, productive research experiences.

I enjoy mentoring a range of projects from mathematical models to empirical analyses. For example, I currently co-advise one student studying comparative genomics in freshwater Alabama mussels. This system is far from my training in ‘organism-free’ theory and I love learning about other facets of our natural world.

I am committed to building a diverse research and educational program but women, students of color and first-generation college students remain underrepresented in Science, Technology, Engineering and Math (STEM). One of my main goals as an Assistant Professor has been increasing diversity in STEM by mentoring and training students from underrepresented groups. 70% of my undergraduate and graduate researchers have been from underrepresented groups.

### **Undergraduate Researchers**

I mentor undergraduate researchers through the BSC 398 Research course and the UA work-study program. I have worked with 16 undergraduate researchers at UA and they have gone on to pursue a number of different paths after graduation. Louis Bubrig remained in my UA lab for graduate school, recently completed his MS degree and will pursue a PhD at the University of Virginia. John Sutton started as an undergraduate researcher and remained in my UA lab for his PhD. Ashlyn Anderson published a first-author paper from her research project (co-authored

with Louis Bubrig) and is pursuing a PhD in Biostatistics at the University of Florida, funded by a 5 year competitive fellowship. Two Computer Science majors went on to work at software engineering firms, helped in part by computing projects they pursued in my lab. One student went on to a Physicians Assistant program and 4 went on to medical school.

### **Graduate Researchers**

My graduate students are active, engaged members of the Department of Biological Sciences, UA and the broader scientific community. Two of my graduate students served as officers of the Department of Biological Sciences Graduate Student Organization and worked to increase social events, informal ties and social support within the graduate student community. My 4 graduate students have together been awarded 1 UA Graduate Council Fellowship, 3 UA National Alumni Association fellowships and multiple smaller research and travel awards. They have presented at 15 national and international scientific conferences and submitted 11 manuscripts.

### **Other Educational Responsibilities**

#### **Academic Advising**

I typically advise 30-50 undergraduates in class planning per academic semester. I have also advised newly enrolling undergraduates through summer 'Bama Bound' programs.

#### **Letters of Recommendation**

I typically write 5-15 letters of recommendation per year.

#### **Graduate Committees**

I have served on 13 dissertation and 3 thesis committees.

## **Professional Service and Outreach**

I have been involved in service within my department, college, university, and broader scientific community. My service has focused around three interconnected goals: (1) Developing computational resources including personnel and support for student training; (2) Developing high-quality training environments for the next generation of scientists; and (3) Broadening the participation of women, first-generation students, students of color and other traditionally underrepresented groups in science.

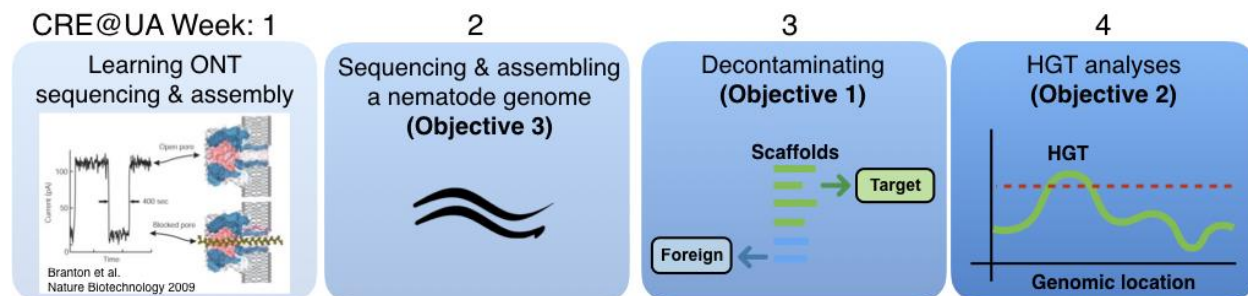
Within UA I serve on the Technology Resource Advisory committee and the College of Arts and Sciences High Performance Computing committee. Both are tasked with developing plans for increasing computational resources within the college and university. This includes identifying needs across a broad range of departments from Modern Languages and Literature to Physics and a range of colleges from Community Health Sciences to Engineering. We meet regularly as interdisciplinary groups to define current computational use and discuss the future of computing in our varied fields. Although our research questions are widely different we have identified core challenges in our fields and computational use. For example, graduate students across the university come in with little practical training in high performance computing and are reticent to seek help. Our committees have defined dedicated support staff that are readily approachable and in regular communication with graduate students to be as vital as physical

resources like high-speed data transfer. We are able to communicate these needs to the UA administration and ensure support that allows students to flourish in computational sciences. This support is important for all students but it is vital for increasing the participation of traditionally underrepresented groups in computing.

I believe one of the largest barriers to increasing the participation of traditionally underrepresented groups in science is a lack of supportive training environments. I serve on the Department of Biological Sciences Graduate Admissions and Recruiting committee and am actively working to create a high-quality environment for our students. For example, I proposed a successful initiative to remove the GRE from our graduate application requirements. Research has identified the GRE as an expensive barrier to underrepresented groups and removing this was a first step in communicating our departmental commitment to broadening participation.

Within the broader scientific community I served on the Society for the Study of Evolution's W.D. Hamilton Award for Outstanding Graduate Student Presentation Selection Committee. Advanced graduate students submit presentation abstracts (typically 50-150 a year) for competitive selection in the Hamilton Symposium and evaluation for the W.D. Hamilton Award. The symposium contains many of the best talks of the annual Evolution meetings and the presentations are judged by Evolution society members beyond the selection committee. The effort and excitement surrounding the W.D. Hamilton Award communicate to graduate students that they are valued members of the society and scientific community. The symposium brings energy to the society as members see the development of the next generation of evolutionary biologists. I am grateful that I was able to serve as a member of the Hamilton Committee for 3 years. In addition to these service commitments I regularly review 9-12 scientific manuscripts per year and grants for agencies within the US and abroad. It is an honor to provide input to the broader scientific community and shape future research objectives.

In order to better the training environment at UA my CAREER award involves the development of an immersive summer Computational Research Experience at the University of Alabama (CRE@UA) for undergraduates. This project will train at least 30 undergraduate researchers (6 per year for each of 5 years). Graduate and postdoctoral researchers will serve as collaborative research mentors during CRE@UA. The program will focus on each undergraduate sequencing, assembling, decontaminating and analysing a nematode genome and follow the curriculum in Figure 4. I am excited that my CAREER award will enable me to develop innovative, integrative training for undergraduate, graduate and postdoctoral researchers.



**Figure 4.** The CRE@UA activities week by week.

## UA Service and Outreach

### Service to the Department of Biological Sciences

- Graduate Admissions and Recruiting Committee
- Facilities Committee
- 3 Minute Thesis (3MT) Judge
- Plant Systematics faculty search committee

### Service to the College of Arts and Sciences and UA

- UA Cyberinstitute member
- Research Software Engineer search committee
- College of Arts and Sciences High Performance Computing committee
- UA Technology Research Advisory Committee
- Alabama's Lectures on Life's Evolution Organizing Committee

### Guest Lectures and Outreach

- Honors Biology Enrichment Section
- Society for Engineers in Biomedicine
- Society of Women Engineers
- NSF Research Experiences for Undergraduates "Fluid Mechanics with Analysis Using Computations and Experiments"

## Scientific Service

### Society for the Study of Evolution

- W.D. Hamilton Award for Outstanding Graduate Student Presentation Selection Committee

### Manuscript Reviews

I review 9-12 scientific manuscripts per year for a diverse set of journals including:

- *Bioinformatics*
- *Briefings in Bioinformatics*
- *BMC Bioinformatics*
- *BMC Evolutionary Biology*
- *Current Biology*
- *Ecology*
- *Evolution*
- *Evolution Letters*
- *G3: Genes, Genomes and Genetics*
- *Genetics*
- *J. of Evolutionary Biology*
- *Molecular Biology and Evolution*
- *PLoS Genetics*
- *Proceedings of the Royal Society, Series B*
- *Science Advances*

**Grant reviews**

Panelist for:

- NIH Early Career Reviewer for the Genomics, Computational Biology and Technology study section

Ad hoc reviewer for:

- NSF Division of Environmental Biology
- Medical Research Council (UK)
- Agence Nationale de la Recherche (FR)
- CONACYT (MX)
- Graduate Women in Science National Fellowship Program (US)

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## EDUCATION

2010	<b>The Florida State University</b> <i>PhD, Biological Science, Section for Ecology and Evolution</i> Advisors: David Houle and Thomas F. Hansen	<b>Tallahassee, FL</b>
2004	<b>California State University, Northridge</b> <i>MS, Biology</i> Advisor: Steven R. Dudgeon	<b>Los Angeles, CA</b>
1998	<b>Pomona College</b> <i>BA, Biology</i>	<b>Claremont, CA</b>

## PROFESSIONAL POSITIONS

2015-Present	<b>The University of Alabama</b> <i>Assistant Professor</i> Department of Biological Sciences	<b>Tuscaloosa, AL</b>
2010-2014	<b>The University of Oregon</b> <i>Postdoctoral Researcher</i> , Institute for Ecology and Evolution Mentor: Patrick C. Phillips	<b>Eugene, OR</b>
2008-2009	<b>The University of Oslo</b> <i>Leiv Eiriksson Mobility Fellow</i> Sponsor: Thomas F. Hansen	<b>Oslo, Norway</b>

## GRANTS AND AWARDS

### Current Funding

National Science Foundation \$1,135,944 8/2020 - 8/2025  
 CAREER: Reproductive mode and horizontal gene transfer in nematode worms: Training early career researchers in computational evolutionary biology  
**Fierst PI**



National Science Foundation	\$2,589,602	5/2020 - 10/2023
Understanding the Rules of Life: Epigenetics 2: Collaborative research: Bumble bee cold tolerance across elevations- From epigenotype to phenotype across space, time, and levels of biological organization		
<b>Fierst co-PI</b> (cost share \$701,211)		

*Proposals In Review*

National Institutes of Health	\$1,835,000	10/2021 - 9/2026
National Institute of General Medical Sciences		
R35 MIRA: Sex and self-fertility: Drivers of genome evolution		
<b>Fierst PI</b>		

*Completed Funding*

National Institutes of Health	\$1,251,600	10/2015 - 5/2019
National Institute of General Medical Sciences		
R01: System genetics of natural variation in stress response pathways		
<b>Fierst subcontract</b> (cost share \$145,625)		

University of Alabama	\$82,446	6/2015 - 2/2017
Research Grants Committee		
Genome-scale model guided metabolic engineering of <i>C. tyrobutyricum</i>		
<b>Fierst co-PI</b> (cost share \$15,666)		

National Science Foundation	\$123,000	10/2010 - 9/2012
Postdoctoral Fellowship in Biological Informatics		
<b>Fierst PI</b>		

Norwegian Research Council	NOK300,000	6/2008 - 6/2009
Leiv Eiriksson Mobility Fellowship		
<b>Fierst PI</b>		

PADI Project Aware	\$5,000	2003
Grant in Aid of Research		

Sigma Xi	\$2,500	2002
Grant in Aid of Research		

Phycological Society of America	\$2,500	2002
Grant in Aid of Research		

## *Proposals Declined*

### **2020**

PI on a NIH National Institute of General Medical Sciences proposal: R35 MIRA: Sex and self-fertility: Drivers of genome evolution (\$1,735,000)

co-I on a NIH National Institute on Aging proposal: R01: Mechanisms underlying aged host-virus interactions (\$1,801,206; cost share \$270,181)

co-I on a NASA Exobiology proposal: Coevolution of desiccation resistance in tardigrades and their symbiotic bryophytic habitats: Implications for earth-like life to adapt to extraterrestrial environments (\$995,000; cost share \$173,478)

### **2019**

co-PI on an internal UA competition for submission to the NSF Major Research Instrumentation competition: MiSeq for UA

PI on a NIH National Human Genome Research Institute proposal: Developing ensemble-based statistical learning methods for Decontamination genome sequences (\$403,000; cost share \$273,000)

Co-I on a NIH National Institute of Environmental Health and Safety proposal: Functional characterization of gene regulatory networks associated with acquired cadmium tolerance and resultant chronic inflammation (\$1,780,000; cost share \$537,642)

co-PI on an NSF proposal: Dimensions US-South Africa: The fig fruit- gatekeeper of obligate mutualism and biodiversity (\$1,775,869; cost share \$533,295)

co-PI on a NSF Integrative Organismal Systems proposal: Linking genomic level approaches to physiological assessment and ecosystem-level responses (\$1,755,770; cost share \$175,577)

PI on a UA College of Arts & Sciences College Academy of Research, Scholarship and Creative Activity proposal: Sex in genome evolution (\$6,000)

### **2018**

PI on a NSF CAREER proposal: Intersexual conflict and genome evolution in nematode worms: Training early career researchers in computational evolutionary biology (\$803,000)

Co-I on a NASA Exobiology proposal: Comparative cryptobiosis: the evolvability of anhydrobiosis across tardigrades, nematodes and rotifers and the implications for advanced life's ability to adapt to extraterrestrial habitats. (\$990,085; cost share \$155,931)

Co-I on a NASA Exobiology proposal: Acetylene, a novel hydrocarbon substrate for supporting primordial microbial food webs and putative microbes on planetoids of the outer Solar System (e.g., Enceladus, Titan, Europa) (\$860,000; cost share \$235,000)

Co-PI on a NSF Dimensions of Biodiversity proposal: Collaborative research: Coevolutionary diversification in Astragalus, the most species rich genus of flowering plants. (\$2,240,425; cost

share \$225,600)

Co-PI on a NIH National Institute of Environmental Health and Safety proposal: Elucidating the gene regulatory network modulating cadmium transformed cells (\$1,780,000; cost share \$448,158)

PI on a Teach Access proposal: Accessibility for bioinformatics education. (\$5,000)

PI on a NASA Earth and Space Science Fellowship: Acetylene Fermentation in Earth's Primordial Atmosphere (\$45,000)

## **2017**

Co-I on a NASA Exobiology proposal: Acetylene Fermentation: A primordial sustenance for developing terrestrial microbial communities and for putative microbes on planetoids of the outer Solar System (e.g., Enceladus, Titan, Europa) (\$800,000; cost share \$200,000)

Senior personnel on a Department of Defense Environmental Security Technology Certification Program proposal: Validation of a molecular biological assay to confirm the abiotic degradation of chlorinated solvents (\$335,000; cost share \$167,920)

PI on a NASA Earth and Space Science Fellowship: Evolutionary History of Acetylene Fermentation and its Viability for Extraterrestrial Life (\$45,000)

## **2016**

PI on a NSF CAREER project: Reproductive mode differences in horizontal gene transfer: Teaching computation effectively to biology students (\$521,091)

Senior personnel (PI Dr. Patrick Phillips, University of Oregon) on a NIH National Institute for General Medical Sciences project: The structure of genetic regulatory systems and the coherence of genomic vacation (\$3,400,035; cost share \$454,481)

PI on a NSF Division of Environmental Biology pre-proposal: Reproductive mode differences in horizontal gene transfer

PI (co-PI Dr. X. Margaret Liu, Chemical and Biological Engineering) on a Simons Foundation Targeted Grants in the Mathematical Modeling of Living Systems project: Linking genotype and phenotype in a metabolic model (\$600,000)

Senior personnel (PI Dr. Matthew Jenny, Biological Sciences) on a Gulf of Mexico Research Initiative – British Petroleum project: Sub-lethal and trans-generational effects of Macondo oil and Corexit dispersant on oyster life history characteristics (\$2,981,819; cost share \$155,316)

## **2015**

Senior personnel (PI Dr. Matthew Jenny, Biological Sciences) on a Gulf of Mexico Research Initiative – British Petroleum project: Gulf of Mexico Health and Assessment Program (\$11,720,786; cost share \$175,519)

PI on an NSF Advances in Biological Informatics proposal: ABI Innovation: 21<sup>st</sup> Century Linkage Maps (\$618,017)

## PUBLICATIONS

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\* An asterisk indicates the publication was co-authored with one or more of my graduate and/or undergraduate researchers

### *Manuscripts in Review and Revision*

\* Baesman, S.M., J.M. Sutton, **J.L. Fierst**, D.M. Akob, and R.S. Oremland. *Pelobacter acetylenovorans*, strain SFB93, sp. nov., a diazotrophic, acetylene-fermenting anaerobe isolated from San Francisco Bay intertidal sediments. *In review*, International Journal of Systematic and Evolutionary Microbiology.

Sheffield, L., N. Sciambra, A. Evans, E. Hagedorn, M. Delfeld, C. Goltz, **J.L. Fierst** and S. Chtarbanova. Age-dependent impairment of disease tolerance is associated with a robust transcriptional response following RNA virus infection in *Drosophila*. *In review*, Aging Cell.

\* Adams, P.E., A.L. Crist, E.P. Young, J.H. Willis, P.C. Phillips and **J.L. Fierst**. Slow recovery from inbreeding depression generated by the complex genetic architecture of segregating deleterious mutations. *In revision*, Molecular Biology and Evolution.

O'Connor, C.H., K.L. Sikkink, T.C. Nelson, **J.L. Fierst**, W.A. Cresko, and P.C. Phillips. Complex pleiotropic genetic architecture of evolved heat stress and oxidative stress resistance in the nematode *Caenorhabditis remanei*. *In revision*, G3.

\* Sutton, J.M. and **J.L. Fierst**. Optimizing experimental design for genome sequencing and assembly with Oxford Nanopore Technologies. *In revision*, iScience.

### *Published*

2020\* Bubrig, L.T., J.M. Sutton, and **J.L. Fierst**. *Caenorhabditis elegans* dauer recovery varies with worm-bacteria interactions. Ecology and Evolution *in press*, doi: 10.1002/ece3.6646

2020\* Heraghty, S.D., J.M. Sutton, M.L. Pimsler, **J.L. Fierst**, J.P. Strange, and J.D. Lozier. *De novo* genome assemblies for three North American bumble bee species: *Bombus bifarius*, *Bombus vancouverensis*, and *Bombus vosnesenskii*. G3: Genes, Genomes, Genetics 10 (8), 2585-2592.

2020\* Adams, P.E., L.T. Bubrig and **J.L. Fierst**. Genome evolution: On the road to parasitism. Current Biology 30, R272-274.

- 2020\* Anderson, A.G., L.T. Bubrig and J.L. Fierst. Environmental stress maintains trioecy in nematode worms. *Evolution* 74-3: 518-527.
- 2018\* Akob, D.M., J.M. Sutton, **J.L. Fierst**, K.B. Haase, G.W. Luther III, and R.S. Oremland. Acetylenotrophy: a hidden but ubiquitous microbial metabolism? *FEMS Microbiology Ecology* 94(8): fiy103.
- 2017 **Fierst, J.L.**, and D.A. Murdock. Decontaminating eukaryotic genome assemblies with machine learning. *BMC Bioinformatics* 18(1): 533.
- 2017\* Akob, D.M., S.M. Baesman, J.M. Sutton, **J.L. Fierst**, A.C. Mumford, Y. Shrestha, A.T. Poret-Peterson, S. Bennett, D.S. Dunlap, K.B. Haase, and R.S. Oremland. Detection of diazotrophy in the acetylene-fermenting anaerobe, *Pelobacter* strain SFB93. *Applied and Environmental Microbiology*. 83: e01198 - 17.
- 2017 **Fierst, J.L.**, D.A. Murdock, C. Thanthiriwatte, J.H. Willis, and P.C. Phillips. Metagenome-assembled draft genome sequence of a novel microbial *Stenotrophomonas maltophilia* strain isolated from *Caenorhabditis remanei* tissue. *Genome Announcements* 5(7): e01646-16.
- 2017\* Sutton, J.M., S.M. Baesman, **J.L. Fierst**, A.T. Poret-Peterson, R.S. Oremland, D.S. Dunlap, D.M. Akob. Complete genome sequences of two acetylene-fermenting *Pelobacter acetylenicus* strains. *Genome Announcements* 5(6): e01572-16.
- 2017\* Sutton, J.M., S.M. Baesman, **J.L. Fierst**, A.T. Poret-Peterson, R.S. Oremland, D.S. Dunlap, and D.M. Akob. Complete genome sequence of the acetylene-fermenting *Pelobacter* strain SFB93.” *Genome Announcements* 5(6): e01573-16.
- 2016 Ma, C., J. Ou, N. Xu, **J.L. Fierst**, S-T Yang and X. Liu. Rebalancing redox to improve biobutanol production by *Clostridium tyrobutyricum*. *Bioengineering* 3(1): 2.
- 2015 **Fierst, J.L.**, J.H. Willis, C.G. Thomas, W. Wang, R.M. Reynolds, T.E. Ahearne, A.D. Cutter, and P.C. Phillips. Reproductive mode and the evolution of genome size and structure in *Caenorhabditis* nematodes. *PLoS Genetics* 11(6): e1005323.
- 2015 **Fierst, J.L.** Using linkage maps to correct and scaffold *de novo* genome assemblies: methods, challenges and computational tools. *Frontiers in*

Genetics 6: 220.

- 2015 **Fierst, J.L.** and P.C. Phillips. Modeling the evolution of genetic systems: the gene network family tree. *Journal of Experimental Zoology (Molecular and Developmental Evolution)* 324B: 1-12.
- 2013 **Fierst, J.L.** Female mating preferences determine system-level evolution in a gene network model. *Genetica* 141: 157-170.
- 2013 Houle, D. and **J.L. Fierst**. Properties of spontaneous mutational variance and covariance for wing size and shape in *Drosophila melanogaster*. *Evolution* 67: 1116-1130.
- 2012 **Fierst, J.L.** and P.C. Phillips. Variance in epistasis links gene regulation and evolutionary rate in the yeast genetic interaction network. *Genome Biology and Evolution* 4: 1080-1087.
- 2011 **Fierst, J.L.** A history of phenotypic plasticity accelerates evolution to a new environment. *Journal of Evolutionary Biology* 24: 1992-2001.
- 2011 **Fierst, J.L.** Sexual dimorphism increases evolvability in a genetic regulatory network. *Evolutionary Biology* 38: 52-67.
- 2010 **Fierst, J.L.**, and T.F. Hansen. Genetic architecture and post-zygotic reproductive isolation: Bateson-Dobzhansky-Muller incompatibilities in a polygenic model. *Evolution* 64: 675-693.
- 2010 **Fierst, J.L.**, J.E. Kubler and S.R. Dudgeon. Spatial distribution and reproductive phenology of sexual and asexual *Mastocarpus papillatus* (Rhodophyta). *Phycologia* 49: 274-282.
- 2009 Hollis, B., **J.L. Fierst**, and D. Houle. Sexual selection accelerates the elimination of a deleterious mutant in *Drosophila melanogaster*. *Evolution* 63: 324-333.
- 2005 **Fierst, J.**, C. Terhorst, J.E. Kubler and S.R. Dudgeon. Fertilization success can drive patterns of phases dominance in complex life histories. *Journal of Phycology* 41: 238-249.



## TEACHING AND MENTORING

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### Teaching

2015-present     **The University of Alabama**     **Tuscaloosa, AL**

*Instructor of Record*

As an Assistant Professor I developed and taught two new cross-listed courses:

#### **Introduction to Bioinformatics**

Undergraduate section BSC 473 (enrollment 15-30 students per term)

Graduate section BSC 573 (enrollment 5-15 students per term)

From the University of Alabama course catalog: “Bioinformatics BSC 473/573 covers the tools and approaches necessary to perform computational analysis of large datasets. We will focus on analyzing high-throughput sequencing data although the tools we will learn are applicable to a wide range of modern biological questions. Specific topics include operating in a UNIX/bash shell environment, scripting, genome assembly, alignment, and algorithms. Writing proficiency is required for a passing grade in this course. A student who does not write with the skill normally required of an upper-division student will not earn a passing grade, no matter how well the student performs in other areas of the course.”

Introduction to Bioinformatics requires one formative and one summative writing assignment and satisfies the writing or ‘W’ requirement for Biological Sciences majors at the University of Alabama.

#### **Computational Biology Lab**

Undergraduate section BSC 426 (enrollment 15-30 students per term)

Graduate section BSC 526 (enrollment 5-15 students per term)

From the University of Alabama course catalog: “Computational Biology Lab introduces the programming skills, statistical methods and conceptual foundations necessary to pursue computational analysis and modeling of biological systems. This course is designed for biology students, and it is not expected that students will have prior with experience with computing or programming.”

Computational Biology Lab is a hands-on class involving a combination of lectures and laboratory activities. The course satisfies the Laboratory or ‘L’ requirement for Biological Sciences majors at the University of Alabama.

2003-2010     **The Florida State University**     **Tallahassee, FL**

*Graduate Teaching Assistant*

Study sections, lectures and lab sessions for Introductory Biology, Animal Diversity and Evolution

2000-2004     **California State University, Northridge**     **Los Angeles, CA**

*Graduate Teaching Assistant*

Lectures and lab sessions for Introductory Biology, Anatomy and Physiology,  
Marine Ecology and Biometry

1998-2000     **Immaculate Heart High School**     **Los Angeles, CA**  
*Science Teacher*  
9<sup>th</sup> grade Introductory Science and 10<sup>th</sup> grade Biology and Honors Biology

### *Mentoring*

2015-present     **The University of Alabama**

#### Current

*Dissertation chair:*

Paula Adams  
Joshua Millwood  
John Sutton

Accepted PhD students (starting 2020-2021):

Alekhiya Kandoor

*Biological Sciences undergraduate researchers:*

Chris Yousseff

*Computer Science undergraduate researchers:*

Tenisha Ciby  
Case McCormack

*Dissertation committee:*

Mustafa Divyapicigil  
Jennifer Fortunato  
Sam Heraghty  
Jacob Loeffelholz  
Sogol Momeni  
Caleb Turberville

#### Past

*Thesis chair:*

Louis Bubrig

*Biological Sciences undergraduate researchers:*

Ashlyn Anderson  
Louis Bubrig  
Kaylee Covan  
Sai Dwarampudi  
Danielle Kem  
Obie Moultrie  
Robert Reis  
Nilsamarie Rodriguez  
John Sutton  
Kloe Timbers  
Mackenzie Valentin

*Computer Science undergraduate researchers:*

Alan Hincey  
A. Houston Wingo

*Dissertation committee:*

Andrei Bombin  
Jason Jackson  
Younji Kim  
Chao Ma  
Jianfa Ou  
Vishal Oza  
Rebecca Varney

*Thesis committee:*

Ryan Lavoie  
Anna Reding  
Grace Scarsella

2012-2013    **The University of Oregon**

Computer and Information Sciences research projects

*Undergraduate students:*

Zeyu Feng  
Katerina Ko  
Jiazhong Liu  
Erick Rogers  
Alexandra Weston  
Ran Zhang

*Graduate students:*

Azad Abbasi  
Dan Everson  
Mahshid Yar Mohammadi  
Yunfeng Zhang

The Institute of Ecology and Evolution graduate student rotation projects

Allison Fuiten  
Andrew Nishida  
Christine O'Connor  
Alex Weimer

## GRADUATE STUDENT INVITED PRESENTATIONS

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- |      |  |
|------|--|
| 2017 | Genome evolution in <i>Caenorhabditis</i> nematode worms. <b>Graduate student invited speaker</b> , Population Biology, Ecology and Evolution Graduate Group. Emory University, Atlanta, GA.   |
| 2016 | Decontaminating <i>de novo</i> genome assemblies. <b>Graduate student invited speaker</b> , Ecology, Evolution and Marine Biology Graduate Group, University of California, Santa Barbara, CA. |

## INVITED PRESENTATIONS

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- |      |   |
|------|---|
| 2020 | Best practices for decontaminating <i>de novo</i> assembled genome sequences. Research Coordination Network: Evolving Seas Genomic Workshop, Catalina, CA. <i>Canceled due to Covid-19.</i> |
| 2020 | Holocentric chromosomes and the locus of evolvability. Center for Advanced Studies, the University of Oslo. <i>Canceled due to Covid-19.</i>  |
| 2020 | Complex systems and genome evolution. Syracuse University, Department of Biology.   |
| 2020 | Complex systems and genome evolution. Tufts University, Department of Biology.  |
| 2019 | A systems approach to studying genome evolution. The University of Alabama at Birmingham, Department of Biomedical Engineering.   |
| 2018 | Sexual conflict in genome evolution. Mississippi State University, Starkville, MS.  |
| 2018 | Sexual conflict in genome evolution. The University of Alabama at Birmingham, Department of Biological Sciences.  |
| 2018 | Genome evolution across worms and microbes. The University of West Alabama, Livingston, AL.   |
| 2016 | Chemical & Biological Engineering Departmental Seminar, The University of Alabama   |
| 2016 | Department of Mathematics, Applied Math Seminar, The University of Alabama  |
| 2016 | Form and function in biological networks. Network study interdisciplinary graduate education research and training, University of California, Santa Barbara, CA.                            |
| 2014 | Computational approaches to genetic evolution. The Florida State University, Tallahassee, FL.   |
| 2014 | Sex and recombination in genomic evolution. San Francisco State University, San Francisco, CA.  |
| 2014 | The influence of sex on genetic and genomic evolution. The University of  |

Alabama, Tuscaloosa, AL.

- 2012 Evolutionary systems biology. The University of Colorado at Denver.
- 2011 Nucleosome occupancy mediates transcription, gene expression, and epistatic fitness effects. Workshop on Systems Biology, Luebeck, Germany.
- 2010 Studying evolutionary processes with models of gene regulatory networks. University of Pretoria, Pretoria, South Africa.
- 2010 Sexual selection determines robustness and evolvability in a computational model of a genetic regulatory network. Gothenburg University, Gothenburg, Sweden.

### SELECTED CONFERENCE PRESENTATIONS

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\* An asterisk indicates the presentation was co-authored with one or more of my graduate and/or undergraduate researchers

- 2020\* P.E. Adams and **J.L. Fierst**. Slow recovery from inbreeding in *Caenorhabditis remanei*. Society for Molecular Biology and Evolution Annual Meeting, Quebec City, CA. Selected for an oral presentation and a Young Investigators Award. *Canceled due to Covid-19*.
- 2020\* T.J. Bushman, J.M. Sutton, **J.L. Fierst**, S.M. Baesman, R.S. Oremland and D.M. Akob. Assessment of acetylenotrophy within the genus *Bradyrhizibium*. Virginia Branch of the American Society of Microbiologists Annual Meeting, Farmville, VA.
- 2020 N. Sciambra, L. Sheffield, A. Evans, M.J. Delfeld, **J.L. Fierst** and S. Chtarbanova. Potent transcriptional response of aged *Drosophila melanogaster* following infection with an RNA virus. The Allied Genetics Conference, Washington, DC (virtual due to COVID-19).
- 2020\* J.M. Sutton, T.J. Bushman, S.M. Baesman, R.S. Oremland, **J.L. Fierst** and D.M. Akob. Southeastern Branch of the American Society of Microbiologists Annual Meeting, Huntsville, AL.
- 2019\* P.E. Adams and **J.L. Fierst**. The genomic architecture of inbreeding and recovery in *Caenorhabditis remanei*. Society for the Study of Evolution Annual Meeting, Providence, Rhode Island.
- 2019\* P.E. Adams, Anna L. Crist, Ellen P. Young, John H. Willis, Patrick C. Phillips

and **J.L. Fierst**. Slow recovery from inbreeding depression generated by the complex genetic architecture of segregating deleterious mutations. Southeastern Population Ecology and Evolutionary Genetics Meeting, Clemson, South Carolina.

- 2019\* D.M. Akob, **J.L. Fierst** and J.M. Sutton. Expanding the distribution of acetylenotrophic microbes. Applied and Environmental Microbiology Gordon Research Conference, South Hadley, Massachusetts.
- 2019\* L.T. Bubrig, A.G. Anderson and **J.L. Fierst**. Fluctuating stress and the maintenance of trioecy. Society for the Study of Evolution Annual Meeting, Providence, Rhode Island.
- 2019\* L.T. Bubrig, A.G. Anderson and **J.L. Fierst**. Environmental stress maintains trioecy. Southeastern Population Ecology and Evolutionary Genetics Meeting, Clemson, South Carolina.
- 2019 S.H. Lye, **J.L. Fierst** and S. Chtarbanova. Inflammaging in *Drosophila*: Identifying novel factors involved in predisposition to age-dependent neurodegeneration. Oklahoma Geroscience Symposium, Norman, Oklahoma.
- 2019\* J.D. Millwood, J.D. Lozier, C.M. Atkinson, M.J. Jenny and **J.L. Fierst**. Hybrid, de novo assembly method results in quality, preliminary freshwater mussel genome drafts. Southeastern Population Ecology and Evolutionary Genetics Meeting, Clemson, South Carolina.
- 2019\* J.M. Sutton and **J.L. Fierst**. Improving the *Caenorhabditis remanei* PX356 genome with long-read sequence data. Oxford Nanopore Technologies London Calling, London, UK.
- 2018\* P.E. Adams and **J.L. Fierst**. The genomic architecture of inbreeding in *Caenorhabditis remanei*. Society for the Study of Evolution Annual Meeting, Montpellier, France.
- 2018 **J.L. Fierst**. Horizontal transfers in gene co-expression networks. Society for the Study of Evolution Annual Meeting, Montpellier, France.
- 2017\* P.E. Adams and **J.L. Fierst**. Computational genomics of inbreeding in *Caenorhabditis*. Society for the Study of Evolution Annual Meeting, Portland, Oregon.
- 2017\* J.M. Sutton and **J.L. Fierst**. Discovery of two methods of acetylene



transformation in a single organism. American Society for Microbiology Annual Meeting, New Orleans, Louisiana.

- 2016 **J.L. Fierst.** Decontaminating genome assemblies with machine learning. Society for the Study of Evolution Annual Meeting, Austin, Texas.
- 2016\* P.E. Adams and **J.L. Fierst.** The genomic architecture of inbreeding in *Caenorhabditis remanei*. Society for the Study of Evolution Annual Meeting, Austin, Texas.
- 2016 D.A. Murdock and **J.L. Fierst.** Comparing computational methods for decontaminating genome assemblies. Society for the Study of Evolution Annual Meeting, Austin, Texas.
- 2016 C.H. O'Connor, **J.L. Fierst** and P.C. Phillips. Systems genetics of natural variation in stress in *Caenorhabditis* worms. Society for the Study of Evolution Annual Meeting, Austin, Texas.
- 2014 **J.L. Fierst.** The influence of mating system on genome evolution in *Caenorhabditis*. EVO-WIBO, Port Townsend, WA.
- 2014 **J.L. Fierst.** The influence of mating system on genome evolution in *Caenorhabditis*. Wellcome Trust, Evolution of Caenorhabditid worms and their relatives, Hinxton, UK.
- 2014 **J.L. Fierst.** The influence of mating system on genome evolution in *Caenorhabditis*. Society for the Study of Evolution Annual Meeting, Raleigh, North Carolina.
- 2012 **J.L. Fierst.** Evolution of genome structure in *Caenorhabditis remanei*. Cold Spring Harbor Laboratory, Evolution of Caenorhabditid worms and their relatives, New York.
- 2011 **J.L. Fierst.** A history of phenotypic plasticity accelerates adaptation. Western Society of Naturalists, Vancouver, WA.
- 2010 **J.L. Fierst.** Sexual dimorphism increases both robustness and evolvability. Society for Integrative and Comparative Biology, Seattle, USA.
- 2009 **J.L. Fierst.** Genetic architecture in reproductive isolation: Evolution of Bateson-Dobzhansky-Muller incompatibilities in a polygenic model. Society for the Study of Evolution Annual Meeting, Moscow, USA.

- 2008      **J.L. Fierst.** Genetic architecture in reproductive isolation. Society for Molecular Biology and Evolution Annual Meeting, Barcelona, Spain.
- 2006      **J.L. Fierst.** Good genes and sexual conflict. Society for the Study of Evolution Annual Meeting, Stonybrook, NY.
- 2004      **J.L. Fierst.** Multilinear epistatic interactions in the Bateson-Dobzhansky-Muller model. Society for the Study of Evolution Annual Meeting, Fort Collins, CO.

### **GUEST LECTURES AND OUTREACH**

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- 2019      Society for Engineers in Biomedicine, the University of Alabama
- 2019      Society of Women Engineers, the University of Alabama
- 2019      Honors Biology Enrichment Section (BSC 118), the University of Alabama
- 2018      Honors Biology Enrichment Section (BSC 118), the University of Alabama
- 2016      NSF Research Experiences for Undergraduates “Fluid Mechanics with Analysis Using Computations and Experiments,” The University of Alabama
- 2015      NSF Research Experiences for Undergraduates “Fluid Mechanics with Analysis Using Computations and Experiments” Guest speaker, The University of Alabama

### **SERVICE**

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- 2020      NIH Early Career Reviewer for the Genomics, Computational Biology and Technology (GCAT) study section
- 2020 - present      Faculty advisor, UA Graduate Women in Science
- 2019 - present      UA Cyberinstitute member
- 2019 - present      Research Software Engineer Search Committee, the University of Alabama
- 2018 - present      Graduate Admissions and Recruiting Committee, Department of Biological Sciences, the University of Alabama
- 2017 - present      College of Arts & Sciences High Performance Computing Advisory

Committee, the University of Alabama

2016 - present	3 Minute Thesis (3MT) Biological Sciences Judge
2014 - present	Technology Research Advisory Committee, the University of Alabama
2016 - 2018	W.D. Hamilton Award for Outstanding Graduate Student Presentation Selection Committee, Society for the Study of Evolution
2015 - 2018	Facilities Committee, Department of Biological Sciences, the University of Alabama
2015 - 2018	Alabama's Lectures on Life's Evolution (ALLELE) Organizing Committee, the University of Alabama
2015	Plant Systematics Faculty Search Committee, the University of Alabama
2013	Organizing Committee, University of Oregon Postdoctoral Association
2012-2013	Constitution and Bylaws Committee, University of Oregon Faculty Union
2006-2008	Graduate representative, Integrating Genotype and Phenotype faculty search committee, Florida State University
2004-2005	President, Ecology and Evolution Discussion Group, Florida State University
2002-2003	President, Biology Graduate Student Association, CSU Northridge

**Articles reviewed for:**

*Bioinformatics*

*Briefings in Bioinformatics*

*BMC Bioinformatics*

*BMC Evolutionary Biology*

*Current Biology*

*Ecology*

*Evolution*

*Evolution Letters*

*G3: Genes, Genomes and Genetics*

*Genetics*

*J. of Evolutionary Biology*

*Molecular Biology and Evolution*

*PLoS Genetics*

*Proceedings of the Royal Society, Series B*  
*Science Advances*

**Grants reviewed for:**

National Institutes of Health (US)  
National Science Foundation (US)  
Medical Research Council (UK)  
Agence Nationale de la Recherche (FR)  
CONACYT (MX)  
Graduate Women in Science National Fellowship Program (US)

**SPECIAL PROGRAMS**

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2011	<b>Pacific-American Studies Institute</b> <i>Scientific Computing: The Challenge of Massive Parallelism in the Americas</i>	<b>Valparaiso, Chile</b>
2006	<b>Santa Fe Institute</b> <i>Complex Systems Summer School</i>	<b>Beijing, China</b>
1997	<b>Semester Abroad in Zimbabwe</b> <i>Pitzer International Programs</i>	<b>Harare, Zimbabwe</b>

**MEMBERSHIPS**

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International Society for Computational Biology  
Society for Integrated and Applied Mathematics  
Society for Molecular Biology and Evolution  
Society for the Study of Evolution