



2019

2019 Conference Abstracts: Annual Undergraduate Research Conference at the Interface of Biology and Mathematics

National Institute for Mathematical and Biological Synthesis (NIMBioS)

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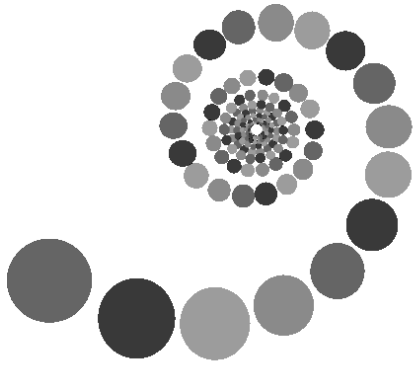
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NIMBioS

National Institute for Mathematical
and Biological Synthesis

Eleventh Annual

Undergraduate Research Conference at the Interface of Biology and Mathematics

November 16-17, 2019

University of Tennessee Conference Center

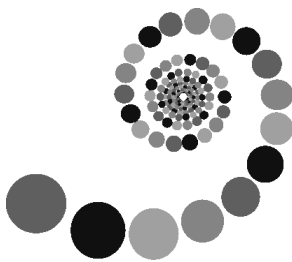
Knoxville, TN

CONFERENCE OVERVIEW

Welcome! This conference is hosted by the National Institute for Mathematical and Biological Synthesis (NIMBioS), housed on the campus of the University of Tennessee-Knoxville. Undergraduate students conducting research in mathematics and biology will present over 65 oral and poster presentations. A keynote address by Dr. Sadie Ryan and featured talk by Dr. Christopher Strickland will take place Saturday afternoon, and a panel discussion on career opportunities will follow. Graduate school training and opportunities will be showcased on Sunday morning. Poster abstracts start on page 6, oral presentation abstracts start on page 19.



NIMBioS



The National Institute for Mathematical and Biological Synthesis is a center that brings together talented researchers in the fields of math and biology from all over the world. At NIMBioS, researchers work to cross the boundaries of their disciplines and address the many questions and challenges of 21st century biology. Currently in its eleventh year, NIMBioS is sponsored by the National Science Foundation, with additional support from the University of Tennessee-Knoxville. NIMBioS also coordinates many educational programs including a summer research experience for undergraduates program and workshops for math and biology faculty. For more information on NIMBioS and its research and educational opportunities please visit www.nimbios.org.

UNIVERSITY OF TENNESSEE & KNOXVILLE

This conference is being held at the University of Tennessee (UT) Conference center, just across town from the university's main campus. UT has an enrollment of over 29,000 and more than 300 degree programs offered. It was founded in 1794 as Blount College but subsequently changed names a few times before becoming the University of Tennessee in 1879.

Knoxville is the second-oldest and third-largest city in Tennessee. The prominent Sunsphere west of the conference center is a remnant of the 1982 World's Fair themed on energy, due to Knoxville's close connections to the Tennessee Valley Authority and Oak Ridge National Laboratory. Also nearby is downtown with restaurants and shops found on Gay Street, Market Square, and the Old City.



INFORMATION FOR HANGING POSTERS

There will be two poster sessions. The first will immediately follow dinner on **Saturday, from 7:30-8:30 pm (posters assigned odd numbers presented)**. The second will precede lunch on **Sunday, from 11:00 am to Noon, (posters assigned even numbers presented)**. Please hang your poster as soon as possible and leave it up for the duration of the conference. Refer to the poster listing in this booklet to find your assigned number. Posters will all be hung in the hallway areas outside room 406. Find your assigned space and use the tacks provided to affix it to the wall or poster board. Poster abstracts and numbering start on page 6.

INFORMATION FOR ORAL PRESENTERS

Refer to the schedule to find your presentation time and room number. You will have 15 minutes to speak and a few minutes to answer questions. Also, note the nearest meal or break before your presentation. At that time, please see a meeting moderator to have your talk loaded onto the appropriate computer in advance.

SOCIAL MEDIA AT URC 2019



Twitter: Check Twitter for live updates, highlights from sessions, and more. Follow us by visiting <https://twitter.com/NIMBioS>. Twitter users -- just login and click "follow."

View and join in conversations about URC 2019 on Twitter by using the hashtag, #nimbiosURC. If you don't have a Twitter account, you can still view our updates or bookmark the NIMBioS Twitter webpage.

KEYNOTE LECTURE

Dr. Sadie Ryan
Department of Geography
University of Florida

Linking vector borne disease to climate at multiple scales with mechanistic and geospatial models

Understanding the impacts of climate and climate change on vector-borne diseases (VBDs)—especially those under current public scrutiny and concern, such as malaria, dengue, chikungunya, and Zika—is a key component of global public health preparedness, and a key component of the ongoing issue of climate change preparedness. In this talk, I will showcase a strategy for applying ecophysiological models of temperature-dependent transmission to current and future climate models at large scales. I will demonstrate how our collaborative team have used these models to explore future scenarios for malaria, and for *Aedes* spp. transmitted diseases, and how we can use mapping approaches as useful visualization tools, and how we tackle describing the multiple potential outcomes. I will also describe some local-scale, city and province level approaches to understanding vectorborne disease dynamics and management, and explore issues of how these two scales come together (or don't) for decision making on the ground and in the boardroom.

FEATURED SPEAKER

Dr. Christopher Strickland
Department of Mathematics
University of Tennessee, Knoxville

Bugs and drugs: Two approaches to modeling systems with social impact in mathematical biology

Modeling in mathematical biology can take on a number of forms depending on the application, with tradeoffs including both complexity versus mathematical tractability as well as issues of perspective. In this talk, I will describe two research projects that demonstrate a total of three mathematical approaches: the study of pattern formation in Australian plague locusts and a population-level analysis of the prescription opioid and heroin epidemic. Locusts gather by the millions to feed on crops, destroying fields of agricultural produce. As juveniles, wingless locusts march together and form a variety of patterns including wave fronts. We examine this collective propagation through two models: an agent-based model and a set of partial differential equations. The agent-based model is directly linked to individual behavior with respect to resource availability, while the PDE model yields insight into the collective, analytic behavior of the aggregate group. In the case of prescription opioid addiction, I will present a first epidemic model for prescription opioid addiction and treatment followed by extensions to the model to examine the effect of heroin and fentanyl on the epidemic. In contrast to the dynamics of a classic disease or illicit drug epidemic, opioid addiction has its roots in legal, prescription medication - a fact which greatly increases the exposed population and mathematically suggests non-contact based routes of infection. Mathematical analysis of the models provides insight into the mechanisms sustaining the epidemic, current trends in the number of individuals suffering from substance abuse disorder, and potential targets for control.

SCHEDULE

Saturday, November 16: Room 413AB (Except where noted)

12:30-12:40 Welcome: Dr. Louis Gross, NIMBioS Director

12:45-1:40 Keynote Lecture:

Dr. Sadie Ryan, Department of Geography, University of Florida

Linking vector borne disease to climate at multiple scales with mechanistic and geospatial models

1:50-2:05

406: Ellie Lochner, Brandyn Ruiz, and Abigail Williams – *The Impact of Climate Change on Environmental Suitability of Buzz Pollinators*

413AB: Leah Mitchell – *Analyzing the Effects of Observation Functions in Nonlinear Filtering for the SIR model*

2:10-2:25

406: Kayleigh Campbell & Laura Staugler – *Estimating Time-Varying Applied Current in the Hodgkin-Huxley Model*

413AB: Ixtacchuatl Obregon – *Minimizing Drug Resistant Cases of Gonorrhea through Cost-Effective Treatment Plans*

2:30-2:45

406: Timothy Hedspeth and Patricia Steinhagen – *Amplifiers and Suppressors of Evolution on Graphs Under Birth-Death Updating*

413AB: Gabrielle Majetic – *A Computational Model of Cell-Type Specific and Pain-Related Neural Activity in the Amygdala During Neuropathic Pain*

2:45-3:00 Snack Break

3:00-3:30 Technology Tools Comparison: Preparing for Data Analysis in Graduate School

Dr. Lou Gross, NIMBioS Director

Dr. Christopher Strickland, Department of Mathematics, University of Tennessee

3:35-4:15 Breakout Sessions

413AB (Right): Dr. Lou Gross – Ecology

413AB (Left): Dr. David Talmy – Microbiology

400A: Dr. Suzanne Lenhart and Dr. Sadie Ryan – Mathematics and Biology

406 (Front): Dr. Albrecht von Arnim and Dr. Tian Hong – Biomedical

406 (Back): Dr. Mona Papeş and Dr. Greg Wiggins – Spatial Ecology

4:25-5:15 Featured Speaker:

Dr. Christopher Strickland, Department of Mathematics, University of Tennessee

Bugs and drugs: Two approaches to modeling systems with social impact in mathematical biology

5:25-6:15 Panel Discussion: Careers in Math-Biology and Transitioning to Graduate School

(Moderator: Suzanne Lenhart, Associate Director at NIMBioS)

Dr. Sadie Ryan, Geography, UF

Dr. Christopher Strickland, Mathematics, UTK

Dr. David Talmy, Microbiology, UTK

Dr. Holly Moeller, University of California, Santa Barbara

6:20-7:25 Networking Buffet Dinner with a Researcher in 404A

7:30-8:30 Poster Session I: Odd numbered posters presented (and desserts)

Sunday, November 17: Rooms 406, 413AB, 413C

7:45-8:00 Continental Breakfast

8:00-8:15

406: Matthew King and Julia Shapiro – *Computing Fixation Probabilities on Graphs Under Weak Selection*

413AB: Bernardo Amenyero and Brian Chau – *The Role of Variation in Mate Choice and Wolbachia Infection on Aedes aegypti Population Dynamics*

8:20-8:35

406: Alex Svetlik – *Investigating the protective effect of nicotine on neurodegeneration in the model organism C. elegans*

413AB: Julia Shapiro – *Predicting Optimal Treatment Strategies for Transplant Patients using Theoretical Modeling*

8:40-8:55

406: Bonnie Smith – *Identification of Lampenflora in Bristol Caverns*

413AB: Kristen Scheckelhoff – *A Game-theoretic Model of Optimal Clean Equipment Usage to Prevent Hepatitis C Among Injecting Drug Users*

9:00-9:15

406: Hannah Schmidt, Taylor Dunlevy, and Peter Wagstaff – *Analyzing the Impact of Weather, Phenotypic Features, and Hybridization to Improve Maize Crop Yield Model Predictions*

413AB: Zahra Rasuli and Valencia Heard – *Using Machine Learning Methods to Diagnose Diabetes Mellitus of Pima Indians*

9:25-10:00 Applying for Graduate Fellowships

Dr. Suzanne Lenhart, Associate Director at NIMBioS

Dr. Maitreyi Das, Biochemistry, Cellular and Molecular Biology, UTK

Shelby Scott, Graduate Student, Ecology and Evolutionary Biology, UTK

Leigh Percy, Graduate Student, Mathematics, UTK

10:05-11:00 Graduate School Opportunities Showcase, Room 413C

11:00-12:00 Poster Session II: Even numbered posters presented

12:00-12:55 Lunch and Career Opportunities Discussions

1:00-1:15

406: Kelly Rivenbark – *BPA and BPF Exposure Alters Brood Size and Decreases Food Availability for Wild Type C. elegans*

413AB: Matthew Clark – *Modeling Blood Glucose for the Detection of Type 2 Diabetes*

1:20-1:35

406: Trent Maddox, Nicholas Karig, and Darien Roach – *Statistical Analysis of Internet Coverage at Different Times of Day for Business to Business Companies*

413AB: Michael Belcher – *Mathematical Modeling of Diabetic Foot Ulcers Using Optimal Design and Mixed-Modeling Techniques*

1:40-1:55

406: Austin Huff – *The Effects of Salinity on Mussel Glochidia*

413AB: Morgan Powers – *Enhanced Antibiotic Resistance in Mobile Bacteria Populations*

Sunday, November 17: Rooms 406, 413AB, 413C (Continued)

2:00-2:15

406: Jerry Magaña – *Topography and Behavior Based Movement Modeling for Missing Persons in Land-Wilderness Settings*

413AB: Vincent Jodoin and Sheridan Payne – *Modeling the Effect of Social Networks on the Spread of Opioid Use*

2:20-2:35

406: Matthew Ashby, Taylor Dennis, and Kyle Wright – *Determining Over-Performing Phenotypic Features in Maize Using Machine Learning Techniques*

413AB: Alan Gan – *A Steady and Near-Steady State Cancer Cell Model*

2:40-2:55

406: Emily Hill – *Role of the YrbE Phospholipid Transporter in Salmonella Typhimurium Infection*

413AB: Joe Tolone – *Lock-In Based Technique for High Sensitivity Probe of Dielectric Modulation*

3:00-3:15

413AB: Kristen Klitgaard – *Leaky or Loyal: Optimizing Plant Investment in Mycorrhizae Fungal Mutualists within a Fluctuating Environment*

3:20-3:25

413AB: Closing Remarks and Adjourn

POSTER ABSTRACTS

- 1. ADEWUNMI, E.¹, A. BECHTEL², G. COLÓN-CABEZUDO³, V. ALEXIADES¹, and C. COLLINS¹. Biochemical Aerotaxis in *Azospirillum brasilense*. ¹Department of Mathematics, University of Tennessee, Knoxville, TN, ²Department of Biochemistry and Cellular and Molecular Biology, University of Tennessee, Knoxville, TN, ³Department of Mathematics, University of Puerto Rico, Rio Piedras, San Juan, PR.** *Azospirillum brasilense* is a nitrogen-fixing bacteria that plays a big role in promoting plant growth. Due to this, it is important to study how this bacterium performs chemotaxis, movement along chemical gradients towards preferred chemical levels. The single biochemical chemotactic pathway of *E. coli* has been studied extensively, but, unlike *E. coli*, *A. brasilense* has two main chemotactic pathways and the connections and interactions between these two pathways is, for the most part, unknown. In this project, we used a mathematical model to identify how these two pathways connect and control the motion of the bacteria. We studied how variations of certain parameters in the model would affect the time for CheYp, the main motor activation protein, to relax after being triggered by a chemical stimulation. We sought to qualitatively recreate the results of experimental papers in order to assess how appropriate the mathematical model is as a tool to study the chemotactic pathways of *A. brasilense*. We concluded that the model has an accurate resemblance to the behavior of the chemotactic pathways, albeit incomplete. The model does show that both pathways play a role and that some level of interaction must exist between them to better match the experimental behavior. Our results also show that to fully match the behavior we need to investigate extending the model to take into consideration the effects of other chemicals, such as CheD and CheC.
- 2. BAI², S., JIA², Y., LI², W., WATSON¹, T., YANG², X., and LI¹, Q. Numerical Simulation of Microchannel Heat Sink. ¹Department of Mathematics and Computer Science, Fisk University, Nashville, TN. ²Department of Mathematical Sciences, Xi'an Jiaotong Liverpool University, Suzhou, Jiangsu, CN.** This research project focuses on the analysis of the impacts of aperture sizes and shapes on heat dissipation performance of microchannel heat sink for chip cooling. In this project, the heat sink is considered to be a porous medium model using air convection. Derivation based on energy equation gives a set of governing partial differential equations describing the model of solid heat transfer. Finite element method and finite difference method are used to develop a finite element solver to solve the derived PDEs with properly defined initial and boundary conditions. Numerical simulation, including thermal analysis, discovers the heat dissipation performance of microchannel heat sink.
- 3. BOGGS, K., and L. URBIETA. Mathematical Study of the Influence of Social Media on Depression Among Young Adults. Arizona State University, Tempe, AZ.** Depression has caused an economic burden in the United States. The CDC reported that 186 billion dollars was spent on health care services to treat mental health disorders in 2014. An association between the use of social media and depression has been indicated in recent studies; therefore, it is necessary to study this problem. A compartmental model focusing on teens and young adults is created to study the use of social media and how it contributes to the cause of depression. The model consists of sub-classes including susceptible, low, moderate, severe depression, and treatment. From mathematical analysis of the model, the depression reproduction number, R_D , is found which represents a threshold value of the epidemic. In order to help minimize the number of depression cases, control strategies are implemented. The number of depression cases can be controlled and converges to the depression-free equilibrium when the threshold is less than one. Control strategies were implemented consisting of four different methods. Numerical simulations show that the depression cases can be controlled via public health counselling and a hybrid strategy of prevention and intervention. The hybrid method is the most effective way to control the epidemic.

4. **BAO, L. Mathematical Modeling and Optimal Control for Malaria Transmission Using Sterile Mosquitoes Technique and Bednets. School of Science and Technology, Georgia Gwinnett College, Lawrenceville, GA.** We consider a malaria transmission model with SEIR (susceptible-exposed-infected-recovered) classes for the human population, SEI (susceptible-exposed-infected) classes for the wild mosquitoes and an additional class for sterile mosquitoes. We derive a formula for the basic reproduction number \mathcal{R}_0 of infection. We formulate an optimal control problem in which the goal is to minimize both the infected human populations and the cost to implement two control strategies: the release of sterile mosquitoes and the usage of bed nets to prevent the malaria transmission. Adjoint equations are derived and the characterization of the optimal controls are established. Finally, we quantify the effectiveness of the two interventions aimed at limiting the spread of Malaria. A combination of both strategies leads to a more rapid elimination of the wild mosquito population. Numerical simulations are provided to illustrate the results.

5. **BROWN, T., and A. WASHINGTON. Mathematical study of the dynamics of prescription opioid misuse, Grand Canyon University, Phoenix, AZ.** Arizona hospitals assisted over 51,000 patients for opioid-related reasons in 2017. The state also saw over 400 lives lost due to prescription-opioid misuse and spent over 431 million dollars to battle the growing issue [ADHS, NIH]. With the growth of prescription opioid-related deaths in Arizona, it is essential to address this concern. We concluded that mathematical investigation of this societal epidemic could provide useful insights and allow us to determine the effectiveness of various control strategies. A compartmental model was constructed to represent the dynamics among subpopulations: susceptible, opioid-prescribed individuals, cessation of prescription, lightly and heavily addicted users, and effectively treated individuals. We discovered a threshold for the stability of the epidemic called the opioid-user generation number, R_0 . The epidemic is stable and converges to an opioid-misuse free equilibrium when the threshold value is less than one; however, it is unstable and converges to an opioid-misuse persistent equilibrium when R_0 is greater than one. The effects of current control strategies were identified by a series of numerical simulations. Public health education and effective treatment, along with hybrid methods that combine education with effective treatment and decreased prescription rates, significantly reduced the number of secondary infections caused by one infected individual. In conclusion, we propose that a combination of prevention and intervention methods would be most efficient in eliminating prescription opioid misuse.

6. **CALIP, A., and B. PEERCY. Chemoattractant Gradient Sensing of Cell Cluster Migration in Drosophila Egg Chambers. Department of Mathematics and Statistics, University of Maryland-Baltimore County, Baltimore, MD.** Chemoattractant gradients can guide motile cells to their destination through a process called chemotaxis. We are interested in the chemotactic forces needed for cell cluster migration in the Drosophila egg chamber. The egg chamber consists of sixteen germ line cells surrounded by a layer of follicle cells. During mid-oogenesis, two non-motile polar cells at the anterior end of the chamber are surrounded by border cells. The cell cluster detaches from the epithelium and begins its migration to the oocyte. We examined how the cell cluster senses and translates the chemoattractant gradient to motion in order to improve our model of chemical gradient sensing and inform the Stonko et al. migration model. We compared the Stonko et al. model with the Cai et al. model. The former viewed the cluster as an aggregate of single cells while the latter viewed the cluster as one large cell. The Cai model integrated the pulling force along the surface, a sphere for simplicity, of the cluster. The chemotactic force was assumed to be only along the x-axis. We aimed to get a fully 3D force generation of this chemotactic force using calculus and MATLAB to inform our migratory force on the Stonko model.

7. **DEBRITO, M.^{1,2}, and N. TOUMBACARIS^{1,3}. The Role of Utility in the Optimal Allocation Strategy of Annual Plants.** ¹National Science Foundation Research Experience for Undergraduates at the University of Houston – Downtown; ²University of Michigan, Ann Arbor, MI; ³Marist College, Poughkeepsie, NY. Annual plants must allocate resources to growth of vegetative mass (roots and shoots) or reproductive mass (flowers and fruits) throughout a season of unpredictable length. We modeled this allocation strategy as an optimal control problem, maximizing the average utility of the plant's reproductive yield at the end of the season as in the seminal model of King and Roughgarden. To model strategies of plants with varying reproduction priorities and growth rates, we solved for optimal strategies using general power utility functions and production functions. With a combination of analytic and numerical computation, we found that a period of mixed allocation to vegetative and reproductive growth in the optimal strategy arises for a range of different utility functions. We also compared solutions of varying production functions on the end-of-season payoff and generated a complete characterization of the optimal control strategy. These models provided insights to the way plants allocate their resources in natural environments.
8. **DAMRAU, Z., A. SANWICK, and M. JONES. Using Machine Learning to Build an Optimal Soil Profile for Corn.** Departments of Mathematics and Statistics, Chemistry and Physics, East Tennessee State University, Johnson City, TN. Many factors affect the yield of corn, such as genetics, weather, and soil. Using data collected by the Genomes to Fields (G2F) initiative together with data from the SoilGrids project, we examine the correlation between the nutrients in the soil and corn yield. Using machine learning methods such as decision trees, random forests, and LASSO, we try to identify the combination of soil factors that best correlate to high output. From these results, we hope to determine which mix of fertilizers and irrigation could potentially produce crops with the greatest yield.
9. **DEROUEN, Z.¹, M. PETERSON², H-H. WANG³, and W.E. GRANT³. The Recent Expansion of Invasive *Tubastraea coccinea* Throughout the Northern Gulf of Mexico.** Department of Ecosystem Science and Management¹, Department of Geography², Department of Wildlife and Fisheries Sciences³, Texas A&M University, College Station, TX. Invasive species have large economic and ecological impacts, including agriculture losses, native species replacement, ecological function modification, and altered community structure. Despite this, invasive marine species are relatively understudied. The orange cup coral, *Tubastraea coccinea*, is the first Scleractinia to invade the Western Atlantic. The coral is shown to have negative effects on native reef corals and has been spreading to natural reefs within the Gulf of Mexico (GoM). Our objective is to document the recent range expansion of *T. coccinea* throughout the GoM and produce a species distribution model to project its potential range of invasion and identify the factors for its distribution. Our results show that potential habitat for *T. coccinea* to be mainly distributed within the western half of the GoM, with the highest probabilities ($0.8 < P < 1.0$) clustered along the Texas and Louisiana borders. Considering the threat that *T. coccinea* presents to native reefs within the GoM, it is important to be able to track and predict its distribution, as well as identify potential factors facilitating its invasion.
10. **FARADJI, D., GARCIA S., and TRINH C. The Metabolic Module Database (MMdb): A Database of Pathways and Simulation Tool for Metabolic Engineering.** Department of Chemical Engineering, The University of Tennessee, Knoxville, TN. Metabolic network modeling can be used to simulate and improve upon production techniques of high value molecules, but simulating new pathways from literature is a difficult process, and there is currently no way to quickly input a novel pathway into simulation software directly from literature. The prevailing manual methods of input have a significant technical and programming knowledge barrier that is time-consuming for many non-computational biologists and other researchers to overcome. Additionally, many metabolic engineering tools have different input requirements despite using

the same metabolic pathway data. The Metabolic Module Database (MMdb) allows researchers to quickly construct pathway inputs to different forms of simulation software using literature references through a guided web interface. No technical knowledge is needed to create simulations from novel pathways. Generated pathways become accessible to the scientific community, and collecting existing pathways in a single location allows data analysis on multiple closely related pathways at once. A robust local storage mechanism allows long-term pathway accessibility, in contrast to many existing databases eventually become derelict after initial publication. Web querying through a browser allows data access by traditional researchers, while the integration of an Application Programming Interface (API) allows data retrieval by computer scientists or computational biologists. MMdb also serves as a more precise online search for publications, as it allows for publication search by target products of interest or reactions. In addition to its advanced querying capabilities, large scale analysis involving both novel pathways and non-model organisms is now possible using MMdb.

- 11. FRANCK, J. Modeling the Effects of Erythropoietin Concentration Levels on Red Blood Cell Production. University of Florida, Gainesville, FL.** Chronic Kidney Disease (CKD) refers to a permanent partial loss of kidney function. As a result of impaired kidney function, many patients with CKD develop anemia as the kidneys can no longer produce a normal amount of the growth factor erythropoietin (EPO) to stimulate red blood cell (RBC) production. For decades, patients with CKD have been treated with recombinant human erythropoietin (rHuEPO), a man-made clone of natural human EPO, and erythropoiesis-stimulating agents (ESAs), to treat CKD-caused anemia. As erythropoietic stem cells differentiate into mature red blood cells, the cells rely on growth factors, namely EPO, to determine whether to continue in the cell cycle or to exit. The purpose of this project is to model the relationship between EPO and RBC population, through the use of a system of delay-differential equations, in order to study the effects of abnormalities in kidney function (improper EPO production).
- 12. GONZALEZ, L.M. Predicting the Evolutionary Trajectories of Mixotrophic Organisms. Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, CA.** Rising oceanic temperatures due to climate change are predicted to influence the rates of carbon cycling, with respiration predicted to increase faster than the rate of c-fixation. It is uncertain whether or not organisms involved in the carbon cycle will evolve to mitigate such changes, and thus modelling approaches aimed at understanding the evolutionary dynamics of carbon cycling organisms could be highly informative. Recently, more attention has been paid towards modelling of mixotrophic organisms, who happen to be major players in oceanic carbon cycling. Mixotrophs are organisms capable of utilizing multiple nutritional modes, typically heterotrophy and autotrophy, thereby acting as biogeochemical “short circuits”. There have been many efforts to model the behavior and dynamics of mixotrophs, however few incorporate evolution. Here, I use a mutant invasion analysis model involving a mixotrophic phytoplankton that feeds on a heterotrophic prey in order to predict the evolutionary stable state (ESS) of mixotrophs with different nutritional specialization (heterotrophic vs autotrophic specialists), and to predict how this ESS shifts with rising temperatures and alternate light intensities. This model suggests that the evolutionary trajectory of a particular mixotroph is dependent on its environment and type of nutritional specialization, having implications for carbon cycling that depends on a community’s reliance on heterotrophy and autotrophy.
- 13. GRAHAM, I.C., and M.W. LANE. Mechanical and Electrical Investigations of the Ternary Au-Sn-Si System. Department of Chemistry, Emory & Henry College, Emory, VA.** Au, Sn, and Si play formative roles in a number of emerging technologies ranging from transparent electrodes in solar cells (Au, Si), catalyst for nanotube growth (Au, Si), and wafer bonding (Au, Si and Sn, Au) to more traditional uses as electrical conductors in microelectronics. Intermetallic phase formation in combinations of these binary systems,

particularly Au/Sn, is well known and the phase diagrams of each binary system indicate relatively low temperature eutectics. Formation of compounds at the interfaces of any two of these materials can lead to reduced conductivity and mechanical failure of the interface under stress. However, little data exists coupling the changes in conductivity with quantitative fracture measurements. This work seeks to understand the phase formation and resultant changes in material conductivity and mechanical properties of both binary (Au/Si, Au/Sn, and Sn/Si) and ternary (Au/Si/Sn) systems. Understanding these changes and the potential tradeoffs between electrical and mechanical properties in these systems may play a key role in the development and enablement of future technologies.

14. GRANDISON, B.¹, H. YIN², and A. KILGORE³. Disease-Driven Dynamics of Evolutionary Rescue. ¹University of Florida, Gainesville, FL, ²Tufts University, Boston, MA, ³Colorado College, Colorado Springs, CO.

Changing habitat ranges and shifting environmental conditions are altering the disease landscapes for hosts, vectors, and pathogens. Epidemiological modeling is an integral aspect of mathematical biology and has greatly furthered research and assessment of at-risk populations by modeling the impacts of pathogens upon a host population. Accurately portraying these epidemiological patterns requires an understanding of the host's behavioral and evolutionary patterns, especially when attempting to capture the dynamics of a population experiencing pressures that impact their shifting environments. Evolutionary game theory has been used previously to analyze the payoffs associated with and predict the results of competing strategies. As one of the first steps in an ongoing project to model the impacts of a shifting climate on the coevolution of vector-borne avian malaria in the Hawaiian Honeycreeper population, we integrated game theoretical breeding dynamics into a diseased population model undergoing environmental changes, representing real-life pressures such as habitat loss and climate change. Our preliminary model explores the evolutionary dynamics of a host population facing selective pressures, focusing in particular on evolutionary rescue. Evolutionary rescue may be defined as rapid adaptation of a species to avoid extinction due to an environmental change. Our goal is to explore and produce population dynamics resembling evolutionary rescue and identify factors that create this phenomenon within the host population. Our preliminary results demonstrate that a robust mutant type population less susceptible to infection grows more successfully than the more susceptible wild type population under the pressure of disease with a high transmission rate.

15. HAMPTON, G.¹, M. CREE-GREEN², and C. DINIZ BEHN^{1,2}. Utilizing Data Assimilation to Determine Optimal OGTT Duration for Estimating Insulin Sensitivity. ¹Applied Mathematics and Statistics Department, Colorado School of Mines, Golden, CO; ²Division of Pediatric Endocrinology, University of Colorado Anschutz Medical Campus, Aurora, CO.

Accurate assessment of insulin sensitivity, S_I , is crucial for characterizing metabolic disease and optimizing patient care. During an oral glucose tolerance test (OGTT), plasma glucose concentrations increase as ingested glucose enters the bloodstream and decrease as glucose is taken up by peripheral tissues. Fitting the Oral Minimal Model (OMM), a differential equations-based representation of glucose-insulin dynamics, with glucose and insulin concentration data from an OGTT allows estimation of S_I . However, in insulin resistant (IR) populations, estimated S_I may depend on OGTT protocol duration with shorter durations typically underestimating S_I . To determine the shortest duration for an OGTT protocol that provides accurate S_I estimates, we applied a Dual Unscented Kalman Filter, a data assimilation technique, to OMM to investigate the convergence of S_I estimates over a six hour OGTT protocol in an IR population of obese adolescent girls. We found that S_I estimates improved with protocol duration, however, for most participants, a shorter protocol was sufficient to estimate S_I within a defined accuracy threshold. This approach provides insight into the relationship between data and OMM parameters across the OGTT, and it may inform OGTT protocol design for other populations with disrupted glucose-insulin dynamics.

- 16. HASLAM, A., J. BRODA, and M.L. ZEEMAN. Resilience in Biological Systems: Analytic Approaches to Flow-kick Dynamical Systems. Department of Mathematics, Bowdoin College, Brunswick, ME.** In light of recent concerns about rapid climate change, there is growing interest in the role that sustainable management strategies could have in maintaining the resilience of ecosystems. We use flow-kick dynamical systems to model periodically managed ecosystems and quantify their resilience to environmental change and management strategies. Flow-kick systems consist of repeated periods of undisturbed, natural growth (flow), each followed by a discrete intervention (kick). When the flow and kick perfectly counteract each other, the system is in flow-kick equilibrium. This raises the following questions: Does the kick represent a viable management strategy? Does the equilibrium represent a desired state of the modeled ecosystem? And, if so, does the system settle at this equilibrium (ie. is the equilibrium stable)? To determine the stability of the flow-kick equilibrium, we must consider the behavior of neighboring trajectories under the flow dynamics. These dynamics can be approximated using the variational equation and measured, in part, by the reactivity. We have shown that in any finite dimension, a flow-kick equilibrium whose trajectory is contained within a non-reactive region of state space is stable.
- 17. HUANG, G. Parameter Identifiability and the Geometry of Parameter Space Using a Wound-Healing Model. Department of Mathematics, Western Kentucky University, Bowling Green, KY.** Wound healing in both acute and chronic wounds is characterized by complex interactions between matrix metalloproteinases (MMPs), their regulators (TIMPs), the extracellular matrix (ECM), and fibroblasts. However, unlike acute wounds, chronic wounds often heal at unpredictable rates due to their prolonged presence in the inflammatory stage. Because the relationship between these three proteins and fibroblast cells is vital to the healing process, a differential equation model was developed and analyzed to determine what factors affect the healing process in chronic wounds, namely diabetic foot ulcers. Using previously gathered de-identified individual patient data, local and global analyses were conducted to determine which parameters were easily identified and most influential. The three-dimensional geometry of parameter space was then visualized to more precisely see how these factors affect individual patients. Knowledge of these factors can, in turn, streamline the treatment of diabetic foot ulcers by allowing us to predict the optimal data collection times for each patient. To further build on previous results, both analyses will be rerun and recurve fitted for the globally sensitive parameters. Through refining the analysis of this mathematical model, we hope to better illuminate the unpredictable nature of wound healing.
- 18. JACKSON, M., and X. LI. The Application of 3-Dimensional Printing in Calculus. Department of Mathematics, Emory & Henry College, Emory, VA.** In learning calculus, students often struggle with visualization. Throughout this research, a Flashforge 3-dimensional printer is used to facilitate the visualization of certain calculus subtopics with an emphasis on tools/aids that can be used in a learning environment. The first subtopic examined is contour maps. Contour maps illustrate the gradient of a surface as a 2-dimensional drawing. By printing the 3-dimensional surfaces represented by contour maps, the connection between the 2-dimensional mapping and the surface can be seen. The 3-dimensional surfaces are then sliced into pieces to create an aid which allows the student to build the surface based on the 2-dimensional contour map provided. The second subtopic is the method of shell approximation, where a 2-dimensional function is rotated about the y-axis to form a solid. The enclosed volume can then be approximated by slicing the solid in multiple cylindrical shells. Each cylindrical shell's volume can be calculated and summed via integration. Using 3-dimensional printing, this research takes an example function, creates the 3-dimensional solid, and then slices it into cylindrical shells. To illustrate the concept that more shells result in a better approximation, the example function's solid has three printed replicas,

each with varying numbers of cylindrical shells. In the future, we hope to study the use of the aids created previously under learning conditions and better understand ways to improve them or implement them. We also hope to find more topics in STEM that could use visualization tools to clarify important ideas.

- 19. LEITNER, K., K.F. MURDOCH, G. CHEN, R.W. MURDOCH, and F.E. LÖFFLER. Using Heterologous Expression Techniques to Explore Chlorinated Organic Compound Degradation by Novel Haloacid Dehalogenases Identified in Pristine Environments. University of Tennessee, Knoxville, TN.** Diverse bacteria from various environments possess putative haloacid dehalogenase (HADase) genes. Some HADases have been characterized and allow their hosts to degrade anthropogenic chlorinated compounds, including dichloroacetate. Interestingly, HADase genes commonly occur on bacterial genomes recovered from pristine environments that have never experienced anthropogenic contamination with halogenated pollutants. Despite their widespread distribution, the function of these HADases, in particular in pristine environments, is poorly understood. A phylogenetic analysis of available HADase gene sequences identified 5 groups, but functional assignments based on grouping could not be made. To shed light on the role of these enigmatic genes, HADase genes were identified in metagenomes from a range of natural ecosystems including forest soils and engineered systems such as wastewater treatment plants. Using gene synthesis and molecular cloning techniques, select putative HADase genes were introduced and expressed in *E. coli*. HADase activity was tested with dichloroacetate and monochloroacetate as substrates. Out of 5 putative HADase genes assayed, 1 converted dichloroacetate and monochloroacetate to glyoxylate and glycolate, respectively. These HADase were recovered from pristine ecosystems, suggesting that chlorinated acetates are natural products and occur in various environmental systems. In future work, I will develop quantitative PCR assays for select HADase genes and monitor the temporal and spatial dynamics of HADase gene expression in environmental systems.
- 20. MARTIN MAYOR, M., K.N. GILBERT, A. REYNOLDS-GRAY, R. FRYE, and L.K. VAUGHAN. The Effect of non-nutritive sweeteners on lipid metabolism in the model organism *C. elegans*. Department of Biology, King University, Bristol, TN.** The mechanism of increased prevalence of global obesity is complex, likely with numerous genetic and environmental factors. To combat this, artificial sweeteners have been suggested as a way to decrease obesity and type II diabetes. However, research suggests that they disrupt both glucose and fat metabolism, which raises concerns as consumption of diet beverages increases. Metabolic anomalies in the Insulin Signaling (IGF-1) pathway, which modulates cell proliferation and growth, are seen as an effect of the consumption of artificial sweeteners. The model organism *C. elegans*, which has 80% homology with humans, was treated with glucose, Sweet and Low[®] (10mM and 30mM) and the active ingredient, Saccharin, to evaluate subsequent lipid accumulation. Oil Red O' was used to quantify the lipid content through image analysis; images were evaluated by quantification of the red pixels. When compared to control, both the active ingredient and the Sweet and Low[®] exposed worms show significantly greater red pixel count; therefore, greater lipid accumulation. Glucose treated worms showed an insignificant amount of lipid accumulation. This data suggests that, unlike glucose, exposure to artificial sweeteners leads to an increase in lipid accumulation in nematodes, indicating artificial sweeteners may play a role in the obesity epidemic.
- 21. MATTHEW, S., S. HODGES, E. WEISGERBER, K. SANFT, and B. DRAWERT. GillesPy2: Stochastic Modeling for Biochemical Systems. Department of Computer Science, University of North Carolina Asheville, Asheville, NC.** Understanding complex biological systems often requires investigation using mathematical and computational models. To facilitate this endeavor, we present GillesPy2: a Python package for creating and simulating computational models of biochemical systems. GillesPy2 is the next-generation of the original GillesPy software, an open source cross-platform Python library. It offers an object-oriented

approach for specifying mathematical models, as well as a variety of advanced algorithms for the simulation of those models. The methods include the Gillespie direct method (SSA), a new hybrid stochastic/deterministic tau-leaping method, tau-leaping, and numerical integration of ordinary differential equations. The solvers support a variety of user environments, with optimized code in C++, Cython, and NumPy. GillesPy2 also supports the industry standard SBML model format specification.

- 22. MCKINSEY, M., and G. ARGYROS Prevalence of Antibiotic Resistance in the Gut Flora (Enterobacteracea) of Wild and Domesticated Horses. Department of Biology, Emory & Henry College, Emory, VA.** A horse's gastrointestinal tract houses a large and diverse microbial community. Antibiotics used for prophylaxis and/or treatment of bacterial infections can lead to the evolution of antibiotic resistance in the horse's gut flora. For this study, fecal samples of wild horses from the Outer Banks, Carova Beach, N.C. were analyzed to determine the prevalence of antibiotic resistance against twelve common antibiotics used in the veterinary treatment of domesticated livestock. We expect the flora of wild horses to be more susceptible to these antibiotics than domesticated horses due to a lower frequency of medical intervention as compared to domesticated horses. We plan to compare degree of resistance of the Carova Beach herd to horses at the Emory & Henry Equestrian Center and the wild ponies of Grayson Highlands State Park, Virginia. We expect the domesticated population to exhibit greater antibiotic resistance due to availability of treatment and human contact. The Carova Beach population was 100% resistant to Bacitracin, Clindamycin, and Penicillin, 4.35% resistant to Ampicillin, 86.96% to Chloramphenicol, and 8.69% to Erythromycin. The population was 100% susceptible to Ciprofloxacin, Doxycycline, Gentamycin, and Tetracycline, and 95.65% susceptible to Vancomycin. These data suggest a moderate degree of exposure of the Carova Beach herd to either antibiotics, or bacteria exhibiting resistance to some of these antibiotics. One possible hypothesis is exposure to drinking water pools contaminated with human feces from septic systems that are periodically inundated during high rain periods in the area of the Outer Banks.
- 23. NG, E.¹, and M. KLUKAS². Understanding the Topology of the Hidden State Space of a Self-Localizing RNN. ¹Department of Mathematics, CUNY Hunter College, New York, NY, ²Department of Brain & Cognitive Sciences, Massachusetts Institute of Technology, Boston, MA.** A common approach to modeling neuron activity is to implement a neural network. A neural network can "learn" to perform complicated spatial tasks, such as navigation and localization, but the solution (its learned ability) is difficult to interpret and explain. We trained a recurrent neural network to self-localize while exploring a 1-D ring environment with scattered, identical landmarks, provided self-motion cues and a map containing landmark placements. At each timestep, the network computes a probability distribution which represents the likelihood that each location in the environment corresponds to the agent's true position. A distribution is obtained by applying a LeakyReLU to an activation of the recurrent hidden layer; these values are referred to as output states and hidden states respectively. We present an approach to understanding the network solution by analyzing the persistent topologies of the manifolds formed by output and hidden states. We also present an a priori argument that the observed manifold is a Möbius strip. This theoretical approach is comparable to the current methodology of recording neural activity, followed by performing data analysis to observe a low-dimensional activity manifold in task-performing animals.
- 24. OKEKENWA, S., S. PATEL, and R. WELNER. The Effect of the Microenvironment on Chronic Myeloid Leukemic (CML) Cells Treated with Drugs. Department of Biology, Fisk University, Nashville, TN.** Chronic Myeloid Leukemia (CML) is formed from the translocation between chromosome 9 and chromosome 22 in stem cells. This oncogene gives rise to the active tyrosine kinase BCR-ABL1 in blood cells. CML results in an abnormally high number of myeloid cells (white blood cells) in the bone marrow and blood. Drug inhibitors

against this active oncogene targets the kinase activity leading to the death of leukemic cells. In some patient's cases, these CML transformed stem cells don't die and become drug resistant. It is reported that the cell environment (stromal cells) provides protection to the CML cells from the effects of Tyrosine Kinase Inhibitors (TKIs). The stromal cells contribute to this resistance through CML-stroma adherence molecules and secretion of cytokines which protect the leukemic cells from the apoptotic effects of drug treatment. Therefore, my hypothesis is that CML cells co-cultured with stromal cells will survive when treated with drugs. The goal of this research is to characterize the reasons that CML cells when co-cultured with stromal cells survive drug treatment. CML cells were cultured and passaged, and the growth curve was made for CML cells and CML cells +/- drug. CML cells without drug grew significantly while CML cells with drug showed a decline in growth. The results show that TKI (drug) leads to the death of leukemic cells. This research project is conducted at the University of Alabama in Summer 2019.

25. PAN, Z., and A. PAVKOV. Using the Method of Regularized Stokeslets to Model Biofilm as a Viscoelastic Network Coupled to a Stokesian Fluid, Department of Mathematics, University of Akron, Akron, OH.

From the plaque on our teeth to the fertilization process of an ovum, biofilms are ubiquitous throughout the biological world. They are formed from a complex network of elastic polymers and filaments with internal rheological properties. Many times, they are immersed in a fluid and their motion is a result of the interaction between the internal elastic process and the surrounding fluid environment. In this work, we form a model of a biofilm as a discrete viscoelastic network coupled to a Stokesian fluid. We employ the method of regularized Stokeslets to study this interaction. The behavior and kinematics of the biofilm under differing elastic properties are examined. The role of the wall is also explored using a method of images formulation for the method of regularized Stokeslets, elevated carbon dioxide compensated for the effects of ozone on aggregate protection of C.

26. PETERSON, M.¹, Z. DEROUEN², S.M. HELDMAN³, A.E. BISHOP³, Y. MARINKOVIC⁴, C. VAZQUEZ³, L. CHILONGO¹, T.E. KORALEWSKI⁶, H.H. WANG⁶ and W.E. GRANT⁶. Determinants of Japanese Honeysuckle (*Lonicera japonica*) Invasion in Southeast United States Forestlands. Department of Geography¹, Department of Ecosystem Science and Management², Department of Biology³, Department of International Studies⁴, Department of Wildlife and Fisheries Sciences⁶, Texas A&M University, College Station, TX. Invasive species modify biogeochemical cycles, inhibit natural regeneration, and decrease biodiversity and productivity. Japanese honeysuckle, *Lonicera japonica*, was introduced to the United States in the early 1800's and was first recorded outside of cultivation in 1882. As a vigorous invader of the southeast United States, Japanese honeysuckle grows rapidly and has an early and lasting reproductive period. Therefore, our objective is to understand the recent range expansion of this invasive species and to identify potential vectors of invasion. To complete our objective, we collected and mapped geospatial data from the Southern Nonnative Invasive Plant data Extraction Tool (SNIPET) and combined it with its associated attribute data collected from the Forest Inventory and Analysis (FIA). We then used multicollinearity regression to identify potential determinants of invasion. Our results indicate the Japanese honeysuckle generally spread southward with a significantly increasing presence of approximately 50% (P-value < 0.05). The presence of Japanese honeysuckle was positively associated with adjacency to water bodies, temperature, and species diversity and negatively associated with slope, forest stand age, distance to the nearest road, and fire disturbance. Our model provides insights into the management of Japanese honeysuckle with which forest managers can develop strategies for effective management.

27. PICKLE, S., J. STURGILL and G. BRESOWAR. Ecological correlations of mosquito communities at the Bartlett-Crowe Field Station. Department of Biology, Emory & Henry College, Emory, VA. The Bartlett-

Crowe Field Station is a 72-acre plot of land consisting of multiple micro-habitats including: wetlands, hardwood forests, and open pastures. *Aedes triseriatus* is the native mosquito species of the Appalachian region. The emergence of two invasive species of mosquitos, *A. albopictus* and *A. japonicus* has raised some ecological questions about species diversity within the mentioned habitats. This research is a statistical analysis of the mosquitos present in these habitats, which were all collected with Bioquip Gravid Traps.

- 28. PIGHINI, J.¹, M. JACKSON¹, J. TOLONE¹, C. FAY¹, D. MOREL¹, and J. DICK². Development of a Night Interruption Light Therapy Delivery Apparatus for Field Treatment of Hop Plants.** ¹Department of Physics, Emory & Henry College, Emory, VA, ²Kelly Ridge Farms, Meadowview, VA. The short-day plant *Humulus lupulus*, or hops, relies on night length to control growth. During relatively long nights, as is the case in Virginia in summer, hop plants do not grow as tall as they do in the northwestern US. Growth triggers in hop plants are partially controlled by photoreceptors called Phytochromes, which respond to light. Of particular interest are those phytochromes sensitive to the red and far-red wavelengths of light. When exposed to red light, the inactive form of phytochrome (Pr - Phytochrome red) is converted to the active form (Pfr - Phytochrome far-red), the latter regulating growth processes. Whereas far-red light triggers Pfr conversion back to Pr. In order to counter the effect of long nights on phytochromes, three types of LED-based, Arduino-controlled, light delivery structures are under development, as well as a structure to manipulate the light array within the field. With the use of spectrometers, measurements of intensity as a function of wavelength give a profile of the illumination delivered by each array. The most efficient type of LED light for hop plants can be determined by comparing spectral data with the desired peak wavelength of red light for the conversion of Pr to Pfr, which is approximately 657 nanometers. Further measurements can verify calculations of the effective intensity of the light at various distances from the source, suggesting treatment regimens.
- 29. POLLACK, M., and F. AGUSTO. Effectiveness of Disease Control Measures in Pathosystems with Co-Infection and Vector Preference.** Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS. Most plant-vector-virus diseases found in nature are caused by the interaction of multiple viruses in organisms, called co-infection. Three main types of co-infection have been identified: helper-dependence, cross protection, and synergism. The vectors that are able to carry the diseases between hosts also tend to prefer certain categories of hosts over others. In this study, we developed a general compartmental disease model that incorporates all three types of co-infections, vector preference, and the transmission of disease in vectors in addition to in hosts. The model was utilized to evaluate the effectiveness of three common disease control strategies that are applied in agriculture: increasing planting of healthy hosts, rouging (removal of diseased plant hosts), and pesticides. When vectors preferred healthy hosts, for all types of co-infections none of these control measures eliminated the disease. For other types of preference, increasing the planting of healthy hosts rarely significantly lowered disease incidence, whereas planting more protected hosts when cross protection was present did lower disease occurrence. Also, when vectors did not prefer healthy hosts, pesticide was the most effective control. Rouging completely eliminated disease in the presence of cross protection but was largely ineffective against helper-dependence or synergism.
- 30. SAUCHUK, R., B. CHEN-CHARPENTIER, F. AGUSTO, O. GAOUE, and M.C.A. LEITE. Study of Sustainable Harvesting of Non-Timber Forest Products in a Fragmented Ecosystem: A Mathematical Framework,** University of South Florida St. Petersburg, St. Petersburg, FL. Fragmentation, degradation, and habitat loss are viewed as important causes of known species extinctions and ecosystem fragmentation is one of the main threats to species persistence. In addition to ecosystem fragmentation, harvesting non-timber

forest products (NTPP) from wild plants species have been recognized to affect significantly the population dynamics of plants. Nowadays with increasing human pressure through land clearing and logging, NTPPs are being harvested from increasingly fragmented landscapes. Despite numerous efforts that have been spent to understand plant sustainability and plant management subject to the two fragmentation and harvesting, there is still a wide range of challenging problems to be faced in order to be better equipped to handle threats posed to plants by these external ecosystems disturbances. We will present a processes-based mathematical framework that integrates data and two plant's endogenous stressors: harvesting and fragmentation. The aim of this on-going project is to use the mathematical models to gain insights on management strategies that sustainably conserve plant species subject to such interactive stressors. We will discuss the proposed mathematical models, how data integration was performed to accomplish the model parametrization, and some interesting results derived from the models.

- 31. SHAO, O., G. DWYER, and S. CARRAN. Late Enough to Be Effective, Early Enough to Be Protective: Optimal Influenza Vaccination Timing. Biological Sciences Division, University of Chicago, Chicago, IL.** Annual vaccination is considered the best course of action for protection against influenza infection. However, recent work suggests that flu vaccine effectiveness (VE) likely wanes within the course of a single flu season, bringing into question the optimal timing for vaccination. If VE wanes quickly enough, greater individual flu protection would be obtained by vaccination closer to the time of highest flu activity. We approach this issue quantitatively: Our mathematical model seeks to determine which week of vaccination results in the greatest protection from the flu. We represent the relative protection provided by vaccination as the product of VE and flu incidence, and integrate over the course of the season to obtain total protection from respective vaccination at each week of the year. We used flu incidence data from the CDC, encompassing the past 21 flu seasons. For realistic waning rates, our model suggests that there may be a protective benefit to delaying vaccination until later in the year than the current average time of vaccination. While the CDC recommends that individuals get their flu shot by the end of October, our analysis suggests that vaccination closer the end of November provides individuals with optimal protection across the season.
- 32. SCHREINER C., S. NUISMER, and A. BASINSKI. When to Vaccinate a Fluctuating Wildlife Population: Is Timing Everything? Department of Biological Sciences and Department of Mathematics, University of Idaho, Moscow, ID.** Wildlife vaccination is an important tool for managing the burden of infectious disease in human populations, domesticated livestock, and various iconic wildlife. Though substantial progress has been made in the field of vaccine designs for wildlife, there is a gap in our understanding of how to time wildlife vaccination, relative to host demography, to best protect a population. We use a mathematical model and computer simulations to assess the outcomes of vaccination campaigns that deploy vaccines once per annual population cycle. Optimal timing of vaccination is an important consideration in animals with short to intermediate lifespans and a short birthing season. Vaccines that are deployed shortly after the birthing season best protect the host population. Vaccinating at the end of the breeding season best reduces the mean abundance of pathogen-infected hosts. Delaying vaccinating until later in the year can facilitate pathogen elimination. Tuning vaccination campaigns to host demography and pathogen traits can substantially increase the effectiveness of a campaign. Our results highlight the need to better understand and predict host demography in wildlife populations that are targeted for vaccination.
- 33. SHEPPARD, L., and G. ARGYROS. Canada Geese (*Branta canadensis*) as Mechanical Vectors of Bacterial Pathogens and Parasitic Protozoa. ¹Department of Biology, Emory & Henry College, Emory, VA.** Birds are known to serve as mechanical vectors for a variety of microorganisms that are infectious to humans. Canada geese (*Branta canadensis*) are migratory waterfowl that are known to vector of variety of

pathogens capable of infecting humans by passing them into the environment through their feces. Due to the increase of Canada Geese populations in recreational and residential areas, there is also an increased risk for humans to become infected with the pathogens they carry. This research investigates the presence of *Salmonella*, *Cryptosporidium*, and other parasitic protozoa. in fecal samples collected from Canada Geese found in North Carolina, Tennessee, and Virginia. A total of 124 samples from seven different localities were tested for presence of *Salmonella* and *Cryptosporidium*. Of the 124 fecal samples tested, 89 (= 71.8%) were positive for *Salmonella*, 24 (=22%) were positive for *Cryptosporidium*, and 19 (=15.3%) were positive for both. As many species of *Salmonella* and *Cryptosporidium* are zoonotic pathogens, these data indicate a potential public health hazard where human-animal (fecal) contact is possible.

- 34. STAPLETON, A.¹, I. ZARETZKI², F. NASRIN¹, and V. MAROULAS¹. EEG Signal Classification Using Topological Machine Learning.** ¹University of Tennessee, Knoxville, TN, ²West High School, Knoxville, TN. This work presents a two topological classification schemes of Electroencephalogram (EEG) signals along with their comparisons. An effective classification scheme of EEG signals is crucial to develop human-machine system. We view the EEG signals through the lens of topology to gain a fresh insight of the shape peculiarities. Persistent homology explores topological and geometric features of point clouds and summarizes them in a descriptor known as persistence diagram. Here we implement two methods to convert the signals to persistence diagrams—Vietoris-Rips filtration and sublevel set filtration. These diagrams enable us to utilize effective classification scheme based on important topological characteristics. The distance-based method utilizes metrics such as the Wasserstein, Bottleneck and d_p^c distance to find the overall distance of persistence diagram. The d_p^c metric accounts for variations in small persistence and in number of features, thus ultimately yielded the best results under certain parameter choices. The Bayesian framework method employs posterior intensities to compute a Bayes Factor, which ultimately determines classification through a predetermined threshold. One important observation is that in most cases, Bayes factor outperforms in presence of high noise than the distance-based classification. For less noisy signals we encounter higher accuracy in distance-based classification.
- 35. TOLBERT, B.¹, Y. OH², L. HOLLINGSWORTH³, and K. KUH⁴. HPV16 E6 Antibody as early Biomarker for HPV OPC.** ¹Fisk University, Nashville, TN, ²Berea College, Berea, KY, ³Vanderbilt University Medical Center, Nashville, TN, ⁴Department of Epidemiology, Vanderbilt University, Nashville, TN. The incidence of oropharyngeal cancer (OPC), a type of head and neck cancer, is rapidly increasing in the US and has been attributed to human papillomavirus (HPV) infection. OPC cases now outnumber cervical cancer cases in the US, approximately 85% of which occur among men. Unlike cervical cancer, where the introduction of highly effective screening has significantly reduced the incidence and mortality of cervical cancer in women, there are no methods for early detection of HPV-OPC in men. Recently, HPV16 E6 antibody positivity has been identified as a promising early biomarker for HPV-OPC. Previous work from our group showed that HPV16 E6 antibodies are present in up to 90% of HPV-OPC patients and appear more than 10 years prior to diagnosis. The object of this study is to use the HPV16 E6 biomarker to develop a cohort of individuals who are at highest risk of HPV-OPC. We will capitalize on the pre-existing infrastructure at Vanderbilt to test residual blood samples from healthy men aged 45-70 without diagnosed cancer for the presence of HPV16 E6 antibodies to estimate the seroprevalence of HPV16 E6 antibodies among men aged 45-70 in the general Nashville population. Determine the association between HPV16 E6 seropositivity and markers of HPV-OPC risk; Residual blood samples from men aged 45 to 70 are being collected from Vanderbilt University Medical Center outpatient clinics (target: 25,000) and tested for the presence of HPV16 E6 antibodies. In hope to create a vaccine for HPV16 E6 OPC.

36. TU, D. Modeling Cell Population and Morphology of Microglia and Dopamine Neurons in the Midbrain of Mice During Aging. Department of Mathematics, University of Florida, Gainesville, FL. In the midbrain, dopamine receptors on microglia alter microglial function to (reciprocally) facilitate neurotransmission. To understand cellular mechanisms of this bidirectional interaction, especially incorporating the factor of aging, accurate mathematical models are needed. This research answers three main questions through modeling: (1) how do numbers of microglia (Ibal+), dopamine neuron (TH+), and their ratio (Ibal+/TH+) change, (2) how does morphology of microglia change, and (3) does physical contact between microglia and dopamine neuron alter. Multiple trials were run on five mice over average life span of 0 – 24 months and observation focused on two midbrain regions SNc and VTA. Based on general features of data, various models were created for each data set, including polynomials, exponentials and fractions. For each model, treating data as Poisson distribution, maximum likelihood functions were created of which parameters were found by multiple least squares regression. Models were evaluated by the Akaike Information Criterion and then selected and weighted based on their Akaike weights. The number of Ibal+ and TH+, contact sites, and Ibal+/TH+ ratio increased in aged mice and the complexity of microglia declined with age. Projection of model to the age of 30 months suggests ultimate scenario for elderly mice which is usually unattainable through experiment.

37. ZUMPARO, F.¹, and E. LUSHI². Separating Motile and Immotile Bacteria Through Confined Chemotaxis. ¹Department of Mathematics and Statistics, The College of New Jersey, Ewing, NJ, ²Department of Mathematical Sciences, New Jersey Institute of Technology, Newark, NJ. The motion and spread of bacteria in complex porous media is an interest with significant implications in health sciences and technology. The vast majority of bacteria move in complicated porous materials, such as tissues or soil, yet their motion in confinement is not completely understood. Bacteria such as *E. coli*, a well-known species that has pathogenic strains, typically swim in a run and tumble fashion, alternating straight swimming runs with tumble reorientations. These bacteria also exhibit chemotaxis, directed motion along a chemical gradient (e.g. food or oxygen), during which bacteria are able to suppress tumbles. Here we investigate the collective motion of chemotactic bacteria in the simplest circular confinement mimicking the drops seen in experiments. Experiments with both immotile and motile bacteria show zone formations that are affected by the oxygen seeping through the drop boundary. These zones include a ring of motile bacteria at the circular boundary, a compact inner core of immotile bacteria, and a clear depletion zone between these two areas. Our model and simulations show that we can capture the eventual phase separation in an initially random mixture of motile and immotile bacteria.

38. GERBER, J., D. HOWARD, and J. QUINN. Modeling Shifts in Acoustic Indices during a Total Solar Eclipse. Department of Biology, Furman University, Greenville, SC. Noticeable changes in soundscapes occur over a 24-hour day. These shifts are based, largely, on cues tied to the sun's movement. For example, at dawn and dusk, Biophony, a measure of the frequency generated from biological noise, is high. Urban development also affects these measures. In 2017, a total solar eclipse resulted in a 3-hour period where the sun was partially covered by the moon, and around 2 minutes of total darkness. We hypothesized measurable, unique changes in different acoustic indices within the path of totality. We placed ARUs across an urban-rural gradient to measure these changes. We used an array of packages in R to process the data and generalized additive models to model and visualize how six acoustic indices changed over time, nesting for development among sites. Biophony peaked immediately before the period of totality, mimicking dusk chorus and when the eclipse ended, mimicking dawn chorus. Anthrophony, however, was lowest before totality, and increased throughout totality. Including development in the models significantly improved fit, where increasing development minimized acoustic change. The solar eclipse

shifted normal acoustic variation expected during 24-hours to a narrow 5-hour period. Thus, an eclipse provides novel insight on temporal and spatial variation in soundscapes.

- 39. RANDALL. N.¹, C. AZEREDO-TSENG², and M. LUO³. Modeling Epithelial Gene Expression in Cell Differentiation.** ¹Austin College, Sherman, TX, ²New College of Florida, Sarasota, FL, ³The College of New Jersey, Ewing, NJ. Epithelial to mesenchymal transition (EMT) is a trans-differentiation process essential to development and wound healing, as well as cancer metastasis. Several regulatory elements that induce EMT, such as TGF β and ZEB1, have been identified to date. These regulatory elements effectively repress epithelial (E) gene expression and activate mesenchymal (M) gene expression. How these factors regulate the M-gene pathway has been previously studied. However, the role of these regulatory elements in the E-gene pathway remains unclear. In this study, we explored the effects of TGF β and ZEB1 on the E-gene pathway in both clinical and experimental settings. Using gene set enrichment analysis, we scored cancer samples based on their overall E- and M-gene expression, and compared them against a time-course of TGF β induced EMT. Finding a similarity, we created a model of E-gene expression during EMT as a function of TGF β and ZEB1 which captures the change in E-gene expression over both the EMT time-course and major clusters in our clinical data. Our model suggests that TGF β can serve as both an activator and suppressor of E-gene expression based on the specific sub-cluster, but that ZEB1 is the primary regulator of E-gene expression during EMT.

ORAL PRESENTATION ABSTRACTS

AMENEYRO, B.^{1,2}, B. CHAU², C. M. PONCE², U. JAIME-YEPEZ², and Z. WANG². The Role of Variation in Mate Choice and Wolbachia Infection on Aedes aegypti Population Dynamics. ¹Department of Mathematics, University of Tennessee, Knoxville, TN, ²The Mathematical and Theoretical Biology Institute Summer Program, Arizona State University, Tempe, AZ. Wolbachia, an endosymbiont bacteria, is common in various invertebrates and known for host reproductive manipulation strategies as well as for slowing the replication of certain viruses. When infected by Wolbachia, Aedes aegypti mosquitoes become resistant to transmitting some mosquito-borne diseases (MBD) such as dengue, diseases prevalent in tropical and subtropical regions. Releasing a large number of Wolbachia infected mosquitoes in the environment is assumed to be a more effective strategy than other various methods to control the spread of MBD. However, evaluation of such Wolbachia-based interventions over a long term temporal scale is limited in the literature. Moreover, the Wolbachia's host manipulation strategy, cytoplasmic incompatibility (CI), benefits the Wolbachia in the form of decreasing the number of non-infected mosquitoes. Additionally, Changes in mating preference could impact the benefit from CI, as it requires that infected males mate with uninfected females. We developed and analyzed models that capture the life cycle and mating preference of mosquitoes with and without Wolbachia. Our research primarily focuses on the effects of non-random mating on the population dynamics of mosquitoes. The analysis of models suggest that Wolbachia persists in the mosquito population as long as a sufficiently large Wolbachia infected mosquito population (critical population size) is released. This critical population size is a function of mating-related factors and stage progression rates. We hope that the results of this modeling study will help in identifying significant change to the dynamics which could better inform us about the effectiveness and sustainability of this method to combat MBD.

ASHBY, M., T. DENNIS, and K. WRIGHT. Determining Over-Performing Phenotypic Features in Maize Using Machine Learning Techniques. Departments of Mathematics and Statistics, Physics, and Computer Science, East Tennessee State University, Johnson City, TN. With the growing population, crops have

become more important than ever. The increasing demand for food has required farmers to push their crops to the limit. The Genomes to Fields (G2F) initiative is a publicly funded partnership in which maize genomic data is being collected in the attempts to better understand genotype-by-environment (GxE) and gene-by-gene (GxG) interactions, potentially leading to a way to produce maximally yielding crops with enough food to feed the growing population. Using the data from the G2F initiative, we seek to model maize crop yield as a function of its phenotypic features and then identify over-performing crops and the commonalities among them. Eventually, we want to map the phenotypic features that correlate with large crop yield back to the genetic sequence to determine which genes produce the strongest, highest-yielding plants.

BELCHER, M. Mathematical Modeling of Diabetic Foot Ulcers Using Optimal Design and Mixed-Modeling Techniques. Western Kentucky University, Bowling Green, KY. A mathematical model for the healing response of diabetic foot ulcers was developed using averaged data. The model contains four major factors in the healing of wounds using four separate differential equations with 12 parameters. The four differential equations describe the interactions between matrix metalloproteinases (MMP-1), tissue inhibitors of matrix metalloproteinases (TIMP-1), the extracellular matrix (ECM) of the skin, and the fibroblasts, which produce these proteins. One approach to implementing this model was to introduce mixed modeling techniques on certain parameters in that model. Mixed effects modeling is an analytical tool useful for the repeated measurement of data with subjects, patients, etc. that have random affects that deviate from a specified norm. Another approach has been to use an optimal design technique to identify which times are ideal for data gathering for the model. Our project worked to combine these techniques by first introducing mixed modeled parameter values into a Standard Error (SE) optimal design algorithm and then comparing the results collected to the standard algorithm. Once this was completed the other optimal design techniques were used with and without these mixed modeled parameters to see if a certain technique was better than the others.

CAMPBELL, K., and L. STAUGLER. Estimating Time-Varying Applied Current in the Hodgkin-Huxley Model. Mathematics Department, Worcester Polytechnic Institute, Worcester, MA. The classical Hodgkin-Huxley model is widely-used for understanding the electrophysiological dynamics of a single neuron. While applying a constant current to the system results in a single voltage spike, it is possible to produce more interesting dynamics by applying time-varying currents, which may not be experimentally measurable. The aim of this work is to estimate time-varying applied currents of different forms given voltage data. In particular, we utilize an augmented ensemble Kalman filter with parameter tracking to estimate three different applied currents, analyzing how the model dynamics change in each case. We further test the efficiency of the parameter tracking algorithm in this setting by exploring the effects of changing the parameter drift variance and the frequency of data available on the resulting applied current estimates.

CLARK, M., G. GREY, and S. HOTA. Modeling Blood Glucose for the Detection of Type 2 Diabetes. Fisk University, Nashville, TN. Diabetes mellitus refers to a category of metabolic disorders characterized by elevated blood glucose levels. Normally, after ingesting a meal, blood glucose levels increase before being reduced to homeostatic levels by hormones such as insulin. In diabetic patients, there is some failing that prevents normal regulation. For type 2 diabetics, this failing usually occurs because of adult-onset metabolic disorder resulting in insulin resistance or relative insulin deficiency. In this project, glucose regulation is considered as a forced spring-mass differential equation with glucose input as the forcing function. Three different input equations are considered for glucose, each one corresponding to a different type of glucose tolerance test. By applying the Laplace transform, explicit solutions for glucose are derived, each one corresponding to a particular form of external glucose input. This leads to the development of

characterizing factors for type 2 diabetes. The model with Dirac-delta function as the forcing function for oral glucose tolerance tests proved particularly interesting and was found to agree closely with clinical data for a patient with type 2 diabetes.

GAN, A. A Steady and Near-Steady State Cancer Cell Model. Department of Mathematics, University of Tennessee, Knoxville, TN. Breast cancer affects around 3.5 million Americans, and metastasis is involved in 70-90% of cancer-related deaths. To better understand cancer cell mechanics in diagnostic microfluidic devices and during metastatic migration, a two-dimensional cancer cell model was developed by Barber and Zhu. To assist with the calibration and development of this more comprehensive model, we present and implement a model of cancer cells in and near steady deformation states. The model represents the internal and membrane forces of cancer cells using a triangular mesh of viscoelastic elements (damped springs), and balancing forces yields an implicit system of differential equations. A steady state solver and implicit time-integrator are implemented in order to consider the equilibrium configuration and time dynamics of the cancer cell. The model is similar to the original Barber and Zhu model except that it is used to consider experiments taking place during extremely slow flow conditions and therefore ignores external fluid forces acting on the cell. Thus, this makes this new model far more efficient in terms of computational runtime. Overall this tool can be used to consider how internal elasticity affects cell behaviors, and in the future, explore more complex and physiologically realistic cytoskeletal structures as well as assist in the calibration of model parameter values for the full-fluid model using experiments available from the literature.

HEDSPETH, T., P. STEINHAGEN, B. ALLEN, M. GONCALVES, M. KING, C. SAMPLE, and J. SHAPIRO. Amplifiers and Suppressors of Evolution on Graphs Under Birth-Death Updating. Department of Mathematics, Emmanuel College, Boston, MA. The spatial structure of a population can amplify or suppress a mutation's ability to become fixed. In this research we applied the Birth-Death update rule to asexual individuals that reside on nodes of a graph. We utilized temperature initialization, where the initial location of the mutant type is chosen in proportion to how often a node is replaced. We analyzed fixation probability using two methods: one that applies to weak selection, and one that applies to arbitrary selection strength in a certain limit. We applied this model to three families of graphs, which we call the fan, spider, and big spider. We then analytically computed the characteristics that would optimize the fixation probability of an advantageous mutant for each structure. We found that all three families of graphs that we studied could yield amplifiers of selection. Notably, we were able to create a very strong amplifier of selection using a graph with no self-loops.

HILL, E.¹, S. VERMA², and B.J. CHERAYIL². Role of the YrbE phospholipid transporter in Salmonella Typhimurium infection. ¹Emory & Henry College, Emory, VA, ²Massachusetts General Hospital for Children, Boston, MA. *Salmonella enterica* serovar Typhimurium causes gastroenteritis that leads to diarrhea, vomiting and fever. This bacterium has a wide host range and annually affects 90 million people worldwide and 40,000 in the United States. *Salmonella enterica* serovar Typhi is 90% genetically identical to *S. Typhimurium*; the symptoms of typhoid fever, however, are much more intense and are fatal in up to 20% of all patients. Both bacteria share the *yrbE* gene and phospholipid transporter that may play a crucial role in their initial adhesive and invasive capabilities. To assess the role of the *yrbE* gene in adhesion and invasion, we used three strains of *S. Typhimurium* to perform adhesion and invasion assays in HeLa epithelium: termed SL1344, SL Δ yrbE, and SL Δ yrbE/pyrbE. The uptake of *S. Typhimurium* in RAW 264.7 cells was also quantified at the 2- and 6-hour time points. Ultimately, we assessed the role of the *yrbE* gene and phospholipid transporter in the role of *S. Typhimurium* infection in comparison with previous work performed with *S. Typhi*.

HUFF, M.A., T. LANE, and J. RUDD. The Effects of Salinity on Mussel Glochidia. Department of Biology, King University, Bristol, TN. Every year, the USA uses nearly 20 million tons of salt to de-ice roads. With the combined effects of snow melt and spring rains, much of this salt is washed into freshwater ecosystems. The Appalachian region of the US contains roughly 400,000 miles of streams and rivers, which support an incredible amount of biodiversity. Among this biodiversity is the freshwater mussels of the Unionidae family. It is estimated that a third of the roughly 1,000 known Unionidae species are endemic to the US, and the Tennessee River basin likely contains more species than China and Europe combined. Researchers have identified a correlation between Unionidae population decline and the application of road salts; however, the exact cause is unknown. Unionids have a complex life-cycle which involves a larval stage (known as glochidia) parasitizing the gills of a host fish. This research exposed the glochidia of *Medionidus conradicus* to increasing brine concentrations to simulate varying degrees of run-off. Preliminary results show that low concentrations of NaCl can prevent the glochidia of *M. conradicus* from successfully attaching to the gills of their host fish, *Etheostoma rufilineatum*. This suggests that even light use of road salts can potentially negatively impact populations of *M. conradicus*.

JODOIN, V.¹, and S. PAYNE². Modeling the Effect of Social Networks on the Spread of Opioid Use
¹Department of Mathematics, University of Tennessee, Knoxville, TN, ²Department of Mathematics, Bellarmine University, Louisville, KY. The opioid crisis has recently become classified as a national health emergency, and in this paper, we investigate the effect of social networks on the spread of opioid use. We are modeling the impact the presence of a highly connected and highly positive individual has on the network in order to see if they can decrease the number of addicts in the overall network, or the rate of users becoming addicts. We built an agent-based model via NetLogo to create our spatially clustered network to model how individuals remain non-users or become users, addicts, or rehabilitated. Our model examines the premise of a mechanism to encourage users or addicts to end the use of opioids by surrounding themselves with a sub-network of positive individuals. This sub-group will encourage a user to have less negative influences.

KING, M., J. SHAPIRO, T. HEDSPETH, P. STEINHAGEN, M. GONCALVES, B. ALLEN, and C. SAMPLE. Computing Fixation Probabilities on Graphs Under Weak Selection. Department of Mathematics, Emmanuel College, Boston, MA. Evolution occurs when there are genetic changes in a population over time. These genetic changes, or mutations, impact an individual's ability to survive and reproduce. In this study, we examined how the spatial structure of a population affects the rate at which mutations accumulate as well as the balance of weak selection versus neutral drift. We modeled the spatial structure as a graph with haploid, asexual individuals occupying vertices. By analyzing the evolutionary dynamics on various structures, we identified extreme amplifiers or suppressors of selection. Amplifying population structures increase the fixation probability of beneficial mutations while reducing that of deleterious mutations; suppressing structures do the opposite. We used MATLAB to exhaustively compute fixation probabilities under weak selection on all simple graphs up to size 10. These calculations identified a family of graphs, which we call Diamond Rings, that are strong relative suppressors of weak selection. For larger graphs, we developed a genetic algorithm to determine structures that are amplifiers and suppressors of selection. We discovered another family of graphs, which we call Spider Islands, that are amplifiers of weak selection.

KLITGAARD, K. Leaky or Loyal: Optimizing Plant Investment in Mycorrhizae Fungal Mutualists within a Fluctuating Environment. Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, CA. More than 75% of plant species form mycorrhizal associations to obtain

nutrients from their environment. These associations may be impacted by various seasonal conditions (e.g., rainfall, temperature). To examine the effect of seasonality on plant-mycorrhizal associations, I created a dynamic, continuous-time model of the interactions between a host tree and fungal partners in a fluctuating environment. In this model, plants provide carbon investments to fungi, which provide soil nutrients in return. The environmental state affects fungal partner quality, determining fungal traits such as mortality, growth rate, and nutrient affinity. I simulated two plant strategies: First, I modeled the optimal investment of a plant in a single fungus, and found that its growth-maximizing investment strategy is a time-weighted average of its strategy in each of the fluctuating environments. Second, I modeled a plant with two partners whose quality switched as a function of the environment. I assumed that the plant could make investments only based on its present-day knowledge. I found that “leaky” investment strategies (in which not all belowground investment goes to the present-day highest quality fungus) produced greater plant fitness. This supports the idea that “imperfect” partner recognition and reward systems may not be optimal in fluctuating environments.

LOCHNER, E.¹, B. RUIZ², and A. WILLIAMS³. The impact of climate change on environmental suitability of buzz pollinators. ¹Department of Mathematics, University of Wisconsin, Eau Claire, WI, ²School of Mathematical and Statistical Sciences, University of Arizona, Tempe, AZ, ³Department of Biology, Salem College, Winston-Salem, NC. Many crops depend on pollinators for fruit and seed production. Several crops, the tomato in particular, rely on buzz pollination, where bees vibrate their indirect flight muscles at the right frequency to release pollen. Managed honey bees do not buzz pollinate which implies a critical relationship between the tomato plant and wild buzz-pollinator species. However, climate change is affecting the distribution of these wild pollinators which could lead to pollination deficits for tomato crops. We expect climate change to force some tomato pollinator species out of the current distribution of tomato crop production areas. Using ecological niche modeling, we assessed potential range shifts for sixteen buzz-pollinators native to North America. We used known species occurrence data and climate change projections based on several circulation models and emission scenarios developed in the Fifth Assessment Report of the Intergovernmental Panel on Climate Change to detect regions where climate change will severely affect buzz-pollinator distribution. Additionally, we assessed areas where a decrease in buzz-pollinator richness will likely impact tomato agricultural activity. Our results highlight areas where tomato pollinator diversity is likely to decrease in the future, specifically in the eastern United States. These areas include counties in states such as Indiana and Ohio that also have dense tomato production. Since tomatoes rely on pollinators for fruit production and increased quality, these maps indicate areas where habitat management and climate change mitigation measures should be prioritized in order to preserve tomato production and quality.

MADDOX, T., N. KARIG, and D. ROACH. Statistical Analysis of Internet Coverage at Different Times of Day for Business to Business Companies. Departments of Mathematics and Statistics, Chemistry, and Computer Science, East Tennessee State University, Johnson City, TN. Because of the growth of the internet as a gathering place of people, it appears that having a presence online would be crucial for businesses, even those marketing themselves to other businesses. In the biological sciences, there come times when a new product or service may be provided to hospitals, universities, or pharmaceuticals in order to better human lives. In some cases, a good idea will only get creators so far, and a budget for advertising may be out of reach. In such a case, personally posting on social media is an option for growing awareness. However, knowing what times to post certain kinds of content on social media platforms could benefit businesses or otherwise in reaching their target audiences. An exploration of the data provided for data analysis with tools such as Google Analytics will be used to explore how factors of time and type of

content affect the growth of an audience. Such methods as one-way ANOVA and t-tests will tell statistical significance of certain methodologies against others.

MAGAÑA, J.^{1,2}, M.M. BROWN^{1,3}, J. ALANIS^{1,4}, J. KITCHENS^{1,5}, C. VELASTEGUI^{1,6}, M. THAKUR¹, B. ESPINOZA¹, A. MURILLO¹, M. RODRIGUEZ MESSAN¹, R. KOESTER⁷, and C. CASTILLO-GARSOW^{1,8}.

Topography and Behavior Based Movement Modeling for Missing Persons in Land-Wilderness Settings.

¹Simon A. Levin Mathematical, Computational, and Modeling Sciences Center: Mathematical & Theoretical Biology Institute. Arizona State University, Tempe AZ, US, ²University of North Georgia, Dahlonega GA, US, ³Scripps College, Claremont CA, US, ⁴San Joaquin Delta College, Stockton CA, US, ⁵Warren Wilson College, Swannanoa NC, US, ⁶Yachay Tech University, San Miguel de Urcuquí Imbabura, EC, ⁷Kingston University London, London, UK, ⁸Eastern Washington University, Cheney WA, US. Search and Rescue (SAR) operations are critical to the safety and well-being of individuals who visit state and national parks. Rescue time is crucial as survival rates dramatically decrease each day, and the cost of each mission increases proportionally. It is estimated that approximately 2000 individuals get lost every year, and the average cost of a SAR operation is \$1,375 per person. There is a need to incorporate a mechanistic mathematical model that takes a parameter of human behavior into consideration also. Data from resources such as the International Search and Rescue Incident Database (ISRID) are analyzed to identify patterns in human behaviors and key geographic environmental influences to develop a mechanistic model of missing persons. We use a discrete-time Markov Decision Process (MDP) where the lost individual's state determines a strategy for being found. The individual then interacts with the environment, where a utility function for that strategy over the geographic environment determines direction of travel. We compare data from various national parks against our model. Implications are discussed for SAR, hiker survival training, and other areas. The proposed model might be extended for other groups of people, including experienced hikers or individuals who suffer from mental illnesses.

MAJETIC, G.^{1,4}, R. MILLER NEILAN^{2,4}, A. ADKE⁵, Y. CARRASQUILLO⁵, and B. KOLBER^{3,4}. A Computational Model of Cell-Type Specific and Pain-Related Neural Activity in the Amygdala During Neuropathic Pain.

¹Department of Engineering, Duquesne University, Pittsburgh, PA ²Department of Mathematics and Computer Science, Duquesne University, Pittsburgh, PA ³Department of Biological Sciences, Duquesne University, Pittsburgh, PA ⁴Chronic Pain Research Consortium, Duquesne University, Pittsburgh, PA ⁵National Center of Complementary and Integrative Health, National Institutes of Health, Bethesda, MD. Injury changes the excitability of pain-related neurons within the right hemisphere of the central nucleus of the amygdala (CeA). An agent-based computational model was created in NetLogo to simulate neural behavior over time and in response to injury. Each of the 625 agents represents one neuron in the right hemisphere of the CeA and is characterized by its protein-expression type (somatostatin or protein kinase C-delta) and spiking frequency (regular or late). During each time step, neurons' firing rates (Hz) are stochastically updated using probability distributions estimated from data collected in laboratory experiments using a neuropathic pain model. A damage accumulation sub-model tracks the damage accumulated by each neuron during injury as the neurons transition from an unsensitized to a sensitized state. Cumulative firing rates of somatostatin and protein kinase C-delta neurons are used to calculate emergent levels of pain attributed to injury. Results demonstrate the model's ability to predict acute and chronic pain along with neurons' contribution to pain. Agent-based modelling is a useful tool in studying the relationship between neural activity and pain.

MITCHELL, L. Analyzing the Effects of Observation functions in Nonlinear filtering for the SIR model. Mathematics Department, Worcester Polytechnic Institute, Worcester, MA. Nonlinear filtering is an approach to solving the inverse problem of estimating unknown states and/or parameters of a system. The

ensemble Kalman filter (EnKF) is one such algorithm that can be used for nonlinear, non-Gaussian systems within a Bayesian inference framework. One component of the EnKF is the observation function, which relates the discrete, noisy data back to the system model. The observation function can take different forms based on assumptions relating to the available data and relevant system parameters. The goal of this research is to explore the effects of selecting different observation functions in the EnKF framework, for both parameter and state predictions in epidemic models. In particular, four different observation functions, of different forms and various levels of complexity, are examined in the SIR model. Results discuss the effects of the observation function selection on the filter outputs.

OBREGON, I. Minimizing Drug Resistant Cases of Gonorrhea through Cost-Effective Treatment Plans.

University of the Incarnate Word, San Antonio, TX. Gonorrhea, caused by the bacterium *Neisseria gonorrhoeae*, is the second most prevalent bacterial sexually transmitted infection (STI) with 87 million new cases reported worldwide, according to the World Health Organization (WHO). Gonorrhea has developed resistance to multiple treatment therapies within the past century due to the introduction and misuse of antibiotics. The decrease of effective treatment plans develops a posing threat of an untreatable gonorrhea infection and a global health crisis. We aim to study a comprehensive treatment strategy with respect to drug resistance in gonorrhea and its cost-effectiveness. We develop a mathematical model of gonorrhea's resistance with respect to two dual treatments recommended by the WHO, ceftriaxone with azithromycin and cefixime with azithromycin. We also perform a cost-benefit analysis which compares the suggested treatment plans to minimize the emergence of drug resistance. We numerically simulate our model and analyze the reproductive number based on estimated parameters, such that, we conclude the costs of treatments are minimized if more than 50% of individuals are successfully treated.

POWERS, M., and P.D. STRAIGHT. Enhanced Antibiotic Resistance in Mobile Bacteria Population, King

University, Bristol, TN. To survive encounters with competitors, bacteria exhibit behaviors like modifying growth patterns and metabolism. Specifically, *Bacillus subtilis* make dormant spores and build biofilms when exposed to chloramphenicol produced by a competitor, initiating defensive mobility. The mobile population increases expression of a subset of genes that are predicted to convey antibiotic resistance, suggesting the sliding population would have enhanced antibiotic resistance over a non-motile population. *B. subtilis* also induces mobility when exposed to additional ribosome-targeting antibiotics, suggesting genes are correlated to antibiotic resistance. To study this, mutant strains that have deletions in multiple antibiotic resistance genes and tested growth and induced mobility. Differences in sensitivity between antibiotics were analyzed. To explore the possibility that the response in antibiotic resistance genes can function as a sensor to detect the translation stress, fusion of relevant promoter fragments to the luciferase operon were made to use as reporter strains. We found that *PyxjB-lux* demonstrates increase in luciferase signal and translation stress when exposed to chloramphenicol. The luciferase signal can also be used to detect spatial patterns of enhanced expression within the colony. The results helped illustrate how exposure to antibiotics induces motility changes and antibiotic resistance to protect *B. subtilis* against competitors.

RASULI, Z., V. HEARD, and L. QIAN. Using Machine Learning Methods to diagnose Diabetes Mellitus of

Pima Indians, Fisk University, Nashville, TN. Diabetes is a disease in which the body's ability to produce or respond to the hormone insulin is impaired, resulting in abnormal metabolism of carbohydrates and elevated levels of glucose in the blood and urine. In this research, we use Machine Learning methods to diagnose diabetes through Glucose, pregnancy, and BMI and other features. The research data is from Pima Indians. The Pima Indians of Arizona have the highest reported prevalence of diabetes of any population in the world. During the 1853 Gadsden Purchase, the Pima Bajo who were residing in Gila

Valley were forced to colonize and in 1959 a Pima reservation in Arizona was created and the number of people with diabetes among the Pima Indians increased 10-fold. The data set has 768 samples with 8 independent variables and a dependent variable. The 8 independent variables are pregnant, number of times pregnant, glucose, plasma glucose concentration, pressure, diastolic blood pressure, triceps, tri-iceps skin fold thickness, insulin, BMI, diabetes pedigree function and age. The dependent variable is diabetes. Our goals for this research project were to determine the best model to diagnose diabetes through those features, and to determine which factors played the most significant role in diagnosing diabetes. The machine learning models used in this research were Support Vector Machine, Logistic Regression, MLP, Decision tree, Random forest and Ensemble Learning methods. The best accuracy was obtained when using Stacking Ensemble method which achieved a score of 78.1. The PCA analysis confirms that a higher testing score would be hard to attain as the data cannot be split into distinct sections. Glucose, pregnancy, and BMI played the most significant role in diagnosing Diabetes.

RIVENBARK, K., R.F. FRYE, and L.K. VAUGHAN. BPA and BPF Exposure Alters Brood Size and Decreases Food Availability for Wild Type *C. elegans*. King University, Bristol, TN. Bisphenol A (BPA) is used in the synthesis of polycarbonate plastics, which compose consumer-based plastic product. Because of concern for the estrogenic effects, some federal governments have implemented regulations on the use of BPA in consumer products, which have increased the demand for bisphenol analogues, like bisphenol F. Because of structural similarity, BPF is hypothesized to induce reproductive toxicity similarly to BPA. Previous studies of BPA toxicity on model organisms have been conducted in polystyrene petri dishes. While no BPA is reported in these dishes, bisphenols may be leaching into the media; to eliminate this potential confounding factor, we also utilized glass petri dishes in our study. Wild type *Caenorhabditis elegans* were chronically exposed to 250 μ M or 500 μ M BPA or BPF solutions for 2 days. After exposure, individual adult hermaphrodites were isolated allow for the quantification of brood size. After exposure, all treatment groups, including those cultured in plastic dishes, displayed a significant decrease in brood size compared to the glass dish control group, suggesting that BPA and BPF display estrogenic activity and induct sterility. Currently, research suggests that BPF is not a safe alternative to BPA and induces toxic effects in the same magnitude as BPA on *C. elegans*.

SCHECKELHOFF, K.¹, and A. EJAZ². A game-theoretic model of optimal clean equipment usage to prevent hepatitis C among injecting drug users. ¹Department of Mathematics and Statistics, ²Department of Chemistry, UNC Greensboro, Greensboro, NC. Hepatitis C is an infectious liver disease which contributes to an estimated 400,000 deaths each year. The disease is caused by the hepatitis C virus (HCV) and is spread by direct blood contact between infected and susceptible individuals. Despite the magnitude of its impact on human populations, hepatitis C has received relatively little scientific attention. In particular, studies targeting disease eradication in the populations most at risk—injecting drug users—are scarce. Here we construct a game-theoretic model to investigate the potential implications of voluntary participation in clean needle exchange programs on the spread of HCV among injecting drug users. Individual drug users weigh the (perceived) cost of clean equipment usage relative to the (perceived) cost of infection, as well as the strategies adopted by the rest of the population, and look for a selfishly optimal level of protection. We find that the spread of HCV in this population can theoretically be eliminated if individuals use sterile equipment approximately two-thirds of the time. Achieving this level of compliance, however, requires that the real and perceived costs of obtaining sterile equipment be essentially zero.

SCHMIDT, H., T. DUNLEVY, and P. WAGSTAFF. Analyzing the Impact of Weather, Phenotypic Features, and Hybridization to Improve Maize Crop Yield Model Predictions. Department of Mathematics and Statistics and Department of Physics, East Tennessee State University, Johnson City, TN. In the field of

agriculture, farmers are consistently asked to grow more with less: less space, less resources, less emissions. Yield per acre for important crops like maize (field corn) and soybeans have steadily increased for the last 80 years due to the introduction of modern breeding practices as well as fertilizers and pesticides. This steady growth cannot continue without advancing our understanding of genetics and environmental factors on crop yield. By combining techniques from mathematics with big data and the knowledge of the agricultural industry, we may be able to aid in this understanding. Using data from the Genomes to Fields (G2F) initiative together with machine learning and regression models, we aim to determine which factors optimize corn yield. Due to the diversity in crop locations, we first use spatial clustering to group locations based on geographical proximity to one another and hold those location-specific weather conditions constant. This allows us to further isolate and identify which phenotypic and genetic factors significantly impact grain yield without sacrificing the impact that environmental variation has on crop yield. The goal of the project is to identify which factors have the biggest impact on crop yield for maize while also comparing the results using some more advanced machine learning techniques to the commonly used best linear unbiased prediction (BLUP) for yield and genome prediction.

SHAPIRO, J., H. SCHMIDT, G. RAIMONDI, and J. ARCIERO. Predicting Optimal Treatment Strategies for Transplant Patients using Theoretical Modeling. Department of Mathematical Sciences, Indiana University-Purdue University, Indianapolis, IN. Immunosuppression is necessary to prevent transplant rejection, but it also makes patients more susceptible to infection, cancer, or diabetes. The development of a treatment strategy that maintains immune competence while preventing graft rejection is important for improving the quality of life and long-term success rate of transplant patients. The adoptive transfer of regulatory T cells (Tregs) has emerged as an alternative treatment that works to boost the regulatory (inhibitory) factors within the host immune system in order to reduce the immune response and promote graft tolerance. In this study, a previous ODE model of murine heart transplant rejection is adapted to include adoptive transfer as a treatment strategy. The Treg dose magnitude, timing, and frequency are varied to determine optimal treatment strategies given a single dose or multiple doses. The model predicts that delivering daily injections of 10^6 activated Tregs into the graft during the first two weeks following transplantation maximizes graft survival. While Treg delivery alone is not predicted to prevent eventual allograft rejection, it allows the graft to survive almost ten times longer than in the absence of treatment while preserving the functionality of the immune system.

SMITH, B., and L. ONG. Identification of Lampenflora in Bristol Caverns. King University, Bristol, TN. Since the beginning of time, man has been interested in caves and the underground world. As our knowledge in science has grown, cave exploration has allowed a greater understanding of cavern ecology. Different organisms have adapted to underground environments despite the fact that conditions are cool and damp. Although caves are normally devoid of light, the introduction of artificial lighting systems for public or “show” caves has made it possible for photosynthetic organisms to colonize the areas surrounding the lights. The name “lampenflora” has been given to algae, moss, ferns and liverworts that grow around artificial cave lighting. Most existing research on lampenflora has been published in Europe, and very little is known about the ones that are predominant in North America. It is important to understand the growth of these lampenflora as the continued growth of these species can damage the underlying rock structures and make preservation of the geological features difficult. The research in the public Bristol Caverns aims at identifying species of lampenflora; only two species of algae have previously been identified in this cave. Identification of these strains will allow for informed decision-making about how they should best be controlled to allow preservation of cave formations.

SVETLIK, A. C. ROGERS, R.L. FRYE, V.A. FITSANAKSIS, and L.K. VAUGHAN. Investigating the protective effect of nicotine on neurodegeneration in the model organism *C. elegans*. King University, Bristol, TN. Though tobacco addiction has long been linked with the development of cancer, epidemiological studies have also linked tobacco use to delay or prevention of onset of Parkinson's disease (PD), a neurodegenerative disease characterized by the loss of function of dopaminergic (DAergic) neurons. Previous studies by our lab have indicated that chronic exposure to environmental toxicants, particularly the fungicide mancozeb, can lead to degeneration of DAergic neurons in the model organism *Caenorhabditis elegans* (*C. elegans*). We hypothesized that pre-treatment with biologically relevant concentrations of nicotine prior to exposure with mancozeb would lead to neuroprotection in the wild-type N2 strain of *C. elegans*. Mechanosensation assays were used to determine loss of function in treated worms. DAergic neuronal function in worms was assessed with nose touch, general behavioral sensation was assessed with body stroke, and nicotinic acetylcholinergic was assessed via harsh touch. Treatment with mancozeb showed a statistically significant decrease in average nose touch response. Pre-treatment with nicotine and treatment with mancozeb showed no significant difference between control and treatment groups. This supports our hypothesis of nicotine having a protective role in DAergic system after being exposed to the fungicide mancozeb. Future studies will utilize mutant knock out mutants to elucidate mechanisms.

TOLONE, J.¹, and Y. ZHANG². Lock-In Based Technique for High Sensitivity Probe of Dielectric Modulation. ¹Department of Physics, Emory & Henry College, Emory, VA, ²Department of Electrical and Computer Engineering, University of North Carolina, Charlotte, NC. The purpose of this research is to develop a system that can detect weak, modulated signals. When taking measurements that are directly concerned with waves, interference and noise can become problematic. A lock-in amplifier is able to extract accurate information about the signal it is measuring and minimize the noise. By modulating incoming signals with an optical chopper, the lock-in amplifier is able to discriminate between modulated signal and un-modulated noise, and it can selectively amplify only the modulated signal. The development of a data acquisition system that uses a lock-in amplifier, optical chopper, laser/light source, and photo detector interfaced with a computer would improve the efficiency and effectiveness of optical-based measurements. In this research, I attempted to develop a data acquisition system using the format outlined above. At first, the system was synchronized with just the lock-in amplifier, optical chopper and photo detector. After testing and optimizing this system, a computer interface was added to try and provide more control and automation for future experiments. This modulation system will be applied to multiple areas of research and experimentation upon completion.