NIMBioS

National Institute for Mathematical and Biological Synthesis

Twelfth Annual

Undergraduate Research Conference at the Interface of Biology and Mathematics

October 31-November 1, 2020

Held Virtually on NIMBioS Interactive

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 60 oral and poster presentations. A keynote address by Dr. Gerardo Chowell and featured talk by Dr. Olivia Prosper will take place Saturday afternoon, and breakout sessions and a panel discussion on career opportunities will follow. A multi-session Graduate School Fair and other opportunities will be showcased. Poster abstracts start on page 6, oral presentation abstracts start on page 13, and for the Graduate School Fair sessions, a schedule and the names of the graduate programs and their representatives is on page 27.

NSF

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 twelfth 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 please visit www.nimbios.org.

TIME CHANGE INFORMATION

There will be a change from Daylight Savings Time to Standard Time on Sunday, November 1 at 2:00 am. Therefore, please note that **times for events before November 1 are in Eastern Daylight Time (EDT)** and **times for November 1 are in Eastern Standard Time (EST).**

INFORMATION FOR HANGING POSTERS

There will be two poster sessions. The first will be on **Saturday from 6:00 to 7:15 pm (EDT) (posters assigned odd numbers presented)**. The second will be on **Sunday, from 3:00 to 4:15 pm (EST), (posters assigned even numbers presented)**. Each poster will have its own room assigned in the NIMBioS Interactive space for the duration of the Conference. Refer to the poster listing in this booklet to find your assigned number; poster rooms in NIMBioS Interactive will have the number of the respective poster in the room name (i.e., 'Post 31' for poster number 31). You can browse the poster rooms in NIMBioS Interactive, or go to a specific poster by clicking on its hyperlink in this program. Poster abstracts and numbering start on page 6.

INFORMATION FOR ORAL PRESENTERS

Refer to the schedule to find your presentation time and NIMBioS Interactive room number. You will have 15 minutes to speak and a few minutes to answer questions. We will be using Zoom for the oral presentations. To display your slides you will share your screen. Please make sure you can share your presentation in Zoom prior to the meeting.

INFORMATION FOR THE GRADUATE SCHOOL FAIR

There will be three Graduate School Fair sessions; the first on **Thursday, October 29 from 4:00 to 5:00 pm (EDT)**, the second on **Friday, October 30 from 5:00 to 7:00 pm (EDT)**, and the third on **Sunday, November 1 from 1:25 to 2:55 pm (EST)**. Each institution has an assigned room in the NIMBioS Interactive space for the duration of the Conference, but representatives will be present at specific times. A schedule of institutions, representatives and the times each institution are assigned to be in their rooms are on the last page of this program.

SOCIAL MEDIA AT URC 2020

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 2020 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. Gerardo Chowell
Chair, Department of Population Health Sciences
Georgia State University School of Public Health, Atlanta

The Power of Mathematical and Statistical Modeling Tools to Combat the COVID-19 Pandemic

The devastating COVID-19 pandemic represents an unprecedented opportunity to test and apply mathematical and statistical modeling approaches to infer key epidemiological and transmission characteristics of the novel coronavirus as well as evaluate the performance of different theoretical models for forecasting the trajectory of the pandemic at various spatial scales. In this context, I will present results from multiple ongoing collaborations involving interdisciplinary quantitative scientists, doctoral students, and public health officials.

FEATURED SPEAKER

Dr. Olivia Prosper
Department of Mathematics
University of Tennessee, Knoxville

Malaria Dynamics within the Mosquito

The malaria parasite *Plasmodium falciparum* requires a vertebrate host and a female *Anopheles mosquito* to complete a full life cycle, with sexual reproduction occurring in the mosquito. While parasite dynamics within the vertebrate host, such as humans, has been studied using mathematical models, less is understood about dynamics within the mosquito, a critical component of malaria transmission dynamics. This sexual stage of the parasite life cycle allows for the production of genetically novel parasites. In the meantime, a mosquito's biology creates bottlenecks in the infecting parasites' development. We developed a two-stage stochastic model of the generation of parasite diversity within a mosquito and were able to demonstrate the importance of heterogeneity amongst parasite dynamics across a population of mosquitoes on estimates of parasite diversity. A key epidemiological parameter related to the timing of onward transmission from mosquito to vertebrate host is the extrinsic incubation period (EIP). Using simple models of within-mosquito parasite dynamics fitted to empirical data, we investigated factors influencing the EIP.

SCHEDULE

Thursday, October 29

4:00-5:00pm Graduate School Fair, Session I

Friday, October 30

3:30-4:30pm Pre-conference Talk: Volker Grimm. Modeling honeybees under stress with BEEHAVE: Lessons for theory and practice

5:00-7:00pm Graduate School Fair, Session II

Saturday, October 31 (Times Eastern Daylight Time)

11:00-11:10am Room 1: Welcome – Lou Gross, NIMBioS Director

11:15am-12:10pm Room 1: Keynote Lecture – Gerardo Chowell. The Power of Mathematical and Statistical Modeling Tools to Combat the COVID-19 Pandemic

12:25-12:40pm
Room 1: Jacob Summers. Mathematical Modeling of *Mycobacterium tuberculosis* Dynamics in Macaques
Room 2: Emily Petroni and Ethan Ashby. Comparison and Application of Sigmoid Model Fitting Algorithms to Time Course RNA-Sequencing Data in *Escherichia coli*

12:45-1:00pm
Room 1: Vivek Jadhav. Effects of Stochasticity and Variable Speed on the Collective Dynamics of Finite Fish Schools
Room 2: Victoria A. Lucero. Application of Fractals in Branching Patterns in Nature

1:05-1:20pm
Room 1: Doménica Garzón. The Transmission Dynamics of COVID-19 in Close-Contact Facilities
Room 2: Charlotte Beckford, Elliott Smith, and Amy Tian. Where's the Buzz? Dispersal Speed as a Limitation to Climate Migration of Bees

1:25-1:35pm Break

1:40-2:25pm Breakout Sessions (in 5 rooms)
Room 1: Dr. Lou Gross – Ecology
Room 2: Dr. Gerardo Chowell – Public Health
Room 3: Dr. Suzanne Lenhart – Infectious Diseases
Room 4: Dr. Albrecht von Arnim and Dr. Tian Hong – Biomedical
Room 5: Dr. Mona Papeş and Dr. Greg Wiggins – Spatial Ecology

2:35-3:25pm Room 1: Featured Speaker – Olivia Prosper. Malaria Dynamics within the Mosquito

3:35-4:25pm Room 1: Panel Discussion (Moderator: Suzanne Lenhart)
Dr. Gerardo Chowell
Dr. Olivia Prosper
Dr. Albrecht von Arnim

4:35-4:50pm
Room 1: Vivek Sreejithkumar. The Evolution of the Identifiable Analysis of the Novel COVID-19 Virus
Room 2: Nathan Tennies. Where will it Grow? Modeling the Distribution of *Nereocystis* Kelp in the Salish Sea

4:55-5:10pm
Room 1: Shruti Sathish and Yu Zhang. Modeling the Effects of HSV-2 Testing on Transmission Dynamics
Room 2: Aarini Panzade. The Effect of TIMP-1 levels, MMP-1 Levels, and Healing Times on the Wound Surface Area

5:15-5:30pm
Room 1: Diksha Satish. Calculating Individual and Population Parameter Values in the Healing of Chronic Wounds through Mixed-Effects Modeling
Room 2: Lief vanSliedrecht. A Computational Approach to Electrostatic Analysis of ATP-Synthase

5:35-5:50pm
Room 1: Alexander Mercier. Contagion-Preserving Network Sparsifiers: Preserving Average Epidemic Dynamics Utilizing Effective Resistance
Room 2: Grace Casarez. An Adaptive Dynamics Approach to Acquired Phototrophy

6:00-7:15pm Poster Session I
Poster rooms: 1 (Bateman), 3 (Brasic), 5 (Crowe), 7 (Dominic), 9 (Guo), 11 (Hsu), 13 (Kingsley), 15 (McAlister), 17 (Ohajunwa), 19 (Queen), 21 (Watanabe)

Sunday, November 1 (Times in Eastern Standard Time)

11:00-11:15am
Room 1: Laurinne Balstad. Privatization of Goods in Biofilms Allows for Successful Cooperation
Room 2: Eileen Figueroa, Michelle Hewson, and James Garrison. The Role of Intercell Coupling in the Development of Rapid Cardiac Rhythm Disorders in the Heart

11:20-11:35am
Room 1: Katie Coe, Marie Neubrander, David Sokolov, and Julie Zhang. Network-Informed Group Testing for Outbreak Surveillance
Room 2: Quenisha Baldwin. The Local Topological Free Energy of Viral Glycoproteins

11:40-11:55am
Room 1: Sarah Wyse. Modeling the Effect of Stochasticity on a Mathematical Predator-Prey System
Room 2: Aisha Seard and Lorhena Antonio. Spatial Structure and Genetic Change in a Northern Pintail Population

12:00-12:20pm Break

12:25-12:40pm
Room 1: Spencer Catron, Sarah Roth, and Francesca Zumpano. Examining Temperature Dependency in Loggerhead Populations
Room 2: Benjamin Brindle. Mathematical Understanding of Red Blood Cell Dynamics

12:45-1:00pm
Room 1: Joseph Drozek. Using Mathematical Models to Predict the Impact of the Coronavirus in the Chicagoland Area
Room 2: Kyle Hart. Lipid Accumulation and Obesogenic Effects of BPA and BPF on *Caenorhabditis elegans*

1:05-1:20pm
Room 1: Matthew Clark, Chelsea Seggern, and Anna Thomas. Integration of Proprioceptive Feedback for Forward Locomotion in *Caenorhabditis elegans* Network Model
Room 2: Patrick Tran. Computational Models of Protein-Protein Phase-Separation on Curved Surfaces

1:25-2:55pm Graduate School Fair, Session III
Rooms in NIMBioS Interactive

3:00-4:15pm Poster Session II
Poster rooms: 2 (Baxter), 4 (Carpenter), 6 (Ding), 8 (Gross), 10 (Ho), 12 (Huang), 14 (Marzen), 16 (Moskal), 18 (Peyton), 20 (Santos), 22 (Westaway)

4:20-4:35pm
Room 1: Emma Brann. Modeling the COVID-19 Outbreak in South American Countries
Room 2: Ilana Goldin. Optimizing a PBPK Model of PFAS for Best Fit

4:40-4:55pm
Room 1: Alex Svetlik and Alexis McDowell. Investigating the Protective Effect of Nicotine on Neurodegeneration in the Model Organism *C. elegans*.
Room 2: Mason McCrury. Evaluating Proteomic Responses to NEK2 Targeted Treatments in DLBCL Cell Lines

5:00-5:15pm
Room 1: Jake Baldauf. Enhancing COVID-19 Transmission Models with Genomic Data
Room 2: Cody Pham. Climate-Mediated Changes in Interactions among Wood Warbler Species

5:20-5:35pm
Room 1: Tamjeed Azad. Recurrent Neural Networks for Covid-19 Prediction: A Cross-Study with Historical Flu Data and Temperature Data
Room 2: Riley Wadehra. Using Simple Models to Examine Pattern Formation on an Alpine Treeline Ecotone

5:40-5:55pm
Room 1: Leah Rolf. Modeling Resistance Emergence in *Aedes albopictus* on a Heterogeneous Landscape
Room 2: Amanda Tran and Aysha Hoang. Modeling the Rates of Genetic Change in Diploid Populations

6:00-6:15pm
Room 1: Jagger Joyner. Modeling Plant-Pollinator Interactions during an Invasion of a Nonnative Plant Species
Room 2: Lauren Mossman and Mei Knudson. Mathematically Modeling the Impact of Adoptive Transfer in Murine Heart Transplant

POSTER ABSTRACTS

1. **BATEMAN, R., A. BEAMS, AND F. ADLER. Mask or JASC? What are the conditions under which SARS-CoV-2 could become "Just Another Seasonal Coronavirus"? University of Utah, Salt Lake City, UT.** In some respects, SARS-CoV-2 resembles its benign cold-causing relatives. Coronavirus NL63 uses the same ACE2 receptor to enter cells, and circumstantial evidence suggests Coronavirus OC43 may have caused a pandemic in the late 1800's. Both are now "common colds." Could SARS-CoV-2 take the same path? We have written models to address how three factors might push SARS-CoV-2 towards becoming "Just another seasonal coronavirus", or JASC. First, evidence suggests asymptomatic cases tend to shed less virus. If viral dose affects disease severity, and vice versa, virulence will decrease. Second, children are less likely to suffer from severe infections, and thus provide a constant reservoir of mild cases. Third, waning immunity could provide another source of mild infections. Our models show that transition to JASC is possible if viral dose correlates with disease severity, and if immunity is sufficiently strong and long-lasting. Although unlikely to ever become as mild as the four existing seasonal coronaviruses, we establish how SARS-CoV-2 could become less severe even without genetic evolution.

2. **BAXTER, E. Growth volumes: Quantifying bleaching resistance in coral symbiosis. University of California, Santa Barbara, CA.** As ocean climates become more variable, coral reefs are experiencing bleaching events that we need to know more about. A paper published in 2017 by Cunning et al. describes a model of coral symbiosis that relies on a number of host and symbiont parameters. Work is being done with that model to identify tolerant symbionts, of which one trait is resistance to bleaching. This poster presents growth volumes as a quantification of bleaching resistance and as a way to identify trends among tolerant symbionts. A proof for the existence of both weak and strong growth volumes is discussed in detail. The model mentioned above returns a steady state value of symbiont to host biomass ratio that will be approached over time, and an indicator function for healthy steady states determines which points belong in the growth volume. A weak growth volume can be calculated using the indicator function and some calculus. The definition of a strong growth volume improves upon the definition of a weak growth volume by taking into account different initial conditions of the model via an expected steady state. Expected steady states are determined from the values of the initial conditions and their likelihood of occurring naturally. The same process from weak growth volumes is applied, which yields an expected, or strong, growth volume. Considerations for computing growth volumes are also discussed on the poster, along with some examples.

3. **BRASIC, C. Testing the effect of acetaminophen overdose on the liver and the role of biomarkers to predict death or survival. University of Wisconsin, Whitewater, WI.** In the United States, acetaminophen (APAP) overdose is the leading cause of acute liver injury, with a third of cases being unintentional. The current model for assessing liver health, The King's College Criteria (KCC), cannot predict APAP dosage or time of overdose—crucial information for selecting treatment in the case of APAP overdose. The Model for APAP-Induced Liver Damage (MALD), however, uses dynamic system of differential equations to model liver injury. By utilizing the three bio-markers aspartate aminotransferase, alanine aminotransferase, and international normalized ratio, MALD estimates the dose of APAP and the time of overdose in order to assess whether treatment with N-acetylcysteine is sufficient or if survivability is contingent on a liver transplant. These biomarkers are indicative of hepatocyte death but are not specific to APAP. In our work we have modeled a fourth biomarker, APAP-protein adduct—specific to APAP—to the existing model, MALD. We validated our model using 59 cases from the Acute Liver Failure Study Group. We also performed sensitivity analysis of the important parameters associated with the updated model. We found the addition of APAP-protein adducts increases the predictive quality for the model.

4. **CARPENTER, S. L., K. E. SWINDLE-REILLY, AND A.N. FORD VERSYPT. Modeling controlled release drug delivery through core-shell microparticles using finite differences for spatially dependent diffusivity. Department of Chemical Engineering, Oklahoma State University, Stillwater, OK.** In order to reduce the number of injections required when treating eye illnesses and increase the efficiency of the treatment of eye illnesses, it is important to insure the correct drug dosage. Our research involves studying controlled release drug delivery from core-shell microparticles with bi-layered drug releasing materials. We use data from our collaborators who conduct the experiments and have determined the material properties, drug properties and conducted the drug release studies. For predicting drug release from the core-shell microparticles, we consider diffusion through a sphere with variable diffusion coefficients. We use the method of lines where the spatial derivatives in the partial differential equation for drug diffusion from the sphere are approximated with finite difference formulas accounting for variable diffusivity, yielding a spatially discretized systems of ordinary differential equations (ODEs) in time that are solved using MATLAB's built-in ODE solvers. We numerically integrated the solution concentration to predict the cumulative release profiles. We used nonlinear least squares optimization to determine the diffusion coefficients and burst release amount of specific drugs within materials from experimental data of similar studies. We determined the cumulative release of drugs in a predictable and repeatable manner from microparticles with different layers consisting of chitosan and polycaprolactone for BSA and bevacizumab release.

5. **CROWE, V. Modelling the quasi-species effects in the immune response to SARS-CoV-2. Department of Mathematics and Statistics, Concordia University, QC, Canada.** SARS-CoV-2 is a positive-sense RNA virus currently causing a pandemic of respiratory illness. Due to rapid replication and selective pressures genetic variation accumulates rapidly and a uniform viral population is an unrealistic assumption. Studying the subset of mutations that leads to functional variation is done on two scales – in isolation, to understand the mechanism of change, and at a systemic level. We have developed a systemic model of the immune response to SARS-CoV-2 infection to integrate knowledge from isolated variant studies. This model considers many important immune players and has already provided insight into how disease severity correlates to the production of inflammatory macrophages by monocyte differentiation and interferon signaling. I contributed to this effort by developing a submodel describe the viral diversity within a host. This allows for the study of the so-called viral quasi-species - the set of all viral strains whose biological characteristics are defined collectively, as opposed to that of a single isolated strain. Our intra-host quasi-species model facilitates more realistic predictions of the immune response to different viral strains, and importantly of drug or vaccine resistance in the both viral and host population. Therefore, our intra-host quasi-species model has implications for assessing treatment efficacy, both in terms of ensuring robust treatment combinations, as well as helping to optimize the timing of such treatments.

6. **DING, L., L. MASTROMATTEO, AND S. REICHHELD. Practical parameter identifiability for partial differential equation models of PTBP3 fluorescence recovery after photobleaching. Division of Applied Mathematics, Brown University, Providence, RI.** Fluorescence recovery after photobleaching (FRAP) is a technique used to observe the diffusion and binding of molecules in a cell. FRAP data, combined with differential equation modeling, can be used to model active transport, diffusion, and protein binding within the cell. Here, we use FRAP recovery data to study the dynamics of PTBP3, an RNA-binding protein that localizes in the granules of Xenopus oocytes (frog egg cells). We develop a two-state partial differential equation model for estimating the diffusion and binding/unbinding rates of the PTBP3 proteins. We then present and compare two approaches for assessing the practical identifiability of the parameters in our PDE model, given experimental FRAP data. One approach, Bayesian Markov Chain

Monte Carlo or MCMC, is used to generate probability distributions for the parameters; however, this method is computationally expensive. The alternative, profile likelihood, is faster than the MCMC technique but still provides useful insights. This strategy assesses the practical identifiability of the diffusion and binding parameters and can be used to generate least-squares and profile relative likelihood plots. In the future, we aim to use these approaches in assessing parameter identifiability for PTBP3 binding mutants and models encompassing multiple binding states.

7. **DOMINIC, A.J., D. DASGUPTA, B. MAHJOUR, AND H. A. CARLSON. Identification of binding hotspots on Med25. Department of Medicinal Chemistry, College of Pharmacy University of Michigan, Ann Arbor, MI.** Structure-based drug discovery relies on the identification of binding sites on protein surfaces. Mixed-solvent molecular dynamics (MixMD) is a technique used to identify druggable sites via simulation of an unbound protein in a 5% cosolvent and water solution. Water soluble cosolvents are used at low concentrations to allow for competition between cosolvent and water molecules at the surface of the protein. Sites mapped by at least two probes at a high signal-to-noise ratio is defined to be a hotspot or a potential binding site. Previous work has used MixMD to successfully identify competitive and allosteric sites on seven protein systems including: ABL Kinase, Androgen Receptor, CHK1 Kinase, Glucokinase, PDK1 Kinase, FPPS, and PTP1B. In this work, MixMD was used to identify two hotspots on the mediator Med25 activator interaction domain protein, a key component of the RNA polymerase type II complex in gene transcription. Docking experiments are underway to further assess the druggability of these identified sites. The molecular dynamics simulations at the heart of the MixMD method rely on integrating Newton's equations of motion over time. The simulations are executed using the software AMBER18.

8. **GROSS, E., B. PUMA, E. SERACINO, AND J. B. HERRICK. Isolation of *Salmonella enterica Meleagridis* with plasmid addiction system genes from stream sediment in the Shenandoah Valley. Department of Biology, James Madison University, Harrisonburg, VA and Center for Genome & Metagenome Studies, James Madison University.** *Salmonella* is a human pathogen responsible for 1.2 million illnesses in the United States each year. Illnesses from *Salmonella* can include diarrhea, fever and abdominal cramps. In recent years, the emergence of antibiotic resistant *Salmonella* has been a serious concern, and may be attributed to the transfer of resistance gene carrying plasmids. We wanted to examine environmental *Salmonella* and investigate the potential effects on creating an antibiotic resistance gene reservoir in the Shenandoah Valley area. Samples of stream sediment were taken from three streams, pre-enriched with modified buffered peptone water (mBPW) for 24 hours, then added to Tetrathionate and Rappaport-Vassiliadis enrichment broth. After 5 days, enrichments were plated onto CHROMagar Plus and XLT4 for 24 hours. Two Salmonella enterica isolates called PSG01 and PSG02 were purified and confirmed as catalase positive, oxidase negative, KOH positive, gram-negative rods. Enterotubes and real time PCR verified the isolates as *Salmonella enterica*. PSG01 and PSG02 were sent to the Virginia state Dept. of Consolidated Laboratory Services for sequencing. A pipeline on GalaxyTrakr was used to assemble quality genomes from the illumina reads. FastQC was used for sequence quality analysis, then filtered and trimmed using the program Trimmomatic. SPAdes assembled the genomes, quality was assessed using QUAST, and Prokka was used to annotate the genome then visualized using Artemis. Visualization of PSG01 and PSG02 genomes displayed the presence of the MazE and MazF genes associated with plasmid addiction systems. The serotypes for PSG01 and PSG02 were determined to be *Meleagridis* using SeqSero and plasmid IncI-1 was found using the PlasmidFinder function from the Center for Genomic Epidemiology. The presence of *Salmonella* in Shenandoah Valley streams may constitute a health hazard and could be contributing to the persistence of antibiotic resistance in environmental bacteria.

9. **GUO, E.[1] AND F. B. AGUSTO[2]. Baptism of fire: Modeling the effects of prescribed fire on tick-borne disease. [1]Washington University, St. Louis, MO, [2]University of Kansas, Lawrence, KS.** Climate change has expanded the northern borders of tick habitats and increased winter tick activity, increasing the prevalence of tick-borne diseases and thus the importance of finding a practical and cost-efficient way of managing tick populations. Prescribed burns, a common and necessary form of land management in many different environments, are appealing due to their time and cost efficiency along with their ability to be applied across large amounts of land. This study developed a compartmental model for ticks carrying Lyme disease to see how they are affected by the intensity of prescribed burns and the duration between fires. Sensitivity analysis was conducted to determine what parameters had the largest effect on R0. The parameters with the largest influence are the tick death rate, the carrying capacity, the larvae development rate, and the transmission possibilities for both ticks and mice. Intensity appears to have a larger impact on tick population reduction than the frequency of burns. Burning at high intensity is preferable to burning at low intensity whenever possible, although high intensity burns may be unrealistic due to environmental factors. Annual burns resulted in the most significant reduction of infectious nymphs, which are the primary carriers of Lyme disease.

10. **HO, K.D.[1], J. TRAUTMAN[2], N. WRIGHT[1], AND J.D. NAGY[3,4]. Predicting approaching castration resistance in advanced prostate cancer using PSA time series data. [1]School of Life Sciences, Arizona State University, Tempe, AZ, [2]Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ, [3]Department of Life Sciences, Scottsdale Community College, Scottsdale, AZ, [4]School of Mathematical and Statistical Sciences, Arizona State University, Tempe, AZ.** Recurrent prostate epithelial cancers are commonly treated with a total androgen blockade via chemical castration. However, tumors under such treatment invariably become resistant. Various resistance mechanisms are known, the most common of which is up-regulation of the androgen receptor. However, it is unknown whether the resistance mechanism arises from natural selection or phenotypic plasticity. Here we show that natural selection is the cause of castration resistance in prostate cancers treated with androgen ablation. We fit simple mathematical models to prostate specific antigen data from patients undergoing intermittent androgen deprivation therapy. Tumor aggressiveness, measured as growth rate of serum PSA concentration, correlates positively with the number of treatment cycles. Additionally, we found a signal of increasing tumor aggressiveness with cycle in both on and off-treatment phases. This result argues against the plasticity hypothesis and is consistent with evolution by natural selection. If plasticity were the mechanism, tumor aggressiveness would not correlate with cycle. This result can help improve clinical management of advanced prostate cancer. Identification of the mechanism responsible for treatment resistance will yield insight into more efficacious treatment schedules and drug combinations, while maintaining patient quality of life and delaying onset of castration resistance.

11. **HSU, V. Management-oriented profit optimization of biocontrol and pesticide use for agricultural pests. Department of Ecology, Evolution and Marine Biology, University of California, Santa Barbara, CA.** *Drosophila suzukii*, an invasive fruit fly originally from southeast Asia, has become a major pest species in America and Europe. This species is especially problematic for agriculture because it infests crops during the ripening phase, while other Drosophila species only infest rotten fruit. The pupal parasitoid *Trichopria dosophilae* has an extremely high parasitism efficiency, and shows potential as a biocontrol to constrain *D. suzukii* populations in the wild and in the field. Our study generated mathematical models to describe management strategies to eradicate *D. suzukii* pests and optimize profits by altering pesticide use and biocontrol release. We found that in the presence of both pest (*D. suzukii*) and biocontrol (*T. dosophilae*), optimal profits results from releasing either entirely biocontrol or pesticide, rather than a combination of both. This is because the pesticide kills off biocontrol, so it is not cost effective to use both eradication

strategies. This model can be used more generally to describe other pest and biocontrol systems to inform management-oriented profit optimization.

12. **HUANG, G. Using the geometry of parameter space to analyze identifiability in a wound-healing model. Department Of Mathematics, Western Kentucky University, Bowling Green, KY.** The treatment of chronic wounds has long been a challenge to wound care professionals and presents a substantial economic burden to healthcare systems globally. To combat this issue, a mathematical model describing the interactions between matrix metalloproteinases (MMPs), their regulators (TIMPs), fibroblasts, and the extracellular matrix (ECM) was analyzed to find the most influential factors in the healing process of diabetic foot ulcers. Using the differential equation model with de-identified patient data, the three-dimensional geometry of parameter space was visualized for all combinations of the twelve parameters in the model to more precisely see how these parameters affect the biological system. Knowledge of the identifiability of parameters can, in turn, streamline treatment by allowing us to individualize treatment for each patient. This approach plots two parameters against the sum of squared errors to generate a three-dimensional graph. By analyzing the minimum of the graph, we can conclude if a parameter is able to be uniquely determined. The identifiability of a parameter signifies its importance in the healing response. This research shows the regulators of MMPs (TIMPs) are the most influential parameters in a wound-healing model. A local sensitivity analysis was used in conjunction with eigenvalues to confirm results.

13. **KINGSLEY, J.L.[1], AND K.A. REJNIAK[2]. Investigating intratumoral short-time oxygen fluctuations with agent-based model. [1]Department of Mathematics and Statistics, University of South Florida, Tampa, FL, [2]Integrated Mathematical Oncology Department, Moffitt Cancer Center, Tampa, FL.** Metabolites in tumor microenvironment can experience both spatial gradients and temporal fluctuations in oxygenation. Using mathematical modeling, we explored how invasive tumors adjust to these microenvironmental changes. Our model of the tumor tissue involved individual tumor and stromal cells, tumor vasculature, and tumor metabolic landscape. The tumor tissue architecture was based on tissue characteristics acquired from electron paramagnetic resonance (EPR) images. We investigated intratumoral oxygen fluctuations that these EPR images recorded in three minutes intervals. We corroborated the experimental hypothesis that the fast cycling hypoxia is caused by changes in the blood supply to the tissue. However, we showed that in certain cases, a change in cell metabolism is necessary to fit the experimental data. We tested these hypotheses by varying the influx of oxygen from vessels, varying oxygen uptake of tumor and stromal cells, and varying all three parameters in the tumor domain. Our results are important for the design of personalized treatments. Understanding the causes and patterns of changes in intratumoral oxygenation can aid the efforts to better cater treatments for patients in order to reduce therapy resistance.

14. **MARZEN, B. Environmental impacts of the space industry in Earth's atmosphere: An analysis on rocket emissions and ozone. Embry-Riddle Aeronautical University, Daytona Beach, FL.** Ozone has been a research topic for a few decades, specifically its depletion in the stratosphere and its production in the troposphere. The space industry burns multiple types of fuel to project spacecrafts possibly contributing to the ozone concerns in both areas of the atmosphere. Data consisting of Cocoa Beach's daily ozone levels from the Florida Department of Environmental Protection's Office of Air Monitoring were used to discover if ozone levels were significantly higher when rockets were launched from Kennedy Space Center from the years 1994 to 2019. After performing a hypothesis test on the ozone levels for those years, there was no evidence in the results to show that rocket launch days had significantly high ozone levels. Furthermore, it is likely that rocket launches do not affect the overall ozone for a specific day, but that does not show the

industry has no impact. These results further emphasize why there are no regulations on the industry even though there is a profusion of articles stating the industry's negative effect. The effects of the industry are likely long-term effects, but there are other contributors that are make it difficult to identify the impact strictly from the rocket industry.

15. **MCALISTER, J., AND I. HAMILTON. An adaptive dynamic model for the vigilance game among group foragers. Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, OH.** There is a well observed relationship between group size and time spent being vigilant in group foragers and there have been many models presented that capture that reality in different ways. These models, however, often fail to capture the way group size depends on vigilance, and most depend on the idea of behavioral monitoring, which lacks wide support. Here I present a model for the vigilance game using adaptive dynamics which captures the biological reality of this relationship, over long time scales, without the need for behavioral monitoring. By approximating a fitness function for an individual using a particular vigilance strategy in a group of some size, I can show when new strategies of vigilance will invade using pairwise invasion analysis. Using this analysis I construct a dynamical system which describes the change in group size and vigilance as they relate to each other. By spanning the entire parameter space I show that at equilibrium, larger groups have far more limited maximum vigilance. Furthermore, by varying intraspecific competition I show an inverse relationship between group size and vigilance. Thus I provide a mechanism in support of the many eyes hypothesis from an evolutionary game theoretical perspective without depending on behavioral monitoring.

16. **MOSKAL, L.[2, 3], L. SINES[1], AND R. NEILAN[3]. Modeling the effects of fentanyl and Narcan on the opioid epidemic in Allegheny County. [1]Department of Biological Sciences, [2]Department of Chemistry and Biochemistry, [3] Department of Mathematics and Computer Science, Duquesne University, Pittsburgh, PA.** As a result of the increased use of prescription opioid pain relievers across the U.S., the number of overdose fatalities has risen drastically and has fueled the current opioid epidemic. One state that has contributed significantly to the epidemic is Pennsylvania, which ranks first for the greatest number of overdose deaths and third for the highest death rate. In fact, Allegheny County has witnessed an overdose death rate that is three times that of the national rate. In collaboration with the Allegheny County Department of Human Services (DHS), we modified an existing mathematical model to describe the opioid epidemic in our community. The model is a system of differential equations describing how the size of each population class–Susceptible, Prescribed, Addicted, and Recovered–changes over time and includes variables that describe the presence of fentanyl (a synthetic opioid) and the use of Narcan (medication used to block the effects of opioids). Model parameters were estimated to reflect the addiction and overdose rates in our community using data provided by the DHS. Model results highlight the impact of fentanyl and Narcan on the annual overdose death rates and indicate the extent to which an increase in the availability of Narcan in the community will result in a meaningful reduction in overdose deaths.

17. **OHAJUNWA, C., K. KUMAR, AND P. SESHAIYER. Mathematical modeling, analysis, and simulation of the COVID-19 pandemic with explicit and implicit behavioral changes. Department of Mathematical Sciences, George Mason University, Fairfax, VA.** As COVID-19 cases continue to rise globally, many researchers have developed mathematical models to help capture the dynamics of the spread of COVID-19. Specifically, the compartmental SEIR model and its variations have been widely employed. These models differ in the type of compartments included, nature of the transmission rates, seasonality, and several other factors. Yet, while the spread of COVID-19 is largely attributed to a wide range of social behaviors in the population, several of these SEIR models do not account for such behaviors. In this project, we consider novel SEIR-based models that incorporate various behaviors. We created a baseline

model and explored incorporating both explicit and implicit behavioral changes. Furthermore, using the Next Generation Matrix method, we derive a basic reproduction number, which indicates the estimated number of secondary cases by a single infected individual. Numerical simulations for the various models we made were performed and user-friendly graphical user interfaces were created. In the future, we plan to expand our project to account for the use of face masks, age-based behaviors and transmission rates, and mixing patterns.

18. **PEYTON, T., C. CALBAUGH, AND H. QIN. Modeling DNA repair gene hierarchy and state change using deep learning neural networks. University of Tennessee, Chattanooga, TN.** Artificial neural networks (ANNs) process information to form relationships using layers of fully connected nodes. However, these ANNs are not easily interpretable. Conversely, visual neural networks (VNNs) are structured to allow for the modeling of a known system to better understand pathways that lead to an output. Using the extensive knowledge of the yeast cells hierarchy, we hoped to model the gene hierarchy and subsystem state change of DNA repair in yeast cells using a VNN. We also hoped to accurately predict single and double mutants' effect on cellular fitness compared to wildtypes. The model was trained using the GO database with DAmP double mutants as inputs and their respective phenotypic fitness as the single output. The trained model was then tested for accuracy and state change of the subsystem. The model was found to predict subsystem changes with varying accuracies, and overall state changes were found for all double mutants. This deep learning modeling is currently one of the first VNNs capable of predicting yeast phenotypic fitness and state change. We plan to expand our model to include more subsystems connected with DNA repair. If successful, subsystems deletions could be examined for possible enhancements or new pathways based on subsystem state changes.

19. **QUEEN, O., AND V. JODOIN. Agent-based social network models of the prescription opioid epidemic. Department of Mathematics, University of Tennessee, Knoxville, TN.** The opioid epidemic is a public health crisis in the United States, with approximately 70% of all drug overdose deaths attributed to opioids. While ordinary differential equation (ODE) models have been used in the past to study this epidemic, these models ignore the underlying social network structure by utilizing the well-mixing principle. This study investigates agent-based models that break down this assumption, allowing for variation in social network structures. Through the implementation of four different network structures – fully connected, Erdos-Renyi, Barabasi-Albert, and Watts-Strogatz – we examine the effects of varying network parameters on the progression of prescription opioid and heroin addiction in a population. In addition, optimization techniques are used to find the corresponding rates needed for an ODE model which compensates for the presence of community structure.

20. **SANTOS, B. N. AND F. L. P. SANTOS. Mathematical and Computational Modelling of the Dynamics of *H. armigera* with Control. Institute of Biosciences, São Paulo State University, Botucatu, São Paulo, Brazil.** *Helicoverpa armigera* (*H. armigera*) is considered a major agricultural pest in the world. It was identified in Brazil in 2013, causing economic damage of R$ 2 billion on crops. Its larvae have a polyphagous characteristic with a high destruction potential of cotton, corn and soybeans. The control of *H. armigera* larvae is far from the ideal and the knowledge of their dynamics is indispensable to the Integrated Pest Management by farmers. Therefore, we developed a mathematical model to describe its dynamics population. The model is described by a non-linear system of ordinary differential equations and a compartmental model was used to represents the compartments of *H. armigera* life cycle: normal eggs (E1), larvae (L), pupae (P) and adult (A) over time t. The biological control, represented by a compartment of parasitized eggs (E2), and insecticide as a chemical control were applied in the model, in order to reduce the larvae density. The local equilibrium points of the model were obtained, as well the computational

simulations were realized, which evidenced that the use of both controls were effective in reducing *H. armigera* population. Thus, we may recommend this investigation as a useful tool to prevent and control the *H. armigera*.

21. **WATANABE, M., CATLETT, C., D. SHENKER, AND R. WANDER. Data assimilation for parameter estimation of a single-compartment Type 1 diabetes ODE model. Harvey-Mudd College, Claremont, CA.** The onset of Type 1 diabetes, an autoimmune disease characterized by an inability to regulate blood glucose, is believed to be determined by the interactions of immune cells in response to a catalyst during weaning. In vivo, it is difficult to collect immune cell population data, but mathematical modeling, combined with data assimilation, allows us to realistically simulate these cell interactions. We explore various methods of data assimilation to estimate parameters for a single-compartment ODE model of pancreatic immune cell response during Type 1 diabetes onset in mice based on experimental glucose measurements. We evaluate and compare the performance and biological feasibility of Markov Chain Monte Carlo (MCMC) methods, Particle Swarm Optimization (PSO), and Unscented Kalman Filters (UKF). All techniques allowed us to effectively tune parameters previously determined for the model. While MCMC showed a preference towards population-level data sets, and the UKF was better adapted to the noise present within glucose data of a single subject, PSO proved versatile for both types of datasets. Our work also suggests that model composition influences the ideal parameterization strategy based on the scale of the model and number of parameters.

22. **WESTAWAY, S.[1], M. LIN[2], U. JOSHI[3], D. TALMY[4], AND A. HINSON[5]. Phytoplankton host-virus modeling. [1]Department of Mathematics and Computer Science, Samford University, Birmingham, AL, [2]Department of Biophysics, Johns Hopkins University, Baltimore, MD, [3]Department of Biology and Computer Science, Xavier University, Cincinnati, OH, [4]Department of Microbiology, University of Tennessee, Knoxville, TN, [5]Department of Microbiology, Utah State University, Logan, UT.** Phytoplankton provide essential nutrients for marine life, although overproduction can lead to bloom formations, some of which can be detrimental to marine life. The predator-prey interactions between phytoplankton and algal viruses are an integral process in contributing to the carbon cycle. In the present work, we investigate the predator-prey interactions between various phytoplankton communities and lytic viruses. We make use of multiple differential equation models to explore the best fit possible for various data sets provided by previous biological experiments. Furthermore, Monte Carlo Markov Chain (MCMC) statistical methods are implemented to determine the optimal parameters and to help select the best model type to use for each data set. We make use of Python to run numerical simulations and optimizations.

ORAL PRESENTATION ABSTRACTS

AZAD, T.[1], AND H. QIN[2]. Recurrent neural networks for COVID-19 prediction: A cross-study with historical flu data and temperature data. [1]Department of Computer Science, Columbia University, New York, NY, [2]Department of Computer Science and Engineering, University of Tennessee, Chattanooga, TN. The spread of the COVID-19 pandemic has led to a tragic loss in human lives and has upended and changed lifestyles in the US and worldwide in unimaginable ways. There is a serious need for effective, accurate prediction models to influence public health policy decisions. Although many methods already exist, this project aimed to apply deep learning to COVID-19 prediction, specifically using recurrent neural networks and historical data. Three different recurrent neural network models across four US States were trained using seasonal historical flu surveillance and temperature data; these models were tested on states' COVID-19 positive cases' data. In the results, it was determined that historical temperature is not an

effective feature for prediction for our models, suggesting that the impact of social distancing and mask-wearing on the pandemic is more significant than temperature's potential impact. Additionally, the use of seasonal historical flu data for prediction was effective only when states had already exhibited a demonstrated peak in cases and was ineffective when states were still early in the progression of their local pandemic peaks. Future potential directions include the incorporation of social distancing data for training and developing models for other geographic locations.

BALDAUF, J. Enhancing COVID-19 transmission models with genomic data. Brigham Young University, Provo, UT. Covid-19 quickly become a global pandemic in 2020. The disease has infected over 35 million individuals and has resulted in over a million deaths worldwide. Researchers have developed a variety of models to understand SARS-CoV-2 transmission. We created an agent-based model to simulate a pandemic similar to the Covid-19 pandemic. Specifically, this simulation creates a genomic RNA sequence for each newly infected individual and creates a complete transmission tree for all cases. Using Nextstrain, a phylogenetic tree reconstruction software, we can sample cases and use the sequences to assemble phylogenetic trees. Using our simulation and phylogenetic tree, we aim to estimate the true prevalence of a virus using genomic data. Our goal is to apply the parameter estimates acquired from the simulation study to genomic data from Utah to estimate the true prevalence of Covid-19 in the state.

BALDWIN, Q. The local topological free energy of viral glycoproteins. Tuskegee University, Tuskegee, AL. Many viruses infect cells by using a mechanism that involves binding of a viral protein to the host cell. During this process, the three-dimensional conformation of the viral binding protein changes significantly. Disruption of this process could be achieved by targeting key locations in the viral protein that are essential in this rearrangement. In this manuscript we propose to use the local geometry/topology of the crystal structure of the viral protein backbone alone to identify these essential locations. Our results show that the local Writhe, local Average Crossing Number and the local Torsion alone can identify "exotic" residues that may be essential in the viral protein infection mechanism. We apply this method to the SARS-Cov-2 Spike protein to propose target residues for drug discovery.

BALSTAD, L. J.[1], J. FOLMAR[2], A. SALLEE[3], L. SANTANA-SOUZA[4], M. D. SWENSON[5], AND S. EDA[6]. Privatization of goods in biofilms allows for successful cooperation. [1]Department of Mathematics and Biology, St. Olaf College, Northfield, MN, [2]Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, [3]Department of Biochemistry, University of Tennessee, Knoxville, TN, [4]Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN, [5]Department of Mathematics, University of Tennessee Knoxville, TN, [6]Department of Forestry, Wildlife and Fisheries, University of Tennessee, Knoxville, TN. Bacteria are social organisms that interact intimately in biofilms through cooperation and competition. Public goods are produced by "cooperators" and provide a collective benefit to all cells in the biofilm. "Cheaters" benefit from public goods but do not endure the cost of producing them. Thus, cheaters are expected to have greater fitness and reduce biofilm growth. However, biofilms are ubiquitous. One hypothesized explanation for biofilm persistence is the existence of mixed goods. Produced by cooperators, mixed goods are partially private and partially public goods that cannot be fully exploited by cheaters. As a result, cheater growth is policed. Our individual-based model analyzes the effect of mixed goods on Pseudomonas aeruginosa biofilms. This model examines how the frequency of cheaters and cooperators change due to the cost, diffusion, and sharing (privatization) of mixed goods. Outcomes incorporated a broad range of scenarios, including complete cheater dominance, cooperator dominance, and coexistence. We demonstrate that increases to communal good production cost and initial cheater frequency can lead to decreased biofilm mass, suggesting a possible health care treatment for biofilm size. Additionally, findings were able to confirm the hypothesis that increased

privatization decreased cheater frequency, suggesting a potential mechanism by which cooperators can police cheaters.

BECKFORD, C.[1], E. SMITH[2], AND A. TIAN[3]. Where's the buzz? Dispersal speed as a limitation to climate migration of bees. [1]Department of Mathematics, Fordham University, The Bronx, NY, [2]Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, [3]Department of Ecology and Evolution, University of Chicago, Chicago, IL. Declining bee populations have fueled global conservation concerns given their importance to pollinating crops. Recent evidence has pointed to climate change as a significant driver of regional extinctions of bee species due to range shifts. While previous studies have modeled these range shifts over time, it is not well known whether bee species will be able to disperse fast enough to maintain a constant climate. In this study, we model how the limited dispersal abilities of bees will affect future ranges by 2050. Our work builds on previously developed ecological niche models, which model baseline (1960-1990) and future (2050-2060) ranges of 15 North American buzz pollinator bee species under RCP 4.5 and 8.5 greenhouse gas emissions scenarios. We projected the required dispersal speeds of each species by calculating the distance between pixels of matching climates from the baseline to future distribution over time. Species distribution maps were created by identifying the areas where the required dispersal speeds were within a threshold of 5 kilometers per year determined from a literature review. Our findings point to conservation areas of maximal benefit to be in Ohio, Indiana, Illinois, and the Northeastern United States. We found, comparing across species, that the median percentage decrease of currently habitable areas was between 0.59% and 14% when considering a limited dispersal ability. Our results suggest that dispersal ability has important implications for future distributions and that modeling with climatic conditions alone is insufficient to predict realistic climate change outcomes.

BRANN, E. Modeling the COVID-19 outbreak in South American countries. Michigan State University, East Lansing, MI. The emergence of COVID-19 has necessitated the development of models that accurately forecast its spread throughout global populations. The long latent period believed to be associated with COVID-19 makes the SEIR model— an extension of the well-known SIR model that accounts for diseases with an extended latent period— an excellent model to study the disease. Here, we focus on developing SEIR models for South American countries. We consider reported case counts, fatalities, and recoveries in each country, and fit the SEIR model with fixed latent and infectious periods and a time-varying constant contact rate. We use ACAPS data outlining the timeline of implementation of non-pharmaceutical interventions (NPIs) in each country to estimate when the individual contact rate within the model might change. Peru, Paraguay, and Ecuador have particularly low testing rates, resulting in inconsistent data that is difficult to fit. We develop a joint model for these countries due to their economic and geographic similarities. We further investigate how varying the contact rate at different time intervals affects the accuracy of the model. We find that, for the most part, NPIs reduce the contact rate and lessen case counts when compared to the scenario in which no interventions are taken.

BRINDLE, B., AND M. TEBOH-EWUNGKEM. Mathematical understanding of red blood cell dynamics. Department of Mathematics, Lehigh University, Bethlehem, PA. Red blood cell dynamics within a human subject involve several stages of precursor cells before a red blood cell fully matures to an erythrocyte. Stem cells, erythroblasts, and reticulocytes are important stages in erythrocyte maturation. When a subject experiences blood loss, a feedback mechanism contingent on the level of erythrocytes causes the production of more erythroblasts to return the blood dynamics to equilibrium. Mathematically, functions describing this feedback, the stem cell recruitment, and the blood loss can be chosen to examine system dynamics. For certain parameter choices a Hopf bifurcation is observed. Numerical integration and plots were used to display bifurcation diagrams and system dynamics. It can be determined what parameters lead to death of the subject, while others result in stable steady states or limit cycles. Methods of

mathematical analysis such as nondimensionalization and proofs of invariance, positivity, boundedness, and uniqueness for arbitrary functions are given. Numerical results are performed for several specific functions.

CASAREZ, G. An adaptive dynamics approach to acquired phototrophy. Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, CA. Mixotrophic oceanic plankton rely on a combination of heterotrophy and phototrophy to obtain the energy necessary for survival. These species acquire photosynthetic equipment from their prey to perform photosynthesis for a limited period of time. However, the extent to which a mixotroph uses phototrophy varies widely; a species' reliance on acquired phototrophy depends on how long they are able to use photosynthetic equipment for (retention) and whether they can pass this equipment to the next generation (replication). My model utilizes an adaptive dynamics approach to illustrate the evolution of acquired phototrophy. The algorithm begins with a fully heterotrophic species and induces small, random mutations in either retention or replication. Over a short ecological timescale, the species either keeps or discards the mutation depending on the mutant's success. Over a long evolutionary timescale, these mutations contribute to a larger pattern of evolution. Preliminary results of this research reveal that acquired phototrophy evolves in conjunction with other traits and external conditions. In particular, the model emphasizes the effects of trade-offs in heterotrophy that may occur as a species improves at phototrophy. This work may be useful in understanding how the spectrum of mixotrophy may tilt in response to changing ocean conditions.

CATRON, S.[1], S. ROTH[2], AND F. ZUMPANO[3]. Examining temperature dependency in Loggerhead populations. [1]Department of Mathematics, University of Tennessee, Knoxville, TN, [2]Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN, [3]Department of Mathematics and Statistics, The College of New Jersey, Ewing, NJ. Florida produces 85% of the Loggerhead turtles (*Caretta caretta*) in the Atlantic Ocean. Therefore, examining the underlying ecological mechanisms behind nesting beach success informs our understanding of the population dynamics in the North Atlantic Loggerhead population. This study explores the relationship between nest temperature, air temperature, and the emergence success across nesting seasons, using data from Boca Raton beach, collected by the Wyneken group. This relationship informs a population model of loggerhead turtles across all life stages, associated with this beach. Loggerhead nests are thought to thrive in narrow thermal ranges, but the particular processes behind this assumption have not been explored systematically. Using aspects of temperature, we built a statistical model to determine emergence success for this population. The statistical relationship is integrated into a discrete mathematical model that describes the progression during each nesting season for three egg development stage-classes and the hatchling stage-class. This within-nest sub-model is then incorporated to a four-stage population predictive model that has a multi-year time scale, which includes the transition of hatchling turtles into juvenile and adult classes coming from our statistical model, sub-model, and other rates from current literature. This combined model provides a more detailed understanding of the drivers behind differences in yearly emergence success and predicts the long time growth rate in the Southeastern Florida Loggerhead population.

CLARK, M.[1], C. SEGGERN[2], and A. THOMAS[3]. Integration of proprioceptive feedback for forward locomotion in *Caenorhabditis elegans* network model. [1]Department of Computer Science, Fisk University, Nashville, TN, [2]Department of Kinesiology, University of Tennessee, Knoxville, TN, [3]Department of Mathematics, Lehigh University, Bethlehem, PA. Understanding the neural network dynamics of *Caenorhabditis elegans* can be valuable for continued research related to complex nervous systems such as the human brain. We integrate proprioceptive feedback of motor neurons into the neural network dynamics of the *C. elegans* connectome, to show how oscillatory responses in forward locomotion are sustained by proprioception after an external input to the system. We observe that

sinusoidal input simulating stretch-receptive proprioceptive feedback within B-class motor neurons drives a phenomenon similar to touch-receptive posterior lateral microtubule (PLM) cells that drive oscillations. Furthermore, the observed transition from the fixed state to the limit cycle in the associated Hopf bifurcation is modeled by a combination of the external input current to the mechanosensory neuron class PLM and the proprioception. Using a bottom-up approach in formulation of models, we find that a single cell model alone does not undergo the oscillations that the cells experience as a network, but rather are caused by the connections and dynamics within the system. As *C. elegans* does not explicitly have a Central Pattern Generator (CPG), its functionality to produce oscillatory behavior is found to be carried out by proprioception. The simplicity and feasibility of our model allows for abstracted network analysis and assists in developing the more extensive parent project OpenWorm.

COE, K.[1], M. NEUBRANDER[2], D. SOKOLOV[3], AND J. ZHANG[4]. Network-informed group testing for outbreak surveillance. [1]Department of Mathematics, Bryn Mawr College, Bryn Mawr, PA. [2]Department of Mathematics, University of Alabama, Tuscaloosa, AL. [3]Department of Mathematics, West Virginia University, Morgantown, WV. [4]Department of Statistics, Stanford University, Palo Alto, CA. Due to the recent outbreak of SARS-CoV-2, many institutions must take precautions to prevent disease re-emergence by conducting frequent testing. However, this presents considerable difficulties in the face of limited time and testing resources. Two methods to address this challenge are group testing---the practice of grouping multiple patient samples into a single test---and network-informed testing---using population contact networks to identify and prioritize high-risk individuals for testing. We investigate the intersection of these two approaches within the context of a reopening college campus, examining group testing efficiencies and their relation to testing time across different disease parameters. We first construct a contact network of student interactions based on Bryn Mawr student housing data. Using a stochastic framework, we simulate disease spread on this network and employ custom-made algorithms to simulate several group testing schemes and estimate their respective testing times. Our preliminary results highlight the importance of testing time when optimizing group testing for outbreak surveillance. Our results also suggest that different combinations of initial disease prevalence and infectivity resulting in the same total infected percentage of the population may lead to different group testing efficiency landscapes, which warrants further investigation.

DROZEK, J., AND B. STEPHENSON. Using mathematical models to predict the impact of the coronavirus in the Chicagoland Area. Department of Mathematics, Lewis University, Romeoville, IL. The rapid spread of the novel coronavirus SARS-COV-2 (aka COVID-19) has created great socioeconomic distress for individuals across the world. A striking number of cases of the SARS-COV-2 coronavirus in the United States, and more particularly the state of Illinois, has highlighted the need to better understand how to reduce its spread while a vaccine is developed. In our paper, we present a basic compartmental model of COVID-19 transmission using data from the Chicago area. We implement the Ordinary Least Squares Method to help estimate our infection parameters. To further improve our model, we introduce quarantine to determine the impact of proper contact precautions on reducing the spread of the virus. From this, we use a combination of the data available to us and the estimated parameters to predict how well different disease prevention scenarios will lower the transmission of the coronavirus. We will perform a rigorous sensitivity analysis of the various parameters involved within the model to determine which, if any, significantly modify our results.

FIGUEROA, E.[1], J. GARRISON[2], M. HEWSON[3], L. MUNOZ[4], AND N. OTANI[4]. The role of intercell coupling in the development of rapid cardiac rhythm disorders in the heart. [1]Department of Electrical, Computer and Telecommunications Engineering Technology, Rochester Institute of Technology, Rochester, NY, [2]Department of Mathematics and Computer Science, Hampden-Sydney College, Hampden-Sydney, VA,

[3]Department of Mathematics and Computer Science, Western Carolina University, Cullowhee, NC, [4]School of Mathematical Sciences, Rochester Institute of Technology, Rochester, NY. Ventricular fibrillation (VF) is a cardiac rapid rhythm disorder that is a leading cause of death in the United States. Discordant alternans, an out-of-phase spatial pattern of electrical waves within the heart, renders the heart susceptible to VF. Many mathematical models fail to replicate the observed small spatial scale of this pattern. The "ephaptic" model of intercellular coupling, a more advanced version of gap junction coupling, which includes effects from the intercellular space, was used to describe the connectivity between cells. An electrical circuit-based computer simulation, based on the ephaptic model, was used to study discordant alternans spacing. Wave velocities and length scales were also obtained from the model, and simplified circuits were created to study the characteristics of the ephaptic connection. Linear differential equations and Fourier analysis were used to identify characteristic time scales. The velocities obtained were consistent with these time scales, and were comparable to those observed in the heart. The length scales compared favorably to the theory of Echebarria and Karma and with experimental observations. The role of the components of ephaptic coupling are thus understood and can be manipulated to reduce the spatial scale of the discordant alternans pattern.

GARZÓN, D. N., A. MUBAYI, AND A. GOSH. The transmission dynamics of COVID-19 in close-contact facilities. Physics School, Yachay Tech, Urcuquí, Ecuador. Close-contact places such as Nursing Homes, Old-age Homes, Long-term facilities and Vacation Cruises have been found to be high-risk and high-morbidity places in US for the COVID-19 outbreaks. Some of the reasons these places might be high-risk are: vulnerable resident population, limited resources in facilities, close contacts with visitors and workers, contaminated resources, and ill trained workers. In this study, single and multiple such places are modeled in order to evaluate the impact of different transmission pathways of the COVID-19 outbreaks in the presence of various types of interventions. The model captures a coupled dynamics between three subpopulations (staff, the residents and the visitors) and incorporates infection from infectious individuals and through environment. Using parameterization of the models via reported cases surveillance data from such facilities in USA, we identified timely adaptive interventions that are critically effective for vulnerable population. Finally, we study the tradeoff between disease burden and prevention cost using cost effectiveness analysis.

GOLDIN, I., AND J. McFADDEN. Optimization and parameterization of PFAS through PBPK modeling of mice. NCA&T State-Elon Universities Joint REU in Mathematical Biology, Greensboro, NC. Per- and polyfluoroalkyl substances (PFAS) are a group of persistent manufacturing byproducts. Several state environmental agencies have found an abundance of PFAS in water sources, given the chemicals' longevity. PFAS have been shown to cause tumors and reproductive, developmental, and immunological effects in mammals. In this project, a physiologically-based pharmacokinetic (PBPK) model is constructed to represent the flow of PFAS through mice. The PBPK model assigns each organ its own "compartment" and differential equation. When taken as a system, the model describes the concentration of toxicant within each compartment. Published values for physiological parameters for mice are used for the model. This research selects four organs (the liver, lung, brain, and kidney) and six parameters: the partition coefficients of each organ, Pi and resorption constants Tm and Kt. Running an optimization scheme, we find a range of optimal values for these parameters and retroactively create a model of better fit for existing experimental data. We present four distinct initial parameterizations and four models that serve as a first step for a perfect retroactive fit.

HART, K. M., K. RIVENBARK, R. F. FRYE, AND L. K.VAUGHAN. Lipid accumulation and obesogenic effects of BPA and BPF on *Caenorhabditis elegans* (*C. elegans*). Department of Biology, King University, Bristol, TN. Obesity has become one of the health concerns in today's society and there is an ongoing search to

identify causative factors. One such proposed factor, bisphenol A (BPA), is used in consumer-based plastics. Previous studies have shown that BPA exposure leads to an increase in lipid accumulation. This is thought to be due to the structural similarity between BPA and estrogens which alters metabolism and increases lipid accumulation. Due to this and other concerns, BPA use is regulated, which has increased the demand for analogues like bisphenol F (BPF). Multiple studies have shown that lipid accumulation in the nematode *Caenorhabditis elegans* has increased when treated with BPA but little to no work has been done with BPF. *C. elegans* have a high homology with humans and because they are transparent allow for the quantification of lipid deposits using the dye Oil Red O'. Wild type *C. elegans* were chronically exposed to BPF and BPA for two days and lipid deposits were quantified. Initial experiments show a trend toward increased lipid accumulation in BPF treated nematodes, although additional experiments are ongoing. Taken together, these and previous studies show that bisphenol based components in everyday plastics may be a contributor to the current obesity epidemic.

JADHAV, V. Effects of stochasticity and variable speed on the collective dynamics of finite fish schools. Indian Institute of Science, Bengaluru, India. Various mathematical models have been developed to understand schooling in fish. Most of these models are built on three main behavioral rules - alignment, attraction, and repulsion. They differ in terms of defining social interactions and individual properties. In most of these models, individuals move at a constant speed, or their speed is independent of neighbors. Also, in most models, the position and orientation of all individuals are updated synchronously. Therefore, neglecting the inherent stochasticity that results in an asynchronous change in the direction of movement and neighborhood-dependent dynamic variation in the speed as observed in fish schools. We develop a two-dimensional model that incorporates both stochasticity and individuals' ability to adjust their speed as a response to neighbors' behavior. We consider school size ranging from 5 to 60. Motivated by empirical evidence, we study if pairwise interactions can alone result in cohesive groups. We find that cohesive groups and high polarization are achieved only through pairwise alignment and attraction. This is in contrast to direction averaging in Vicsek-like models. We also show that schools of all sizes are oblong, and the density is equally distributed about the center of the group.

JOYNER, J. Modeling plant-pollinator interactions during an invasion of a nonnative plant species. Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, CA. Invasive species are organisms present in an environment they are not native to that cause economic or ecological harm, and they are a large threat to the biodiversity and overall functioning of ecosystems around the world. Invasive plants are especially problematic as they can have far reaching ecological effects by altering the food and habitat resources available for other organisms, in addition to competing directly with native plants. *Carpobrotus edulis* (Ice Plant) is a plant species from South Africa that has been able to invade many coastal ecosystems around the world due to its intense vegetative and clonal growth patterns that allow it to spread quickly and without the help of pollinating species. I used a system of ODEs to explore the dynamics between *C. edulis*, native plants, and pollinator communities and test methods of restoration in invaded areas, modeled after a site currently being restored on the UC Santa Barbara campus. My theoretical model found that pollinators can intensify competition between natives and invasives, removing the possibility of coexistence, but that active bioremediation efforts (i.e. native replanting and ice plant solarization) are effective at returning a system to a more natural state.

LUCERO, V. Application of fractals in branching patterns in nature. Department of Mathematical, Physical, and Engineering Sciences, Texas A&M, San Antonio, TX. Spatial patterns, such as organic branching structures, exist widely in nature and their biological properties reveal questions potentially encompassing fractal theory. Fractal theory may be a foundation for the explanation of these biological patterns in nature. The objective of this independent study is to review current trends of research into

fractal theory and its relation to organic branching systems in nature, specifically related to applications in mathematical biology. This review focuses on the introduction and definitions of fractals and relative concepts needed to assist the biology community and to set parameters for determining the system as a fractal in nature, or only similar in structure, but not kind. Secondarily, concepts regarding the formation of these systems through fractal generation will be discussed as well as a review of the concepts and methods for calculation in practical application. With the mechanics described and the potential of fractals, the specific biological process of branching systems will be examined for their fractal properties. This review and study would be novel in its effort to determine if the optimization of coverage by an organism is done so by fractal properties in mathematical biology.

MCCRURY, M., AND S. KENDRICK. Evaluating proteomic responses to NEK2 targeted treatments in DLBCL cell lines. Department of Biochemistry and Molecular Biology, University of Arkansas for Medical Sciences, Little Rock, AR. One-third of patients under 18 years old experience severe acute adverse events in response to the standard Diffuse Large B-Cell Lymphoma chemotherapy cocktail. This suggests that targeted therapies could mitigate toxicity associated with non-specific care. Analysis of patient-derived samples suggests young patients have increased transcription of the NEK2 gene compared to adults, which was correlated to lethal disease progression. NEK2 is a kinase involved in cell cycle progression and regulation. This study utilizes phosphoproteomics to generate molecular profiles in cell lines treated with NEK2-targeting molecules. Four DLBCL lines were treated with a NEK2 kinase inhibitor, a proteolysis targeting chimera, or DMSO as a control. Mass spectrometry then quantified protein presence and phosphorylation. MS outputs were analyzed using Ingenuity Pathway Analysis to obtain a gene expression profile. ProteoViz dashboards were generated for the visualization of protein levels, phosphorylation, and gene set enrichment. Analysis of over 3700 differentially expressed proteins and 3330 differentially phosphorylated sites suggests that both molecules have a significant effect on proteins involved in cell cycle progression, cell proliferation, and apoptosis. Because it is difficult to discern what the data signify in terms of disease progression, future studies include performing cell viability and apoptosis assays on treated cell lines.

MERCIER, A. Contagion-preserving network sparsifiers: Preserving average epidemic dynamics utilizing effective resistance. Integrative Biology Department, University of South Florida, FL. Large, complex networks have become increasingly utilized in a variety of fields, including computer science, biological sciences, sociology, and epidemiology. Infectious disease epidemics are a class of dynamics that have become of particular interest on networks where network topology can influence the spread of a contagion. However, the increased size and complexity of networks has incurred a computational cost for performing dynamics on such networks and a decreased intuitive understanding of the underlying network backbone. We explore contagion-preserving sparsifiers which seek to reduce the number of edges in a network while simultaneously approximating average epidemic dynamics. Focusing on SI and SIR contagion models, we draw parallels between the linear flow conceptualization of a network and contagion processes and utilize an effective resistance spectral sparsification algorithm running in $O(n \log^c n)$ time. In order to test contagion-preserving sparsification, we conduct a range of experiments on a variety of real-world networks. We find that the sparsifier can be used to remove up to 50% of the edges while approximately preserving the same average SI dynamics through time.

MOSSMAN, L., AND M. KNUDSON. Mathematically modeling the impact of adoptive transfer in murine heart transplant rejection. St. Olaf College, Northfield, MN. Due to the body's innate immune response, organ transplant patients must receive lifelong immunosuppression treatment to prevent graft rejection. However, immunosuppression compromises the quality of life of patients by putting them at risk for life threatening conditions such as opportunistic infections, heart disease, and cancer. This study examines the

effect of a promising treatment alternative known as adoptive transfer (AT). The adoptive transfer of regulatory T cells (Tregs) delivers activated Tregs to the organ recipient, thereby reducing the destructive immune response and promoting graft survival. A system of ordinary differential equations was used to analyze the impact of dosing magnitude, frequency, and timing of adaptive transfer treatment on immune cell populations and graft survival. The model suggests that administering 13 evenly-spaced doses of Tregs (starting on the day of transplantation) delays rejection more effectively than administering a single large dose on the day of transplantation. Furthermore, the model predicts that it is more advantageous to administer a smaller dose of Tregs two days after transplantation than to administer a larger dose of Tregs on the day of transplantation. However, the model results show that treatment with AT alone is not sufficient to prevent transplant rejection. Therefore, the model is adapted to investigate combined AT and immunosuppression therapy strategies that aim to minimize the amount of immunosuppression delivered to the patient.

PANZADE, A. The effect of TIMP-1 levels, MMP-1 levels and healing times on the wound surface area. Western Kentucky University, Bowling Green, KY. Matrix metalloproteinases (MMPs) are enzymes that degrade all kinds of extracellular matrix proteins during the wound-healing process. TIMP-1 is a tissue inhibitor of metalloproteinases (MMPs). In this work, we are investigating how MMPs and TIMPs, and the ratio of MMPs to TIMPs affect the wound surface area and the healing time. The data that was used for this work was of sixteen patients with diabetic foot ulcers in which measurements were taken of MMPs and TIMPs during a 12-week period. A multilinear regression analysis was performed on the interaction terms of different variables and compared to the wound surface area and compared to the regression analysis done in the spring semester on just the individual variables. It was concluded that the linear regression analysis done by the interaction terms was more beneficial to the wound surface area than the one done on individual variables.

PETRONI, E.[1], E. ASHBY[2], D. M. STOEBEL[1], AND J. HARDIN[2]. Comparison and application of Sigmoid model fitting algorithms to time course RNA-Sequencing data in *Escherichia coli*. [1]Department of Biology, Harvey Mudd College, Claremont, CA, [2]Department of Mathematics, Pomona College, Claremont, CA. RpoS is a sigma factor that coordinates the stress response of *Escherichia coli* bacteria. Genes in the RpoS regulon display three responses to varying levels of RpoS: expression levels can increase linearly with increasing levels of RpoS (linear), dramatically in response to a little RpoS (sensitive) or very little in response to a similarly small amount of RpoS (insensitive). To identify a possible difference in transcriptional timing between sensitive and insensitive genes, we analyzed the onset time parameters of sigmoid models fit to time course (TC) RNA-Seq data for *E. coli* exposed to three RpoS-inducing stressors. ImpulseDE2 is a differential expression method that fits sigmoid models to time course (TC) RNA-Seq data by maximizing the negative binomial likelihood. However, the temporal sparseness of TC RNA-Seq data and ImpulseDE2's naive parameter initializations often generate models that are incongruent with visual inspection of expression trajectories. We revised ImpulseDE2 to include random parameter initializations, consequently improving the fits of these models. Sicegar is another method designed for high-throughput fitting of sigmoid models to biological intensity data by minimizing the sum of squared residuals. Sicegar employs random parameter initializations to guarantee robust fitting. We apply Sicegar to TC RNA-Seq data normalized to a [0,1] scale. It was found that, upon entrance into stationary phase, sensitive genes were induced significantly earlier than insensitive genes.

PHAM, C. H.[1], D. N. KAROWE[2], J. P. PRICE[3], AND J. M. TALLANT[4]. Climate-mediated changes in interactions among Wood Warbler species. [1]Pomona College, Claremont, CA, [2]Western Michigan University, Kalamazoo, MI, [3]St. Mary's College of Maryland, St. Mary's City, MD, [4]University of Michigan, Ann Arbor, MI. Anthropogenically-induced climate change will dramatically alter species distributions. The

magnitude of change, however, will be differential between species, resulting in altered patterns of species co-occurrence. These changes can alter competition, mutualism, and hybridization between species, and determining which species are must vulnerable to these impacts is critical. We examined the potential for climate-mediated changes in interactions among species in the Wood Warbler (Parulidae) family, as these changes may be especially detrimental for these birds. To do this, we used species distribution models to compare range overlap between pairs of warbler species in the present to range overlap under 1.5 °C, 2.0 °C, and 3.0 °C of average global warming. For all warblers, range area, number of overlapping species, and proportion of range overlap decreased significantly in at least one warming scenario. Warbler communities also changed, with all warblers gaining up to an average of one novel interaction and losing up to two interactions between the three warming scenarios. These changes in range overlap and community composition were differential among groups of warblers associating with different habitat types. These results suggest that climate change is likely to alter species interactions, and conservation efforts within different ecosystems must consider the consequences of differentially changing interactions.

ROLF, L. Modeling resistance emergence in *Aedes albopictus* on a heterogeneous landscape. North Carolina State University, Raleigh, NC. In the United States, *Aedes albopictus* is considered a nuisance mosquito due to its peridomestic habitat and propensity to feed on humans. However, in much of the world, they are known to be vectors of diseases such as dengue, Zika, and chikungunya. There are two major methods to eliminate *Ae. albopictus*: adulticides and larval habitat reduction. However, it is feared that resistance to treatment will emerge in *Ae. albopictus* mosquitoes in the US. Resistance emergence occurs rapidly and needs to be explored further within *Ae. albopictus*. We use a population genetics model with multiple patches to model a metapopulation of mosquitoes as they move within a landscape of treatments of different strengths and placement. Using this framework, we look at how treatments affect resistance of the mosquitoes. We also examine the effects of fitness cost on our metapopulations of the model is to help determine effective control strategies that reduce populations without giving rise to resistance.

SATHISH, S., Y. ZHANG, S. KREHBIEL, AND J. WARES. Modeling the effects of HSV-2 testing on transmission dynamics. Division of Mathematics, University of Richmond, Richmond, VA. In the United States, herpes simplex virus (HSV)-2 infections are commonplace and the most likely cause of genital ulcers. Even so, there is also a large degree of unrecognized infection. Although HSV-2 often goes unrecognized, the Center for Disease Control and Prevention (CDC) recommends testing only for individuals who display symptoms, citing in part the lack of evidence that a positive diagnosis changes the sexual behavior of asymptomatic individuals. This has motivated the use of mathematical models to understand the effects of testing on transmission dynamics. In this study, we developed HSV-2 transmission models using differential equations and assessed the impact of testing, diagnosis, and symptomaticity on the behavior of population groups separated by their belief about whether they were infected and their true infection status. We start with a basic SI model, which depicts how susceptible members of the population become infected at a transmission rate beta. This model is expanded upon throughout the study, with additional parameters, and subdivided according to symptomaticity and testing. Ultimately, this study proved to reject the CDC's unrejected null hypothesis that testing does not influence the behavior of asymptomatic individuals by indicating that an increased testing rate generally reduces the equilibrium infection.

SATISH, D. Calculating individual and population parameter values in the healing of chronic wounds through mixed-effects modeling. Western Kentucky University, Bowling Green, KY. In previous work, four differential equations were used to model the relationships between matrix metalloproteinases (MMP-1),

their inhibitors (TIMP-1), and the extracellular matrix (ECM) using averaged patient data during the diabetic foot ulcer healing process. The patient data was acquired from a study that collected data on the concentration of these three factors from sixteen patients over the course of twelve weeks. The aim of this study is to curve-fit individual patient data using mixed-modeling effects. Mixed-effects modeling splits each parameter into two parameters. The population parameter is the same for each patient representing an average response for all patients, while an individual parameter represents the individual patient response and varies across patients. Mixed-effects modeling is implemented in MONOLIX, where its Stochastic Approximation Expectation-Maximization Algorithm is used to calculate population parameters from the patient data. The generated population parameter values were then used as a starting point to calculate individual parameters specific to each patient's data. Through MONOLIX, all sixteen patients were successfully curve fit using this approach generating both population and individual parameter values. Future work will include applying the generated parameter values in a sensitivity analysis to identify the parameters that most affect an individual patient's healing response.

SEARD, A., AND L. ANTONIO. Spatial structure and genetic change in a Northern Pintail population. Emmanuel College, Boston, MA. Previous research has shown that the spatial structure of haploid, asexually reproducing, populations can change the rate of neutral evolution. In our work, we investigate whether the spatial structure and mating patterns of diploid, sexually reproducing, populations can affect the rate at which neutral mutations accrue in the population. We apply our model to *Anas acuta* (northern pintail), a migratory species that has three core breeding and two wintering areas in northern America. To model the spatially structured pintail population, we use a graph where each node is an individual, and edges represent mating and replacement. We derive mating and replacement probabilities from data in the literature, and then calculate the overall fixation probability of a neutral mutation from a set of general equations. We found that the ratio of the fixation probability for the pintail population to that of a well-mixed population is 0.9529; close to 1. Thus, the spatial structure of the pintails marginally slows the rate of neutral evolution. Our model is general and can be applied to other diploid, sexually reproducing, populations.

SREEJITHKUMAR, V., AND N. TUNCER. The evolution of the identifiable analysis of the novel COVID-19 virus. Florida Atlantic University, Boca Raton, FL. The objective is to establish the epidemiologically important parameters for the COVID-19 virus as the virus spread throughout the Floridian population in 2020. For this project, data is obtained weekly from the Florida Department of Health, which reports the numbers of daily COVID-19 cases and disease-induced casualties in Florida. Then, two mathematical models that consist of a system of ordinary differential equations were used to simulate the spread of the coronavirus, and MATLAB computer software was used to fit the models to the data. One mathematical model is a standard SEIR (susceptible-exposed-infected-recovered) epidemiological model, while the second model is a modified SEIR model to represent social distancing in the population. The parameter values that provided the best fit between the epidemiological model and the data were recorded as results, and then the identifiability of the mathematical model was investigated using Monte Carlo simulations. By introducing error into the data and observing how the parameter estimations react to the introduced error, the identifiability of the epidemiological model and the reliability of the parameter estimations can be measured. By using two epidemiological models in this project, the effectiveness of social distancing in preventing incidences and saving lives from disease can be determined.

SUMMERS, J. Mathematical modeling of *Mycobacterium tuberculosis* dynamics in macaques. University of Tennessee, Knoxville, TN. *Mycobacterium tuberculosis* (Mtb) is the causative agent of tuberculosis (TB), infecting a large proportion (~30%) of the world's population. Only a small proportion of infected individuals develop clinical disease, and factors determining why some individuals remain asymptomatic

and some become sick remain unknown. Unfortunately, understanding disease progression in humans remains challenging because most people do not know they are infected. Instead, several different animal species such as mice and monkeys can be infected with Mtb, thus, providing potential explanations for progression of humans to TB. Several recent studies provided interesting insights into early Mtb dynamics in monkeys. In particular, it was found that infection of monkeys with a set of individually barcoded Mtb strains resulted in most local foci of infection (called granulomas) to contain a single barcode. This suggested that individual granulomas were started by a single bacterium. We used stochastic mathematical models to understand whether this observation is also consistent with the hypothesis that multiple strains cause granuloma formation but most die during early dynamics. Our model included the simplest possible way to describe early stochastic dynamics (linear birth-death model); interestingly, we could not find one set of model parameters that allowed us to accurately describe both mean number of bacteria per granuloma and distribution of founder strains in different granulomas. This suggests early Mtb dynamics in monkeys are unlikely to be described by a simple birth-death model, and other biological aspects must be included in the model, in particular, impact of the immune response on rates of Mtb replication and death.

SVETLIK, A.S.[1], R. L. FRYE[1], A. MCDOWELL[1], E. DEROUIS[1], M. MCCURRY[1], C. ROGERS[1], V. A. FITSANAKSIS[2,3], L. K. VAUGHAN[1]. Investigating the protective effect of nicotine on neurodegeneration in the model organism *C. elegans*. [1]Department of Biology, King University, Bristol, TN. [2]Pharmaceutical Sciences, Northeast Ohio Medical University, Rootstown, OH, [3]Robson Forensic, Charleston, SC. Epidemiologic studies have linked nicotine to the reduction of neurogenerative diseases characterized by functional loss of dopaminergic (DAergic) neurons responsible for neural addiction, reward, and satisfaction pathways. Normally acetylcholine binds to DAergic neurons; however, nicotine has higher binding affinity to acetylcholine receptors (nAChRs) resulting in an activation of the DAergic system. Previous studies in our lab established that exposure to environmental toxicants, particularly the fungicide mancozeb, result in degeneration of DAergic neurons in the model organism *Caenorhabditis elegans*. We hypothesized that pre-treatment with biologically relevant concentrations of nicotine prior to exposure with mancozeb would lead to neuroprotection of *C. elegans*. We pretreated wild-type *C. elegans* (Bristol N2) with nicotine and followed by mancozeb to observe the potential neuroprotective effect of nicotine via mechanosenation assays. Touch-insensitive NY7 nematodes were used as a negative control. RB918 nematodes, a transgenic knock-out of the acetylcholine receptor acr-16, were treated and assayed to assess if neuroprotection was reduced with decreased acetylcholine binding. Finally, BZ555 nematodes with green fluorescent protein tagged DAeric neurons were used to directly observe neuronal morphology and health following treatment. Our results suggest a trend toward neuroprotection from nicotine pretreatment, suggesting a potential therapeutic role for nicotine in neurodegenerative disorders.

TENNIES, N. Where will it grow? Modeling the distribution of *Nereocystis* kelp in the Salish Sea. University of Wisconsin, Milwaukee, WI. The bull kelp, *Nereocystis luetkeana*, is a foundational species for aquatic ecosystems in the Salish Sea on the border of Washington and British Columbia. Its ecological importance, population contractions, and the present environmental pressure in these bodies of water require an increased research effort on bull kelp dynamics in the Salish Sea. We're approaching this issue by developing a species distribution model (SDM) to predict, in a spatially explicit way, the probability of *N. luetkeana* occurrence across the Salish Sea. SDM models are built from presence and absence species occurrence data (the response variable) and its association with a set of spatially explicit environmental data (the predictor variables). Environmental data were obtained from the Aqua-MODIS NASA satellite, the Bio-ORACLE global marine dataset, and local digital elevation models. Model development started summer 2019 and will be finished fall 2020. The main technique we're using is generalized linear modeling,

a form of multiple regression analysis better suited for presence-absence responses. Our top four predictors of presence are depth, photosynthetically active radiation, maximum spring sea surface temperature, and maximum primary productivity. An SDM model will be valuable to guide current restoration efforts by helping allocate resources more effectively to populations with long-term promise.

TRAN, A., AND A. HOANG. Modeling the rates of genetic change in diploid populations. Emmanuel College, Boston, MA. The population structure of a species, including spatial structure and mating patterns, can affect rates of neutral genetic change. In this work, we investigated whether the rate of genetic substitution in a sexually reproducing diploid population can be greater than or less than the mutation rate of an individual. We analyzed the effect of population structure on the rates of neutral genetic change in a sexually reproducing diploid population using two models: a bipartite model and a reproductive skew model. A general system of equations was derived to analyze fixation probabilities and applied to both models. In the bipartite model, two sexes randomly mate to produce an offspring, and each male (or female) has an equally likely chance to randomly mate with a female (or male). We found a wide variety of cases where the rate of neutral genetic change was either accelerated or slowed down, and the rate of change was maximized at a factor of 2. The reproductive skew model is an extension of the bipartite model where one subgroup of males (or females) has more favorable reproductive opportunities than another subgroup of males (or females). The results of this model show that the rate of neutral genetic change can be accelerated by any factor.

TRAN, P.[1], and P. ATZBERGER[2]. Computational models of protein-protein phase-separation on curved surfaces. [1]Physics, College of Creative Studies, University of California, Santa Barbara, CA, [2]Department of Mathematics, University of California, Santa Barbara, CA. Biological liquid-liquid phase-separation plays an important role in the formation of cellular microstructures and protein organization. For example, experiments have shown that proteins (SynGAP and PSD-95) exhibit liquid-liquid phase transitions in neuronal structures and may influence the formation of postsynaptic densities (PSD). We develop theoretical descriptions and practical numerical methods for investigating phase separation at the particle and continuum levels on curved surfaces. We develop a Markov-Chain model of drift-diffusion processes for modeling protein dynamics and coupling to phase field models (such as Ginzburg-Landau fields) to account for phase transitions within cellular membranes. We perform studies of the roles of geometry in protein phase separation toward better understanding protein kinetics within neuronal dendritic spines.

VANSLIEDRECHT, L. A computational approach to electrostatic analysis of ATP-synthase. University of North Carolina, Asheville, NC. Adenosine triphosphate (ATP) is often referred to as the energy currency exchanged by all forms of life. Its maker, ATP synthase, has proven difficult to fully understand. The enzyme complex we are examining consists of two rotarymotors: F_o, the ion pump, and F_1, the assembler. To better understand the electrostatic interactions within the F_o motor, we have utilized computational software that solves the Poisson-Boltzmann equation. In an attempt to understand the driving mechanism of the system, experiments have been done both in a wet lab setting as well as in a computational simulation environment. Amino acid residues have been selected, mutated, and analyzed for a particular set of parameters giving us a unique look into the complex. In this talk, we will present visualizations of the electrostatic potential and a method to quantify, comparing these results for various mutations. Improved understanding of this motor could give valuable insight into the world of nano-mechanics and potentially allow us to repurpose the long tested engine of life.

WADEHRA, R. Using simple models to examine pattern formation on an Alpine treeline ecotone. Colorado College, Colorado Springs, CO. Gradients force environmental changes, altering species composition and distribution. Both regular and irregular patterns may emerge on ecotones through local

interactions, however, exactly how these patterns are formed on an external gradient is not fully understood. Because changes in ecosystem boundaries may act as a warning for large scale climate change, it is useful to understand the mechanisms driving the structure of a boundary. I developed three cellular automata models that use different types of local interactions (1. Linear facilitation and competition, 2. Nonlinear density dependence, 3. Nonlinear stress gradient hypothesis) on an external gradient to analyze these dynamics in an alpine treeline environment. I identified three main structure types: abrupt, diffuse and island treelines. I found that different types of neighbor effects determine what type of irregular pattern emerges. Diffuse treelines are found at low levels of interaction, while facilitation by neighboring trees often produces alternating island and abrupt structures over time. Different structures can emerge without environmental forcing, implying that pattern types may not be static in one location. These models lack long-distance inhibition therefore no regular pattern formation is found, and other environmental factors not included in this model may produce different structures.

WYSE, S. Modeling the effect of stochasticity on a mathematical predator-prey system. Department of Computer Science, Mathematics, Physics and Statistics, University of British Columbia-Okanagan, Kelowna, BC, Canada. In mathematical modeling there rarely exists a single best-fit curve to describe a data set, and similar curves are typically considered interchangeable. Recent work, however, shows that similar predation curves may nonetheless result in different tipping points for the Rosenzweig-MacArthur predator-prey system. These tipping point behaviours include destabilising oscillations and extinction; predicting the occurrence of such behaviours is clearly important. I have extended this existing work by finding that the difference in tipping points also occurs in the Leslie-Gower-May predator-prey system. Additionally, I added stochasticity to both models to determine whether the convergence of tipping points can be achieved.

GRADUATE SCHOOL FAIR SCHEDULE

Lastname	Firstname	Institution	Room Name	Day	Time
Strychalski	Wanda	Case Western Reserve Univ	CWRU	Oct. 29	4:00-5:00pm EDT
Leiderman	Karin	Colorado School of Mines	CSM	Oct. 29	4:00-5:00pm EDT
Samuels-Crow	Kimberly	Northern Arizona Univ	NAU	Oct. 29	4:00-5:00pm EDT
Otani	Niels	Rochester Institute of Technology	RIT	Oct. 29	4:00-5:00pm EDT
Barreiro	Andrea	Southern Methodist Univ	SMU	Oct. 29	4:00-5:00pm EDT
Zhang	Haimeng	Univ of North Carolina Greensboro	UNCG	Oct. 29	4:00-5:00pm EDT
Armbruster	Dieter	Arizona State Univ	ASU	Oct. 30	5:00-7:00pm EDT
Fricks	John	Arizona State Univ	ASU	Oct. 30	5:00-7:00pm EDT
Bewick	Sharon	Clemson Univ	Clemson	Oct. 30	5:00-7:00pm EDT
Pimsler	Meaghan	Department of Justice	DOJ	Oct. 30	5:00-7:00pm EDT
Arciero	Julia	Indiana Univ/Purdue Univ at Indianapolis	IUPUI	Oct. 30	5:00-7:00pm EDT
Davis	Lisa	Montana State Univ Bozeman	MSU	Oct. 30	5:00-7:00pm EDT
Sutich	Katie	Montana State Univ Bozeman	MSU	Oct. 30	5:00-7:00pm EDT
Foxall	Eric	Univ of British Columbia-Okanagan	UBC-OK	Oct. 30	5:00-7:00pm EDT
Tyson	Rebecca	Univ of British Columbia-Okanagan	UBC-OK	Oct. 30	5:00-7:00pm EDT
Kilpatrick	Zachary	Univ of Colorado Boulder	UC-Bould	Oct. 30	5:00-7:00pm EDT
Blinov	Michael	Univ of Connecticut-School of Medicine	UConn	Oct. 30	5:00-7:00pm EDT
Rubin	Jonathan	Univ of Pittsburgh-Math	Pitt-Math	Oct. 30	5:00-7:00pm EDT
Gross	Lou	Univ of Tennessee Knoxville-EEB	UTK-EEB	Oct. 30	5:00-7:00pm EDT
Lenhart	Suzanne	Univ of Tennessee Knoxville-Math	UTK-Math	Oct. 30	5:00-7:00pm EDT
Adler	Fred	Univ of Utah	UUtah	Oct. 30	5:00-7:00pm EDT
Reynolds	Angela	Virginia Commonwealth Univ	VCU	Oct. 30	5:00-7:00pm EDT
Long	Hongwei	Florida Atlantic Univ	FAU	Nov. 1	1:25-2:55pmEST
Gumbart	JC	Georgia Institute of Technology	GIT-Qbio	Nov. 1	1:25-2:55pmEST
William	Ratcliff	Georgia Institute of Technology	GIT-Qbio	Nov. 1	1:25-2:55pmEST
Porter	Kristi	National Institutes of Health (NIH)	NIH	Nov. 1	1:25-2:55pmEST
Matveev	Victor	New Jersey Institute of Technology	NJIT	Nov. 1	1:25-2:55pmEST
Melara	Luis	Shippensburg Univ of Pennsylvania	SUP	Nov. 1	1:25-2:55pmEST
Thomases	Becca	Univ of California Davis	UC-Dav	Nov. 1	1:25-2:55pmEST
Pierce	Kristin	Univ of Pittsburgh-School of Medicine	Pitt-Med	Nov. 1	1:25-2:55pmEST
Hong	Tian	Univ of Tennessee Knoxville-BCMB/GST	UTK-BCMB	Nov. 1	1:25-2:55pmEST
von Arnim	Albrecht	Univ of Tennessee Knoxville-BCMB/GST	UTK-BCMB	Nov. 1	1:25-2:55pmEST
Armentrout	Pam	Univ of Tennessee Knoxville-Math Biology	UTK-MathB	Nov. 1	1:25-2:55pmEST
Childs	Lauren	Virginia Tech	VT	Nov. 1	1:25-2:55pmEST