

NIMBioS

National Institute for Mathematical
and Biological Synthesis

Tenth Annual

Undergraduate Research Conference at the Interface of Biology and Mathematics

October 27-28, 2018

University of Tennessee Conference Center

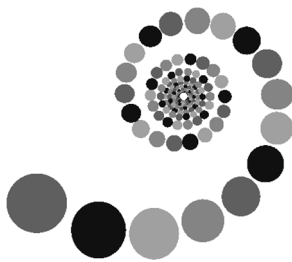
Knoxville, TN

CONFERENCE OVERVIEW

Welcome! This conference is hosted by the National Institute for Mathematical and Biological Synthesis (NIMBioS), housed on the campus of the University of Tennessee-Knoxville. Undergraduate students conducting research in mathematics and biology will present over 50 oral and poster presentations. A keynote address by Dr. Holly Gaff and featured talk by Dr. Nina Fefferman will take place Saturday afternoon, and a panel discussion on career opportunities will follow. Graduate opportunities will be showcased on Sunday morning. Poster abstracts start on page 5, oral presentation abstracts start on page 16.



NIMBioS



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

UNIVERSITY OF TENNESSEE & KNOXVILLE

This conference is being held at the University of Tennessee (UT) Conference center, just across town from the university's main campus. UT has an enrollment of over 27,000 and more than 300 degree programs offered. It was founded in 1794 as Blount College but subsequently changed names a few times before becoming the University of Tennessee in 1879.

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



INFORMATION FOR HANGING POSTERS

There will be two poster sessions. The first will immediately follow dinner on Saturday, from 7:30-8:30 pm. Presenters whose posters are assigned odd numbers will present at this time. The second will precede lunch on Sunday, from 11:00 am to Noon, when posters assigned even numbers will be presented. Please hang your poster as soon as possible and leave it up for the duration of the conference. Refer to the poster listing in this booklet to find your assigned number. Posters will all be hung in the hallway areas outside room 406. Find your assigned space and use the tacks provided to affix it to the wall or poster board. Poster abstracts and numbering start on page 5.

INFORMATION FOR ORAL PRESENTERS

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

SOCIAL MEDIA AT URC 2018



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 2018 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. Holly Gaff
Department of Biological Sciences
Old Dominion University

Mapping the Range Expansion of Ticks: Modeling and Surveillance

Ticks and tick-borne diseases are on the move worldwide. Tracking these movements is critical to understanding the risks of the diseases. Mathematical models can be used to explore tick-borne pathogen dynamics, quantify risk of tick-borne disease, and identify optimal strategies to reduce that risk. Long-term surveillance data are needed to build ecologically valid models. In order to build such a dataset, ticks have been collected since 2009 using a variety of techniques from a set of locations in Virginia. This surveillance project has collected, identified, and cataloged more than 175,000 ticks. While the vast majority of these ticks are the expected three tick species, this study also found two tick species moving into the area. We have carefully tracked these ticks through annual surveys of the majority of the eastern half of the state, and we are using that data in combination with the long-term local data. Agent-based models have been parameterized using these data to explore the future disease dynamics in the region as a result of each type of invasion. The models predict that the population front and pathogen prevalence are highly dependent on the host dynamics. This has led us to shift more focus on identifying hosts in these expansion areas.

FEATURED SPEAKER

Dr. Nina Fefferman
Departments of Ecology and Evolutionary Biology and Mathematics
University of Tennessee, Knoxville

Evolving Efficient Solutions: How Simple Natural Systems Solve the Most Complicated Problems

Nature is replete with biological systems of very simple agents that need to solve incredibly complicated problems in order to survive. Contrary to popular belief, evolutionary systems rarely produce algorithms that find optimal solutions – instead, they produce efficient algorithms to find sufficient solutions. We'll discuss some of the mechanisms at work in nature for how this is accomplished and explore a case study in cyber-security designed by the communication system of honey bees.

SCHEDULE

Saturday, October 27: Room 413AB (Except where noted)

12:45-1:00 Welcome: Dr. Louis Gross, NIMBioS

1:00-2:00 Keynote Lecture:

Dr. Holly Gaff, Biological Sciences, Old Dominion University

Mapping the Range Expansion of Ticks: Modeling and Surveillance

2:10-2:25

406: Nicolas Gort Freitas – *Scaling of Information in Biochemical Systems*

413AB: Sarah Brock, Yi Dai, and Brielle Kwarta – *Economic Modeling of Free-Roaming Cats in Knox County, TN*

2:30-2:45

406: Allison Torsey – *Analyzing the Dynamics of an Inflammatory Response to a Bacterial Infection in Rats*

413AB: Eeman Abbasi, Kevin De Angeli, and Alan Gan – *Modeling Hunting and Harvesting Interactions Between Plants and Their Seed Dispersers*

2:50-3:05

406: Brianna Alred, Benjamin Reber, and Benjamin Schenck – *Ecological Niche Modeling and Risk Assessment of Thousand Cankers Disease*

413AB: Alyssa Petroski – *Investigating Density-Dependent Effects on Fitness of the Dengue and Zika Vector *Aedes aegypti* and Possible Consequences for Wolbachia-Based Control Strategies*

3:10-3:25

406: Leah Andrews – *Modeling Optimal Treatment Strategies for Transplant Patients*

413AB: Annastashia Blesi and Samantha Brozak – *La Crosse Virus Spread Within the Mosquito Population in Knox County, TN*

3:30-3:45 *Opportunities at NIMBioS and Explanation of Networking Activity*

Greg Wiggins, Education & Outreach Coordinator at NIMBioS

3:55-4:25 Networking Activity and Snack Break

4:30-5:20 Featured Speaker:

Dr. Nina Fefferman, Ecology and Evolutionary Biology and Mathematics, University of Tennessee

Evolving Efficient Solutions: How Simple Natural Systems Solve the Most Complicated Problems

5:30-6:20 Career Panel (Moderator: Suzanne Lenhart, Associate Director at NIMBioS)

Dr. Holly Gaff, Biological Sciences, ODU

Dr. Nina Fefferman, Ecology and Evolutionary Biology and Mathematics, UTK

Dr. Olivia Prosper, Mathematics, University of Kentucky

Dr. Karin Leiderman, Applied Mathematics and Statistics, Colorado School of Mines

6:25-6:35 Introduce Kristin Jenkins, Director, BioQUEST, and Stacey Kiser, Professor, Lane Community College

6:40-7:30 Buffet Dinner in 404A

7:00 Turn in SET game sheets to Wiggins or Lenhart at Dinner

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

Sunday Morning, October 28: Rooms 406, 413AB, 413C

8:00 Continental Breakfast

8:30-8:45

406: Tyler Helton – *Applications of the Monte Carlo Method for Problem Solving*

413AB: Kimberlyn Eversman – *Division of Labor in Hygienic Behavior of *Apis mellifera*: Experimental Investigation to Simulation*

8:50-9:05

406: Kelly Rivenbark – *Manzate Exposure Alters Mitochondrial Membrane Potential in Genetically Modified *C. elegans**

413AB: Mariya Savinov – *Entrainment of Forced Oscillators with Flexible Periods*

9:10-9:25

406: Abdullah Ateyeh and Rithik Reddy – *Using Global Sensitivity Analysis to Find Influential Parameters in a Wound-Healing Model*

413AB: Alena Turner – *Simulating an Outbreak of Zika Virus in Climates with Seasonal Mosquito Patterns*

9:30-9:45

406: Nastasha Gilbert – *Using *C. elegans* as a Model for Non-Nutritive Sweetener and Glucose Metabolism*

413AB: Noah Rosenbalm – *Disease Progression on Social Networks*

9:50-10:50

413C: Graduate School Opportunities Showcase

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

12:05-12:55 Lunch

1:00-1:15

406: Rebekah Waters – *3D Printing and Microfluidics*

413AB: Jordan Pellett – *Efficacy of Control in a Spatially Dynamic Model of White-nose Syndrome*

1:20-1:35

406: Amanda Ignacz – *Chronic Exposure to Manzate Formulation in Genetically Modified *Caenorhabditis elegans* Leads to Mitochondrial Dysfunction*

413AB: Jerry Yang – *Estimating Rates of Homologous Recombination in Bacteria*

1:45-2:00

413AB: Closing Remarks

2:00 Adjourn

POSTER ABSTRACTS

1) ALOISO, M, and B. G. FITZPATRICK. Modeling Ecological Federalism in a Pest Control Context.

Department of Mathematics, Loyola Marymount University, Los Angeles, CA.

Recent changes in the federal government's approach to environmental regulation suggest a rolling back of environmental policies to leave management to state and local authorities. Economic federalism concerns the balancing of centralized (federal) and decentralized (regional) decision making. While environmental federalism has seen much debate and theorizing, quantitative modeling and analysis is in the nascent stages. In this project, we pose a regulatory problem in which two neighboring areas are controlled by distinct regional governments and a federal government to explore the outcomes of differing regulatory regimes. We develop a dynamic model of a pest population that grows within regions and disperses across a regional boundary. Regulatory control is implemented by a combination of harvesting and border control, allowing decision makers to focus on preventing pest immigration and/or on reducing the existing population. Using optimal control and game theory techniques, we seek cost-efficient pest control strategies under different regulatory frameworks and data feedback strategies.

2) ANDRADE, A., S. NAIK, and M. WERBICK. Identifying and Evaluating the Impact of On- and Off-Campus Context Dependent Ecological Factors on the Patterns of Health Risk Behaviors Among Arizona State University Students. School of Human Evolution and Social Change, Arizona State University, Tempe, AZ.

Ecological model systems can be used to analyze behaviors and their correlations to ecological factors, which is useful in determining how social environmental factors influence an individual's decisions. Environmental interactions shape the way that humans behave throughout the day, either through observation, action, or consequences. A research study was conducted in the form of a survey to determine and evaluate the impact of ecological factors in drinking and smoking behaviors among Arizona State University students. Ecological factors such as demographics, living conditions, social interactions, and where students spend the most time were used to evaluate the correlations between drinking and smoking behaviors and environmental interactions, both on- and off- campus. A 27 question survey was administered to 539 Arizona State University students to conduct this research. Summary statistics, correlation techniques, linear regression, and logistic regression models were used to find correlations and relationships between patterns of health risk behaviors and ecological factors.

3) ANDRADE, C.¹, A. DAWADI¹, M. JACKSON¹, N. GRIFFIN¹, J. TOLONE¹, C. FAY¹, D. MOREL¹, and J. DICK². Development of a Night Interruption Light Therapy Delivery Apparatus for Field Treatment of Hop Plants.

¹Department of Physics, Emory & Henry College, Emory, VA, ²Kelly Ridge Farms, Meadowview, VA.

The short-day plant *Humulus lupulus*, or hops, relies on night length to control growth. When night length is relatively long, as is the case in southwestern Virginia in summer, hop plants do not grow as tall as they do in the northwestern US. Growth triggers in hop plants are partially controlled by photoreceptors called phytochromes. Of particular interest are those phytochromes sensitive to the red and far red wavelengths of light. When exposed to red light, the inactive form of phytochrome (Pr - Phytochrome red) is converted to the active form (Pfr - Phytochrome far red), the latter regulating growth processes. At night, only Pr phytochromes are synthesized. To counter the effect of longer night lengths and promote conversion of Pr to Pfr, three types of LED-based, Arduino-controlled, light delivery structures are under development. With the use of spectrometers, measurements of intensity as a function of wavelength give a profile of the illumination delivered by each array. The most efficient type of LED light for hop plants can be determined by comparing spectral data with the desired peak wavelength of 657 nm red light for conversion of Pr to Pfr. Further measurements can verify calculations of the effective intensity of the light at various distances from the source, suggesting treatment regimens.

4) BUTLER, C.¹, J. CHENG², L. CORREA³, M. PRECIADO⁴, A. RIOS⁵, B. ESPINOZA⁶, V. MORENO⁶, C. MONTALVO⁶, and C. KRIBS⁷. Comparison of Screening for Methicillin-Resistant *Staphylococcus aureus* (MRSA) at Hospital Admission and Discharge. ¹Department of Mathematics and Statistics, University of Maine, Orono, ME. ²College of Science, Shanghai University, China. ³Escuela de Ciencias Matemáticas y Tecnología Informática, Universidad Yachay Tech, Ecuador. ⁴Escuela de Física y Nanotecnología, Universidad Yachay Tech, Ecuador. ⁵Departamento de Estadística, Universidad Nacional de Colombia, Colombia. ⁶Simon A. Levin Mathematical Computational and Modeling Sciences Center, Arizona State University, Tempe, AZ. ⁷Department of Mathematics, University of Texas, Arlington, TX.

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a significant contributor to the growing concern of antibiotic resistant bacteria, especially given its stubborn persistence in hospital and other health care facility settings. In combination with the general persistence of *S. aureus* (colloquially referred to as staph), MRSA presents an additional barrier to treatment and is now believed to have colonized two of every 100 people worldwide. According to the CDC, MRSA prevalence sits as high as 25-50% in countries such as the United Kingdom and the United States. Given the resistant nature of staph as well as its capability of evolving to compensate antibiotic treatment, controlling MRSA levels is more a matter of precautionary and defensive measures. The subject of the following research is the method of "search and isolation" which seeks to isolate MRSA positive patients in a hospital to decrease infection potential. Although this strategy of search and isolate is straightforward, the question of just whom to screen is of practical importance. We compare screening at admission to screening at discharge. To do this, we develop a mathematical model and use both stochastic and deterministic simulations to determine MRSA endemic levels in a hospital with either control measure implemented. The more successful control measure will better control endemic potential and proliferation of MRSA.

5) CHIDAMBARAN, S.¹, D. CASTEDO PENA², and A. BERLE³. Applying Phylogenetic Tools to Understand Cancer Tumor Evolution. ¹Rutgers University, New Brunswick, NJ, ²North Carolina State University, Raleigh, NC, ³Lewis and Clark College, Portland, OR.

Because of the high speed of replication and mutation in cancer cells, cancer can be modeled as a within host evolutionary process. Here we apply a new model of evolution, Selection on Amino acids and Codons (SelAC), to cancer data and compare it with previously accepted models. In our analysis, SelAC was comparable to the alternate models tested, FMutSel0 and GY94. However, we will need to continue testing if this applies across a broader range of genes. Additionally, we created R scripts to extract relevant data from .maf files and use it combined with information from the human reference genome to simulate cancer sequences. We also conducted a principal component analysis (PCA) to determine which of 30 physicochemical properties best explain the variance in amino acid residues. Our results point to SelAC being an accurate model of evolution for cancer, but future work needs to be done in testing and improving the model to confirm these initial results.

6) COLLINS, R. Investigating Anti-Angiogenesis Therapy for Cancer with a Mathematical Agent-Based Model. Texas Tech University, Lubbock, TX.

Cancer modeling can be used to better understand the growth and metastasis of cancer cells by investigating how individual parameters influence growth dynamics. Tumor growth and metastasis depend on angiogenesis, the development of blood vessels to supply the tumor with the oxygen and nutrients needed to proliferate. Antiangiogenic therapy, using angiogenic inhibitors which prevent blood vessel growth to the necrotic core of the tumor, can ideally slow the spread of cancer cells by essentially starving the tumor of the nutrients needed to survive. Here, an agent based mathematical model was developed to investigate tumor responses to antiangiogenic therapy. The model tracks the distribution of healthy and cancer cells while exploring the efficiency of using different levels of angiogenic inhibitors. The process of introducing antiangiogenic therapy

was simulated by lowering the cell efficiency of cancer cells compared to healthy cells so it is more difficult for cancer cells to take up glucose, as it would be if there were no blood vessels to supply glucose to the core of the tumor. As the level of antiangiogenic factors is increased, the tumor ceases to grow or grows at a much slower rate. The applications of math based modeling for cancer help shed light onto complex dynamics that allow tumor proliferation.

**7) DAWADI, A.¹, M. JACKSON¹, ANDRADE, C.¹, N. GRIFFIN¹, J. TOLONE¹, C. FAY¹, D. MOREL¹, and J. DICK².
Assessing the Efficiency of Night Interruption Light Therapy on the Growth of Short-Day Plants in Virginia.**

¹Department of Physics, Emory & Henry College, Emory, VA, ²Kelly Ridge Farms, Meadowview, VA.

The per plant production of *Humulus lupulus*, or hops, in the northwest of the United States far exceeds that of Virginia. Hops are short-day plants dependent on night length to reach maturity before flowering. Lower latitude regions have longer nights during the growing season which influences the flowering process. Implementation of Night Interruption can mitigate this impact and thus increase production, leading to a more competitive hops industry in the region. Night Interruption is the use of artificial light to mislead the plants' photoreceptors, causing the plants to register night as day-time. This process targets two different forms of phytochrome photoreceptors: the active form (Pfr - phytochrome-far-red) which controls flowering, leaf and chloroplast development; and the inactive form (Pr - phytochrome red). At night, only the Pr form is synthesized. When red light with peak wavelength at 657 nanometers is applied, Pr phytochromes convert to Pfr. The implementation of night interruption enables the plants to convert Pr to Pfr thus promoting growth. As part of a larger project, we propose to study night interruption light therapy in hops and biological equivalents. This experiment will include field testing with delivery of red light over different time intervals throughout the night on hop plants to provide information on the most efficient application of night interruption in this region.

8) GEORGE, S., L. MORA, C. OROZ, and D. TALLANA. The Effect of Gonadotropin-Releasing Hormone (GnRH) on the Regulation of Hormones in the Menstrual Cycle: A Mathematical Model. Mathematical and Theoretical Biology Institute, Arizona State University, Tempe, AZ.

Gonadotropin Releasing Hormone (GnRH) is the driving force for hormonal regulation during the menstrual cycle. GnRH signals the anterior pituitary gland to secrete follicle stimulating hormone (FSH) and luteinizing hormone (LH) which promotes the release of estradiol (E_2) and progesterone (P_4). Interferences in the cyclic interactions have been shown to cause irregularities in the menstrual cycle. In this study, the non-linear dynamics of GnRH, FSH, LH, E_2 , and P_4 are examined. A simplified model of six non-linear ordinary differential equations is developed to model the effect of GnRH on the dynamics of hormones in the menstrual cycle. A mathematical analysis is performed to observe the regulation of GnRH in a monthly cycle. Our findings suggest that the relationship between E_2 and GnRH plays an important role in concentrations and patterns of release of the hormones involved in the menstrual cycle.

**9) GRIFFIN, N.¹, J. TOLONE¹, ANDRADE, C.¹, A. DAWADI¹, M. JACKSON¹, C. FAY¹, D. MOREL¹, and J. DICK².
Implementation of Night Interruption Light Therapy on Short-Day Plants via a Mobile Delivery System.**

¹Department of Physics, Emory & Henry College, Emory, VA, ²Kelly Ridge Farms, Meadowview, VA.

The growth of hop plants (*Humulus lupulus*) depends on the duration of night. Because of different day lengths, hops cultivated at lower latitudes do not produce the same yield as those grown in the Pacific Northwest. This lack of growth can be mitigated by what is known as night interruption light therapy. This is the process of shining specific wavelengths of light on the plants at night to make their biochemistry react as if it were daytime. To effectively and efficiently implement this concept, an automated mobile delivery system is under development. The primary goal is to evenly deliver light across acres of hop plants while keeping costs within reach of farmers. One challenging aspect of the project is that the plants grow to heights of up to

twenty feet. For this reason, cables are suspended down the rows of plants for the machine to use like a track. The mechanism will support a lighting module that will traverse the rows. The motion of the unit will be remotely controlled to move along the track in order to evenly distribute light to the plants.

10) GUY, K., and D. ERNST. Reanalyzing the NEOS Experiment Through Computational Modeling. Department of Mathematics and Computer Science, Fisk University, Nashville, TN.

A phenomenon called the “reactor neutrino anomaly” reports a disappearance of neutrinos with respect to the number that is expected being emitted from reactors. The existence of a fourth, sterile neutrino has been proposed as the possible solution to this problem. A recent experiment, named NEOS (Neutrino oscillations at short baseline) sees evidence of disappearance. The purpose of this work is to create a computer model of the new NEOS experiment which would first follow as closely as possible the analysis performed by the experimentalists. Reproducing the results of the experimentalists would verify and calibrate our model. We would then investigate possible improvements in the model. Our best model would be combined with twenty other models under construction by the Vanderbilt Theoretical Neutrino group. The implications of this analysis would clarify the possible existence of the fourth sterile neutrino, as well as provide the parameters that would govern the oscillations of the known neutrinos into the new sterile neutrino should we find evidence for its existence.

11) HILL, E., and M. JACKSON. The Distribution of Neutral Hydrogen in the Milky Way Galaxy. Emory and Henry College, Emory, VA

The Milky Way is a spiral galaxy composed of neutral hydrogen (HI) gas. The Milky Way's can be represented by plotting blue-shifted and red-shifted neutral HI gas which is concentrated in four spiral arms. To locate HI in the galaxy, we collected data along the 21 cm hydrogen line using a small radio telescope (SRT) at Virginia Tech. In the laboratory, the 21 cm line occurs at a frequency of 1420.4 Mhz. Red-shifted gas moving away from the Sun displayed frequencies lower than the HI emission line while blue shifted displayed higher frequencies. We then used these frequencies to calculate the radial velocities of the gas. These calculations assumed that the orbital velocity of HI gas beyond the orbit of the Sun was equivalent to that of the Sun. This assumption was based on evidence from galactic rotation curve data (see poster by Madison Jackson et al.). The distance from the HI clumps to the Sun were then calculated utilizing trigonometric equations. This, along with the galactic longitude at which the data were taken, represented the galactic coordinates of the gas. When the HI gas was plotted, the data appeared to reveal spiral arms, indicating that the Milky Way is a spiral galaxy, in general agreement with previous high-resolution data.

12) HOARD, E. Using graph theory to evaluate size-structured food webs. Department of Biological Science. Department of Mathematics and Statistics, Murray State University, Murray, KY.

Graph theory has the potential to elucidate food web interactions because of the logical similarity between them. A particularly interesting problem in this regard is the impact of size-structure, the variation in size within a population, on food webs. Size-structure is common within animals, but the impacts of such variation on food web interactions are not well understood. To evaluate this question, we studied several size-structured populations of a top aquatic predator, the tiger salamander (*Ambystoma mavortium*). Paedomorphic tiger salamanders are keystone predators in subalpine ponds, but how size variation affects their predatory impacts is unknown. We sampled salamanders in three ponds at the Mexican Cut Nature Preserve in south-central Colorado, which provides an ideal location to study how salamander prey choice is affected by size-structure. Using non-invasive gastric lavage, we sampled the stomach contents of salamanders across a representative range of sizes in each pond. We also sampled the abundance of invertebrate prey and phytoplankton in order to evaluate possible trophic cascades. By analyzing these data

using graph theory, we will quantify the strength of the predator-prey relationships between each size class and their prey species, and describe how size variation affects predator-prey dynamics of these communities.

13) JACKSON, M., and E. HILL. Producing a Galactic Rotation Curve for the Milky Way Galaxy. Emory and Henry College, Emory, VA.

A galactic rotation curve is a graph of the velocity of intergalactic objects from the center of the galaxy. The orbital velocities of are related to the mass of the intergalactic object's orbit. In this study, a galactic rotation curve was created for the Milky Way galaxy using the 21 cm line of neutral hydrogen. When neutral hydrogen's electron has an antiparallel spin, the energy level is lower than the hydrogen with a parallel spin – when the spin transitions to antiparallel the energy is released as electromagnetic radiation. This radiation was detected with a small radio telescope (SRT) at Virginia Polytechnic Institute with a rest frequency of 1420.42 MHz. The SRT took samples every two degrees longitude from 20°- 260° for a duration of 300 seconds each. The points 20°-90° were used for this rotation curve. The remaining data were used as a continuation of related research for mapping of the neutral hydrogen clumps throughout the galaxy (after establishing assumptions from the rotation curve). Trigonometric equations were applied to calculate the distance of the hydrogen gas from the galactic center. By assessing the Doppler shift of the gas' maximum orbital velocity was calculated. The distance and orbital velocity resulted in a galactic rotation curve for the Milky Way Galaxy.

14) JOHNSON, A.¹, and A. WALKER². Parameter Estimation in Models of *Sphagnum* Gross Primary Production using Advanced Markov Chain Monte Carlo Methods. ¹University of Tennessee, Knoxville, TN, ²Environmental Sciences Division and Climate Change Science Institute, Oak Ridge National Laboratory, Oak Ridge, TN.

Peatlands harbor large stockpiles of carbon, which are vulnerable to rising temperatures and increasing precipitation in northern wetlands. Peatlands account for ~ 0.2 – 0.33 of the Earth's soil carbon, and this peatland carbon is vulnerable to recent and future climate change. The potentially large feedback of CO₂ and CH₄ on climate change as this carbon degrades makes predictive understanding of peatland carbon dynamics imperative. We contribute to this predictive understanding by establishing formal parameter estimation methods in models of *Sphagnum* gross primary production (GPP). In this study, we implemented advanced Markov chain Monte Carlo methods in the Multi-Assumption Architecture and Testbed (MAAT), a modeling software. We then compared alternative *Sphagnum* GPP models. The Dynamic Leaf Area Index model of *Sphagnum* GPP incorporates a hypothesis on the interaction between photosynthesizing tissue surface area and water table height. In contrast, the Constant Leaf Area Index model does not include this hypothesis. By analyzing data from Oak Ridge National Lab's Spruce and Peatland Responses Under Changing Environments (SPRUCE) experiment in northern Minnesota, we concluded that the Dynamic Leaf Area Index model better explains the nuances in the observed data due to its direct connection of *Sphagnum* photosynthesizing tissue to water table height.

15) LI, Q., and M. RIEHL. Predicting the Stability of Profiling Signals of Small RNAs. Rose-Hulman Institute of Technology, Terre Haute, IN.

Different RNA secondary structures have different free energies, and typically those with lower energies are more likely to be found in nature. Boltzmann sampling samples an RNA's possible secondary structures with likelihoods derived from their free energies. Profiling is a process that finds similarities between different RNA secondary structures by extracting signals from this Boltzmann sampling. The reproducibility of profiling can be identified by the standard deviation of number of features among Boltzmann samples. We found a strong relationship between the frequency of a helix class and its standard deviation upon repeated Boltzmann sampling. We used this relationship to develop a perturbation technique which predicts the stability of these features without repeated Boltzmann sampling. Our technique predicts stability with accuracy between 84%

and 94%, depending on the type of RNA, and only requires 0.2% of the computation time compared to one profiling process.

16) MALAGON, D. A.¹, L. MELARA², S. LENHART¹, O. F. PROSPER³, E. D. CARTER¹, R. KUMAR¹, D. L. MILLER¹, and M. J. GRAY¹. Role of Density and Habitat Structure on Eastern Newt Contact Rates and Pathogen Transmission. ¹University of Tennessee, Knoxville, TN, ²Shippensburg University, Shippensburg, PA, and ³University of Kentucky, Lexington, KY.

Batrachochytrium salamandrivorans (*Bsal*) is a fungal pathogen that is emerging in Europe and appears to be highly pathogenic to salamander species in the family Salamandridae. The Eastern Newt (*Notophthalmus viridescens*) is a member of Salamandridae, and known to be susceptible to *Bsal*. This species is one of the most widely distributed salamanders in North America. Given their widespread distribution and high abundance, this species has the potential to significantly influence *Bsal* epidemiology if the pathogen emerges in the USA. We designed two studies to estimate contact rates given different densities and habitat structure, and the probability of transmission from infected to susceptible individuals. We found that *Bsal* transmission due to contact was very efficient between infected and susceptible newts even at early stages of infection when pathogen loads were low. We also found that contact rates were density dependent, and that adding habitat structure (i.e., plants) reduced contact at higher newt densities. Simulations from a system of ordinary differential equations show rapid transmission of *Bsal* among individuals, such that an entire population can become infected quickly under most scenarios. Moreover, disease-induced mortality of susceptible individuals following contact with an infected individual averaged 2 –3 weeks post-contact at 14 C water temperature. These results demonstrate that *Bsal* can potentially have severe population effects on eastern newts. Reducing newt density or increasing habitat structure at *Bsal* positive sites might reduce transmission and outbreak size.

17) MATTAMIRA, C. and J. WILLIAMS. Modeling DNA Self-Assembly with Graph Theory. Department of Mathematics, Converse College, Spartanburg, SC.

Targeted drug delivery, biomolecular computing, and biosensors are just a few of the many recently discovered applications of DNA nanostructures. Laboratories are eager to find the most efficient and cost-effective ways to form certain complexes from various pieces of DNA. In particular, laboratories often seek to construct DNA nanotubes, which have an especially useful structure. This problem can be tackled using an area of mathematics called graph theory. The pairing of graph theory with the well-known complementary properties of DNA strands has resulted in new insights about ways DNA nanostructures can form. The key concept underlying DNA nanotechnology is the formation of complete DNA complexes out of a given collection of branched junction molecules. These molecules can be viewed as portions of graphs made up of vertices and half-edges, where bond-edges are double-stranded DNA pieces that have joined together. Previously known results include optimal construction solutions for cycles, trees, complete graphs and complete bipartite graphs. We provide results for gear graphs, which are a family of graphs having the potential to wrap and form DNA nanotubes.

18) MATTHEW, S., D. NICKERSON, G. HALL, K. SANFT, and B. DRAWERT. Gillespy2: Stochastic Modelling for Biochemical Systems. Division of Computer Science, University of North Carolina, Asheville, NC.

Every living thing is composed of complex interlocking systems. Systems are composed of a variety of biochemical compounds that interacting in complex ways, creating or breaking into new compounds in response to the environment. Quantifying and observing the behavior of these systems requires us to abstract the behavior of these interactions. Software libraries exist to assist researchers in this field, but many are so complex in operation that require an in-depth understanding of computer science to utilize or they do not offer specific capabilities that the system of inquiry requires. We present GillesPy2, a software library intended

to solve the needs of many scientists; from the result seeking wet-lab biologist to the performance seeking bioinformatician. GillesPy2 is a next-generation of the original GillesPy library, an open source cross-platform Python library used for creating statistically correct trajectories for biochemical ordinary differential equations. GillesPy2 has been designed with a focus on providing both ease of use and clarity to the end user, using a unique modular solver system that allows the end user to specify the algorithm to solve their system of inquiry. This granularity is coupled with high-level functionality allowing the researcher to communicate and export their findings seamlessly.

19) NELSON, B. Correlation of CO₂ Levels with Human Population, Deforestation, and Global Temperature Anomalies. Murray State University, Murray, KY.

Almost every news channel in the USA has mentioned climate change at least once in the past few years. According to many scientists, if something is not done about this problem soon, the effects may be irreversible. One of the main contributors to this world ending problem is carbon dioxide, but what contributes to the rise in CO₂ levels and what do humans have to do with it? Some leading causes of the CO₂ increase include deforestation and car exhaust. These factors have a significant correlation with CO₂ levels. In this presentation, these correlations will be compared to one another. The correlation between CO₂ levels and both human population and global temperature change will be calculated.

20) GLASS, K. E., B. KRISTY, K. LEITNER, J. S. DIXON, M. E. LANDON, N. A. REAVILL, C. E. YOUNG, M. T. STREET, R. PENUMADU, M. A. BIAN, W. GULLEDGE, T. E. KEYES, E. B. LIST, J. PAN, S. S. PATEL, M. M. PAYNE, G. T. STATUM, R. B. LAUREL, J. C. CLEMENTS, G. CHEN, R. W. MURDOCH, D. C. GARCIA, N. JIANG, S. A. RIPP, and F. E. LÖFFLER. Biological Degradation of Dichloroacetate via Synthesized Haloacid Dehalogenases. International Genetically Engineered Machine, University of Tennessee, Knoxville, TN.

Chemical pollution resulting from large-scale industrial practices can result in volatile organic compounds (VOCs) in the water. One VOC of interest is dichloroacetate (DCA), a chlorinated contaminant that has negative implications towards human health. DCA is largely found to occur as an environmental pollutant, specifically in water, as a direct result of manufacturing processes. Therefore, the goal of our team is to engineer a biological system (*E. coli*) that is able to degrade the DCA effectively. If this is successfully realized, the applications for environmental conservation will be transformative.

21) PIGHINI, J. Mining the Sloan Digital Sky Survey Database for Quasar Outflows with Possible Distance Indicators. Emory and Henry College, Emory, VA.

The focus of our project is to identify outflows within quasar spectra from the Sloan Digital Sky Survey (SDSS) that exhibit key characteristics and warrant follow-up observations. Quasars are the most energetic objects in the universe and are connected with the supermassive black holes in the center of galaxies. These objects emit powerful outflows that influence the formation and evolution of the host galaxy. The research goal is to find outflows with specific characteristics that allow us to calculate number density and determine the distance of the outflow from the source, thus forming implications for quasar feedback. Currently, our project director Dr. Nahum Arav is looking for quasars with discernable S IV, N III and P V absorption troughs. These troughs are identified with software developed using the Interactive Data Language (IDL). The IDL software is used in conjunction with Java programs to find the velocity of the outflow relative to the quasar rest frame and its velocity spread. Moreover, it is used to check identifications of excited states and compare outflow troughs. Following our analysis, Dr. Arav then sorts through the proposed candidates to find viable follow-up targets. After mining through 2,187 objects in the SDSS database, we found 55 objects that justified a follow-up. With our total being 10,218 objects over a 1,000 hour period, we expect 245 to qualify as interesting. These may be added to proposals for observation time using larger telescopes such as the Hubble Space Telescope (HST) within the coming year.

22) ROSENSTEEL, G. Defining an Epidemiological Geography of the United States: Influenza as a Case Study. Department of Biology, Georgetown University, Washington, DC.

Influenza is a major human pathogen that causes massive morbidity and mortality around the globe and displays complex spatiotemporal patterns in the areas it effects. Flu epidemic patterns vary across the United States as they are influenced by biological, environmental, geographic, and socio-demographic factors. Current disease surveillance, vaccination policies, and resource allocation for influenza are designed and communicated at the level of ad-hoc health administration megaregions (consisting of multiple U.S. states). Instead, we propose basing flu surveillance and vaccine distribution on underlying epidemiological dynamics, while still heeding pragmatic concerns of feasibility and efficiency. Here, we present an empirical network approach to this problem. Based on influenza time series data from 2002-2009 for the United States, we generate networks in which nodes represent locations and edges represent similarity in influenza epidemics. We then apply a community detection algorithm to identify locations in the U.S. that experience comparable influenza dynamics. Our results suggest that there are indeed communities specified by disease dynamics. Our data-driven approach to define epidemiologically relevant regions demonstrates an application of complex network to inform spatial public health policy for infectious disease surveillance and control.

23) SHORTREED, B., A. HINSON, J. NISSIMOV, and D. TALMY. Modeling the Kinetics of *Emiliana huxleyi* CCMP 274 and Coccolithovirus EhV207 Under Changing Phosphate Conditions. Department of Microbiology, University of Tennessee, Knoxville, TN.

Relatively little is known about the kinetics behind viral infection even though marine viruses impact oceanic biogeochemical cycles. We developed a mathematical model of *Emiliana huxleyi* CCMP 374 infected by EhVs under changing phosphorus conditions. The model has six parameters that represent host growth rate, clearance rate, lysis rate, burst size, viral decay, and chronic release. Model parameters were optimized to experimental population data using the Metropolis-Hastings algorithm. When grown under phosphorus-limited conditions, hosts grow at comparable rates whether infected or uninfected. It is speculated that host growth is similar under these conditions because without enough phosphorus available, viruses are defective and cannot inhibit the growth of their host due to virus' large nucleic acid, and thus phosphorus, requirements. The addition of a chronic release parameter also significantly increases the accuracy of our model fit, which before the inclusion, underpredicted viral concentrations. This translates to a hypothesis that viral particles are escaping their host early in the infection process. Thus, through the modeling of this host/virus interaction, one can gain more detailed insight into the dynamics of viral infection.

24) MILLER, P., P. SPELL, R. AUSTIN, S. BOTHWELL, S. RUSK, O. ROSALES, B. D. WAGNER, P. M. MOURANI, and S. H. ABMAN. Effects of Maternal Complications on Circulating Protein Profiles in Preterm Infants. Department of Biostatistics & Informatics, Colorado School of Public Health, Aurora, CO.

The purpose of this research was to prospectively examine the relationship between prenatal events and circulating blood protein profiles in preterm infants. Blood plasma samples collected at day 7 (48 hours) during the first week after birth from 102 preterm infants were processed for a proteomic profile using a SOMA-scan assay. Random forests of classification trees were made to assess relationships between identified proteins and maternal complications. Protein analysis shows that there are inflammatory and angiogenic proteins that can discriminate between the maternal complications of pre-eclampsia and chorioamnionitis. Pre-eclampsia shows decreased concentration of anti-angiogenic and proinflammatory proteins. Chorioamnionitis shows increased concentration of proangiogenic and anti-inflammatory proteins. Proteins involved in angiogenesis discriminate best between the complication groups. Circulating protein profiles in seven days old preterm infants are associated with the antenatal events chorioamnionitis and pre-eclampsia.

These relationships may suggest specific adaptive responses to these disorders in the infants and reveal mechanisms of how maternal complications impact the course and outcomes of preterm infants.

25) STATUM, G. T., J. S. DIXON, M. E. LANDON, B. D. KRISTY, K. D. LEITNER, R.P. PENUMADU, N. A. REAVILL, C. E. YOUNG, M. T. STREET, K. E. GLASS, M. A. BIAN, W. GULLEDGE, T. E. KEYES, E. B. LIST, J. PAN, S. S. PATEL, M. M. PAYNE, R. B. LAUREL, J. C. CLEMENTS, G. CHEN, R. W. MURDOCH, D. C. GARCIA, N. JIANG, S. A. RIPP, and F. E. LÖFFLER. Biological Sensing of Dichloromethane via *E. coli* Expression Vector. International Genetically Engineered Machine, University of Tennessee, Knoxville, TN.

The halogenated organic compound dichloromethane (DCM) is widely used for industrial applications such as paint removal, metal cleaning, chemical processing, and pharmaceutical manufacturing. Accumulation of DCM in water systems poses a threat to aquatic organisms and is considered a hazard to human health, having a carcinogenic effect on the liver and kidneys. Therefore, the goal of our team is to genetically engineer *E. coli* as an expression system in the presence of DCM. The DCM biosensor will be a valuable tool in understanding DCM degradation under anoxic conditions, leading to further applications in the bioremediation of highly contaminated anoxic environments.

26) SUSSWEIN Z., and S. BANSAL. Characterizing the Interaction Between Sensitive and Resistant Breast Cancer Cell Populations. Department of Biology, Georgetown University, Washington DC.

While some forms of breast cancer are highly responsive to treatment, endocrine therapy-resistant breast cancers are disproportionately lethal. There has been significant progress in understanding how endocrine therapy-resistant strains evolve from therapy-susceptible strains, but little is understood about how resistance then proliferates through the population of cancer cells. We examine the spread of resistance by characterizing the nature of the ecological interaction between populations of resistant and susceptible breast cancer cells. Using in vitro data on cell growth, we fit coculture data of the two strains to a Lotka-Volterra competition model. Lotka-Volterra models allow for estimation of the net interaction between the competing populations, folding complex biological mechanisms into a simpler overall effect. We fit the model using a Bayesian methodology, carrying uncertainty through the model into final estimation of the net effect. We found a net interaction between the susceptible and resistant cancer strains, demonstrating that there are ecological dynamics to cancer resistance.

27) TANAKA, S. and R.E. GASPER. Effects of Obesity on Essential Cardiac Action Potentials: Modeling and Bifurcation. Department of Mathematics, Creighton University, Omaha NE.

Obesity is an epidemic that poses major risk factors such as Type 2 Diabetes, coronary heart disease, hypertension, stroke and forms of cancer. Previous studies investigated subcellular effects of obesity on various species of mammals to better understand obesity. This study applies previous clinical mammal obesity studies to DiFrancesco and Noble models of Sino Atrial Node and Purkinje Fibers in attempt to model the complications of obesity on cardiac action potentials. We find that the selected model was robust in demonstrating asystole resulting from obesity.

28) THOMAS, J. Structural Optimization of $Cs_2HfX_5X_1$ Scintillators. Department of Life Sciences, Fisk University, Nashville, TN.

The primary premise of my summer project was to find the lattice constant in various compositions of crystalline structures and to compare a lattice constants percent error when calculated with the Broyden–Fletcher–Goldfarb–Shanno algorithm. The specific type of crystals that were studied were scintillators. A scintillator is a type of luminance where there is a high energy source just as gamma, alpha, or x-rays that excites electrons within a crystal and causes them to release photons. For this research the controlled scintillator was Cesium Hafnium Chloride ($Cs_2Hf_2Cl_6$) or CHC because of its high light yield resolution. The

Chlorine in CHC was altered to make a mixed combination with Bromine, Iodine, and Chlorine to make $Cs_2HfX_5X_1$ compositions. The substitutions were made in hopes that it will lead to a better functioning scintillator. I used density functional theory which is one of the many complex theories to calculate the optical, mechanical, vibrational properties, to help predict the compounds energy minimization. The computer code for DFT was ran on a supercomputer at Vanderbilt University (ACCRE). The lattice constant of experimental CHC to the lattice constant of CHC calculated with Broyden–Fletcher–Goldfarb–Shanno algorithm had a percent error of 26.7% with a correction factor of 1.267. Lattice constants of the other $Cs_2HfX_5X_1$ were also documented and recorded with the same correction factor.

29) VASQUEZ, P., J. MACHADO, and E. CHERRY. Controlling Alternans in a Discrete Cardiac Cell Model. Department of Pure Mathematics, University of Puerto Rico at Mayaguez, PR.

In this study, we consider a condition called alternans, a period-2 heart rhythm characterized by oscillations between strong and weak heartbeats known to precede serious heart disorders. Several studies have analyzed methods to prevent or terminate alternans, but in those cases alternans occurred primarily because of instabilities in the cell membrane potential. Alternans also can arise from instabilities in intracellular calcium cycling related to contraction. Here, we use a discrete model of four coupled difference equations to examine whether suppression or complete elimination of alternans is possible using two classes of control methods, one that applied feedback terms directly to individual state variables and another that modifies the timing of heartbeats. To study alternans suppression, we use direct iteration of the model along with a linear stability analysis to provide a theoretical basis for our findings. We present results on the effectiveness of these control methods as well as the observed dependence on the instability underlying alternans.

30) WALLACE, K.¹, C. LEWIS², S. ADAMS², N. PARKS², and B. MATHEW³. Modeling Dielectrophoresis Based Flow Separator. ¹Department of Chemistry, Howard University, Washington, DC, ²Department of Chemical Engineering, Howard University, Washington, DC, ³Department of Biomedical Engineering, United Arab Emirates University, Al-Ain, UAE.

Vascular diseases impact the functioning of organs by affecting the arteries and veins through atherosclerosis; and prior to a heart attack or stroke, the inflammation within the walls of arteries trigger desquamation of endothelial cells, which are then released into the bloodstream and classified as (CECs). If the presence of CECs can be separated and detected within a blood sample, an accurate predication of future vascular problems can be constructed. The aim of this research is to conceptualize and design a novel microfluidic device that allows for the separation of mixtures, like blood, into smaller, distinct components such as circulating rare-blood cells. To develop the model, a MATLAB code was formulated that takes into consideration the forces associated with inertia, drag, gravity, buoyancy, and dielectrophoresis. The proposed make-up of the device incorporates interdigitated transducer electrodes for separating a heterogeneous sample into homogeneous samples by employing multiple trap and release steps on the bottom surface of the microchannel. The electrodes are in direct contact with the sample solution and run over the entire width of the microchannel. In the flow separator, one type of microparticle is subjected to nDEP and are levitated while the other type is subjected to pDEP and is captured at the electrodes, thereby achieving separation contingent upon the permittivity, conductivity, and density of the microparticles.

31) WATSON, T. Using Machine Learning Methods to Diagnose Breast Cancer. Department of Mathematics and Computer Science, Fisk University, Nashville, TN.

Each year it is estimated that over 252,710 in the United States will be diagnosed with breast cancer and more than 40,500 will die. One of eight women will be diagnosed with breast cancer in her life time. In the last few years, breast Cancer has taken its decline because of the advanced technology being able to predict the state of the cancer and gain an immediate medication for the patient. The data set is retrieved from a Wisconsin

study that consisted of 569 patients, where 32 different factors were observed from a tumor gained by fine needle aspiration. There are multiple machine learning methods used to predict whether a tumor is malignant or benign and the contribution of each factor. After testing Linear, Support Vector Machine, Artificial Neural Network, and decision tree, we created multiple conclusions about which attributes contribute to the malignancy of a tumor. The most successful method compared to the results of previous studies was the Artificial Neural Method with a 97.02% accuracy for predicting whether a tumor will be malignant or benign.

32) WHITE, Z. Opioid Misuse Among Incarcerated: A Mathematical Approach. Department of Biomedical Engineering and Mechanics, Virginia Tech, Blacksburg, VA.

Costing U.S. over 500 billion dollars in 2015, prescription opioid has become a well-known modern-day epidemic. In 2018, the National Institute on Drug Abuse documents over 115 deaths per day from opioid overdose. Studies show opioid epidemic rise is caused by advancement in medical treatment resulting in the title iatrogenic epidemic. The National Academies Press published a census report showing the three most vulnerable population being young adults, pregnant woman, and incarcerated individuals. Numerous studies, policies, and intervention programs were introduced to mitigate usage and overdose; however, few targeted the development of addiction inside incarcerated facilities. This presentation constructs a five-class compartmental model for to study incarcerated individual's opioid dynamics. The reproductive number, R_0 , is employed to determine spread and suppression of prescription opioid. We focus on low and high prescription opioid users and their transition into and out of treatment. By developing a formal definition of parameters and variables, it is possible to observe other solutions to reduce the opioid crisis through observation and simulation. Complete eradication of prescription opioid is not viable; however, increasing duration of treatment, encouraging substance treatment, and informing the population of symptoms can reduce new incarcerated individuals from getting infected to disease.

33) ZENKOV, V. When We Measure T Cell Attraction to the Site of an Infection, Does It Matter How It Is Estimated? Department of Electrical Engineering and Computer Science, University of Tennessee, Knoxville, TN.

Malaria causes hundreds of thousands of deaths a year. Malaria parasites, replicating in the liver, can be eliminated by vaccine-induced T cells. However, how T cells find the infection site - whether randomly or with attraction towards the infection site - remains largely unknown. Our teammates performed two photon microscopy imaging experiments which provide data consisting of positions over time of malaria-specific T cells, control T cells, and malaria parasites. To test the attraction of a set of cells, we examined three different metrics: an angle metric, a change of distance metric, and an angle distribution metric. We analyzed the metrics using simulated position data created with a known level of attraction. We investigated biases in each metric and reinterpreted the manifestations of attraction to best test each metric. We analyzed the weaknesses of each metric and the possible ways to expand their applications and even create new metrics. Finally, we tested the metrics on the simulated data to determine which metric most accurately identifies attraction. We found that each metric's efficacy depends on different parameters, such as the number of available observations. An agreement between all the tests is the most sure way to deduce attraction.

34) ZHU, J., and M. HOLINSTAT. The Mechanism of 12-LOX Regulation. Pennsylvania State University, State College, PA.

Blood clotting is a serious problem, which kills up to 1 in 3 people each year in the United States. Platelets play a vital role in blood clotting, hemostasis, and some other cardiovascular disorders. Platelets are activated following injury, and can cause the formation of an occlusive thrombus. Thus, studying platelets is essential to develop new strategies for the prevention of arterial thrombosis. 12-Lipoxygenase (12-LOX), which is an enzyme found in the platelet and megakaryocyte, was shown to have an important role in platelet activation.

However, the mechanism of how 12-LOX regulates platelet activation is still unknown. In this study, we sought to determine the key biochemical steps in platelets that are regulated by 12-LOX, especially whether the ADP secretion pathway is involved in 12-LOX signaling. Human platelets will be treated with ML355, a selective 12-LOX inhibitor, or the combination of ML355 + ADP receptor inhibitors including P2Y₁ and P2Y₁₂ receptor inhibitors. The treated platelets will be stimulated with thrombin, and assayed for activation using aggregation, western blotting, and flow cytometry. Aggregation, α Granule secretion, and integrin activation data will be collected and analyzed. This research could provide a deeper mechanistic understanding of platelet reactivity and its role in maintaining hemostasis.

35) ROGERS, D. Mobile Phone Malware Epidemiology with Quarantine and Removal Classes. Department of Engineering, Grand Canyon University, Phoenix, AZ.

In 2018, about 500,000 desktop computers were infected with cryptocurrency mining malware in less than 24 hours. In addition to attacking desktop computers, malware also attacks laptops, tablets, mobile phones. That is, any device connected via internet, or the network is at risk of being attacked. In recent years, mobile phones have become extremely popular that places them as a big target of malware infections. In this presentation, the effectiveness of treatment of infected mobile devices is examined using compartmental modeling. Many papers have considered malware infections which also include treatment effectiveness. However, in this study the treatment of the mobile devices are based on the type of malware infections (hostile or malicious malware). This model considers six classes of mobile devices based on their epidemiological status: susceptible, exposed, infected by hostile malware, infected by malicious malware, quarantined, and recovered. The basic reproductive number, \mathscr{R}_0 , was identified to discover the threshold values for the dynamics of malware infections to become both prevalent or absent among mobile devices. Various parameters and variables help to define and indicate the dynamics of malware infections to construct viable simulations. Based on our constructed simulations, the best way to avoid getting an infected phone is installing an ideal anti-virus software and raising awareness of avoiding third-party websites that are unknown.

ORAL PRESENTATION ABSTRACTS

ABBASI, E.¹, K. DE ANGELI², and A. GAN³. Modeling Hunting and Harvesting Interactions Between Plants and Their Seed Dispersers. ¹Computer Science, Mount Holyoke College, South Hadley, MA, ²Department of Mathematics, Texas A&M University, Kingsville, TX, ³Department of Mathematics, University of Tennessee, Knoxville, TN.

The unsustainable harvest of wild animals and plants presents grave biodiversity conservation and livelihood challenges. In particular, non-timber forest products are crucial for the viability of the ecosystem in addition to the economic livelihood for millions of people who rely on them for income. Previous research on plant-animal harvesting has mainly focused on seed dispersal failure under defaunation but neglects the hunting and harvesting interactions between plants and their seed dispersers. To that end, we investigate and represent this interaction by formulating a discrete-time mathematical model. Through various analysis of sensitivity and growth rate, we determine that adult survivorship under harvest as well as hunting are critical parameters for ensuring the population persistence of both the plant and their seed dispersers. Furthermore, we illustrate the broad application of our model by using the Brazil nut-agouti as an example system. Overall, we conclude that conjoined management of co-harvested species is crucial when determining conservation decisions.

ALRED, B.¹, B. REBER², and B. SCHENCK³. Ecological Niche Modeling and Risk Assessment of Thousand Cankers Disease. ¹Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN, ²Mathematics Department, Houghton College, Houghton, NY, ³Applied Mathematics and Biology, College of William and Mary, Williamsburg, VA.

Thousand Cankers Disease (TCD) is an arboreal disease complex which causes mortality in eastern black walnut trees (*Juglans nigra*). TCD is caused by the fungus *Geosmithia morbida*, which is vectored by the walnut twig beetle (*Pityophthorus juglandis*). Maxent models were created to predict niche shift of *P. juglandis* and *J. nigra* under conditions predicted by multiple GCMs using RCP 4.5 and RCP 8.5 in order to help determine high risk areas for TCD. The niche of *P. juglandis* was predicted to have a wide extent which was largely plastic to future scenarios. A northward shift was predicted for the niche of *J. nigra* in future scenarios. The highest risk areas for TCD were predicted to be in the southern U.S. due to more stressful conditions on the trees.

ANDREWS, L.¹, M. LAPP², G. RAIMONDI³, and J. ARCIERO⁴. Modeling Optimal Treatment Strategies for Transplant Patients. ¹Department of Mathematics, Statistics, and Computer Science, St. Olaf College, Northfield, MN, ²Department of Mathematics and Computer Science, The College of Wooster, Wooster, OH, ³Department of Plastic and Reconstructive Surgery, Johns Hopkins School of Medicine, Baltimore, MD, ⁴Department of Mathematical Sciences, IUPUI, Indianapolis, IN.

Solid organ transplantation is a lifesaving procedure that requires lifelong immunosuppression to prevent organ rejection by the host immune system. While this treatment protects the graft, it often leads to complications including hypertension, nephrotoxicity, and cardiovascular disease. Thus, an improved treatment regime is needed to promote long-term graft tolerance and health of the host. Regulatory T cells (Tregs) are a key component of the host immune system that have the capacity to target specific antigens and inhibit inflammation. Thus, increasing host Treg levels through adoptive transfer has been proposed as an alternative method for promoting graft tolerance. This study adapts a previous ODE model of murine heart transplant rejection to include Treg adoptive transfer and immunosuppression via calcineurin inhibitors (CNI) and mechanistic targeting of rapamycin (mTOR). The model predicts that an optimal delivery of Tregs can extend graft lifetime ten times longer than without treatment. Since increased Treg levels alone cannot prevent eventual graft rejection, combinatorial treatment strategies are explored by varying Treg dose magnitude, timing, and frequency and immunosuppressant class, timing, and frequency to maintain graft survival with minimal immunosuppression. These theoretical results can guide in vivo experiments aimed at promoting graft tolerance while minimizing complications presented by immunosuppression.

ATEYEH, A., R. REDDY, and R. SCHUGART. Using Global Sensitivity Analysis to Find Influential Parameters in a Wound-Healing Model. Department of Mathematics, Western Kentucky University, Bowling Green, KY.

To formulate a mathematical model that accurately represents the physiology of a wound, the model must easily predict the most influential factors that affect the wound-healing process. Using a differential-equation model that describes the interactions among matrix metalloproteinases, their inhibitors, the extracellular matrix, and fibroblasts (Krishna et al., 2015), this work focuses on two approaches using global sensitivity analyses. The first approach computes relative “sensitivity” indices for each parameter, and then evaluates the results. The second method is Morris screening, which measures the change in the state variables when a specific parameter is slightly modified from the predicted value. This change can be obtained by finding the difference between the original model and the model with the modified parameter. A sum of squares of these differences can be used to give the overall influence each parameter has on the model. Overall, these methods have allowed for the finding of the most significant factors in the wound-healing process, which can further be used to more accurately predict the healing process for individual patients.

BLESI, A.¹, S. J. BROZAK², H. REED³, R. T. TROUT FRYXELL⁴, and S. LENHART.⁵ La Crosse Virus Spread Within the Mosquito Population in Knox County, TN. ¹Department of Physics and Astronomy, University of Tennessee, Knoxville, TN, ²School of Mathematical and Statistical Sciences, Arizona State University, Tempe, AZ, ³Department of Mathematics, University of Central Florida, Orlando, FL, ⁴Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN, ⁵Department of Mathematics, University of Tennessee, Knoxville, TN.

La Crosse virus (LACV) is one of the leading pediatric arboviruses and a public health concern for children under 16 years, most commonly found in Appalachia. Because LACV is transmitted via the bite of an infected *Aedes* mosquito, it is imperative to understand the dynamics of the local vector population in order to assess risk and transmission. Using entomological data collected from Knox County, Tennessee in 2013, we formulate an environmentally-driven system of ordinary differential equations to model mosquito population dynamics over a single season. Further, we include infected compartments due to LACV transmission within the mosquito population. Findings suggest that the model, with dependence on degree days and accumulated precipitation, can closely describe field data. This model confirms the need to include these environmental variables when planning control strategies.

BROCK, S.¹, Y. DAI², and B. KWARTA³. Economic Modeling of Free-Roaming Cats in Knox County, TN.

¹Department of Mechanical, Aerospace, and Biomedical Engineering, University of Tennessee, Knoxville, TN,

²Data Analytics, The Ohio State University, ³Mathematics Department, Houghton College, Houghton, NY.

Unowned free-roaming cats live outdoors and have little contact with humans. The unowned free-roaming cat population is a global problem due to predation on wildlife, the spread of infectious diseases, and causing other nuisances. Programs such as Trap, Neuter, and Return (TNR) and Trap-Euthanize (TE) have been used to control cat populations. This study involves building a discrete-time mathematical model that represents the free-roaming cat population in Knox County, TN based off given data. The economic costs associated with possible management strategies of the cats are coupled with this model to give guidance about policy decisions. For all time horizons, no control is the most expensive and results in the largest cat population. For a short-term solution, the TE program has the lowest population and is the least expensive. However, whenever the TE program ends, the cat population quickly rises to that of the no control scenario. For a long-term solution, the TNR program is the least expensive and results in the lowest population. Therefore, for this model and chosen parameters, the most cost-effective solution of the unowned free-roaming cat population is a TNR program.

EVERSMAN, K., K. BARRS, M. ANI, and O. RUEPPELL. Division of Labor in Hygienic Behavior of *Apis mellifera*: Experimental Investigation to Simulation. Department of Biology, University of North Carolina, Greensboro, NC.

Honey bees (*Apis mellifera*) are eusocial insects known for their complex colony structure and contribution to agriculture through pollination. In recent years, the health of honey bee colonies has declined. Currently, the *Varroa* mite (*Varroa destructor*), a highly specialized parasite, is considered one of the most dangerous factors affecting *Apis mellifera* colonies. Hygienic behavior, the process of removing diseased or dead brood from the hive, is a natural defense against *Varroa*. Numerous studies have addressed hygienic behavior, but the mechanistic process of this behavior is still poorly understood. By implementing direct observations from an experimental assay into an agent-based model, we explored division of labor within hygienic behavior. Our model simulates a bee colony by incorporating both bee and mite lifecycles. We compared the efficacy of hygienic behavior in models that either allowed bees to differentially perform the tasks associated with hygienic behavior or not. Experimentally, we have found evidence of division of labor within hygienic behavior: a few bees perform the majority of one task and do not participate in the other. Our simulation suggests that hygienic behavior is improved by the bees' ability to divide their labor into different tasks by

decreasing the frequency of erroneously performed hygienic behavior. Our combination of empirical observation and theoretical modeling thus finds division of labor in hygienic behavior to exist and to be adaptive. These insights into hygienic behavior can help breeding programs for hygienic behavior to combat a major factor of declining honey bee health.

GILBERT, K.N., A. REYNOLDS-GRAY, R. FRYE, and L.K. VAUGHAN. Using *C. elegans* as a Model for Non-nutritive Sweetener and Glucose Metabolism. Department of Biology, King University, Bristol, TN.

Some of the most common diseases facing today's U.S. population are Type 2 Diabetes and Obesity. Since the intake of sugar is largely associated with the occurrence of these diseases, people have tried to find health alternatives to sugar without losing the great taste. One popular solution, non-nutritive sweeteners such as Splenda and Sweet'N'Low, offers a possible healthy choice with an appealing taste. However, there is large debate on whether these sweeteners are helping or hurting the situation. This study aims to compare the effects of non-nutritive sweeteners and glucose on metabolism pathways in *C. elegans* for comparison to human medicine. Specifically, the effects of the upregulation/downregulation of the insulin signaling pathway will be examined. After evaluating the insulin signaling pathways of *C. elegans* via fluorescent microscopy, it was found that the nematodes exhibited GFP morphology in response to various glucose concentrations. Additionally, 5-fluoro-2'-deoxyuridine (FUDR) caused the nematodes to exhibit GFP morphology when exposed at the L1 life stage. However, non-nutritive sweeteners may not have an adverse effect on nematode lifespan. Finally, lipid accumulation was observed in nematodes exposed to a high dosage of glucose.

GORT FREITAS, N. A., A. KOLCHINSKY, A. and C. KEMPES. Scaling of Information in Biochemical Systems. Santa Fe Institute, Santa Fe, NM.

Cellular environments are complex and dynamic. The temporal and spatial concentration profiles of external molecules encode information that cells can harness through networks of interacting molecules, which allow them to learn about their environment. Despite the numerous sources of intrinsic and extrinsic noise that limit the capacity of cells as information channels, cells manage to thrive, replicate and maintain chemical equilibrium. In this work, I studied how the inherent stochasticity in protein synthesis limits the transmission of the compositional information of the cell over time, and how this stochasticity scales with respect to cell size through the usage of stochastic simulation methods. Taking a two-species dynamical model of ribosomes and proteins, we unveiled a novel relationship between the initial count distribution of each species, the cell size and the conservation of compositional information over time, defined as the mutual information between the initial state vector and the state vector after a generation of cell division. This has implications on the extent to which a cell needs to regulate its inner environment to maintain chemical equilibrium.

HELTON, T., and W. LINDERMAN. Applications of the Monte Carlo Method for Problem Solving. Department of Mathematics and Physics, King University, Bristol, TN.

This work presents a possible solution using the Monte Carlo (MC) method to the problem proposed by Julien Sorei and Piatra Neamt from PNI, Romania, in Mathematics Magazine, Volume 90 Number 5, in a section of original problems meant to appeal to students and teachers interested in undergraduate mathematics. The problem states, "Letting two points on the circumference of the unit circle, A and B be chosen uniformly at random, and letting two further points C and D be chosen independently and uniformly at random on the inside of the unit circle, what is the probability that D will lie inside the triangle formed by A, B, and C?" This problem could be restated as the following: "What is the chance that a dart thrown at a dartboard will hit a triangle of arbitrary size given two points of the triangle lie on the dartboard's edge, given the third point lies somewhere within the circumference of the dartboard, given that the dart is guaranteed to hit somewhere on the dartboard." Computer simulation using the MC method provides similar results to the exact mathematical solution, illustrating the utility of simulations in mathematics education. The MC program simulated

“throwing” millions of “darts” at triangles of random shape and size as given by the above parameters, providing an easy way to visualize problem. The solution generated by this work has been selected for publication in an upcoming issue of Mathematics Magazine.

IGNACZ, A., J. ELDER, N. EISEL, L.K. VAUGHAN, and V.A. FITSANAKIS. Chronic Exposure to Manzate Formulation in Genetically Modified *Caenorhabditis elegans* Leads to Mitochondrial Dysfunction. Department of Biology, King University, Bristol, TN.

Commercial manzate is a common fungicide used for agricultural purposes, and it has been linked to the development of neurodegenerative diseases, such as Parkinson’s disease (PD). Since gene-environment interactions can influence the formation of PD, manzate exposure studies were conducted using *Caenorhabditis elegans* (*C. elegans*), a nematode model organism, to determine the mechanism for the development of Parkinsonian neurodegeneration. To determine the effects of the fungicide on worms that are already genetically vulnerable to parkinsonism, the worms were acutely exposed to manzate in a three-day protocol. The worms were then assessed for proton gradient potential, death, and ATP production. Hyperpolarization occurred in the mitochondria of *Irrk2* mutant *C. elegans* due to a Ca^{++} efflux in response to mitochondrial damage. In an ATP assay, fluorescence measurements indicated an increase in worm death in response to the manzate treatment. Luminescent signals readings suggested that the worms may be increasing ATP production in response to the hypothesized Ca^{++} -induced hyperpolarization. These data support that manzate exposure in *C. elegans* leads to mitochondrial dysfunction, characteristic of PD.

PELLETT, J.¹, DUAN, J.², M. MALAKHOV³, and I. PHADKE⁴. Efficacy of Control in a Spatially Dynamic Model of White-nose Syndrome. ¹Department of Mathematics & Statistics, University of Wisconsin- La Crosse, La Crosse, WI, ²Department of Mathematics, Bryn Mawr College, Bryn Mawr, PA, ³Department of Mathematics, Andrews University, Berrien Springs, MI, ⁴Department of Mathematics, Pennsylvania State University, State College, PA.

White-nose syndrome (WNS), caused by the invasive fungal pathogen *Pseudogymnoascus destructans*, is a virulent disease that has plagued North American bat populations since 2006. Over the past decade, WNS has rapidly spread throughout much of the eastern United States, leading to mass mortality and threatening range-wide extinction in a number of bat species. Thus, the need for development and implementation of effective control strategies has become increasingly exigent. Previous studies have explored disease dynamics and control in a single hibernaculum model. Here, using a continuous-time two-hibernacula model, we incorporate spatial dynamics to investigate the effects of seasonal bat dispersal on the efficacy of five developing control strategies. We demonstrate that informed management decisions must take interpopulation movement into account, and find the effects of dispersal on control efficacy to be dependent on both the control combination and the primary mode of disease transmission.

PETROSKI, A., and M. ROBERT. Investigating Density-Dependent Effects on Fitness of the Dengue and Zika Vector *Aedes aegypti* and Possible Consequences for *Wolbachia*-Based Control Strategies. Department of Mathematics, Physics, and Statistics, University of the Sciences, Philadelphia, PA.

The mosquito *Aedes aegypti* is responsible for transmitting arboviruses like Zika and dengue, which primarily affect tropical and subtropical areas of the world. This mosquito carries out its early life processes in artificial water containers, and juvenile mosquito populations can be regulated by density dependence. Density dependence is often assumed to increase death rates of mosquitoes, but other life history characteristics such as birth and development rates can also be impacted. Understanding the impact of density dependence on life history traits is critical for developing control programs aimed at eliminating mosquito-borne diseases. We develop an ordinary differential equation population model that incorporates density-dependent fitness (reproductive success) into rates associated with different life history traits. Through analysis and numerical

simulation, we investigated the impacts of fitness advantages and disadvantages on mosquito control involving releases of mosquitoes infected with *Wolbachia*, a maternally transmitted bacterium that affects the lifespan of *Ae. aegypti* and its ability to transmit dengue. We considered various combinations of functional forms and parameters in the fitness term, and we found differential impacts on population dynamics and *Wolbachia*-based control. The results of our study help provide insight into appropriate control measures under different assumptions about the impacts of density dependence.

RIVENBARK, K., J. ELDER, N. EISEL, L.K. VAUGHAN, and V.A. FITSANAKIS. Manzate Exposure Alters Mitochondrial Membrane Potential in Genetically Modified *C. elegans*. Department of Biology, King University, Bristol, TN.

Exposure to the commercial formulation of manzate has been connected to the development of numerous neurodegenerative diseases, including Parkinson's disease. The development of Parkinson's disease is a complex mechanism, likely influenced by gene-environment interactions rather than solely genetic or environmental factors. *Caenorhabditis elegans* with a genetic predisposition of developing parkinsonian-like signs, like mitochondrial dysfunction, were exposed to manzate to assess and clarify this complex gene-environment interaction. Nematodes were exposed to various concentrations of manzate for thirty minutes for three consecutive days, specifically assaying for signs of altered membrane potentials and changes in mitochondrial content compared to control nematodes. Analysis of the membrane potential assay suggested that the treated groups showed a significant increase in fluorescent dye accumulation compared to control worms ($p=0.0025$). Examination of the literature suggests the increased fluorescence could be due to increased cytosolic Ca^{2+} , or an increase in the amount of mitochondrial content. Future research is necessary to confirm increased mitochondrial numbers and to assess the levels of cytosolic Ca^{2+} .

ROSENBALM, N.¹, and C. FAY². Disease Progression on Social Networks. ¹King University, Bristol, TN, ²Physics Department, Emory and Henry College, Emory, VA.

The deterministic SIR and SIS models are generally accepted as an efficient way to represent the theoretical number of people in a population infected by a disease over a certain period of time. The goal of this study was to find another method of representing these outbreaks, specifically a stochastic model. To find a stochastic alternative to the SIR and SIS models, graph population and node states were observed as simulators of disease on four different graph types; random, scale-free, configuration model, and hierarchical configuration model. Each node on the graph represented a person and each edge between two nodes represented an interaction between two people. A disease was then introduced into the population and the spread simulated. Once the simulation was completed, a plot of data was constructed comparing the evolution of the number of susceptible, infected and recovered or dead nodes versus time. This stochastic model was then compared to the deterministic SIR and SIS models, and was found to be a viable alternative on each of the four graph types. Data for an outbreak of Dengue in Puerto Rico was then compared the stochastic SIR model that had been tested. This data was also used to compare how each of the four graph types compared to real world disease spread data.

SAVINOV, M., B. ERMENTROUT, and D. SWIGON. Entrainment of Forced Oscillators with Flexible Periods. Department of Mathematics, University of Pittsburgh, Pittsburgh, PA.

Entrainment is the process by which any two interacting oscillating systems may assume the same period. Experiments have shown that some oscillating systems are able to change their periods. Studying this type of coordination, Loehr et al. asked human subjects—playing on pianos—to follow the beats of a varying metronome sequence; the responses were fit to a nonlinear oscillator model. Unlike previous models, their oscillator model has the ability to change its period of oscillation as well as shift its timing. The discrete model is quantitatively described using a circle map defined by phase and period with sinusoidal coupling terms. This

project focuses on the analysis of this model as well as three proposed variations, two of which feature a preferred period. We focus on the stability of fixed points of N:M locking, where for every N stimuli, the oscillator's phase rotates M times. The types of locking investigated are 1:1, 1:2, 2:1, 2:3, and 3:2. For all four variations, numerous parameter sets were found where the models exhibited multi-stability, including some sets where all investigated types of locking had stable fixed points. This multi-stability is not generally possible when the natural period is not malleable.

TORSEY, A. Analyzing the Dynamics of an Inflammatory Response to a Bacterial Infection in Rats.

Department of Mathematics, Buffalo State College, Buffalo, NY.

Sepsis is a serious health condition defined by an overactive immune response that causes severe damage to healthy tissue, often resulting in death. Mathematical modeling has emerged as a useful tool to investigate key elements of the immune response and thus offers a useful method for studying sepsis. Here, a system of four ordinary differential equations is developed to simulate the dynamics of bacteria, the pro-inflammatory immune response, anti-inflammatory immune response, and tissue damage. The model is used to assess the conditions under which health, aseptic (inflammation-driven) death, or septic (bacteria-driven) death is predicted in both the presence and absence of an induced E. Coli bacterial infection in rats. Model parameters are fit to experimental data from rat sepsis studies. The model is used to predict the survivability range for an infection while varying the initial amount, growth rate, or virulence of the bacteria in the system. For highly virulent strains of bacteria, aseptic or septic death is predicted for very small levels of initial bacterial loads. Model predictions are also used to explain the experimentally observed variability in the mortality rates among rats.

TURNER, A., M.P. KNAPP, D. IVANKOVIC, and D. PRAGER. Simulating an Outbreak of Zika Virus in Climates with Seasonal Mosquito Patterns. Departments of Biology and Mathematics, Anderson University, Anderson, SC.

Zika virus is associated with the development of neurological disorders, such as Guillain-Barré syndrome and congenital microcephaly. A model to simulate the spread of the Zika virus was developed by Carrie Manore, in which she used seven differential equations to simulate outbreaks in climates with year-round mosquito activity. However, Manore's model is not accurate for areas with seasonal mosquito activity, and it does not account for human-to-human transmission. We will describe the adjustments we made to Manore's model in order for a simulation of an outbreak in South Carolina to be accurate. We replaced a term in Manore's susceptible human differential equation to allow for mosquito seasonality and included a term in her exposed human differential equation to account for human-to-human contamination. Since we do not have an empirical value for the rate of human-to-human transmission, we performed different simulations, all showing that the maximum number of infected humans becomes significantly higher and is reached more quickly with our adjustments. In addition, our findings show that an outbreak will occur in annual waves, with the sequence of waves lasting for several years. Sensitivity analysis will be performed to determine which transmission parameters have the greatest influence on model results.

WATERS, R. 3D Printing and Microfluidics. Emory and Henry College, Emory, VA.

Microfluidics is a field combining both scientists and engineers. Due to its small size microfluidics creates faster results and cheaper lab equipment. This is beneficial not only for scientists, but also for the environment. The advancements in 3D printing have made microfluidics more practical now than ever. Some of the smaller applications of the technology have been overlooked in the last couple of years. Revisiting basic science problems such as pollution we see there are new ways to deal with old problems.

YANG, J.¹, Z. BILLINGS², and K. SCHATZ³. Estimating Rates of Homologous Recombination in Bacteria.

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Bacteria are commonly regarded as clonal organisms, inheriting genetic information from a single parent cell. However, evidence shows that bacteria undergo homologous recombination where they incorporate foreign DNA into their genomes. Recombination is most impactful when transferring genes that increase survivability. For example, the transfer of genes for antibiotic resistance can lead to “superbugs:” strains that are resistant to many classes of antibiotics. Recombination is not yet well understood as several studies have come to inconsistent conclusions regarding the rate at which it occurs. However, homoplasies, which are sections of shared DNA not inherited from a common ancestor, are easier to detect, and they arise from either recombination or convergent mutation. Thus, estimating convergent mutations allows us to indirectly infer the rate of recombination. Employing a probabilistic model verified by simulation, we gain insight into which bacterial species undergo recombination and how frequently they do so. Ultimately, an accurate metric for recombination rate provides a better understanding of bacterial evolution and adaptation.