Conference Proceedings

National Institute for Mathematical and Biological Synthesis (NIMBioS)

2017

2017 Conference Abstracts: Annual Undergraduate Research Conference at the Interface of Biology and Mathematics

National Institute for Mathematical and Biological Synthesis (NIMBioS)

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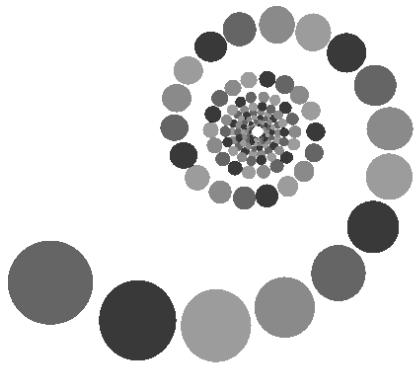
NIMBioS

National Institute for Mathematical and Biological Synthesis

Ninth Annual

Undergraduate Research Conference

at the Interface of

Biology and Mathematics

November 11-12, 2017

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 60 oral and poster presentations. A keynote by Dr. Kiona Ogle and featured talk by Dr. Katherine Evans 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 6, oral presentation abstracts start on page 16.

NIMBioS
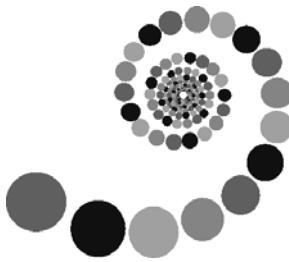
The National Institute for Mathematical and Biological Synthesis is a center that brings together talented researchers in the fields of math and biology from all over the world. At NIMBioS, researchers work to cross the boundaries of their disciplines and address the many questions and challenges of 21st century biology. Currently in its ninth year, NIMBioS is sponsored by the National Science Foundation and the Departments of Homeland Security and Agriculture, 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 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 a revitalized portion of downtown known as Market Square: a pedestrian mall with restaurants and shops.

INFORMATION FOR HANGING POSTERS

There will be two poster sessions. The first will immediately follow dinner on Saturday, from 7:00-8:00 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 auditorium room 406. Find your assigned space and use the tacks provided to affix it to the wall or poster board. Poster abstracts and numbering start on page 6.

INFORMATION FOR ORAL PRESENTERS

Refer to the schedule to find your presentation time and room number. You will have 15 minutes to speak and including a few minutes for 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 2017

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 2017 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.

Facebook: NIMBioS is on Facebook: http://www.facebook.com/nimbios
Look for pictures and blog posts from the URC shared on this medium – or share your own.

KEYNOTE LECTURE

Dr. Kiona Ogle
School of Informatics, Computing & Cyber Systems
Northern Arizona University

Application of Mathematical and Statistical Modeling to Understand Plant and Ecosystem Memory

In this talk, I highlight different statistical and mathematical modeling approaches to quantifying ecological memory. In general, these approaches allow us to understand how ecological responses of interest are governed by exogenous (e.g., environmental) and endogenous (e.g., intrinsic feedbacks) drivers, and their time-scales of influence. I use "memory" to broadly refer to these time-scales of influence, including lagged responses and the importance of antecedent (past) conditions. I focus on applications to soil carbon fluxes and net ecosystem exchange of carbon and water, and highlight other applications to annual tree growth (via tree rings) and sub-daily plant physiological responses. All applications combine field data and models, and the models range from fairly empirical statistical models to process-based differential equation models. The statistical models often employ Bayesian methods that allow integration of diverse data and non-linear models that explicitly quantify time-scales of influence. In all applications, which are mostly focused on arid and semi-arid systems, we find that antecedent conditions are critical to understanding plant and ecosystem processes, and important time lags are revealed. Together, we find that ecological memory is an important process governing plant and ecosystem responses to environmental perturbations.

FEATURED SPEAKER

Dr. Katherine Evans
Climate Change Science Institute
Oak Ridge National Laboratory

Using Computational Science to Understand Earth's Climate

Understanding the myriad of ways in which global warming will affect our planet over the next century requires large-scale and complex global Earth system models. With this tool, scientists are delving into the atmosphere, ocean, land surface, and cryosphere and how these facets of Earth couple together at regional and local scales as part of a larger background of global climate variations. Within the U.S. Department of Energy, we leverage the use of multi-petascale computing facilities to execute and analyze global models that resolve weather scale phenomena in space and time. Scientifically, our efforts include the identification and characterization of atmospheric phenomena at multiple scales, the prediction of sea level rise due to ice sheet and glacier melt, and changes to global biogeochemical cycles. We also prioritize the development of novel testing, evaluation, and determination of uncertainties as models and analysis grow more complex so that we can best inform stakeholders for planning and action.

<u>SCHEDULE</u>

Saturday, November 11: 413AB (Except where noted)

1:00-1:10 Welcome: Dr. Suzanne Lenhart and Dr. Louis Gross, NIMBioS

1:10-2:10 Keynote Lecture:
   Dr. Kiona Ogle, School of Informatics, Computing & Cyber Systems, Northern Arizona University
   Application of Mathematical and Statistical Modeling to Understand Plant and Ecosystem Memory

2:20-2:35
   406: Jordan Pellett – *Modeling Chronic Vascular Responses Following a Major Arterial Occlusion*

   413AB: Erick Oduniyi and Brad Gibbons – *Modeling Ebola Transmission Dynamics with Media Effects*

2:40-2:55
   406: Hannah Dille, Mary Peyton Knapp, and Jonathan Low – *Modeling Breast Cancer Cell Growth and the Effects of Selected Cancer Therapies*

   413AB: Brielle Kwarta and Ben Reber – *Optimal Growth Allocation in Sarracenia purpurea in Varying Environments*

3:00-3:15
   406: Anthony Clear – *Ion Dynamics in The Neurovascular Unit: Analyzing the Affects of Neuronal Seizures on Astrocytes and Blood Vessels*

   413AB: Noah Rosenbalm – *Graph Population and Node States as Viable Simulators of Disease Infection Models*

3:20-3:30 *Opportunities at NIMBioS and Explanation of Networking Activity*
   Greg Wiggins, Education & Outreach Coordinator at NIMBioS

3:35-4:05 Networking Activity and Snack Break

4:10-5:00 Featured Speaker:
   Dr. Katherine Evans, Climate Change Science Institute, Oak Ridge National Laboratory
   Using Computational Science to Understand Earth's Climate

5:10-6:00 Career Panel (Moderator: Suzanne Lenhart, Associate Director at NIMBioS)
      Dr. Kiona Ogle, School of Informatics, Computing & Cyber Systems, NAU
      Dr. Katherine Evans, Climate Change Science Institute, ORNL
      Dr. Albrecht von Arnim, Professor of Biochemistry & Cellular and Molecular Biology, UTK
      Dr. Christopher Strickland, Associate Professor of Mathematics, UTK

6:00-7:00 Buffet Dinner in 404A

6:30   Turn in SET game sheets to Wiggins or Lenhart at Dinner

7:00-8:00 Poster Session I: Odd numbered posters presented (and desserts)

Sunday Morning, November 12: Auditorium 406, 413AB, 413C

8:00 Continental Breakfast

8:30-8:45

406: Aisling Power and Caitlin Nicholson – *Investigating the Mechanical Response of Stress in Coronary Arteries*

413AB: Patrick Pruckler – *A Reaction-Diffusion Model of Acid-Mediated Tumor Invasion with Chemotherapy Intervention*

8:50-9:05

406: Kyle Goryl – *Modeling RNA Secondary Structures Using Matchings*

413AB: Alison Adams, Owen Dougherty, and Quiyana Murphy – *Within-host Mathematical Models for Orthohantavirus Infections*

9:15-9:30

406: Joshua Baktay – *A Computational Model of the Central Nucleus of the Amygdala During Bladder Pain*

413AB: Andrew Brettin and Kyle Weishaar – *Ebola could be Eradicated through Voluntary Vaccination*

9:35-9:50

406: Erin Jennings – *Examining the Contribution of the Microbiota to the Healthy Aging AC5KO Phenotype*

413AB: Jonathan Machado – *Optimal Vaccination Strategies to Reduce Endemic Levels of Meningitis in Africa*

9:55-10:50
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: Ashley Reynolds – *Evaluation of the Cytotoxicity of Tin Dioxide Nanofibers*

413AB: Camille Hankel – *Long-Time Behavior of Two Competing Sub-Species on a Discrete Periodic Habitat*

1:20-1:35
406: Rachel French – *Using Mixed Effects Modeling to Quantify Differences between Patient Groups with Diabetic Foot Ulcers*

413AB: Emily Cosgrove and Eddie Lindsey – *Effects of Competition-Mediated Dispersal on the Persistence of a Population*

1:40-1:55

      406: Kaiying Mo – *Phenomenological Models for the Relationships Among Occupancy, Mean, and Variance of Species Abundance Spatial Distribution*

      413AB: Javier Urcuyo and Matt Ghatak – *Modeling the Spread of La Crosse Virus in Knox County, Tennessee*

2:00-2:15

      406: Sharee Brewer and Kimberly Dautel – *Density Dependence and Multiple Matings Lead to Sexual Conflict in Territorial Migratory Songbirds*

      413AB: Justin Garagnani – *Optimal Advertising Strategies for Use in Popular Media*

2:20-2:35

      406: Jaclyn Pescitelli – *Turing Instability in a Predator-Prey Model for Zooplankton Grazing on Competing Phytoplankton Species*

      413AB: Arjun Kanthawar and Nikhil Krishna – *Accurately Modeling the Wound Healing Process*

2:40-2:55

      406: Sunny Kennedy, Sam Cole, and Rebekah Frye – *Mechanistic Toxicology of Neurodegeneration Induced by the Pesticide Manzate in the Model Organism Caenorhabditis elegans*

      413AB: Jingzhen Hu – *pKa Computation Based on Poisson-Boltzmann Equation*

3:00-3:15

      413AB: Jacob Menix – *Using Computational Bayesian Statistics to Analyze Parameters in a Differential Equations Model*

3:20-3:30

      413AB: Closing Remarks

3:30 Adjourn

POSTER ABSTRACTS

1) BAKTAY, J., R. NEILAN, M. BEHUN, and B. KOLBER. A Computational Model of the Central Nucleus of the Amygdala during Bladder Pain. Department of Mathematics and Computer Science, Duquesne University, Pittsburg, PA.

Chronic bladder pain (CBP) activates neurons in the central nucleus of the amygdala in the brain which exhibits asymmetric behaviors across each hemisphere. To better understand CBP, an agent-based computational model was created using Netlogo software to replicate neuronal behavior observed in bladder distension experiments on mice. In the simulation agents represent individual neurons with unique firing rates updated stochastically at each time step. In total, the model represents the behaviors of four neuron types and an organism's overall perceived pain in response to different noxious stimuli. A damage accumulation feature was added to the model to track the organism's long-term pain history. The model interface provides a dynamic framework for viewing neural activity as it evolves over time and allows the user to predict different pain states by controlling model parameters. Ongoing work will account for the topology of the neural network, cell-type specificity, and three spatial dimensions.

2) BARKER, S., and B. LINDERMAN. Dominance Domains and the 17-Year Cicada. Department of Biology, King University, Bristol, TN.

The lifecycle of the 17-year Cicada has stumped biologists for seemingly eons. But what if the answer to this mysterious puzzle lies in the sky above? Using the cycles of the moon and the changes of that cycle over the millennia, it has been noted that the 17-year Cicada follows eerily close to the moon's cycle. About 250 million years ago there was about 12 + 9/19 moons in a year, with a moon cycle of about 19 years. Now the moon has a cycle of 17 years. Using the dominance domains of these continued fractions, the 17-year Cicada's lifecycle can be seemingly modeled to fit into these intervals.

3) BAUTISTA, A.R., A Mathematical Model for the Potential of a Zika Outbreak in Oahu. University of Hawaii-West O'ahu, Kapolei, HI.

The Zika Virus (ZIKV) is an arbovirus that is known to cause flu/cold-like symptoms and microcephaly, a birth defect where the primary characteristic is the child being born with a smaller than average head. This is caused by an improper development of a child's brain. ZIKV is especially dangerous in the ability for it to not only be passed along during sexual contact, but primarily for its ability to pass along through *Aedes* mosquitoes. Should an uninfected mosquito bite an infected human, they can proceed to infect other humans a small time after the initial bite. This study intends to explore the potential ability for an outbreak in the island of Oahu. Oahu is the central island in the state of Hawaii, also known to be the social hub and primary tourist destination of the islands. Being the home of the *Aedes albopictus* mosquito and just under one million humans, this densely packed island could potentially be a perfect breeding ground for the ZIKV virus. In this study, we will investigate the likelihood of an outbreak in the island of Oahu, as well as the parameters in which an outbreak could be possible.

4) BEIHOFF, J. and A. HONTS. Street View Imagery Based High-Resolution and High-Accuracy Human-Environment Vegetation Mapping: How Green is our County? Department of Mathematical Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.

Measuring the amount of vegetation in a given area has long been accomplished using satellite and aerial imaging systems. However, a primary limitation of these methods has been their ability to measure vegetation coverage accurately only at the top of the canopy, often neglecting green vegetation located beneath canopy cover. Measuring the amount of urban and suburban vegetation beneath canopy cover along the street network is now possible through the use of Google Street View (GSV) images, made accessible by the Google Street View Image API. We developed a multi-filter image processing technique to extract green vegetation

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pixels from GSV images, and computed a green index associated with each image location. Analyzing green vegetation through the use of GSV images provides a comprehensive representation of the amount of green vegetation found within an area, and facilitates an analysis rarely performed on a large scale at the street-level. We use this high-resolution GIS data to map the green index of Milwaukee County in Wisconsin. Such data can be used in statistical comparisons between urban greenery and other known health and socioeconomic outcomes for possible health, social, and urban planning benefits.

5) BURKE, T. The Impact of Recombination on Evolutionary Inference of *Cryptococcus neoformans*. Department of Mathematics, Howard University, Washington, DC.
Cryptococcus neoformans is an opportunistic fungal pathogen found throughout the world, and one of the leading killers among HIV+ people in sub-Saharan Africa. Previous population genomic analyses of *C. neoformans* revealed that there was a large amount of recombination. As recombination can introduce sequences not inherited by vertical descent and therefore skew evolutionary analysis, we decided to re-analyze the impact of recombination with our dataset using two different methods. In the first method, we identified and quantified recombinant regions and estimated phylogenies of the dataset before and after the recombinant regions were removed. One lineage, VNI, had considerably more recombinant regions than was originally measured. Notably, we observed differences in the estimation of phylogenies before and after recombinant regions were removed. In an independent approach, we modeled the recombination of 9 marker genes to find which loci show evidence of recombination between lineages. Interestingly, we observed that SOD1, a super oxide dismutase and known virulence factor, was one of the shared genes. Given our results, we hypothesize that recombination plays a more crucial role in the evolution of *C. neoformans* than previously assumed and it could be misleading to conduct evolutionary studies without taking into account the impact of recombination.

6) CALDES, H.[1], K. RUDDY[1], A. LI[1], and P. DORN[2]. Graph Connectivity Indices Applied to the Evolutionary Analysis of Chagas Disease Vectors. [1]Department of Mathematical Sciences, Montclair State University, [2]Department of Biological Sciences, Loyola University New Orleans, LA.
Trypanosoma cruzi, otherwise known as Chagas disease is currently at epidemic levels in Central America. The disease is carried by the insect *Triatoma dimidiate*, which transmits the disease to the host. It commonly leads to heart and digestive problems. In order to understand the evolutionary relationships between species, DNA sequences can be analyzed using the pKa value of each of the bases and the Randic connectivity Index. By calculating the pKa connectivity indices as well as the ratio of the number of A and T to the number of G and C, a phylogenetic tree is constructed to help with the species analysis. For this analysis 120 different haplotypes with DNA sequences with a length of 489 base characters have been analyzed to create a phylogenetic tree for the ITS-2 sequence series.

7) DELBRIDGE, K.[1], J. NGUYEN[2], J. MONDAL[2], and B.D. BRUCE[1,2]. Optimization of High-throughput PAM (Pulsed Amplitude Modulated) Fluorescence Analysis of Aquatic Cyanobacteria for Detection of Herbicides in the Environment. [1]Department of Chemical and Biomolecular Engineering, University of Tennessee, Knoxville, TN, [2]Department of Biochemistry and Cellular & Molecular Biology, University of Tennessee.
Many herbicides have their primary effect on the process of photosynthetic electron transport. This effect is often associated with an alteration of the chlorophyll fluorescence form PSII. This can be measured using pulsed fluorescent measurements providing rich data on the change in fluorescence and the effect on photosynthesis. We have begun using several different cyanobacteria to see how they response to the common herbicide Diuron™ or DCMU ((3-(3,4-dichlorophenyl)-1,1-dimethylurea). Application of DCMU will be tested on three cyanobacteria, two thermophilic cyanobacteria *Thermosynechococcus elongatus* BP-1 and *Chroococcidiopsis* TS-821, and the mesophilic cyanobacteria, *Synechocystis* PCC 6803*.* Fluorescence data is

captured using a FluorCam instrument, from a suspension of cyanobacteria in custom designed 96-well plate*s*. The 96-well plate was created with 3D printing to maximize the detection of the fluorescence signal. This improvement was done by decreasing the plate depth and minimizing fluorescence from the plate material and by optimizing the optical configuration of the LEDs and detectors. In pursuit of quantifying the fluorescence data and measuring stress tolerance, a program was developed to rapidly calculate the parameters and standard deviation for F_0, F_v, F_m, and Qy. The program executes its commands as a function of well plate location so that multiple variables can be tested at once, as the eventual goal is to have a high-throughput system for testing multiple variables at once.

8) DIXON, E. Developing an Introductory Computer Science Course for Scientists and Mathematicians in Python and R. Department of Computer Science, University of North Carolina, Asheville, NC.
The role of computational software within nearly all scientific fields is growing. As the amount of data available to us continues to increase, the ability to summarize, organize, and visualize large data sets has become extremely important. In the summer of 2017, we designed an introductory programming course to be taught in Python and R. Many of the students who will take this course will be natural science and math majors, rather than computer science majors. Therefore, it was designed to be immediately useful for people who may not take another computer science course. Modeled after a similar course that was designed by Kevin Sanft and Olaf Hall-Holt at St. Olaf College, our course was designed to impart students with foundational knowledge in programming and logic with an emphasis on the skills necessary to collect, organize and visualize data using Python and R. This course is currently (Fall 2017) being offered for the first time. We describe the course content and rationale, initial feedback (quantitative and qualitative) from students and faculty, and recommendations for future offerings at UNC Asheville and other institutions.

9) DUTKOSKI, M. A Mathematical Model of the 2015 Dengue Outbreak on the Island of Hawaii. University of Hawaii-West O'ahu, Kapolei, HI.
The dengue virus is estimated to effect 50 million people yearly worldwide. The dengue virus is not endemic in the state of Hawaii. In the 2015-2016 dengue outbreak on Hawaii Island, 264 confirmed cases of the vector-borne disease were reported to the Hawaii Department of Health. This outbreak was transmitted through the vector species *Aedes albopictus* and *Aedes aegypti* mosquitoes, which are endemic to certain areas on the Hawaii Island. With the heavily trafficked tourist destination of the Hawaiian Islands, habit ranges for *Aedes albopictus* and *Aedes aegypti* may expand, resulting in a far more serious epidemic than the 2015-2016 outbreak or possibly dengue becoming endemic and establishing itself in Hawaii. In this project, we develop a mathematical model to describe the spread of dengue using a system of differential equations. This model should be able to predict the conditions that would enable dengue to become endemic or have another outbreak in Hawaii.

10) FALGOUT, E.[1], and R. SCHUMM[2]. The Investigation of Small Worldness in Pancreatic Islets. [1]Departments of Mathematics and Computer Science, Louisiana State University, Baton Rouge, LA, [2]Marquette University, Milwaukee, WI.
Diabetes occurs when the body's blood sugar levels are in a state of sustained elevation. The pancreatic beta cells, organized in the islets of Langerhans, secrete a hormone called insulin that is responsible for maintaining blood glucose at appropriate levels. Oscillations in insulin levels, which are thought to require beta cell synchronization, are necessary for proper regulation of glucose. To study the properties of the cell network that establishes synchronization, the Single Slow Channel Model was used to compute the calcium and electrical dynamics during insulin secretion of a single beta cell. An islet was modeled by coupling the cell cluster according to a hexagonal-close-packed lattice. The small worldness of the functional network derived by correlating calcium traces was quantified and cells acting as hubs were identified using methods from graph

theory. To observe the effect of hub dysfunction on islet synchronization, network hubs were electrically silenced through the activation of a chlorine channel and the dynamics of the resulting network were re-simulated. Synchronization was quantified using an index that reflects the degree to which the calcium oscillations were in phase. Statistical learning techniques were then used to infer cell and structural network properties conducive with hub function.

11) FERRER, L. and A. PALOMINO. Free Swell Potential of a "Tunable" Clay-Composite: Investigation of Behavioral States. Civil & Environmental Engineering, University of Tennessee, Knoxville, TN.
Understanding soil expansion is essential for soil improvement and will lead to more reliable building foundations, prevention of landfill breakthroughs, and slope stabilization. New geo-materials may aid in improving the design of such structures. Materials that are adaptable to changing environmental conditions may be better suited for some applications in which swelling may be problematic. "Tunable" clay-polymer composites are adaptable geo-materials and are synthesized by combining a responsive polymer with clay mineral particles, thus producing a material with modifiable properties. For this study, montmorillonite (Mt) was combined with polyacrylamide (PAM), a polymer responsive to pH and ionic concentration, to form the clay-polymer composite Mt-PAM. The purpose of this study is to investigate the relationship between the free swell potential and the behavioral states of the composite in the presence of different surrounding fluid chemistries by measuring the swell factor and the Atterberg limits. Results indicate that the swell factor is not influenced by changing salt concentration, but increases with increasing pH. The liquid limit decreases with increasing salt concentration and varies with increasing pH. Thus, the swell factor does not give a clear indication of the behavioral states when the solids content reaches that of the Atterberg limit tests.

12) FLORIDA, R. Mathematical Modeling and Optimal Control of Two Competing Strains of Methicillin-Resistant *Staphylococcus aureus* in a Community Setting. Department of Mathematical Sciences and Physics & Astronomy, Middle Tennessee State University, Murfreesboro, TN.
Mathematical models of community-acquired and hospital-acquired Methicillin-Resistant *Staphylococcus aureus* have been constructed in the community setting. We have equations for both colonized and infected populations. We study the transmission dynamics of MRSA and would like to find optimal strategies to eliminate, or control the spread of the disease.

13) FRIEL, K.D. MgsD (Mannosylglycerate Synthase) from *Dehalococcoides mccartyi* and *Dehalogenimonas lykanthroporepellens's* Impact on Salty Environment Adaptation. Department of Biological Sciences, University of Tennessee, Knoxville, TN.
We constantly contaminate our environment with toxins in our everyday lives. One way to clean up after continuous pollution is using microorganisms, such as bacteria, that thrive off using the toxins we produce and turn them into something nontoxic. However, not all bacteria capable of cleaning up can survive in extreme environments. Things such as drastic temperatures, acidic conditions, and abnormally high salt concentrations can deter bacteria from cleaning up. For our experiment, we focused on salty environments. We took a gene called mgsD from *Dehalococcoides* and *Dehalogenimonas* and tested it in *E. coli* to see what its function was in its native bacteria. We used the mgsD to make new plasmids that we predicted would help *E. coli* adapt to a more extreme environment. We then induced both unmodified and modified *E. coli* in 5% NaCl for 21 hours. The mgsD reacted differently than we anticipated and we had surprising results.

14) GINTHER, A., Z. GOHARI, and K. SALTER. Predictive Modeling of *E. coli* Levels at Urban Beaches along Lake Michigan. Department of Biological Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.
Escherichia coli (*E. coli*) is a bacterium commonly found in natural bodies of water. All warm-blooded animals have *E. coli* in their feces, so high levels of *E. coli* in beach water indicates a probable chance of fecal matter.

Studies show that *E. coli* and/or Enterococci are the best bacterial indicators to assess the risk of acquiring a gastrointestinal illness because of using recreational waters. Colilert-18 test kit is used to simultaneously detect total coliforms and *E. coli* in water. This test requires 18 hours for the results to return, and advisories depend on how often samples are taken. Therefore, advisory postings can only indicate the previous day's *E. coli* sample results, and are not indicative of the current conditions. In our study, we have sampled Lake Michigan's water over the summer of 2017 in order to monitor *E. coli* levels at popular beaches. We also created predictive statistical models with Virtual Beach using *E. coli* data from 2015-2016 and paired it with hourly recorded environmental conditions obtained from a nearby buoy and documented by Environmental Data Discovery and Transformation (EnDDaT). We will present a comparison between measured data and our models, and discuss potential changes that can be made to improve predictions.

15) GUAJARDO, H.,[1] and F. AGUSTO[2]. How Breeding Peak Phenology Affects Arbovirus Transmission. [1]Biology Department, Brigham Young University, Provo, UT, [2]Department of Ecology and Evolutionary Biology, Kansas University, Lawrence, KS.
Arboviruses infect millions of people worldwide each year and are of serious concern to public health care officials. In this study, we examine how synchrony vs. asynchrony of vector and host species' breeding peaks can change the incidence of new infections. We developed a compartmental SIR model for arboviral disease transmission that incorporates phenological synchrony and asynchrony between the breeding peaks of a wildlife host and a vector by using a sinusoidal function. Our findings indicate that the incidence of new arboviral infections in the host is lowest when the vector's breeding peak is shifted earlier in the season or the host's is shifted later. We also found that the greatest incidence of new infections corresponds to synchronized breeding peaks between the wildlife host and the vector. We conclude that shifting the breeding peaks can significantly alter the incidence of new arboviral infections in a wildlife host. Specifically, our model predicts that factors which cause early vector breeding or late host breeding will result in lower numbers of new arboviral infections in the host. These insights will help public health care officials accurately predict the severity of future outbreaks and implement better prevention and control measures.

16) HAKIZIMANA, M., and S. JACOBSON. Mathematical Modeling of Oncolytic Virotherapy. St. Olaf College, Northfield, MN.
An oncolytic virus is designed to specifically target and kill cancer cells while leaving normal cells alone. Oncolytic Virotherapy uses oncolytic viruses as a form of therapy to treat cancer. Previous models have used ordinary differential equations in their modeling process. Our model implements a system of delay differential equations to incorporate the time delay in the adaptive immune system. The model assumes that the adaptive immune system is completely dependent on infected tumor cells created by timed injections of an oncolytic adenovirus. The model was fit to data obtained from Zhang et al. (2011) using the statistical program R-studio. Numerical simulations were implemented in order to find key parameters that could control the extinction of Cancer. A univariate local sensitivity analysis was performed to see which parameters were most sensitive to a slight perturbation. It is hoped that the model can be used in clinical trials to help determine the best course of treatment for individual patients.

17) HOMMES, A.[1], SAROJ DUWAL[2], and AXEL HRANOV[3]. Developing an Educational Simulation of the Cambrian Sea. [1]Department of Mathematics, Vanderbilt University, Nashville, TN, [2]Department of Computer Science, University of New Orleans, LA, [3]Department of Computer Science, University of Tennessee, Knoxville, TN.
In a world that has been revolutionized by the introduction of internet-based technology in day-to-day life, many educational systems are trying to translate their resources into the virtual world in order to economize on physical resources and capture the attention of their students. The Biology in a Box program, a biological

outreach program created in conjunction with UT, is no different. In our project, we strove to create additional virtual resources, such as educational games and worksheets, for Biology in a Box to use with its lessons to help students engage with biological concepts. The fact that this game is playable over the internet means that it is more readily and easily accessible by more school districts across not only Tennessee, but the entire world. I will offer a live-play demo of the game my group created.

18) KRATTS, N.[1], and S. KOMARNYTSKY[2]. A Poisson Binomial Distribution Model for Bitter Taste Perception in the *Brassica oleracea* Species. [1]Lenoir-Rhyne University, Hickory, NC, [2]Department of Food, Bioprocessing and Nutrition Sciences, North Carolina State University, Raleigh, NC.
Glucosinolates are chemical compounds found in *Brassica oleracea* known to give these cruciferous vegetables their bitter taste. In this investigation, a Poisson Binomial Distribution was used to find the probability of the various compounds binding with taste receptors identified in humans, and a mixture of distributions was applied to predict how the glucosinolates work together in different proportions within the vegetables to give them their bitter taste. The prediction scores were compared with data from taste trials to validate the predictions.

19) LAUREL, J., K. MAXIMUS, J. FORD, C. DEVINE, and P. NEPAL. Investigating Correlations in Intermitotic Time Variability. Middle Tennessee State University, Murfreesboro, TN.
The initiation of cellular replication varies among individual cells, so that the time it takes for a cell to divide (or intermitotic time (IMT)) is highly variable. To learn more about IMT variability and the mechanisms behind it, correlations in the IMTs of related cells can be studied. The current research investigates how inheritance influences the distribution of IMTs within a population. We process data that tracks cell lineages in order to compute correlations between the IMTs of related cells and develop and test models for explaining the correlations that we observe.

20) MERCER, A.,[1] and F. AGUSTO[2]. Effects of Phenological Shifts in Breeding Peaks on Arboviral Transmission. [1]Department of Biology, Southwestern Oklahoma State University, Weatherford, OK, [2]Department of Ecology and Evolutionary Biology, Kansas University, Lawrence, KS.
Arboviruses such as the West Nile Virus have been responsible for over 40,000 illnesses with over 1,000 mortalities since 1999. Our goal in this study is to investigate how the transmission of arboviruses is affected by different wildlife host and vector breeding peaks. Matching and mismatching in vector and host breeding peaks can greatly alter the prevalence of a virus. To look at breeding peak shifts, we created an SIR compartmental model for the transmission of an arbovirus between the vector and wildlife host and incorporating a sinusoidal function for the birth rates. We found that for a system where the host's breeding peak was fixed, an early mismatch in the vector's breeding peak led to lower disease prevalence compared to a late mismatch. However, when the vector's breeding peak was fixed, an early mismatch in the host's breeding peak resulted in higher disease prevalence compared to a late mismatch in the host's breeding peak. When we ran a scenario where there was a match in the vector and host's breeding peaks, the virus' prevalence stayed almost constant. The results show that arbovirus prevalence is lowest when the vector's breeding peak occurs earlier than that of the host. measures.

21) MO, K. Phenomenological Models for the Relationships Among Occupancy, Mean, and Variance of Species Abundance Spatial Distribution. Pace University, Staten Island, NY. Phenomenological models derived from negative binomial distribution and Taylor's law were commonly used in ecology to describe relationships of the occupancy, mean, and variance of species abundance. However, the mathematical properties of these models have not been adequately investigated. In addition, the scales, methods, and measures used in the model fitting and evaluation are often arbitrarily chosen, casting doubts on the result of

model comparisons. Here we evaluated six phenomenological models of occupancy-mean-variance relationships empirically and analytically. Using 12 empirical data sets (eight interspecific and four intraspecific), we showed that Taylor's law, negative binomial, and He-Gaston model for variance were equally well in predicting variance, except when the models were fitted under arithmetic scale and assessed using root-mean-square error of log-transformed values. When predicting occupancy, negative binomial and a unified negative binomial model performed equally well, with negative binomial showing a slight advantage. Moreover, we proved analytically that the He-Gaston model for occupancy was theoretically incorrect since it mixed two mathematically independent mean-variance relationships of negative binomial distribution and Taylor's law. We provided recommendations of using phenomenological models in empirical work and discussed the ecological relevance of our theoretical finding.

22) MORRIS, J.[1], B. GARLAND[1], M. SAME[2], and X.J. ZHOU[3]. Study of Normalization Methods and Binning Definitions for the Joint Analysis of Illumina 450k Microarrays and Whole Genome Bisulfite Sequencing Data. [1]BIG Summer Program, Institute for Quantitative and Computational Biosciences, University of California, Los Angeles, CA, [2]Bioinformatics Interdepartmental Graduate Program, UCLA, [3]Department of Pathology and Laboratory Medicine, UCLA.
In whole genome bisulfite sequencing (WGBS), methylation information is obtained for every cytosine that gets mapped to the genome, including over 28 million CpG sites. The 450k microarray provides methylation information for only ~450,000 CpG sites, but is relatively inexpensive. Many models that make use of methylation status are trained using the massive amounts of 450k data found on public repositories, but these models often need to be applied to WGBS data. Direct comparison between the 450k data and WGBS data neglects many of the sites present in the WGBS data and is complicated by differences in platform. The problem this study confronts is how to best process 450k and WGBS data so that they are directly comparable. Three WGBS samples and 59 microarray samples from matched age groups, disease status, and tissues were used to determine the best microarray processing procedures. Several microarray normalization methods and binning techniques were used, and changes to the correlation and mean absolute difference (MAD) between the WGBS and 450k data were observed. Quantile normalization followed by beta-mixture quantile normalization (QN.BMIQ) was found to be the best normalization method, and the binning procedure from CancerLocator [Kang S. et al. Genome Biology. 2017] was found to yield the highest correlation and lowest MAD. In the future, models involving methylation status can be constructed from microarray data by first using QN.BMIQ normalization and then collapsing to the CancerLocator bins to improve results on sequencing platforms.

23) NAIDUGARI, J. Latin Hypercube Sampling as Applied to a Mathematical Model in Wound Healing. Department of Mathematics, Western Kentucky University, Bowling Green, KY.
A global sensitivity analysis is comprised of Latin Hypercube Sampling and Partial Rank Correlation Coefficient (LHS and PRCC) in order to determine the parts of a healing process of a diabetic foot ulcer after the analysis is related to differential equations. LHS is used to determine parameter values; it is divided into unbiased regions where the parameters chosen are all equally probable without repetitions. PRCC is focused more on the distributions that result from the change in these parameters. This study currently focuses on the how three different differential equations, each of which pertains to a certain biological aspect of the foot ulcer, can be manipulated with different parameters in order to replicate past distribution results. The purpose of this research is to understand to what extent past research with this focus can be altered to produce similar results, allowing us to test the boundaries of the variations that can be performed.

24) NGUYEN, D[1]., and T. WAKHARE[2]. Seasonality in Multi-host Disease Systems. [1]Department of Biology, Eastern Washington University, Cheney, WA, [2]Department of Mathematics, University of Maryland, College Park, MD.

Demographic processes have long been known to critically impact population-level epidemic dynamics. Within a single ecosystem, a novel pathogen may circulate among multiple species, each with different seasonal demographic patterns. We investigate the synergy between these different seasonal demographic processes and epidemic dynamics in a two-host disease system. While differences in disease burden between hosts are often explained by immunological differences, behavior, or social contact structures, we find that different demographic patterns alone can also drive differences in disease burden over time, even with only two host species.

25) NGUYEN, P. Inferring Community Structures in Dominance Hierarchy in Networks. Department of Mathematics, Statistics, and Computer Science, Macalester College, St. Paul, MN.

Dominance hierarchies in animals provide behavioral ecologists with a framework to study casual factors of social hierarchies. In addition to ordinal ranks, community structures such as tiers or overlapping sub-hierarchies often exist in dominance hierarchies. For instance, among northern male elephant seals, three groups, the 'alpha', 'beta', and 'peripheral' males exist in their hierarchy, distinguished by their access to female seals during mating seasons. We propose a technique to detect these community structures by clustering the correlations between rankings calculated by a novel, physical ranking model. Using synthetic data, we demonstrate that applying k-means to rankings' correlations can recover tiers in a hierarchy. In addition, we introduce a null model for the overlapping sub-hierarchy structure. By comparing the rankings' correlations of the null model and the original network, we can recover overlapping sub-hierarchies in synthetic examples. Finally, we test our technique's ability to detect tiers and overlapping sub-hierarchies in real data by applying it to dominance hierarchies in northern elephant seals and free-ranging dogs.

26) PAK, D. Estimating Protein Synthesis and Codon-Specific Translation Rates from Ribosome Footprint Data. Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN. Ribosomal foot-printing (RFP) provides important information to identify the location of translation start sites and can be used by researchers in the life sciences as a tool to study the process of protein synthesis, one of the most fundamental processes for living organisms. Identifying patterns in large genomic sequences can be used to learn more about the process. With the emergence of big genomic datasets, RFP data has become more available. However, as the size of genomic data increases, so does external noise and variance making it harder to find meaningful patterns using classical techniques. To analyze this information, a computational model is being developed to make RFP data accessible from a Bayesian statistical perspective. Using a Monte Carlo Markov Chain to gather statistical information about codon translation rates and protein synthesis rates, researchers can better understand the meaning of the large data to which they have access. Such a model could also be used to account for nonsense errors to gather information about nonsense error rates and simulate Genomes with less variation and noise. The model is being designed as an open-source R library that can be used by Biologists to find the underlying statistical patterns behind RFP datasets.

27) REED, J.[1], Z. HAQUE[1], and S. HOTA[2]. Mathematical Modeling for H1N1 Flu Pandemic. [1]NSF-Fisk TIP summer research program 2017, Fisk University, Nashville, TN, [2]Department of Mathematics and Computer Science, Fisk University.

Abstract: The H1N1 virus, a subtype of the influenza A virus, is a type of flu that affects humans, pigs, and birds. This H1N1 virus caused the 2009 swine flu pandemic. In this project a SIR mathematical model of the H1N1 pandemic is developed using the system of ordinary differential equations. Data was collected from the CDC site for the number of reported incidences of the human H1N1 flu in the United States from April 2009

until March 2010. Using the model equations, a formula was developed to determine the contact rate of the disease and the number of infectives during the course of the epidemic. Python was used for computation and simulation and the mathematical model was compared against the data. Comparison shows that this model, even very basic in nature, matches with the characteristics of the data.

28) ROUSE, K., H. GUO, and H. QIN. The Effect of Dietary Restriction on *Saccharomyces cerevisiae* Lifespan. Computer Science and Engineering Department, SimCenter, University of Tennessee at Chattanooga, Chattanooga, TN.

Dietary restriction (DR) increases lifespan in many organisms; however, its effect on individuals in genetically heterogeneous populations is unclear. Here, we are determining the effect of DR on lifespan for 106 gene deletion strains in *Saccharomyces cerevisia* with sample sizes greater than 30 cells. These genetic backgrounds have been used to describe association factor in yeast cells between 2% glucose (YPD) and 0.05 glucose (a form of DR) conditions. Here we present an overview of yeast lifespan data as a model to study aging and describe an approach by fitting yeast lifespan data with Gompertz aging model. We compare both mortality rate parameter (G) using genotype backgrounds and increase in mortality rate parameter (R) between YPD and DR conditions. Data-mining approaches are performed to find association factors with yeast aging to be used for generating predictive models of underlying lifespan, genotype-dependent responses to dietary restriction.

29) SANCHEZ, G.[1,2], MILLER, N.[1,3], D. LEFAUDEUX[4], and A. HOFFMANN[4]. Estimating mRNA Half-life in Naive and Tolerized Macrophages using Actinomycin D RNA-seq Data. [1] BIG Summer Program, Institute for Quantitative and Computational Biosciences, University of California, Los Angeles, CA, [2]Biology, Department of Life and Physical Sciences, Fisk University, Nashville, TN,[3] The Department of Biological and Environmental Engineering, Cornell University, Ithaca, NY, [4]Department of Microbiology, Immunology, & Molecular Genetics, UCLA.

Gene expression dynamics are regulated by mRNA transcription and degradation. Together they determine how long mRNA transcripts of a given gene can actively be translated, producing the proteins that determine biological function. While many studies have elucidated mechanisms of transcriptional control, far fewer studies have addressed mRNA degradation, in part because there is no accepted method for measuring mRNA half-lifes. Here, we analyzed RNAseq datasets produced following a block of transcriptional elongation with Actinomycin D. In this study, bone marrow-derived macrophages (BMDM) were cultured and either tolerized by LipidA (LPA) pre-stimulation or kept naive. The cells were then stimulated with LPA (time 0) to induce an immune response. Transcription was then blocked by adding Actinomycin D (ActD) at 0, 60 and 180 minutes after LPA treatment. RNA was sequenced for all conditions and at 7 different timepoints after ActD. Reads counts were normalized using spike-in RNAs (external controls) to account for diminishing mRNA amount over time. We generated counts for each mRNA and assessed the quality of the RNAseq datasets. A linear model was used to fit a decay rate of each gene and the corresponding half-life was derived for a given experiment. Half-lives of 235 LPA-induced genes were calculated. For example, Tnf, Nfkbia and Mmp13 yielded a mRNA half-life at basal of 20, 17.8, 86.3 minutes respectively. We also derived confidence intervals and assessed the statistical significance of changes in the derived halflifes in different conditions.

30) SMILEY, A. Preparation of Poly Proton Exchange Composite Membranes Using Phosphonated Additives: 2,4,6-Triphosphonicacid-1,3,5-Triazine (TPAT) and Benzyl Phosphonic Acid (BP). Division of Physical and Life Sciences, Fisk University, Nashville, TN.

Polymer electrolyte membrane fuel cells (PEMFC) equipped with a proton exchange membrane (PEM) converts chemical energy of fuel to electrical energy through an oxidation potential. Inadequacies in membrane performance and properties at high temperatures (> 180 Â°C), low relative humidity (RH) and high

sulfonation levels limit the widespread commercialization of these membranes. The current studies describe the synthesis and characterization of 2,4,6-triphoshphonicacid-1,3,5-triazine (TPAT) and benzyl phosphonic acid (BP) for use as an additive in poly copolymers for applications PEM in PEMFCs. Membranes of acidified disulfonated biphenol based polymer arylene ether sulfone) copolymers (BPS-35) with varying concentrations of TPAT (BPSH-35/TPAT) and BP (BPSH-35/BP) were prepared by solution casting and examined after 5 months of storage in DI water. Non-linear thermal properties, water performance, and proton conductivity under relative humidity conditions were observed for either set of membranes. The highest proton conductivity was 3.1 x 10-2 S/cm in the 7 wt% BPSH-35/TPAT membrane at 90% RH. The lowest conductivity was demonstrated by the 3 and 5 wt% BPSH-35/TPAT membranes and the 7 and 10 wt% BPSH-35/BP membranes possibly due to the presence hydrogen bonding which restrict the conduction of proton at high relative humidity. Interestingly an increase in proton conductivity above 10-2 S/cm was also observed for BPSH-35/TPAT between 5 to 30 wt% RH.

31) SUMMERS, J. Mathematical Model and Optimal Control of Malaria using a Sterile Insect Technique Departments of Physics & Astronomy and Mathematical Sciences, Middle Tennessee State University, Murfreesboro, TN.

My research project will be focused on constructing a mathematical model to study the influence that a Sterile-Insect-Technique (SIT) has on a population affected by malaria. This model will build upon the model found in Chitnis et al. which makes use of a Susceptible-Exposed-Infected-Recovered (SEIR) population model for humans, and an SEI model for mosquitoes. Our model introduces a fourth biological compartment to this model in the form of sterile mosquitos. Implementing this new biological compartment will have a drastic impact on the system. With this model, we aim to find the optimal releasing strategy for the new sterile mosquitoes that will minimize the infected population of humans, while also minimizing the number of sterile mosquitoes needed to be produced and introduced.

32) WATSON, T., S. BREWER, and Q. LI. Modeling and Optimization of Reach and Exposure in TV. Division of Mathematics and Computer Science, Fisk University, Nashville, TN.

Advertising agencies (buyers) place television advertisements orders with the networks (sellers) for their desired commercial slots which will expose their products to a particular target audience. Typically, an advertiser needs information on a certain amount of impressions (i.e., views) for each advertising campaign. This project applies two ways, impression based approach and demographic approach, in evaluation of the advertisements orders for a specific company with modified data provided by Clypd. The results show that the impression-based method is more stable while the demographic-based method is more sensitive to different types of customers, prime-time slots, and non-prime time slots. In comparison, the advertising companies should choose the demographic-based method for more accurate results to maximize the profits for both the advertising companies and the networks.

33) WHITAKER, A. [1], A. NETMATBAKHSH [1], J. ZARTMAN [3], and M. ALBER [1,2]. Studying the Nonlinear Elasticity of Epithelial Cells at the Tissue Level Using a Computational Sub-Cellular Element Model. [1]Department of Mathematics, University of California, Riverside, CA, [2]Department of Applied and Computational Mathematics and Statistics, University of Notre Dame, Notre Dame, IN, [3]Department of Chemical and Biomolecular Engineering, University of Notre Dame.

Epithelium, one of the four basic types of animal tissues, works as a barrier between the environment and the body by covering the surfaces of organs, blood vessels, and cavities. Studying the mechanisms involved in proliferation of epithelial cells are of particular interest considering ninety percent of tumors originate from epithelium. To better understand the mechanical behavior of epithelial cells, we have extended a subcellular element computational model, by including the cell's nonlinear elastic behavior. The motivation for this

extension is drawn from experimental mechanical stretching tests of a single cell in which the cell behaved as an active material that stiffened to resist further strain and deformation. We performed simulations of epithelial cell of the *Drosophila* wing disc and showed that the nonlinear elasticity of cells has limited effects for interphase cells but significantly reduce the size of, pre-division cells. Because of the difficulties in performing experimental studies on singular epithelial cells, we instead calibrate the nonlinear elasticity of our cells using experimental data of an epithelial tissue. Applying external stretching forces at the tissue level reveals the elastic properties of individual cells. By comparing our simulated tissue mesh with that of experimental data, the influence and strength of nonlinear elasticity in individual cells can be observed. This investigation of cellular stiffness ultimately deepens the understanding of the mechanical properties of epithelium, and would help make further inferences about the mechanical behavior of epithelial cells at tissue level.

ORAL PRESENTATION ABSTRACTS

ADAMS[1], A., O.P. DOUGHERTY[2], and Q. MURPHY[3]. Within-host Mathematical Models for Orthohantavirus Infections. [1]Department of Mathematics, University of Georgia, Athens, GA, [2]Department of Biochemistry and Molecular Biology, University of Tennessee, Knoxville, TN, [3]Department of Mathematics, University of Kentucky, Lexington, KY.
Orthohantaviruses, family Hantaviridae, are harbored by mice, rats, shrews, moles and bats. Intriguingly, only those viruses harbored by rodents cause disease in humans with up to 40% fatality for cases within the Americas. Infection of humans occurs through inhalation of rodent excreta into the lung. Orthohantaviruses target the endothelial cells of the lung or kidney but eventually spread throughout the body in lethal cases. Understanding the replication kinetics of these viruses in various cell types and how replication is abrogated by the host is critical to the development of effective therapeutics for treatment for which there are none. We formulated a series of mathematical models using ordinary differential equations to examine the viral kinetics of Orthohantavirus within cells. Our models were fit to experimental data of Black Creek Canal Virus infecting Vero E6 cells and then analyzed using Latin Hypercube Sampling. We also determined the basic reproduction number, R0, and the final size relation. Our models provide the basis for further research into mathematical models for Orthohantavirus.

BAKTAY, J., R. NEILAN, M. BEHUN, and B. KOLBER. A Computational Model of the Central Nucleus of the Amygdala during Bladder Pain. Department of Mathematics and Computer Science, Duquesne University, Pittsburg, PA.
Chronic bladder pain (CBP) activates neurons in the central nucleus of the amygdala in the brain which exhibits asymmetric behaviors across each hemisphere. To better understand CBP, an agent-based computational model was created using Netlogo software to replicate neuronal behavior observed in bladder distension experiments on mice. In the simulation agents represent individual neurons with unique firing rates updated stochastically at each time step. In total, the model represents the behaviors of four neuron types and an organism's overall perceived pain in response to different noxious stimuli. A damage accumulation feature was added to the model to track the organism's long-term pain history. The model interface provides a dynamic framework for viewing neural activity as it evolves over time and allows the user to predict different pain states by controlling model parameters. Ongoing work will account for the topology of the neural network, cell-type specificity, and three spatial dimensions.

BRETTIN, A. and K. WEISHAAR. Ebola Could Be Eradicated Through Voluntary Vaccination. Department of Mathematics and Statistics, University of North Carolina, Greensboro, NC.
Ebola virus disease (EVD) is a severe infection with extremely high fatality rate spread through direct contact

with body fluids. A promising Ebola vaccine (rVSV-ZEBOV) may soon become universally available. We constructed a game theoretic model of Ebola incorporating individual decisions to vaccinate. We found that if a population adopts selfishly optimal vaccination strategies, then the population vaccination coverage falls negligibly short of the herd immunity level. We concluded that eradication of Ebola is feasible if voluntary vaccination programs are coupled with focused public education efforts. We conducted uncertainty and sensitivity analysis to demonstrate that our findings do not depend on the choice of the epidemiological model parameters.

BREWER, E. and J. PELLETT. Modeling Chronic Vascular Responses Following a Major Arterial Occlusion. Rose-Hulman Institute of Technology, Terre Haute, IN, University of Wisconsin-La Crosse, La Crosse, WI.
Peripheral arterial disease is a serious health concern characterized by a full or partial occlusion of a major artery in the systemic vasculature. Following an occlusion, blood supply to peripheral tissues is significantly reduced, causing patients to experience severe pain and reduced mobility. This study uses mathematical modeling to investigate the role of different vascular segments in restoring blood flow following a major occlusion. Vascular adaptations to collateral arteries and the microcirculation distal to the occlusion have been observed to occur on both acute and chronic time scales. Here two chronic vascular responses, arteriogenesis (increased diameter of existing vessels) and angiogenesis (new vessel formation), are investigated in a single vessel and a complex network. By coupling these chronic responses to acute responses, the model provides a framework for understanding the time frame and significance of vascular responses that help restore flow. Preliminary results suggest the number of collaterals increases following an occlusion while fewer vessels distal to the occlusion are required for optimal flow restoration. Ultimately, the model can be used to identify the most important vessels to target for future therapies.

BREWER, S.[1], and K. DAUTEL[2], Density Dependence and Multiple Matings lead to Sexual Conflict in Territorial Migratory Songbirds. [1]Division of Mathematics and Computer Science, Fisk University, Nashville, TN, [2]Department of Mathematics, Marist College, Poughkeepsie, NY.
Breeding strategies in conspecific territorial migratory songbirds vary between sexes and play a crucial role in reproductive success. We employ a game theoretic model to determine the effect of various mating strategies on fitness. Males first play a priority game, where the costs of early arrival are based on male quality. Males who arrive sooner obtain the best available territory, but incur an early-arrival cost. The best territory is the one with the most surrounding territories, or sides, which increases the opportunity for extra pair copulations (EPC). The female game theoretic model consists of strategies for choosing a territory that are based on a male quality and female population density. Concern for male quality may increase the number of offspring resulting from a single mating. However, concern for female population density may enable a female to avoid competition. The model finds that, whether or not all females play the same strategy, sexual conflict occurs.

CLEAR, A. Ion Dynamics in The Neurovascular Unit: Analyzing the Affects of Neuronal Seizures on Astrocytes and Blood Vessels. Department of Biology, King University, Bristol, TN.
Homeostasis in the neurovascular unit (NVU) relies on key ion regulators such as potassium (K+), sodium (Na+), and calcium (Ca2+). The interrelated dynamics affect the excitability of neurons and the occurrence of seizures. In order to properly elucidate the full range of affects of seizures on the entire NVU (i.e. Neurons, Astrocytes, and blood vessels) we have created a simple mathematical model coupling ion flow in the NVU between all three subunits. Here we provide a detailed model of the K+, Na+, and Ca2+ dynamics through various channels connecting the NVU. We are able to reproduce phenomena such as neuronal seizure dynamics, Ca2+ release in astrocytes from the endoplasmic reticulum, and mechanistic descriptions of K+ buffering by astrocytes in the intracellular space and the perivascular space by blood vessels. We find the

increased K+ activity in the perivascular space dilates the blood vessel, causing strain in the NVU.

COSGROVE, E., and E. LINDSEY. Effects of Competition-mediated Dispersal on the Persistence of a Population. Department of Mathematics and Computer Science, Auburn University, Montgomery, AL.
Dispersal of an organism plays an important role in individual fitness, population dynamics, and species distribution. In the literature, dispersal is loosely applied to movement over different spatial scales, e.g. movement between habitat patches separated in space from other areas. Recently, ecologists have found that the presence of a competitor can have a major impact on the dispersal of an organism, a phenomenon known as competition-mediated dispersal. Little is known regarding the patch-level consequences of habitat fragmentation of competing species in the presence of competition-mediated dispersal. In this talk, we will develop a patch-level model built on the reaction diffusion framework to explore effects of habitat fragmentation and competition-mediated dispersal. Our results will focus on a one-dimensional patch and methods from nonlinear analysis such as time map analysis (quadrature method) and linearized stability. We will also briefly explain the biological importance of our results.

DILLE, H., M.P. KNAPP, J. LOW, D. R. WEINBRENNER, D. IVANKOVIC, and D. PRAGER. Modeling Breast Cancer Cell Growth and the Effects of Selected Cancer Therapies. Departments of Biology and Mathematics, Anderson University, Anderson, SC.
Breast cancer is the most common cancer in women in the United States and worldwide as stated by the American Cancer Society. Breast cancer cells begin as cancer stem cells (CSCs), which then divide to form progenitor cells (PCs) and eventually terminally differentiated cells (TDCs). In Nonlinear Growth Kinetics of Breast Cancer Stem Cells: Implications for Cancer Stem Cell Targeted Therapy, Liu, Chen et. al., developed a system of differential equations that describes the growth patterns of these cells. We have modified Liu's research model, by adding a feedback loop in order to more accurately estimate the number of cancer stem cells. This feedback loop represents the inflammatory response produced when dead terminally differentiated cells release cellular components that induce malignant cells to spread to other parts of the body. At the Anderson University Center for Cancer Research, MCF7 breast cancer cells were grown, fed, and counted daily for 21 days. Live and dead cell counts were recorded and modeled using our modified differential equations. After the initial 21-day period, indigo and red clover, were used as treatments to slow the rate of cell division and mimic possible cancer therapies. With this significantly more accurate method of modeling stem cell growth, stem cell targeted therapy becomes a more viable option for patients.

FRENCH, R. Using Mixed Effects Modeling to Quantify Differences between Patient Groups with Diabetic Foot Ulcers. Department of Mathematics, Western Kentucky University, Bowling Green, KY.
Medical treatment of diabetic foot ulcers remains a challenge for clinicians. A quantitative approach using patient data and mathematical modeling can help researchers understand the physiology of chronic wound healing. In this work, nonlinear mixed effects modeling is used to attribute wound healing variability to either fixed effects, parameters that are more likely to remain constant across patient groups, or random effects, parameters that vary for patient to patient. Identifying these random effects would allow for sensitive parameters to be taken into special consideration when treating diabetic foot ulcers. These actions could lead to improved patient care and diagnostic methods.

GARAGNANI, J., and M. KELLY. Optimal Advertising Strategies for Use in Popular Media. Department of Mathematics, Transylvania University, Lexington, KY.
In today's world, information is disseminated quicker and to a wider audience than ever before. We investigate the role information hubs, such as social media and internet news sites, play on the spread of such media. We formulate a mathematical model, structured after a Susceptible-Infected-Recovered (SIR) epidemic

disease model. After parametrizing our model, we use optimal control methods to determine best advertising strategies that maximize exposure while minimizing the associated costs. We parameterize our model using data from popular media and our solutions are approximated using numerical simulations.

GORYL, K. Modeling RNA Secondary Structures Using Matchings. Department of Mathematical Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.
RNA's single-helix structure gives it a greater range of movement than DNA. This freedom allows the molecule to bend, fold, and bond to itself. These bonds have been modeled using a variety of graph-theoretical matching families proposed by biologists in previous literature. We explore the intersections of different matching families, then introduce their respective sequences and prove our proposed equations for enumeration.

HANKEL, C. Long-Time Behavior of Two Competing Sub-Species on a Discrete Periodic Habitat. Department of Mathematics, Georgetown University, Washington, DC.
We model Leslie-Gower competition between two subtypes of a species in a discrete periodic habitat where two different environment types alternate within the habitat. Using numerical simulations, we observe several possible long-term outcomes: traveling waves, pinning of one or both types, and extinction of one or both types. We describe how these outcomes depend on the length of one of the environment types in the periodic habitat, the root mean squared dispersal distance, and the intrinsic growth rates of the two subtypes. We observe that competition can induce pinning of one subtype that would spread indefinitely in the absence of a competitor. We also observe that increasing the intrinsic growth rates of both subtypes can actually lead to the extinction of the weaker competitor. This suggests that increased resources in the habitat could benefit the species overall, but could hurt biodiversity by driving a subtype to extinction.

HU, J. pKa Computation Based on Poisson-Boltzmann Equation. Department of Mathematics, Southern Methodist University, Dallas, TX.
Protein molecules in the human body are naturally surrounded by water containing dissolved salt. The ability of a protein active site to exchange protons with the surrounding solvent is characterized by the acid dissociation constant pKa. The pKa value can be obtained from the electrostatic free energy of the system by solving the Poisson-Boltzmann equation (PBE) for the electrostatic potential with appropriate boundary conditions. We use the treecode-accelerated boundary integral (TABI) solver which employs a well-conditioned boundary element formulation on the linearized PBE, and GMRES iteration to solve the linear system with matrix-vector product cost reduced from $O(N2)$ to $O(N \log N)$. The computed pKa of ovomucoid third domain (OMTKY3) is close to the experimental result.

JENNINGS, E, L. MCGUINNESS, L.J. KERKHOF, S.F. VATNER, J. GUERS, P.J. WISNIEWSKI, DOWDEN, and S.C CAMPBELL. Examining the Contribution of the Microbiota to the Healthy Aging AC5KO Phenotype. King University, Bristol, TN.
Healthy aging, including protection against diabetes, obesity, cardiovascular stress and enhanced exercise tolerance, have been observed in our adenylyl cyclase type 5 knock out (AC5KO) mouse model. This is a critical observation since the aging population would not enjoy extra years if they were accompanied by chronic conditions. Since the gut microbiota has been shown to be an important determinant of age-associated pathological states such as inflammation, diabetes, obesity and cardiovascular disease, we propose to conduct a head to head comparison of microbial communities (species and strains) between AC5KO and wild type (WT) mice to reveal whether there are differences that promote longevity and healthful aging (protect against disease states). Male and female AC5KO and WT mice were fed a normal diet and randomly assigned to exercise or sedentary groups. DNA extraction, PCR amplification, and data analysis tools were used

to compare the microbial communities of different groups. After analysis, our data revealed different strains and compositions of microbiota between the AC5KO and WT mice. In future studies, our data will show that AC5KO mice demonstrate unique microbial species that are associated with healthful aging and that exercised AC5KO mice will have either an increase in their unique microbial species or new species present that are a result of exercise training.

KANTHAWAR, A., and N. KRISHNA. Accurately Modeling the Wound Healing Process. Department of Mathematics, Western Kentucky University, Bowling Green, KY.
In order to formulate a mathematical model that accurately represents the physiology of a wound, the model and its parameters must be identifiable when given actual data. Practical identifiability is a method used to determine whether parameters in a model can be uniquely determined given actual data. This work uses a differential equation model that describes the interactions among matrix metalloproteinases, their inhibitors, the extracellular matrix, and fibroblasts. A singular value decomposition technique with a QR factorization combined with a correlation analysis is used to find an identifiable subset of parameters. Subsets are analyzed through model prediction intervals and parameter Markov chains and posterior densities. The goal of this work is to formulate a model that can accurately predict the healing process for individual patients.

KENNEDY, S, S. COLE, R. FRYE, L.K. VAUGHAN, and V. FITSANAKIS. Mechanistic Toxicology of Neurodegeneration Induced by the Pesticide Manzate in the Model Organism *Caenorhabditis elegans.* King University, Bristol, TN.
Exposure to the fungicide Manzate (CMZ) has been associated with the development of neurodegenerative diseases. The mechanisms by which this occurs remain unknown, although there are studies that suggest manganese increases the risk of Parkinson's disease. Investigation of which components of CMZ lead to neurodegeneration was implemented by chronically treating (24-hours) strains of *Caenorhabditis elegans* (Bristol N2s, VC1024s, NW1229s, and WLZ3s) with 3mM (CMZ LC25) concentrations of CMZ, mancozeb (MZ), maneb (MB), and zineb (ZB). MZ is the active ingredient in CMZ, the commercially available formulation of the fungicide. MB and ZB were included since these compounds are structurally similar to MZ, meaning they are all ethylene-bisdithiocarbamates with associated manganese (Mn) and/or zinc (Zn) ions. After chronic treatment, the functionality of the mitochondrial proton gradient was assayed using tetramethylrhodamine ethyl ester (TMRE) along with GFP analysis, quantified with fluorescent microscopy. These data demonstrated no differences in overall fluorescence, but variable punctuated patterns in the WLZ3s and the VC1024s. A statistically significant difference between CMZ and other treatment groups was seen in the nerve ring region, predominately composed of dopaminergic neurons. Further analysis will be done using higher concentrations of each compound. These data will assist in developing the protocol for future studies in which groups of *C. elegans* are exposed to higher treatment concentrations.

KWARTA, B., and B. REBER. Optimal Growth Allocation in *Sarracenia purpurea* in Varying Environments. Department of Mathematics, Houghton College, Houghton, NY.
Sarracenia purpurea, also known as the Northern Pitcher plant, is a perennial carnivorous plant found in nutrient poor bogs in the Eastern part of the United States, the Great Lakes region, and most of Canada. *S. purpurea* has modified pitcher-shaped leaves which collect prey and rainwater for nutrient consumption, with nitrogen being the most important nutrient, and rainwater being the primary means of obtaining it. These modified leaves are photosynthetically less efficient than other leaf structures (phyllodia) that are produced by the plant. *S. purpurea* is phenotypically plastic, and so the plant can allocate growth between carnivorous and non-carnivorous structures depending on environmental nitrogen conditions. Previous research has shown that an increase in phyllodia production is a direct and rapid response to nitrogen availability. Using optimal control theory, we created a model to show optimal growth allocation of *S. purpurea* in such a way

that plant morphology represents a prediction of atmospheric nitrogen levels. Our model predicted a difference in carnivorous to non-carnivorous biomass ratios given different nitrogen uptake rates.

MENIX, J. Using Computational Bayesian Statistics to Analyze Parameters in a Differential Equations Model. Department of Mathematics, Western Kentucky University, Bowling Green, KY.
The purpose of this project is to use Bayesian statistics to analyze values of parameters for a previously developed system of ordinary differential equations which describes the healing process of diabetic foot ulcers. The model describes the relationships between matrix metalloproteinases, their inhibitors, and extracellular matrix. A Bayesian approach is used when the availability of data is sparse, as it is in this case. Delayed Rejection Adaptive Metropolis (DRAM), a MATLAB implementation of a Metropolis-Hastings algorithm, is used to estimate parameters. Using this approach with the individual patient data allows us to refine the parameter estimates, find associated confidence intervals using parameters' posterior distributions, and compare pairwise plots of parameters. This will help improve the wound-healing model in order to better predict wound-healing outcomes for individual patients.

MACHADO, J. Optimal Vaccination Strategies to Reduce Endemic Levels of Meningitis in Africa. Department of Mathematics and Statistics, University of North Carolina, Greensboro, NC.
Meningococcal meningitis is an acute bacterial infection caused by the *Neisseria meningitidis* bacterium that affects the membrane covering the brain and spinal cord. If left untreated, this disease can lead to severe complications or mortality. The most effective way to combat meningitis is through the use of vaccines. We constructed a game-theoretic model of meningitis in which individuals choose to either vaccinate or not vaccinate under assumed costs. We identified conditions under which an individual should vaccinate. We found that with voluntary vaccination protocol, meningitis could be reduced to very low endemic levels (provided the cost of vaccination relative to the cost of the disease is sufficiently low), but not eliminated. We also performed uncertainty and sensitivity analysis of our model.

MO, K. Phenomenological Models for the Relationships Among Occupancy, Mean, and Variance Of Species Abundance Spatial Distribution. Pace University, Staten Island, NY.
Phenomenological models derived from negative binomial distribution and Taylor's law were commonly used in ecology to describe relationships of the occupancy, mean, and variance of species abundance. However, the mathematical properties of these models have not been adequately investigated. In addition, the scales, methods, and measures used in the model fitting and evaluation are often arbitrarily chosen, casting doubts on the result of model comparisons. Here we evaluated six phenomenological models of occupancy-mean-variance relationships empirically and analytically. Using 12 empirical data sets (eight interspecific and four intraspecific), we showed that Taylor's law, negative binomial, and He-Gaston model for variance were equally well in predicting variance, except when the models were fitted under arithmetic scale and assessed using root-mean-square error of log-transformed values. When predicting occupancy, negative binomial and a unified negative binomial model performed equally well, with negative binomial showing a slight advantage. Moreover, we proved analytically that the He-Gaston model for occupancy was theoretically incorrect since it mixed two mathematically independent mean-variance relationships of negative binomial distribution and Taylor's law. We provided recommendations of using phenomenological models in empirical work and discussed the ecological relevance of our theoretical finding.

ODUNIYI, E.[1,2], B. GIBBONS[1,2], M. OH[1], and F.B. AGUSTO[3]. Modeling Ebola Transmission Dynamics with Media Effects. [1]Department of Mathematics, University of Kansas, Lawrence, KS, [2]Department of Electrical Engineering & Computer Science, University of Kansas, [3]Department of Ecology and Evolutionary Biology, University of Kansas.

Historically, modeling disease transmission at both the global and local scale has been particularly difficult because of the variety of factors that are in play. To begin with, it is necessary to account for human-disease dynamics within both susceptible and infected populations for a specific disease since the biology of a disease uniquely affects the way the disease transmission model is constructed. In addition to the complexity of accurately simulating how a disease traverses within a population, local health-care infrastructure, and even media coverage provide added challenges for successful prediction. In this study, we develop a system of ordinary differential equations to model the Ebola virus disease in the three affected West African countries; the model incorporates sexual transmission, isolation of infected individuals and media effects. Our result shows that as media effect increases, the number of individuals isolated increases, ultimately decreasing the total number of infections. Thus, our results indicate the potential positive impact of media on reducing the overall spread of Ebola within the three affected West African countries.

PESCITELLI, J. Turing Instability in a Predator-prey Model for Zooplankton Grazing on Competing Phytoplankton Species. Department of Mathematics, Georgia College and State University, Milledgeville, GA.
We consider a predator-prey system modeling the interactions between a freshwater zooplankton herbivore and two types of competing freshwater phytoplankton species. The zooplankton grazes on one of the species of phytoplankton while the other phytoplankton species secretes a toxin that deters the zooplankton. Taking the motility of the species also into account, we formulate a mathematical model governing their interactions via a three-component reaction-diffusion system of equations under homogenous Neumann boundary conditions. We will prove that the spatially homogenous model admits a stable coexistence equilibrium state for a suitable choice of parameter values. We will then investigate Turing instability at this equilibrium state and find sufficient conditions on the diffusion coefficients that would lead to diffusion-driven instability. We also perform numerical simulations to study the spatial patterns generated by the system.

POWER, A., and C. NICHOLSON. Investigating the Mechanical Response of Stress in Coronary Arteries. Departments of Mathematics and Physics, University of North Carolina, Asheville, NC.
While the biomechanics of vascular smooth muscle (VSM) is very j understood, VSM tone seems to play an important role in arterial regulation. Such regulation is especially important in maintaining appropriate blood pressure under non-normotensive disease states such as hypertension and age-related intimal plaque deposition. This research investigates the mechanical response of individual layers of the arterial wall tissue to different levels of stress due to internal blood pressure and the contractile activity produced by the VSM. COMSOL Multiphysics was used to build a physically accurate, three-layered, axial symmetric cross section of a coronary artery, in order to better understand arterial tissue biomechanics. The composite tissue materials were defined using experimental data from studies done on human coronary arteries. The model provides a better understanding of arterial stress dynamics in relation to muscle contraction, intimal thickening, blood pressure, and material properties.

PRUCKLER, P. A Reaction-Diffusion Model of Acid-Mediated Tumor Invasion with Chemotherapy Intervention. Department of Mathematics, Georgia College and State University, Milledgeville, GA.
It has been studied that most cancer cells rely on aerobic glycolysis, a phenomenon termed the "Warburg effect" to generate energy needed for cellular purposes. Warburg effect is a phenomenon wherein cells ferment glucose to lactic acid using glycolysis even in the presence of normal levels of oxygen. This altered metabolism results in an acidic extracellular tumor environment leading to destruction of normal tissue at the tumor-host interface, while promoting proliferation of cancer cells against normal cells. In this talk, I will present a four-component reaction diffusion system of equations describing the effect of chemotherapy intervention on the spatial distribution and temporal development of tumor tissue and excess H^+ ion

concentration. Our model is an extension of the seminal work by Gatenby and Gawlinski. We perform mathematical analysis and as well as numerical simulations to investigate how treatment affects the strength of the acid-mediated invasion and intervene the progression of cancer cells.

REYNOLDS, A, T. PIERRE, E. WORLANYO, R. MCCALL, and J.W. GATO. Evaluation of the Cytotoxicity of Tin Dioxide Nanofibers. King University, Bristol, TN.
Tin dioxide nanofibers (SnDNFs) are small fibers with many applications in areas such as cosmetics, solar cells, toxic gas release sensors, and air pollution control. There have been few studies on the cytotoxicity of SnDNFs. The goal of this research was to evaluate the toxicity of electrospun SnDNFs in a lung cancer cell line (A549). Occupational exposure to SnDNFs, primarily through inhalation, has been linked to pulmonary disease, making the A549 cell line a relevant model in this study. Synthesized SnDNFs were characterized using scanning electron microscopy (SEM), Raman spectroscopy, and powder X-ray diffraction (PXRD). SEM images confirmed that the fibers were 200-300 nm in diameter, which is consistent with the fiber size used in industry. Raman spectroscopy and PXRD verified that the fibers were also in the rutile phase, a smaller and more stable crystalline structure. Following confirmation of the physical properties, A549 cells were treated with fiber concentrations ranging from 0.02-500 µg/mL. Cell proliferation was measured with the MTT assay, which showed an IC50 of 0.02 mg/mL. Furthermore, cytotoxicity was determined using lactate dehydrogenase (LDH) assay, which showed that toxic effects did not appear until the fifth day of exposure ($p=0.05$). Expression analysis, qRT-PCR, of genes linked to oxidative stress, inflammation, and apoptosis was conducted and showed inflammatory genes to be differentially expressed compared to controls. These results suggest mild toxicity in the A549 cancer cell line via inflammation after at least a five-dayexposure to rutile SnDNF.

ROSENBALM, N.[1], and C. FAY[2]. Graph Population and Node States as Viable Simulators of Disease Infection Models. [1]Department of Biology, King University, Bristol, TN, [2]Emory and Henry College, Emory, VA.
The SIR model is generally accepted as an efficient way to represent the theoretical number of people infected by a disease over a certain period of time. The goal of this study was to find another method of representing these outbreaks. To find an alternative to the SIR model, graph population and node states were observed as simulators of disease on both random and scale free graph. Each node on a graph represented a person and each edge between two nodes represented an interaction between two people. Two sets of trials were run; for the first set, each node had a state, either healthy, sick or dead. For the second set, each graph had an immunity switch, which led to immune as a fourth possible node state. The differential equations used in the SIR model were then matched to graphs found in this study, and the SIR model differential equations compared favorably to the data. The method of using graph population and node states as simulators of disease is a viable alternative to using the SIR model.

URCUYO, J.[1], M. GHATAK[2], and P. WISE[3]. Modeling the Spread of La Crosse Virus in Knox County, Tennessee. [1]Departments of Applied Mathematics and Biology, Arizona State University, Tempe, AZ, [2]Department of Mathematics, University of Tennessee, Knoxville, TN, 3Department of Biological Sciences, University of Delaware, Newark, DE.
La Crosse Virus (LACv) is an arbovirus found in eastern Appalachia that can cause pediatric encephalitis in prepubescent children. To assess the risk and transmission of this disease, it is particularly important to study the spread of *Aedes* mosquitoes, which are the primary vectors of this virus. We use a deterministic SEIR model to study the effects of environmental factors on the population dynamics of *Aedes* mosquitoes in the Knox county area, including infected mosquitoes. We use locally-collected mosquito population data to adjust our model outputs and find that model predictions are heavily dependent on the fluctuations of both temperature and accumulated precipitation. These findings should be considered for mosquito management in southern Appalachia, as well as other regions with slight modifications.