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2014 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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National Institute for Mathematical
and Biological Synthesis

Sixth Annual

Undergraduate Research Conference at the Interface of Biology and Mathematics

November 1-2, 2014

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 by Dr. Joseph Tien and featured talk by Dr. Jeremy Smith will take place Saturday afternoon and a panel discussion on career opportunities will be featured on Saturday evening. Graduate opportunities will be showcased on Sunday morning. Poster abstracts start on page 6, oral presentation abstracts start on page 13.

NIMBioS

So what is 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 seventh 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 am to noon, and posters assigned even numbers will be presented. Please hang up your poster as soon as possible. Refer to the poster listing in this booklet to find your assigned number. Posters will all be hung in the hallway 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 (Dr. Suzanne Lenhart or Kelly Sturner) to have your talk loaded onto the appropriate computer in advance.

Social Media at URC 2014

Twitter

Check Twitter for live updates, highlights from sessions, and more. Follow us by visiting https://twitter.com/NIMBioS. Twitter users -- just log in and click “follow.”

View and join in conversations about URC 2013 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 LECTURES

Dr. Joseph Tien
Assistant Professor, Department of Mathematics
The Ohio State University

Cholera Dynamics: Blackboard, Bedside, Bench

Cholera is a disease with a long history, with John Snow's celebrated investigations of London cholera in the 19th century marking a seminal step in establishing the germ theory of disease. Despite this long history, cholera remains a serious public health concern today in areas lacking adequate water and sanitation infrastructure, with the ongoing cholera outbreak in Haiti as one stark example.

In this talk, I will discuss three examples of mathematical biology research on cholera dynamics that illustrate some of the ways that mathematical modeling can stimulate new biological work, and how biological questions can motivate the development of new mathematics. First, we will revisit the cholera outbreaks of John Snow's time, and see how mathematical models can help generate hypotheses that lead to preserved cholera specimens and reconstructing ancient cholera genomes. Next, we will consider cholera dynamics in Haiti, and discuss how modeling efforts can be used to help understand cholera seasonality and intervention efforts such as vaccination. Finally, I will discuss the role of mobility networks on cholera dynamics, and some mathematical results that arise from examining how network structure and community characteristics combine to affect the ability of disease to invade a network.

Dr. Jeremy Smith
Governor’s Chair, University of Tennessee
Director, Center for Molecular Biophysics, Oak Ridge National Laboratory

Computer Simulation for Renewable Energy, Environmental Science and Drug Design

We will examine how computer simulations help us understand why plants resist being used for cellulosic biofuel production. We will also look at the cycling of toxic mercury in the environment. The use of supercomputers in designing the next generation of targeted medicines will also be discussed.

SCHEDULE

Saturday, November 1: 413AB (Except where noted)

1:00-1:10 Welcome: Louis J. Gross, Director of NIMBioS

1:10-2:10 Keynote Lecture:
Dr. Joseph Tien, Associate Professor of Mathematics, The Ohio State University
Cholera Dynamics: Blackboard, Bedside, Bench

2:20-2:35

406: Winode Handagama, Nitin Krishna, Margaret McDaniel: *Quantifying Limits on Replication, Death, and Quiescence of Mycobacterium tuberculosis in Mice*

413AB: Michael Kelley: *Friend or Foe? A Continuous Ideal Free Distribution Approach to Dynamics of Individualistic, Cooperative, and KleptoparasiticPopulations.*

2:40-2:55

406: Michael DeBellevue: *Determining optimal vaccination strategies for the BCG vaccine in combating tuberculosis with a mathematical model of resistance and altered diagnosis*

413AB: Ian Kotthoff and Nathan Wikle: *Inferring the Evolutionary Processes Acting in a Population Based on Genetic Diversity*

3:00-3:15

406: Jennifer Houser: Modeling *Latency of Thalamocortical Fast-Spiking Interneurons in Schizophrenia*

413AB: Brittany Boribong and Michelle Cruz: *A meta-analysis of coastal populations' genetic diversity of species throughout their range*

3:20-3:50 Networking Activity and Snack Break

4:00-4:10 *Opportunities at NIMBioS*
Kelly Sturner, Education & Outreach Coordinator at NIMBioS

4:10-4:55 Keynote Lecture:
Dr. Jeremy Smith, Governor’s Chair University of Tennessee and Director Center for Molecular Biophysics at Oak Ridge National Laboratory
Computer Simulation for Renewable Energy, Environmental Science and Drug Design

5:05-6:00 Career Panel (Moderator: Suzanne Lenhart, Associate Director at NIMBioS)
Dr. Jeremy Smith
Dr. Joseph Tien

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

6:30 Turn in SET game sheets to Sturner or Lenhart at dinner

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

Sunday Morning, November 2: Auditorium 406, 413AB, 413C

8:00 Continental Breakfast

8:30-8:45

406: Vivian Anyaeche, Taylor Kuramoto, Taylor Nelsen: *An epidemiological model of Bovine Respiratory Syncytial Virus (BRSV) dynamics.*

413AB: Kendrea Bufford: *Fish Harvesting.*

8:50-9:05

406: Marina Massaro and Kelly Moran: *An Analysis of the Coherence Between Experiential and Behavioral Response During Ambiguous Emotional Stimuli*

413AB: Brennan Bean and Victoria Kelley: *The Effect of Prey Dispersal on a Two-Patch Predator-Prey System*

9:10-9:25

406: Oladipo Oyediran: The Effects of the Immune System on Bacteriophage Therapy on Cholera.

413AB: Alexander White: Parameter Estimation of Conductance-Based Neuron Models Using Current Clump Data: An Algorithmic Approach

9:30-9:45

406: Marina Romadan: Model *Comparison for Cholera over Multiple Data Sets.*

413AB: Zoe Vernon: *H-Representation of the Kimura-3 Polytope*

9:55-10:50

413C: Graduate School Opportunities & More Showcase

413AB: Faculty Networking (faculty only invited)

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

Sunday Afternoon: Rooms 403, Auditorium 406 and 413AB

12:05-12:55 Lunch

1:00-1:15

406: Katie Sipes: *Understanding the Locomotory Gait of Caenorhabditis elegans in a Viscous Fluid*

413AB: John Mooney: The Effect of Contact Lens Suction Pressure on the Shape of the Human Cornea

1:20-1:35

406: Ross Sausa: *Game Theory: If you are trying to avoid extinction or survive cancer, it's not just a game*

413AB: Hannah Pennington: *A Mathematical Model for the Interaction of the Proteins MMP-1, TIMP-1, and ECM in a Wound*

1:40-1:55

406: Jasmine Rivers and Jose Torres: *A New Approach to Understanding Evolutionary Relationships among Chagas Disease Vectors in Latin American Countries*

413AB: Veronica Go and John Shamshoian: *Unveiling cardiac disorders using a data-driven technique for eigenvalue estimation*

2:00-2:15

406: John Marken, Nicole Rooks, Brian Whyte: *Could Diminishing Aggression in the Invasive Argentine Ant cause Supercolony Collapse?*

413AB: Anthony Olivos: *Predictive models for dysphagia after spine surgery*

2:20-2:40: Break and Snacks

2:45-3:00

406: Kailong Mao: *Modeling the Population of Off-host Larval* A. americanum *in the Forest*

413AB: Alexis Bury and McKenzie Pickett: *Seasonality in Vibrio Bacteria Population Structure - A Practical Application of the Lotka-Volterra Competition Model*

3:05-3:20

413AB: Shelbie Burchfield: *Treatment of Caenorhabditis elegans with a Glyphosate-Containing Herbicide Leads to Mitochondrial Inhibition.*

3:25-3:35

406: Closing Remarks

3:40 Adjourn

POSTER ABSTRACTS BY SEQUENCE

1. BARTON, G., and WILD, G. Next Generation Methods in Invasion Analysis.Department of Applied Mathematics, University of Western Ontario, London, ON.

The traditional tools of linear stability analysis in invasion fitness calculations are often difficult to carry out, and as such the often overlooked next-generation tools can often be a useful framework for the performance of invasion analysis. We aim to illustrate the correspondence between the next-generation framework and linear stability analysis, in order to demonstrate the utility of these methods to a larger audience. The next-generation methods are differentiated from the methods of non-linear analysis by the examination of a decomposition of the Jacobian system rather than the Jacobian system itself. This decomposition is strictly characterized, and often has deep biological interpretations. We use the example of a Lotka-Volterra Predator-Prey system to illustrate the correspondence between these two methods, and utilize Gillespie's Algorithm to justify the resulting predictions. In demonstrating the validity of next generation tools as an alternative approach to linear stability analysis in invasion fitness calculations we aim to allow performance of invasion analysis in new contexts that were otherwise computationally intractable due to the nature of the linearization.

2. BERSIE, L., NEUBAUER, K., SCHMIDT, A., CHEONG, S., PINTER, G., LAUKO, I., KLINGLER, R., and M. CARVAN. Development of an automated assay for quantifying visual startle response in zebrafish exposed to methylmercury. Department of Mathematical Sciences, School of Freshwater Science, University of Wisconsin-Milwaukee, Milwaukee, WI.

Methylmercury pollutes bodies of water and bioaccumulates in food chains and is a well-documented and serious risk to environmental and human health. Small doses of methylmercury during gestation can have adverse effects on development, resulting in congenital diseases and behavioral problems. This study examines the effects of methylmercury exposure using zebrafish as an experimental model as they exhibit similar teratological and toxicological effects as humans. Prior studies have shown that methylmercury treated zebrafish show a dose-dependent decrease in response to visual stimuli, as well as abnormal retinal electrophysiology. However, determination of this startle response was not automated and required visual analysis and human interpretation of the response. These disadvantages left the possibility for inaccurate interpretation of responses, as well as bias and variability between observers.

We aim to improve upon this previous assay through the use of a novel observation setup, motion tracking software and specialized analysis algorithms. Our automated approach produces locomotion data, including velocity and angular velocity data, which can be used to quantitatively identify the startle response. By comparing the results of this new assay to the gold standard of the previous assay, we examine the validity of the new experimental design through descriptive statistics.

3. CAHILL, L. Have You Finished Growing? Why does it matter? University of Delaware, Newark, DE.

The purpose of this research was to model the Bertalanffy Growth Equation using Excel for the Biological ESTEEM (Excel Simulations and Tools for Exploratory, Experiential Mathematics) Program. The Bertalanffy Growth Equation models the body length of an individual over time. This is determined by time, the rate of growth, and the final length that the individual will eventually grow to be. The derivative of this equation explains how the rate of growth of an individual decreases over time until it eventually goes to zero. This is because over time an individual cannot grow without bounds, so as the length of an individual increases, the rate of growth will continuously decline until the individual reaches its eventual height. The function of this model is to help students and teachers visualize the equation as well as see how the equation is utilized when actual data is being utilized. This equation is most commonly used in fisheries for experimental purposes, but it has been very broadly used to study other organisms. Additionally, it has been applied medically for modeling tumor growth and estimating functional brain size from fMRI data. Actual data from several species will be included and compared to with the model.

4. CHAPINA, R. J., RAMOS-CHAVEZ, J., and E.J. WALSH. Population Structure of a Widespread Caribbean mysid Mysidium gracile. Department of Biological Sciences, The University of Texas, El Paso, TX.

Genetic variation is essential for populations to respond to changing environments. Seawater temperatures are rising while pH is dropping. Thus, there is concern about the ability of coral reef-associated organisms to withstand these changes and overall reef health. The mysid *Mysidiumgracile* commonly aggregates into swarms near reefs, and occupies an important intermediate level in marine food webs. The objective of this study is to determine levels of genetic variation in Caribbean *M. gracile* populations. Mysids from 15 swarms were collected and the COI DNA barcoding gene was sequenced for 50 mysids representing 5populations. An uncorrected genetic distance (p) matrix was constructed using PAUP. Genetic variation among swarms varied from 4-33% and distances within swarms ranged from 0-25%. Mysids comprised four clades based on Neighbor-Joining analyses. Additional individuals representing swarms isolated from three other islands are in the process of being characterized. Overall, these results show that there is high levels of genetic variation with and among mysid swarms, thus potentially facilitating their ability to adapt to environmental changes.

5. CRUICKSHANK, Z. and K. SCOTT. The Link Between Cellular Aging and Network Robustness. Spelman College, Atlanta, GA.

The budding yeast Saccharomyces cerevisiae is a model for cellular aging. Yeast aging is often measured by its replicative life span or (RLS), which is determined by the number of cell divisions that occur prior to senescence (when cells can no longer divide). We recently showed that cellular aging is an emergent property of gene networks and the aging dynamics are influenced by network robustness. Here, we studied the role of robustness on replicative aging in S. cerevisiae. As a cell's network robustness decreases, it will be less able to adapt against external perturbations. Several measures of robustness measure are examined, including morphological robustness, network connectivities, growth fitness and gene expression plasticities. Our studies show that the yeast replicative aging correlates with these robustness measures.

6. FRELIGH, A. Cooperation at the Molecular Level Affects your Performance and Health. University of Delaware, Newark, DE.

Many biological macromolecules are composed of subunits that function synergistically due to cooperativity. I have generated a spreadsheet model of the Hill Equation for the Biological Excel Simulations and Tools for Exploratory Experiential Mathematics (ESTEEM) modules page:http://bioquest.org/esteem/esteem_result.php in order for users to interactively develop a sense of nonlinear behavior of such macromolecules. This software is accessible to students and professors both nationally and internationally. Originally, the Hill equation represented the cooperative binding process of oxygen to hemoglobin molecules. Although Hill's model is not precise for modeling all forms of biological cooperativity, it is accurate enough that it is frequently utilized to describe the cooperative behavior of enzymes. In the model the parameters of the Hill equation are adjustable so that students can monitor the effects of adjusting such parameters. Additional spreadsheets will incorporate real world data about the binding of oxygen to hemoglobin under various conditions, the binding of ligands to enzymes, and genetic repressors whose data also fit the Hill equation. Medically, this model is relevant to the cooperativity of hemoglobin during intense anaerobic physical activity and is important to understanding the development of drugs for treating diabetes, sickle cell anemia, and thalassemia.

7. GUTH, B, LYNCH, S. and K. KOHLER. Mathematical Modeling of Blood Coagulation. University of Tennessee, Knoxville, TN.

Blood coagulation is a series of biochemical reactions that, in part, leads to blood clot formation and the cessation of bleeding. Many players involved in these reactions are known as clotting factors. Blood platelets are vital to clot formation; clotting factors must bind to platelet surfaces for many of the reactions to occur. Early reactions in coagulation produce catalysts, known as enzymes, which speed up the rates of other reactions and allow for clotting to occur in a feasible timespan. Many in vitro tests of coagulation involve closed systems that employ lipids in place of cell surfaces for the reactions to occur. These lipids are thought to function analogously to cellular-surface binding sites found on platelets in blood, but are typically in much higher concentrations than the number of binding sites on platelets. Mathematical models have been developed to simulate these lipid-based experiments but fail to include the concept of cellular-surfaces, despite platelets being instrumental to blood clotting. In this study we will extend a current mathematical model of the lipid-based in vitro tests to include a limited number of binding sites on platelet surfaces. The purpose of this investigation is to better understand the role of platelet binding sites in coagulation and to quantify the sensitivity of the extended model to the number of surfaces.

8. HALL, E. and S. HOTA. A Quantitative Analysis of SIR-type Malaria Models. Department of Mathematics, Austin Peay State University, Clarksville, TN. and Fisk University, Nashville, TN.
Malaria is a parasitic infection transmitted by female Anopheles mosquitos which can be fatal if not treated. The CDC reports Malaria had killed more than 627,000 people and created 207 million clinical episodes in 2012 alone. With approximately 1,500-2,000 cases reported every year, America is far from being isolated from this disease.
Sir Ronald Ross was the first to create an analytical model of Malaria and received a Nobel Prize for his work in 1902. Others such as Macdonald and Lotka have built upon this basis to give a refined view of the behavior of Malaria and treatment options. Ross' model, a general Kermack-McKendrick SIR-type model, is still being used as a basis to create further models of the Malaria epidemic.
This project is a comprehensive analysis of Ross and Ross-Lotka models including determining the equilibrium points, reproduction numbers and stability of the equilibrium point. Further study is done to compare/contrast both models

9. KELLEY, M. Friend or Foe? A Continuous Ideal Free Distribution Approach to Dynamics of Individualistic, Cooperative, and Kleptoparasitic Populations. Appalachian State University, Boone, NC.

10. KIRKLAND, M. Quantifying the Effect of Calorie Restriction on Yeast Replicative Lifespan. Spelman College, Atlanta, GA.
Cellular aging, the basis of physiological aging can be studied by using a organism similar to human cells known as Saccharomycescerevisiae. In this study, we investigate how calorie restrictions affect the longevity of a cell's life span. Here we measure the cell's life span by counting the number of cell divisions that it has. We compare the lifespan of wildtype, YBR053C null mutant, IZH4 null mutant, and Pvac8ERG2 over-expression under normal and calorie restricted conditions. We then applied student test, the t-test, evaluate the significance of lifespan differences.

11. KUWONU, D. and B. CAIN. Mathematical Model Transmission Dynamics of West Nile Virus in Bald Eagles. Austin Peay State University, Clarksville, TN.
In this project we derived a system of ordinary differential equations for the dynamics of West Nile Virus in the Bald Eagles, Eared Grebes and mosquitoes populations. The result of the basic qualitative analysis of the model shows that the system has a locally stable disease free equilibrium when the reproduction number is less than one. Furthermore, the results of the sensitivity analysis show that the death rate of mosquitoes, the rate that susceptible mosquitoes and Eared Grebes become infected and the interaction between the mosquitoes and Eared Grebes has the most impact on the reproduction number. We implemented some control strategies such as mosquito reduction, protection and universal strategy.

12. MAGRUDER, D.S. and P. MILLER. Dual Homeostasis: Preserving Information. Rhodes College, Memphis, TN.
Maintenance of an average firing rate on a large timescale is crucial for information that is conveyed by the fluctuations on a short timescale. Hebbian plasticity is a destabilizing force modifying the strength of specific synapses of a neuron, whereas homeostatic plasticity is a stabilizing force scaling the strength of all synapses of a neuron to maintain an average firing rate. Most theoretical models currently establish stability via a single

homeostatic sensor. It is likely that homeostatic plasticity is effectuated via two sensors. Here we investigate the stability requirements of a theoretical model with dual homeostatic functions modulating independently intrinsic and synaptic conductances.

13. MARTINEZ, J., BROOKER, J., and M. DELORENZO. Effects of Antimicrobial Exposures on Grass Shrimp, *Palaemonetes pugio*, and Associated Vibro Bacterial Density and Development of Antibiotic Resistance. Department of Biology, College of Charleston, Charleston, SC.

Although not usually thought of as pollutants, antimicrobials are widespread in the aquatic environment and may threaten ecosystem and human health. To study the impact of antimicrobials, grass shrimp, Palaemonetes pugio, were exposed to 0.11 mg/L and 0.33 mg/L triclosan (TCS), 30 mg/L and 60 mg/L sulfamethoxazole (SMX), and additive mixtures of the two compounds for 96 hours. Effects on survival and sublethal effects on glutathione and lipid peroxidation activity, two biomarkers of cellular stress, were measured in the grass shrimp. Antimicrobial effects on the bacterial community of the shrimp were assessed by measuring Vibrio spp. density and testing bacterial community of the shrimp were assessed by measuring Vibrio spp. Density and testing bacterial isolated for the presence of antibiotic resistance. TCS (0.33 mg/L) and the high mixtures of TCS and SMX caused significant shrimp mortality and significant increase in lipid peroxidation activity. Glutathione activity was not significantly altered by antimicrobial exposure. TCS significantly increased Vibrio density compared to control, while SMX and the mixture decreased Vibrio density. Also, antimicrobial exposures changed the proportion of V. vulnificus and V. parahaemolyticus found in shrimp. An increase in Vibrio antibiotic resistance was observed with shrimp antimicrobial treatment. For TCS, there was > 80% Vibrio resistance in the control treatment, thus the presence of TCS in coastal waters may preferentially increase the abundance of pathogenic bacterial species. The result of this study indicated the need for careful regulation of antimicrobial use and disposal to safeguard against ecological and human health risks related to pathogenic bacteria and development of antibiotic resistance in the environment.

14. MAXWELL, L. and J. PASCAL. Mathematical Modeling of Electroosmotic Flow in Tumor Cells for Tumor Treating Fields (TTF) Therapy. Tennessee Technological University, Cookeville, TN.

Tumor treating fields (TTF) is a new type of cancer therapy that was recently approved by the Food and Drug Administration (FDA) in March 2011 for use in glioblastoma multiforme (GBM) patients that dramatically increases quality of life, while still being just as effective as traditional chemotherapy. TTF therapy uses alternating (AC) applied electrical fields to interfere with tumor cell division by disrupting mitosis via the movement of charged molecules within the cells, altering their internal structure. The processes of electrophoresis, electroosmosis and dielectrophoresis play a key role in the effectiveness of this therapy. Thus, here we will present a mathematical model that describes electroosmotic flow within a single, dividing tumor cell during anaphase and cytokinesis by using idealized geometrical structures to describe the cell. Time dependent velocity profiles as a function of electrical field, cell phase and geometrical parameters indicate situations in which flow reversals can occur within the cells. These results can aid in ultimately predicting and optimizing tumor cell response to TTF therapy.

15. MOORE, K. Hydrogen Peroxide Increases the Amount of Intracellular Reactive Species and Decreases Cellular Robustness in Saccharomyces cerevisiae. Spelman College, Atlanta, GA.

Saccharomyces cerevisiae, also known as the budding yeast, can be used to study the cellular aging process as a model for aging of human cells. Past studies have concluded that there is a strong connection between the presence of superoxides and cellular aging. This study investigates how the presence of hydrogen peroxide on the outside of the cell influences the amount of hydrogen peroxide inside of the cell. The hydrogen peroxide represents stress which causes the cell to aim for a balance between intracellular and intercellular levels. The intracellular levels of superoxide anions are monitored by dihydroethidium (DHE; red) and that peroxide levels are monitored by dihydrorhodamine (DHR; green). DHR and DHE are florescent probes that can be detected by flowcytometry. The presence of hydrogen peroxide increases the coefficient variation that represents the DHE and DHR. Those increases cause a decrease in the robustness of the cells.

16. MYERS, N., PINTER, G., LAUKO, I. and T MILLER. Cyanobacteria Bloom Model Dynamics and Calibration Using Parameter Selection Techniques. Zilber School of Public Health and the Department of Mathematics, University of Wisconsin, Milwaukee, WI.
Harmful algal blooms, especially those related to Microcystis, can be toxic to humans and freshwater biota. Managing this growing problem will depend upon the existence of accurate modeling approaches. In this work, a model described by a system of nonlinear integro-partial differential equations (including convective and diffusive terms and non-local light-limited growth) is modified to represent the ecosystem of a lake in central Wisconsin. The model developed for predicting Microcystis algal blooms incorporates light intensity, nutrient densities, water column mixing, and interspecies competition. Parameter selection techniques tested include global sensitivity measures and Bayesian methods. In addition, these techniques examine the importance of individual parameters to the dynamics of the system and their relationships to each other.

17. NGUYEN, C., COX, B. and Z. Pang. Spatial Reef Competition in the Florida Keys: The Modeling of Various Dominance Scenarios. University of Texas, Arlington, TX.
Coral reefs play a vital role in maintaining the balance of the ocean's ecosystems. In the past few decades, these diverse ecosystems have sustained substantial damages from environmental stress such as elevated temperatures, ocean acidification, and pollution. Consequently, the interactions between corals and their competing species have become imbalanced. As a result, coral coverage has experienced immense declines, allowing the competitors to become more dominant in the reefs.

To contribute to resolving this ongoing issue, we are modeling changes in the populations of stony corals and two of their major competitors near Florida Keys: macroalgae and gorgonian corals. Gorgonian corals have become more abundant, which endangers the biodiversity that is organic to the natural reef ecosystems. Using parameters to represent the effects of environmental factors on these species, we will run simulations to estimate how these species behave and compete with each other under various stressors.

Further, to gain a better understanding of the competition dynamics, we are conducting analysis on our model of three ordinary differential equations by solving for equilibria values and determining their stabilities. Doing so, we can find sets of parameter values that correspond to biological conditions under which each of the species will become the dominant population, especially the currently disadvantaged stony corals.

18. ONABOLU, O.O. and S. HOTA. A discrete dynamic model of oxygen absorption with different breathing patterns. Department of Mathematics and Computer Science, Fisk University, Nashville, TN.
Breathing is a process that is fundamental to the survival of the living species on earth. Different living organisms have their means of achieving their physiological respiration. In human beings, the two lungs are the major organs responsible for this vital process. In this project, a mathematical model is developed in discrete dynamical systems to analyze the mechanism of oxygen absorption in the human body.

This project determines quantitatively, supported by numerical simulation through Mathematica, the chemical concentration of a particular substance in the body after each breath and also how variations in the chemical concentrations of the substance in the outside air, fraction of air exchanged, quantity of oxygen absorbed into the blood and different breathing patterns affect the dynamics of the model.

19. PEDERSON, J., C. STIEZ and F. ALBERTO. A Mathematical Approach for the Estimation of Inbreeding Rate in a Kelp Metapopulation.Division of Biological Sciences, University of Wisconsin, Milwaukee, WI.
Giant kelp (*Macrocystispyrifera*) is among the world's largest macroalgae. Living in dynamic coastal populationsfrom Alaska to New Zealand, giant kelp abuts much of the world's temperate coastal reefs. In southern California, giant kelp constitutes a true metapopulation of sub-patches.

The extinction and re-colonization dynamics of this metapopulation is the focus of ongoing research. Although environmental conditions and associated stochasticity play a predominant role in determining metapopulation dynamics, there is considerable uncertainty about genetic contributions—e.g. inbreeding depression. Inbreeding

depression is well documented for this species using controlled laboratory crosses. However, little is known about its expression in nature where it is a function of naturally occurring selfing rates.
Here, we use a lattice simulation model that makes use of a25year long time series of satellite (LANDSAT) data, a particle transport model based connectivity matrix,a probability density function for the dispersal of spores and a graph theory based subpopulation identification to quantify the variation in selfing rate for the entire Southern California Bight. These quantifications can be used as a predictor variable to model patch dynamics throughout the time series and will contribute to our understanding of genetic contributions in giant kelp population dynamics.

20. PRICE, K., KING, R. and C. RIN. Isolation and Characterization of Gansey, a New Member of the Cluster K Mycobacteriophages. Division of Biological Sciences, Western Kentucky University, Bowling Green, KY.
Bacteriophages are viruses that infect bacteria and can be found anywhere a suitable host exists. The purpose of this research was to gain insight into the diversity of the bacteriophage population by isolating and characterizing new bacteriophages from the environment. Mycobacteriophage Gansey was isolated from a soil sample collected from Hodgenville, Kentucky. Gansey's morphology was viewed by electron microscopy, and preliminary information about its DNA sequence was determined by restriction analysis and gel electrophoresis. Gansey phage particles have an average 162.4 nm long, non-contractile tail and a icosahedral head with an average diameter of 37.6 nm. DNA restriction analysis suggested that Gansey belongs to the K1 sub-cluster of mycobacteriophages and full genomic sequencing verified this. The DNA sequence is 59,708 bp long, and includes a 11 bp 3' overhang (CTCGTAGGCAT). Using DNA Master, GeneMark, Glimmer, BLAST, and HHPRED, Gansey's genome was predicted to have 95 genes and is most similar to other K1 mycobacteriophages JAWS, Adephagia, Angelica, CrimD, Anaya, and BarrelRoll.

21. QUIJANO, A. J., JOYNER, SEIER, E., M., HANCOCK, N., LARGENT, M., JONES, T., An Aggregate Stochastic Model Incorporating Individual Dynamics for Predation Movements of AnelosimusStudiosus. Department of Mathematics and Statistics, East Tennessee State University, Johnson City, TN.
In this poster, we discuss methods for developing a stochastic model which incorporates behavior differences in the predation movements of AnelosimusStudiosus (a subsocial spider). Stochastic models for animal movement and, in particular, spider predation movement have been developed previously; however, this poster focuses on the development and implementation of the necessary mathematical and statistical methods required to expand such a model in order to capture a variety of distinct behaviors. A least squares optimization algorithm is used for parameter estimation to fit a single stochastic model to an individual spider during predation resulting in unique parameter values for each spider. Similarities and variations between parameter values across the spiders are analyzed and used to estimate probability distributions for the variable parameter values. An aggregate stochastic model is then created which incorporates the individual dynamics. The comparison between the optimal individual models to the aggregate model indicate the methodology and algorithm developed in this paper are appropriate for simulating a range of individualistic behaviors.

22. VERNON, Z. MUAHAR, M. and J. RUSINKO. H-Representation of the Kimura-3 Polytope. Winthrop University, Rock Hill, SC; Lenior-Rhyne University, Hickory, NC.
Given a group-based Markov model on a tree, one can compute the vertex representation of a polytope, which describes the associated toricvariety. Thehalf-space representation, however, is not easily computable. In thecase of$\mathbf{Z}_2$ or $\mathbf{Z}_2$ **X** $\mathbf{Z}_2$, these polytopes haveapplications in the field of phylogenetics. We provide a half-spacerepresentation for the m-claw tree, for G=$\mathbf{Z}_2$ **X** $\mathbf{Z}_2$**,** which corresponds to the Kimura-3 model of evolution.

23. WHITE, A. J. Waveform Fitting Algorithm: A Framework for Parameter Estimation in Neural Conductance Models Using Current Clamp Data. Case Western Reserve University, Cleveland, OH.

Determining the underlying dynamics of a neuron is computationally expensive and requires a large quantity of experimental data. Often the calculations require using voltage clamps and many different channel blockers to tease out the ion channels present in the cell membrane. This process is often averaged over many neurons to produce a conductance based model. However, the parameters of an individual neuron may differ from its neighbors, or even itself, given enough time. Models based on averaged parameters can fail to reproduce the behavior of the individuals [Golowasch et al 2002]. In this project, I develop an algorithm that finds certain parameters (conductances, capacitance, and driving potentials) of a neuron from a single current clamp experiment. Using the recorded voltage, we calculate the hidden gating variables by solving a system of non-homogeneous linear differential equations, assuming the gating variable dynamics take a known form. Having determined the gating variables, we calculate the conductance of each type of ion channel in the membrane by using a least squares method. The efficiency and accuracy of my method compares favorably with existing methods in the literature [Lepora et al. 2012][Huys et al. 2006].

24. WILLIAMS, B. and QIAN, L. Using Machine Learning Techniques to Predict the Secondary Structure of Protein. Department of Mathematics and Computer Science, Fisk University, Nashville, TN.
It is from the structure of the protein, that scientists are able to gain an understanding of protein function and its role in the body. In this project, we focused on using artificial neural networks, a pattern recognition technique, to predict the secondary structures of proteins. Our goal was to investigate different neural network architectures to determine the best configuration for predicting the secondary structures of proteins from their primary sequences. We also investigated different techniques to run neural network in computers with low memory. Using the proteins dataset from the CullPDB database, we tested different neural network architectures in a computer cluster and also developed algorithms to train the network in our own personal computers with less memory. Their performances are compared.

25. YAGBOYAJU, S., QIAN, L. and B. NELMS. Developing Effective Algorithms For Biological Data Access and Sequence Analysis of C-Elegans. Department of Mathematics and Computer Science and Department of Biology, Fisk University, Nashville, TN.
Real time access to biological data and information has become increasingly important in the modern day world. Biological data has helped improve the quality of research, the standard of medical care and also the production of drugs and vaccines. Many biological databases such as Worm-base and NCBI have been built to allow access through web browsers however using web browsers may be difficult and inefficient especially when we have to synthesize data from multiple sources or we have to do batch queries .In this project, We will be using Python to develop a tool to simulate a web search and automatically parse the web pages to extract data, analyze data and generate required primers. The ultimate goal of this project will be to develop web services and applications to seamlessly access and analyze data from biological databases.

26. ZELLMER, J. Determining Sufficiency for Comparison in the Friction Ridge Impression Examination Process. University of Wisconsin, Milwaukee, WI.
Friction ridge impressions, better known as “fingerprints”, have gained recognition for their use in identification purposes due to their uniqueness among individuals and their persistence throughout an individuals’ lifetime. Two characteristics that are used in the identification process are: the quality of the print and the quantity of unique characteristics of the print. Previous research has focused on the lack of examiner consistency in the determination of sufficiency for comparison based on the quality and the number of minutiae (unique characteristics) of the fingerprint. Sufficiency of determination is a subjective calculation of the examiner that states whether the print in question has enough unique characteristics and is of good enough quality that it will likely yield a match when comparing prints. This research developed an ordinal logistic regression model and examined the predicted usefulness of fingerprints (measured by their ordered categorical rank when searching a database for a potential match) in an effort to determine a sufficiency standard for a fingerprint to be considered

useful in casework. The results of this project determined that the minimum standards for the quality and quantity of minutiae of a print may be higher than those currently recommended.

ORAL PRESENTATION ABSTRACTS (Alphabetical)

ANYAECHE, V., KURAMOTO, T., NELSEN, T., JAMES, T., CHEN, S., LANZAS, C., LENHART, S. An Epidemiological Model of Bovine Respiratory Syncytial Virus (BRSV) Dynamics. Department of Life and Physical Sciences, Fisk University, Nashville, TN; Department of Mathematics, Augsburg College, Minneapolis, MN; Department of Geography, University of North Carolina, Chapel Hill, NC; Department of Natural and Mathematical Sciences, LeMoyne Owen College, Memphis, TN; College of Veterinary Medicine and the National Institute of Mathematical and Biological Synthesis, University of Tennessee, Knoxville, TN.
Bovine Respiratory Syncytial Virus (BRSV) is one pathogen in the larger Bovine Respiratory Disease Complex that causes damage to the respiratory tract, facilitates bacterial growth and compromises the immune system. Negative effects of BRSV include costs stemming from death, reduced performance, poor growth and administration of vaccines and treatments. Understanding the effect of cattle contact networks on the transmission of the virus will help reduce unnecessary treatments, costs and public health concerns of growing drug-resistance. A stochastic agent-based epidemiological model has been developed to predict the outcome of infection under different circumstances. The model simulates the spread of BRSV using a spatially implicit contact network generated by a real time location system and visualized in NetLogo. The underlying theory relies on basic Susceptible-Infected-Recovered compartmental principles. Simulations were completed under varying initial conditions and compared susceptibility, incidence proportion, maximum prevalence and cumulative centrality to see how disease dynamics and emergence differ under given initial conditions. Qualitative observations from the model interface and preliminary quantitative analysis indicate that cows' social behavior and interactions affect how the virus spreads through a population. These findings indicate that decreasing the number of cows in a herd will not decrease the transmission rate but if the network structure and sociality of the cows can be controlled so can the transmission.

BEAN, B., KELLEY, V., RICHARDSON, J., TALIS, E., and WELLS, C. The Effect of Prey Dispersal on a Two-Patch Predator-Prey System. Brigham Young University, Provo, ID.
We consider the effect of prey dispersal in a two-patch predator-prey model in which the two patches are qualitatively different. In particular, we assume patch two has a significantly smaller carrying capacity and a correspondingly higher predation rate. Scaling the model under these assumptions introduces a parameter of arbitrarily small order, allowing for an asymptotic analysis. We show that the predator and prey will always coexist for biologically reasonable parameter values. Furthermore, we prove the existence and uniqueness of a coexistence equilibrium and determine the stability regions in the parameter space. Using numerical simulations, we illustrate the varying effects of prey dispersal on the stability of the coexistence equilibrium and find parameter values for which a Hopf bifurcation occurs.

BORIBONG B., CRUZ M., and F. HONG. Meta-analysis of Coastal Populations' Genetic Diversity of Species Throughout Their Range. University of Scranton, Scranton, PA; California State University, San Marcos, CA; Mount Holyoke College, South Hadley, MA; National Institute for Mathematical and Biological Synthesis (NIMBioS), University of Tennessee, Knoxville, TN.
Along a species' distribution, its location in either the center or edge of the range may affect various characteristics of the populations, such as fitness, genetic diversity, and adaptability. Higher genetic diversity in the centers of many species' ranges have been thought to account for the abundant-center hypothesis, which states that populations found in the center of their natural distribution are more abundant than those found at the edges. Despite the prevalence of the abundant-center hypothesis in population studies, the assumption of differential genetic diversity throughout ranges has rarely been tested in a rigorous way across many taxa. On

the other hand, studies that have tested the genetic variation in plants and animals along their species' ranges did not account for variation in sample sizes among studies. To better test the validity of the abundant center hypothesis, this study investigated how genetic diversity of populations distributing along world's coastlines is affected by location within the species' range using a meta-analysis. This study focused only on coastal populations, where range shapes are often less complex, and thus the genetic signal is likely clearer. As an explanatory factor of genetic diversity among populations, populations' distance to the center of a range is hypothesized to be positively correlated with the genetic diversity. An effect size of correlation coefficient (Pearson's r) for each genetic measurement of each species versus distance to center was calculated from the meta-analysis. Results showed positive correlations for most species and insignificant correlations for others. By determining if there is a difference in genetic diversity among populations throughout their ranges, conservation efforts can target individual populations, as opposed to protecting the entire species as one entity. The study can potentially give insights and directions for developing more effective and feasible coastal conservation practices.

BUFFORD, K. Fish Harvesting. Department of Mathematics, Tennessee State University, Nashville, TN.
Understanding the dynamics of fish harvesting is one of the challenging and important issues in marine ecology pertaining to protecting the ocean's ecosystem. In this talk, Predator-Prey type model with Holling Type II interaction is developed to study the dynamics of the populations of the prey and predator during the controlled harvesting period. Qualitative analysis of the model is studied and all parameter values are determined from the literature reviews. The optimal control problem is stated to maximize the profit from harvesting both populations under the different harvesting policies. The solution algorithm is developed to solve the optimal harvesting problem using the forward-backward sweep method with forward-backward Runge-Kutta 4 solvers. All codes were developed in MatLab. The presentation summarizes the results of the "Control Theory Summer Workshop 2014" hosted by the Department of Mathematical Sciences at Tennessee State University under the support of the NSF, Undergraduate Program for Historically Black College Universities (HBCU UP) grant #1238775.

BURCHFIELD, S., TODT, C., BAILEY, D., NEGGA, R., and FITSANAKIS, V. Treatment of *Caenorhabditis elegans* with a Glyphosate-Containing Herbicide Leads to Mitochondrial Inhibition. Department of Biology, King University, Bristol, TN.
It is well-documented that patients with Parkinson's disease (PD) exhibit Complex I mitochondrial inhibition. Interestingly TouchDown® (TD), a widely-used glyphosate-containing herbicide, is suspected of adversely affecting mitochondrial function. Previous work in *Caenorhabditis elegans* (*C elegans*) treated with TD showed dopaminergic neurodegeneration similar to that observed in PD patients. To determine whether exposure to TD results in mitochondrial inhibition, we treated N2 (wild-type) *C elegans* with varying concentrations (LC_{25}, LC_{50}, LC_{75}) of the commercial-grade herbicide. Studies using an acute (30 min) exposure paradigm were conducted. Following treatment, a luminescent probe was used to determine relative ATP amount. Results indicated a statistically significant decrease (***$p<0.001$) in ATP production in the LC_{75} group compared to controls. To determine the site of inhibition, further studies specifically assayed for function of Complexes I-IV. Although Complex I was statistically significantly decreased (*$p<0.05$) in oxygen consumption studies, colorimetric assays indicated increased Complex II and Complex IV activity. This suggested electron deficiency rather than inhibition of these latter complexes. Furthermore, TMRE accumulation, a measure of an intact proton gradient, was also increased. Taken together, these data suggest Complex I inhibition may be responsible for the observed ATP decrease. This provides a possible mechanism for the previously reported neurodegeneration.

BURY, A. and M. PICKETT. Seasonality in Vibrio Bacteria Population Structure- a Practical Application of the Lotka-Volterra Competition Model. Departments of Biological Sciences and Mathematics, University of Wisconsin-Milwaukee, WI.

The bioluminescent bacteria *Vibrio harveyi* and *V. chagasii,* are found in the Gulf Coast of Florida where their relative abundance varies between winter and summer. This study aims at examining the hypothesis that seasonal variations in the relative abundance of *Vibrio harveyi*and *V. chagasii* populations off the coast of Florida are due to changes in growth rate and competitive ability caused by seasonal variations in temperature. We conducted growth experiments with the two bacteria populations at six different temperatures to identify temperature dependent growth rates. Time series cell-count population data were also collected in competition experiments at the same temperature range. The experiments conducted qualitatively exhibit the behavior observed in nature. Experimental results are used to parameterize a Lotka-Volterra competition model to test the presence of factors influencing the competitive dynamics additional to the individual temperature dependent growth parameters.

DEBELLEVUE, M., NGUYEN, D.H., NYANGANI, I. and C. KRIBS-ZALETA. Determining optimal vaccination strategies for the BCG vaccine in combating tuberculosis with a mathematical model of resistance and altered diagnosis. Departments of Mathematics and Biology, The University of Texas of Arlington, Arlington, TX.
The commonly used Bacille Calmette-Guerin (BCG) vaccine is not completely effective, and renders ineffective the tuberculin skin test, a common tool in areas without adequate laboratory facilities, complicating diagnosis. A modified SIR model consisting of a system of five nonlinear differential equations was created to represent the two effects of the BCG vaccine in order to understand the proper role of the BCG vaccine in fighting tuberculosis. Analysis yielded a simple criterion under which vaccination increases the reproductive number of the disease. When applied to a particular setting, the model can predict whether a strategy of tuberculin skin test use is superior to vaccination. Our results predict that the vaccine is less effective at fighting the disease than indicated merely by the immunity conferred to the user, as it is also dependent on the availability of laboratory diagnosis techniques.

GO, V. SHAMSHOIAN, J., COMER, M., and R. MCDOWELL. Uncovering Cardiac Dynamics Using a Model Independent Technique for Eigenvalue Estimation. National Institute for Mathematical and Biological Synthesis, University of Tennesse, Knoxville, TN; California Polytechnic University, San Luis Obispo, CA; Campbell County High School, Jacksboro, TN; West High School, Knoxville, TN.
Cardiac alternans, a beat-to-beat alternation in action potential duration in cardiac cells, is a harbinger of ventricular fibrillation. Ventricular fibrillation is a fatal arrhythmia and leads to sudden cardiac arrest, which takes the lives of about 300,000 Americans each year. Alternans is characterized by an eigenvalue of the Jacobian approaching -1. Unfortunately, specifying a model to fully describe cardiac dynamics may be impossible. Furthermore, the full state space may not be physically measured. Petrie and Zhao [2012] developed statistical data-driven statistical techniques to estimate dominant eigenvalues and their standard errors by measuring action potent duration values. This work expands the previous technique by introducing random disturbances to the pacing rate. The added disturbance proves to improve the robustness of the technique, rendering it more suitable for experimental analyses, which noises and measurement errors impose challenges to data analysis.

HANDAGAMA, W., KRISHNA, N. and M. MCDANIEL. Quantifying Limits on Replication, Death, and Quiescence of Mycobacterium tuberculosis in Mice. University of Chicago, Chicago, IL; Maryville College, Maryville, TN; National Institute for Mathematical and Biological Synthesis, University of Tennessee, Knoxville, TN.
According to the World Health Organization, an estimated 2.3 billion people are infected with Mycobacerium tuberculosis (Mtb). Despite decades of research, the physiology of tuberculosis remains poorly understood. Current models for Mtb hold that the total bacterial burden approaches a static equilibrium during chronic infection. A recent study of Mtb-infected mice by Gill et al. (2009) used a mathematical model to show that bacterial replication and death rates do not necessarily remain constant. In our study, we extend this model by investigating the effects of a time-dependent segregation rate and the inclusion of quiescence to find limits on

growth rates that are consistent with bacteria counts. We find that there are alternative hypotheses to tuberculosis pathogenesis that lead to lower predictions of Mtb replication and death rates. We also show that replication and death rates of Mtb may be higher than initially predicted when bacterial quiescence is added into the model.

HOUSER, J. Modeling Latency of Thalamocortical Fast-Spiking Interneurons in Schizophrenia. East Tennessee State University, Johnson City, TN.
Neural thalamocortical circuits relay external sensations from the thalamus to the cortex where sensory information is then processed. Feedforward inhibition involving a subtype of fast-spiking interneurons, which are marked by the calcium-binding protein parvalbumin, reduce the chance that a postsynaptic neuron will fire an action potential. Consequences on the circuit due to the absence of parvalbumin expression in fast-spiking neurons in schizophrenia patients are caused by fast-spiking latency. In this presentation, we present a conventional neuron model. We will show how to develop a mathematical model to incorporate a latency effect as well as show numerical simulations.

KELLEY, M., REDING, I. and ROWELL, J. Friend or Foe? A Continuous Ideal Free Distribution Approach to Dynamics of Individualistic, Cooperative, and KleptoparasiticPopulations. Department of Mathematics Math-Bio REU, University of North Carolina Greensboro, Greensboro NC.
Populations distribute themselves throughout their habitat based upon a range of environmental factors. In this paper, we extend a reaction-advection model of ideally motivated populations to describe the local and regional consequences of interactions between three populations distinguished by their levels of intraspecific cooperation and interspecific competition and exploitation. These populations are taken as three stereotypical expressions of cooperative-exploitative behavior in resource collection and include: a baseline non-cooperative population that engages in interference competition, obligate cooperators who initially benefit from the presence of conspecifics, and - in a pathological example of defection - kleptoparasites who require heterospecifics to extract resources from the environment. Using both analytic techniques and simulations, we determine where different populations can coexist within the environment and investigate under what conditions one population will invade another. Kleptoparasites can initiate a long term dynamic instability when invading cooperators at high resource levels. Non-cooperators and cooperators are primarily allopatric with respect to one another and capable of resisting low-level invasions.

KOTTHOFF, I. and N. WIKLE. Inferring the Evolutionary Processes Acting in a Population Based on Genetic Diversity. Truman State University, Kirksville, MO.
Tajima’s D is a statistical test used to infer the evolutionary processes acting in a population based on patterns of genetic diversity. This test may be used to distinguish the evolutionary mechanisms of neutral evolution, population subdivision, negative frequency-dependent selection, and purifying selection that are present in a population. Although this process seems straight forward, similarities in Tajima’s D statistic for different evolutionary mechanisms requires the use of various summary statistics and statistical learning techniques in pursuit of an accurate predictive model. In this study the use of Tajima’s Dsyn and Dnon statistics, and Fu and Li’s D, F, D* and F* statistics as predictor variables for distinguishing evolutionary mechanisms will be explored, with particular emphasis placed on their relevance to principal component analysis and random forests. This study seeks to demonstrate that the implementation of random forests can lead to an accurate predictive model for observations influenced by population subdivision, purifying selection and negative frequency-dependent selection. Further improvements are needed to distinguish between the neutral model of evolution and population bottleneck.

MAO, K. Modelling the Population of Off-host Larval *A. americanum* in the Forest. Truman State University, Kirksville, MO.
In order to assess the possibility of some vector-borne diseases it is essential to understand what determines the number of Amblyomma americanum. The objective of our research was to model the population of off-host larval A. americanum in the forest habitat. Four regression models (Poisson, negative binomial, zero-inflated

Poisson and zero-inflated negative binomial) were evaluated based on Akaike Information Criterion (AIC) and Pearson Dispersion. Eight variables (temperature, saturation deficit, precipitation, wind speed, day length, extreme high temperature, extreme low temperature and adult lag) were evaluated based on AIC, Kullback Information Criterion (KIC) and their corrected and quasi versions (AICc QAIC, QAICc, KICc, QKIC and QKICc). The negative binomial model was chosen as a "best" model and several variables were identified as important factors to explain larval load based on the variable selection criteria. Finally, the model was modified via a dynamic component to incorporate potential autocorrelation. This model would be significant within vector ecology because the activity of the larval stage impacts later stages that carry diseases.

MARKEN, J., ROOKS, N. and B. WHYTE. Could Diminishing Aggression in the Invasive Argentine Ant Cause Supercolony Collapse? College of William & Mary, Williamsburg, VA; University of Tennessee, Chattanooga, TN; SUNY Plattsburgh, Plattsburgh, NY; National Institute for Mathematical & Biological Synthesis, University of Tennessee, Knoxville, TN.
Supercolonies are collections of ant colonies whose workers treat each other as kin despite being effectively unrelated. Applying inclusive fitness theory suggests that supercolonies are structured upon inherently unstable social behaviors, leading many to predict that supercolonies will collapse from exploitative "cheats" invading the group. Here we propose a new theory on supercolony collapse focusing instead on behavioral and ecological constraints which support the supercolony structure, and we examine how these might change over time with a spatially explicit agent-based model of invasive Argentine ant supercolonies in their environment. Invasive populations of Argentine ants assemble the largest supercolonies ever recorded, forming collections of colonies up to 6,000 km wide that avoid aggression with each other. Conspecific aggression in Argentine ants is avoided only when ants bear similar enough chemical recognition cues. Rival supercolonies use distinctly different recognition cues, leading to intense intraspecific aggression. Within a supercolony this aggression towards outsiders selects against variations in recognition factors, but if aggression were to diminish over time, recognition factors would be free to vary, allowing supercolonies to fragment. Our model simulates how cases like gene drift in aggressive behaviors, as well as other scenarios, can lead to the collapse of supercolonies.

MASSARO, M., MORAN, K., and B. ROBERSON. An Analysis of the Coherence Between Experiential and Behavioral Response During Ambiguous Emotional Stimuli. SUNY Geneseo, Geneseo, NY; Clemson University, Clemson, SC; National Institute for Mathematical & Biological Synthesis, University of Tennessee, Knoxville, TN.
In 1971, Paul Ekman published that the six basic emotions (anger, happiness, surprise, disgust, sadness, and fear) have distinct, universal facial expressions; we smile when we are happy, frown when we are sad, and wrinkle our noses in disgust. Past studies confirm that high levels of coherence exist between emotional experience and facial expression when subjects are shown poignant film clips. But what happens to the tie between emotional experience and facial response when the eliciting event isn't purely of one sentiment? In this study, data collected from video recordings of individuals watching ambivalent film clips are used to examine the relationship between emotional experience and facial response when mixed emotion is elicited. Cross-correlations between data sources measuring positive and negative emotional response indicate low to moderate amounts of coherence between response systems. Contributors to coherence are being investigated, including the degree to which emotion is "mixed" at a given time, individual personality characteristics, and attitude toward various emotions. Furthering the understanding of response coherence and mixed feelings will shed light on various psychiatric disorders, where emotional dysfunction skews the normal emotional experience and response.

MOONEY, J. The Effect of Contact Lens Suction Pressure on the Shape of the Human Cornea. Rochester Institute of Technology, Rochester, NY.
The field of orthokeratology is concerned with using special contact lenses to reshape one's cornea in order to change its refractive properties. When a contact lens is inserted, the lens stretches to conform to the eye. The deformed contact lens acts to assume its undeformed shape and generates a suction pressure. Consequently, the

cornea deforms. By controlling the way the cornea deforms, contact lenses can be used to correct vision errors such as nearsightedness, farsightedness, and astigmatism. In this work, we develop a mathematical model to predict the corneal deformation. We model the human cornea as an isotropic linear elastic material. By relating stress-equilibrium equations to strain-displacement equations from elasticity theory, we develop a system of coupled partial differential equations. We approximate solutions of the partial differential equations associated with the suction pressure produced by a contact lens using the method of finite differences. We also explore the influence of contact lens design parameters on corneal deformations.

OLIVOS, A. Predictive Models for Dysphagia after Spine Surgery. Washington State University, Pullman, WA.

After spine surgery, many patients develop a condition called dysphagia, which is a condition where the patient has difficulty in swallowing. The goal of this research is to find factors that could mathematically predict if a patient will develop dysphagia. A set of 194 patients underwent surgery at the Oregon Health & Science University (OHSU), with a subset developing dysphagia. Over 30 different factors were measured and recorded for each patient, including age, sex, BMI, blood lost during procedure, time of procedure, etc. We develop robust nonlinear predictive models for dysphagia using support vector machines (SVM) under cross validation. Some of the most predictive factors were diagnosis code (ICD), upper level of fusion, age, and time. We also investigated combinations of these factors. The group of easy to measure factors BMI, Smoking (Y/N), and Alcohol (Y/N) turned out to be the most predictive.

OYEDIRAN, O. and M. NASHAWI. The Effects of the Immune System on Bacteriophage Therapy on Cholera. University of Texas, Arlington, TX.

Cholera is a bacterial infection of the small intestine that results in excessive water loss through diarrhea, which can be fatal under some circumstances. Water loss is caused by a toxic secretion of the bacteria that inhibits the small intestine’s ability to eradicate sodium. Individuals who consume water contaminated with infective strains of the Vibrio cholera bacterium become infected with this disease. Countries such as Bangladesh, India and other Sub-Saharan African countries have frequent cholera outbreaks, and in order to limit the severity of cholera outbreaks, phage treatment is a treatment of considerable interest. Phage treatment consists of inoculating a patient with a virus, in hopes that the virus would infect and destroy the bacteria, while the immune system will eradicate the virus. In order to understand the dynamics of this physiological interaction, a mathematical model that combined the behaviors of the bacteria, bacteriophage and the immune system was analyzed. Equilibria and stability was assessed on a theoretical basis with respect to combinations of model parameters. The notion that the immune system has an effect on the bacteriophage treatment was found, as is bolstered by numerical simulations with concrete parameter values found in scientific literature.

PENNINGTON, H. A Mathematical Model for the Interaction of the Proteins MMP-1, TIMP-1, and ECM in a Wound. Western Kentucky University, Bowling Green, KY.

This study aims to formulate, quantify, and analyze a mathematical model describing interactions among matrix metalloproteinases (MMP-1), their inhibitors (TIMP-1), and extracellular matrix (ECM) in the healing of a diabetic foot ulcer. De-identified patient data for modeling were taken from Muller et al. (2008), a research outcome that collected average physiological data for two patient subgroups: ``good healers" and “poor healers," where classification was based on rate of ulcer healing. Model parameters for the two patient subgroups were estimated by minimizing the least-squares residual between the data and model output using Matlab's GlobalSearch and fmincon routines. The model and parameter values were analyzed by conducting steady-state and sensitivity analyses. Both global and local sensitivity analyses were conducted and compared. The global sensitivity analysis was performed using Latin hypercube sampling, while local analysis was conducted through a classical sensitivity analysis followed by an SVD-QR subset selection. Model and clinical implications are discussed based on our results.

RIVERS, J. and J. TORRES. A New Approach to Understanding Evolutionary Relationships among

Chagas Disease Vectors in Latin American Countries. Montclair State University, Newark, NJ.
Our research applies a graph connectivity index to DNA sequence data of Chagas disease vectors from Latin American countries. It provides a new approach to understanding the evolutionary relationships among the insect vectors. We perform normalization and principle component analysis on the graph indices of the DNA data and then build phylogenetic trees in order to answer scientific questions about the disease.

ROMADAN, M. Model Comparison for Cholera over Multiple Data Sets. Mathematics Department, Marymount University, Arlington, VA.
Researchers have considered a wide variety of models for cholera in recent years, however the most simple of these do not account for various known disease transmission pathways. This research has looked at several more complex, mechanistic models for cholera; however, here, the concern of “overfitting” the data arises because there is doubt whether the model created is simply fitting the data due to increased numbers of parameters, and is therefore not appropriate for predicting behavior for future cholera outbreaks. To account for this issue, there are various criteria for model selection, the most widely used of which is the Akaike information criterion (AIC). This method measures the relative quality of a statistical model by creating a trade-off between the goodness of fit and the number of parameters (i.e. the more parameters a model has the greater the penalty). In the literature, the variation of AIC that is used for time series data is AIC for the Least Squares Case. While the application of AIC criteria is clear for a single data set as a tool for model comparison, it is less clear how one might compare model performances over multiple data sets.

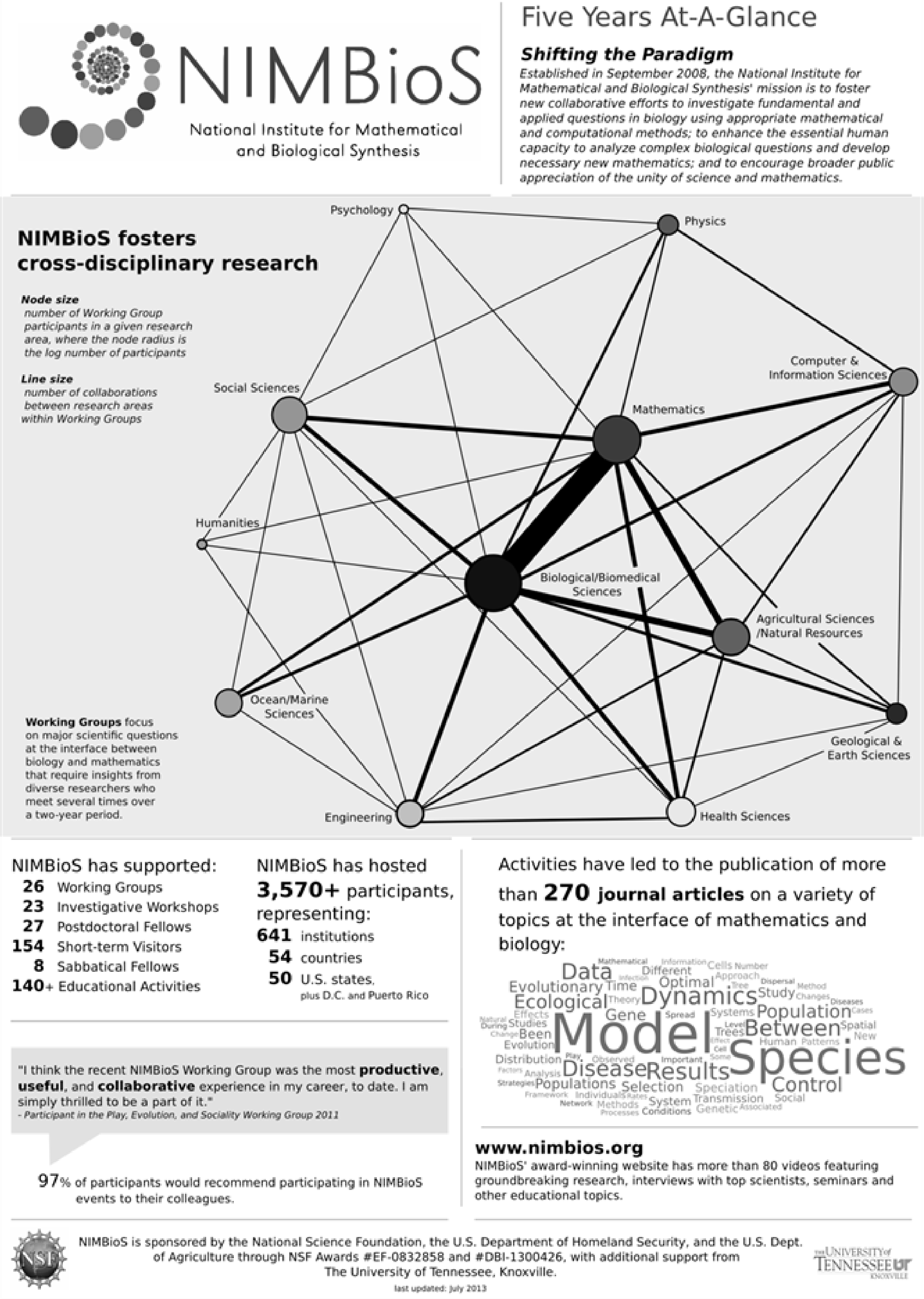
SAUSA, R. Game Theory: If You Are Trying to Avoid Extinction or Survive Cancer, It's Not Just A Game. University of Delaware, Newark, DE.
I have developed game theoretic modules that are well instantiated with actual biological data that will engage professors and students internationally. Specifically, I am concentrating on game theory applied to strategies for maintaining biodiversity in ecosystems susceptible to invasive species, development of new antibiotic treatments, avoidance of resistance to cancer chemotherapy by appropriate combinations of multiple drugs or simultaneous or asynchronous combinations of chemotherapy, radiation, and surgery, or invasiveness of tumors. Game theory analyzes competitive situations where participants seek to maximize personal gains, resulting in the descent and demise of opponents. Traditionally, most focus has been on the prisoners dilemma hypothesis. All options in prisoners dilemma leads the individual to improve their position, which happens to influence them to hurt either their opponent or friend. In this metaphor a hawk tries to fight, while risking injury, a dove relinquishes its resources, however does not get injured, since it doesn’t fight. Recently, more attention has been given to the non-transitive game: “rock-paper-scissors” because there is no clear hierarchy; multiple complex scenarios will illustrate how to maintain diversity, avoid the evolution of resistance, or provide cancer treatments. Analyzed are the effects of “rock-paper-scissors” on the environment and the relation to the “moose-caribou-wolf”.

SIPES, K. Understanding the Locomotory Gait of *Caenorhabditis elegans* in a Viscous Fluid. James Madison University, Harrisonburg, VA.
Viscosity is a measurement of a fluid's resistance to the rate of deformation. An example of a liquid with high viscosity is tree sap, or a homogeneous mixture of mud. Both of these liquids run very slowly when acted upon by gravity. In contrast, water has a very low viscosity and flows readily. So how does a liquid's characteristics effect the locomotion of a swimming organism? Do higher viscosities change the dynamics that an organism implements in order to move in a solution? The Reynolds number is defined as the ratio of inertial to viscious forces and is given by rho V L\mu where rho is the fluid density, V is characteristic velocity, L is the characteristic length of the system, and mu is kinematic viscosity. In particular, I am interested in measuring these different scales in a system where the worm C. elegans is swimming in fluids of different viscosities. We will compare these measurements to different modes of locomotion.

VERNON, Z. MUAHAR, M. and J. RUSINKO. H-Representation of the Kimura-3 Polytope. Winthrop

University, Rock Hill, SC; Lenior-Rhyne University, Hickory, NC.
Given a group-based Markov model on a tree, one can compute the vertex representation of a polytope, which describes the associated toricvariety. Thehalf-space representation, however, is not easily computable. In thecase of$\mathbf{Z}_2$ or $\mathbf{Z}_2$ **X** $\mathbf{Z}_2$, these polytopes haveapplications in the field of phylogenetics. We provide a half-spacerepresentation for the m-claw tree, for G=$\mathbf{Z}_2$ **X** $\mathbf{Z}_2$**,** which corresponds to the Kimura-3 model of evolution.

WHITE, A. J. Waveform Fitting Algorithm: A Framework for Parameter Estimation in Neural Conductance Models Using Current Clamp Data. Case Western Reserve University, Cleveland, OH.
Determining the underlying dynamics of a neuron is computationally expensive and requires a large quantity of experimental data. Often the calculations require using voltage clamps and many different channel blockers to tease out the ion channels present in the cell membrane. This process is often averaged over many neurons to produce a conductance based model. However, the parameters of an individual neuron may differ from its neighbors, or even itself, given enough time. Models based on averaged parameters can fail to reproduce the behavior of the individuals [Golowasch et al 2002]. In this project, I develop an algorithm that finds certain parameters (conductances, capacitance, and driving potentials) of a neuron from a single current clamp experiment. Using the recorded voltage, we calculate the hidden gating variables by solving a system of non-homogeneous linear differential equations, assuming the gating variable dynamics take a known form. Having determined the gating variables, we calculate the conductance of each type of ion channel in the membrane by using a least squares method. The efficiency and accuracy of my method compares favorably with existing methods in the literature [Lepora et al. 2012][Huys et al. 2006].



Five Years At-A-Glance

Shifting the Paradigm

Established in September 2008, the National Institute for Mathematical and Biological Synthesis' mission is to foster new collaborative efforts to investigate fundamental and applied questions in biology using appropriate mathematical and computational methods; to enhance the essential human capacity to analyze complex biological questions and develop necessary new mathematics; and to encourage broader public appreciation of the unity of science and mathematics.

NIMBioS fosters cross-disciplinary research

Node size
number of Working Group participants in a given research area, where the node radius is the log number of participants

Line size
number of collaborations between research areas within Working Groups

Working Groups focus on major scientific questions at the interface between biology and mathematics that require insights from diverse researchers who meet several times over a two-year period.

NIMBioS has supported:

26	Working Groups
23	Investigative Workshops
27	Postdoctoral Fellows
154	Short-term Visitors
8	Sabbatical Fellows
140+	Educational Activities

NIMBioS has hosted **3,570+** participants, representing:

641	institutions
54	countries
50	U.S. states, plus D.C. and Puerto Rico

Activities have led to the publication of more than **270 journal articles** on a variety of topics at the interface of mathematics and biology:

"I think the recent NIMBioS Working Group was the most **productive**, **useful**, and **collaborative** experience in my career, to date. I am simply thrilled to be a part of it."
- Participant in the Play, Evolution, and Sociality Working Group 2011

97% of participants would recommend participating in NIMBioS events to their colleagues.

www.nimbios.org
NIMBioS' award-winning website has more than 80 videos featuring groundbreaking research, interviews with top scientists, seminars and other educational topics.

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