



2015

## **2015 Conference Abstracts: Annual Undergraduate Research Conference at the Interface of Biology and Mathematics**

National Institute for Mathematical and Biological Synthesis (NIMBioS)

Follow this and additional works at: [https://trace.tennessee.edu/utk\\_nimbiosconf](https://trace.tennessee.edu/utk_nimbiosconf)

---

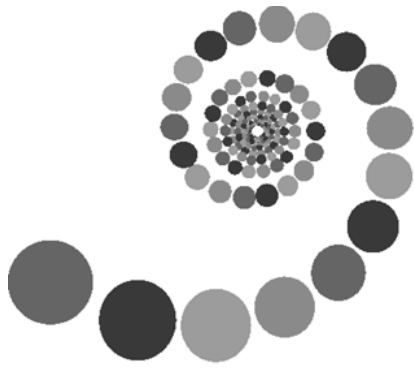
### **Recommended Citation**

National Institute for Mathematical and Biological Synthesis (NIMBioS), "2015 Conference Abstracts: Annual Undergraduate Research Conference at the Interface of Biology and Mathematics" (2015).

*Conference Proceedings.*

[https://trace.tennessee.edu/utk\\_nimbiosconf/6](https://trace.tennessee.edu/utk_nimbiosconf/6)

This Conference Proceeding is brought to you for free and open access by the National Institute for Mathematical and Biological Synthesis (NIMBioS) at TRACE: Tennessee Research and Creative Exchange. It has been accepted for inclusion in Conference Proceedings by an authorized administrator of TRACE: Tennessee Research and Creative Exchange. For more information, please contact [trace@utk.edu](mailto:trace@utk.edu).



# NIMBioS

National Institute for Mathematical  
and Biological Synthesis

*Seventh Annual*

## **Undergraduate Research Conference at the Interface of Biology and Mathematics**

*November 21-22, 2015*

**University of Tennessee Conference Center  
Knoxville, TN**

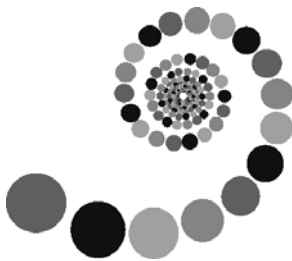
### **CONFERENCE OVERVIEW**

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 50 oral and poster presentations. A keynote by Dr. Robert Smith? and featured talk by Dr. Rachel Lenhart 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 along with a second talk by Dr. Smith?. Poster abstracts start on page 6, oral presentation abstracts start on page 15.



## **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 21<sup>st</sup> 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](http://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, when posters assigned even numbers will be presented. Please hang 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 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 (Dr. Suzanne Lenhart or Kelly Sturner) to have your talk loaded onto the appropriate computer in advance.

## **Social Media at URC 2015**

### **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 2015 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. Robert Smith?**

**The Department of Mathematics**

**The University of Ottawa**

### **Neglected Tropical Diseases and the Next Disease to be Eradicated**

We survey the current state of a group of parasitic and microbial diseases called the Neglected Tropical Diseases (NTDs). These diseases currently infect a billion people, primarily in socioeconomically depressed areas of the world, are a leading cause of world- wide disability, and are responsible for approximately 534,000 deaths per year. We focus on several subcategories: protozoans, helminthes and bacterial diseases. We identify the populations most at risk from these diseases, and outline symptoms and other disease burdens. We examine the progress being made in controlling NTDs, including the current state of drug development. We also examine mathematical modeling of NTDs. While mathematical modeling is not bound by many of the strictures of access, data collection and infrastructure funding, we nevertheless demonstrate that few NTDs have received much attention from mathematical models, and that some have received no attention at all. Simple mathematical models could contribute significantly to our understanding of these diseases and the efforts required to control them, at very little cost. Further investment in prevention, treatment and awareness of NTDs is urgently warranted. As an example, we illustrate the power of modelling to examine Guinea Worm Disease, the next disease to be eradicated.

### **When Zombies Attack! Mathematical Modeling of an Outbreak of Zombie Infection**

Zombies are a popular figure in pop culture/entertainment and they are usually portrayed as being brought about through an outbreak or epidemic. Consequently, we model a zombie attack, using biological assumptions based on popular zombie movies. We introduce a basic model for zombie infection, determine equilibria and their stability, and illustrate the outcome with numerical solutions. We then refine the model to introduce a latent period of zombification, whereby humans are infected, but not infectious, before becoming undead. We then modify the model to include the effects of possible quarantine or a cure. Finally, we examine the impact of regular, impulsive reductions in the number of zombies and derive conditions under which eradication can occur. We show that only quick, aggressive attacks can stave off the doomsday scenario: the collapse of society as zombies overtake us all.

## **FEATURED SPEAKER**

**Dr. Rachel L. Lenhart**  
**UW Neuromuscular Biomechanics Lab**  
**University of Wisconsin, Madison**

### **Influence of Surgery on Musculoskeletal Mechanics in Children with Crouch Gait**

Cerebral palsy (CP) is the most common motor disability of childhood with approximately 1 in 323 affected. Many of these children adopt abnormal walking patterns, with crouch gait being one of the most common. Crouch, characterized by excessive knee flexion (i.e. bending) during stance, is fatiguing and often requires surgical correction to allow patients to continue to walk as they mature. A new surgical technique, the distal femoral extension osteotomy and patellar tendon advancement (DFEO + PTA), is a promising approach for reducing crouch and restoring quadriceps strength in these children. While short term outcomes are generally good, little is known about why the coupled procedures are better than either procedure alone, and which surgical parameters are most efficacious. Perhaps more importantly, the long term implications of the procedures on skeletal growth and cartilage health are unclear.

To explore these questions, we utilized computational approaches designed to help enhance understanding of human movement. Specifically, musculoskeletal modeling, dynamic simulation, and machine learning techniques were used to investigate the influence of DFEO + PTA on knee mechanics. A model was created that allowed for prediction of 3D motion of the knee during walking. Surgical simulations performed on the knee model provide insights into how the degree of DFEO and amount of PTA affect how the muscles operate during walking. Specifically, patellar (i.e. kneecap) position and walking posture are demonstrated to be important determinants of muscle forces and joint contact pressure patterns during gait. Further, DFEO surgical parameters have a large impact on post-surgical muscle lengths, particularly of the quadriceps and hamstrings. Finally, a machine learning technique, the random forest algorithm, reveals the pre-surgical factors that are most predictive of improvement in walking posture after DFEO+PTA surgery. As a whole, this work will help surgeons better understand and refine their treatment of children with crouch gait.

## **SCHEDULE**

### **Saturday, November 21: 413AB (Except where noted)**

**1:00-1:10** Welcome: Dr. Colleen Jonsson, Director of NIMBioS

**1:10-2:10** Keynote Lecture:

Dr. Robert Smith?, The University of Ottawa

*Neglected Tropical Diseases and the Next Disease to be Eradicated*

**2:20-2:35**

406: Wesley Falk and John Williams - *Modeling Ebola Using an SEIR Network*

413AB: Ivanti Galloway and Charles Tyler Allee - *The Effect of Mutation Levels on the Evolution of Cooperation*

**2:40-2:55**

406: Haley Felts - *Effects of Proprioception on Balance and Ankle Injuries in Athletes at King University*

413AB: Nathan Wikle and Ryan Yan - *Projecting Terrestrial Species Invasion Spread Using Commodity Flow Pathways*

**3:00-3:15**

406: Timothy Ireland - *An Agent-Based Model of Interacting Feral Cat Colonies for Analysis of Spatial Population Control Strategies*

413AB: Rebecca Frye - *From the Laptop to the Bench Top: A Bioinformatics Approach to the Identification of Parkinson's Disease Gene Candidates*

**3:20-3:30** *Opportunities at NIMBioS*

Kelly Sturner, Education & Outreach Coordinator at NIMBioS

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

**4:10-4:55** Featured Speaker:

Dr. Rachel L. Lenhart, University of Wisconsin, Madison

*Influence of Surgery on Musculoskeletal Mechanics in Children with Crouch Gait*

**5:05-6:00** Career Panel (Moderator: Suzanne Lenhart, Associate Director at NIMBioS)

Dr. Robert Smith?

Dr. Rachel Lenhart

Dr. Louis Gross, University of Tennessee

Dr. Annalise Paaby, Georgia Tech

**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 22: Auditorium 406, 413AB, 413C**

**8:00** Continental Breakfast

**8:30-9:00** Featured Talk

413AB: Dr. Robert Smith?, The University of Ottawa

When Zombies Attack! Mathematical Modeling of an Outbreak of Zombie Infection

**9:15-9:30**

406: Curtis Lamp - *Atherosclerosis and Social Influences*

413AB: Amanda Patrick - *A Mathematical Model of Recycling*

**9:35-9:50**

406: Paezha McCartt and Rebekah White - Development of a PBPK Model to Study the Effects of BMI on Effectiveness of Antibiotic

413AB: MaLyn Lawhorn - *Comparative Analysis of Transcriptomic Data: Modeling Gene Overlap Using Gene Flexibility*

**9:55-10:50**

413C: Graduate School Opportunities & More Showcase

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

**12:05-12:55** Lunch

**1:00-1:15**

406: Kenneth Moody - *Impact of Organization and Community Retention Programs on Gang Activity*

413AB: Wyatt Goff, Christopher Murphy and Samantha Pulido - *Reevaluating Classical SEIR Models in the Context of the Ebola Epidemic*

**1:20-1:35**

406: Zakar White - *The Effects of Government Intervention and Rehabilitation on Prostitution*

413AB: Elizabeth Swallow - *Astrocyte Maturation: A Possible Implication in Arterial–Venous Specification*

**1:40-1:55**

406: John Lagergren - *Mathematical Demographic Analysis of Enrollment Trends at a Regional University*

413AB: Anh Vo - *Numerical Methods for an Auditory PDE*

**2:00-2:15**

406: Kara Montgomery - *Transport of Glyphosate in Caenorhabditis elegans is Not Mediated Via Presynaptic Neurotransmitter Transporters*

413AB: Jinchuan Wei - *Discriminating between alternative mechanisms of in vitro mycobacterial granuloma formation in Johne's disease*

**2:20-2:35**

413AB: Adam Byerly - *Experiments and Simulations of Heterologously Expressed Mouse Melanopsin*

**2:40-2:50**

413AB: Closing Remarks

**2:55 Adjourn****POSTER ABSTRACTS BY SEQUENCE****1. AGABA, P. Incorporating a Discount Factor in an Optimal Control Model of Chronic Wound Healing. Western Kentucky University, Bowling Green, KY.**

A chronic wound is a wound that does not heal in an order and on time. The analysis in this research project focuses on treating chronic wounds using both mathematical and biological models. These models primarily focus on the amount of oxygen supplied to the wound. This amount should be optimal since too much oxygen is toxic to the body, and can potentially lead to death. Some other models focus on capturing the significance of the length of therapy in wound treatment. Our goal is to minimize the time used in therapies since longer periods make treatments more costly. In order to do this, we are incorporating discount factors into several models of wound healing.

**2. BIELICH, D. LAUKO, I. and PINTER, G. A Mathematical Model for Light and Nutrient Modulated Multi Species Competitive Phytoplankton Growth in a Water Column Under the Influence of Benthic Grazing and Nutrient Forcing. Department of Mathematical Sciences, University of Milwaukee, Milwaukee, WI.**

It is well documented that the recent colonization of Lake Michigan by dreissenid bivalves lead to a dramatic reconfiguration of the lake's ecosystem. These changes resulted in benthification, which is a transport of a substantial part of the ecosystem's biomass to the bottom of the lake's water. While various datasets support this observation, a quantitative evaluation of overall ecosystem productivity, its spatial distribution and its effects on the dynamics of the lake ecosystem is not fully understood. The formulation, parametrization and numerical solution of mathematical models representing the major components of the altered lake ecology could help the understanding and quantitative evaluation of the new ecological dynamics. We present a detailed formulation of a simplified mathematical model, as well as a method for its numerical solution, that takes into account the competition among primary producer species for the varying light and two different nitrogenous nutrient sources in the pelagic, as well as the impact of the grazing and nutrient recycling by a substantial and changing dreissenid mussel population in the benthos.

**3. BURKE, T. Fusiform Face Area Activation During Image Recognition. Howard University, Washington, DC.**



Recently functional Magnetic Resonance Imaging (fMRI) has been widely used in neuroimaging. This is achieved through the application of statistical analysis to fMRI data to obtain distinctive activated regions in brain when humans recognize faces and other man-made objects. In our study, we analyze a face and three other objects which have been viewed by subjects while being scanned by fMRI and contrasts between face and other objects. In this way, we can detect specific locations in ventral temporal cortex and we can determine whether fusiform face area (FFA) or parahippocampal place area (PPA) has more activation when face is recognized compared with other objects.

#### **4. BREWER, S., QIAN, L., and NELMS, B. A Bioinformatics Approach for Investigating Genes Involved in Dopamine Neuron Function and Degeneration. Department of Life and Physical Sciences, Department of Mathematics and Computer Science. Fisk University, Nashville, TN.**

*Caenorhabditis elegans* (*C. elegans*), is a powerful model system for biological studies and inquiry. Though this organism is relatively simple, much of its molecular and cellular function is homologous to that of *Homo sapiens*. Understanding the molecules present in the various cell types of this nematode worm can give insight into the analogous cells in humans. In order to gain insight into relationships from *C. elegans* gene expression datasets, I used Python to develop a program to automate the retrieval of information about *C. elegans* genes, known functions, and their human homologs. I aimed to link and retrieve information from the databases WormBase ([www.wormbase.org](http://www.wormbase.org)) and Online Mendelian Inheritance in Man ([www.omim.org](http://www.omim.org)) to compiled lists of selected *C. elegans* gene expression datasets. To manually navigate and to decipher all of the information would be very time-consuming and inefficient. The initial dataset was a list of over 1200 *C. elegans* genes whose expression was enriched in dopamine (DA) neurons (generated by Spencer et al., 2011). This program can now easily be applied to other large *C. elegans* gene lists, such as recently generated datasets from deep-sequencing of mRNAs (RNA-Seq) performed in our lab.

In a related, but independent project, I analyzed dopamine neuron degeneration in *C. elegans* that have been exposed to copper. Patients with Parkinson's disease (PD) not only have dopaminergic neurodegeneration, but also tend to have higher levels of metals (such as iron, copper, and manganese) in their systems. With the hypothesis that exposure to metal can lead to neurodegeneration associated with early onset of PD, my goal was to analyze the effect that copper has on dopamine degeneration in *C. elegans*, and find what genes are involved. I completed one trial during my Fisk-TIP2015 summer research work and it is still on progress for completing several more trials for a conclusive result. Our preliminary data from the first trial correlates with the hypothesis. So I am hopeful that this study will provide insight into Parkinson's disease and other diseases that involve dopaminergic neurodegeneration.

#### **5. BRYANT, M.L. Mechanism of the Drug-mediated inhibition of ATP Hydrolysis by P-Glycoprotein: Studies on the Role of Tyrosine and Glutamine Residues. Spelman College, Atlanta, GA.**

The human ATP-binding cassette (ABC) transporters, ABCB1 (P-glycoprotein, P-gp), ABCG2 and ABCC1 are drug efflux pumps that transport cytotoxic anticancer agents, thereby conferring resistance to chemotherapeutic agents in most cancers. They utilize energy from ATP hydrolysis for the efflux of a great variety of amphipathic compounds (polyspecificity), including anticancer drugs. It is proposed that P-gp functions through an alternate access mechanism involving two different conformations. Drug binding occurs when the protein adopts an inward-facing conformation (inverted V appearance, open), followed by a significant structural change to an outward-facing conformation (V-shaped in appearance, closed), when drug release takes place. The formation of the P-gp-ATP (E-S) and post ATP hydrolysis reaction intermediates (E + P) during catalytic cycle are accompanied by conformational changes in the drug-binding site, in the transmembrane domain. These changes result in the high affinity site for substrate binding, being transformed to the low affinity site for substrate release. Previous data suggests that the inhibition of basal ATP Hydrolysis is due to hydrogen bonds being formed in the drug binding pocket of P-glycoprotein. These hydrogen bonds causes P-glycoprotein to be locked in the open conformation, thus preventing P-glycoprotein from effluxing the drug out of the cell. Tyrosine and glutamine residues in the drug binding pocket of P-glycoprotein are, among others, capable of forming these hydrogen bonds with certain drugs. The hypothesis was that the addition of tyrosine residues in the drug-

binding pocket of P-gp will inhibit (or at least decrease stimulation) of the basal ATP hydrolysis in P-gp, due to increased hydrogen bonding to drugs. Consequently, the removal of glutamine residues in the drug-binding pocket of P-gp will stimulate (or at least decrease inhibition) of the basal ATP hydrolysis in P-gp, due to decreased hydrogen bonding to drugs. To test this statement, crude membranes were prepared by hypotonic lysis and differential centrifugation. Afterwards ATPase activity was measured by determining liberation of inorganic phosphate from ATP. The results showed that there was a drastic difference in the tyrosine mutants however little to no change in the glutamine mutants. The addition of 3 tyrosine residues in the drug-binding pocket of P-gp (F336Y/F343Y/F957Y) decreases the typical stimulation of the basal ATP hydrolysis of P-gp by drugs, due likely to increased hydrogen bonding to drugs. The removal of up to 3 glutamine residues in the drug-binding pocket of P-gp (Q195A/Q725A/Q838A) did not change the typical inhibition of the basal ATP hydrolysis of P-gp by drugs. These data suggest that glutamine residues (in contrast to what was observed for tyrosines) may not directly interact with drugs or the interaction is weak.

#### **6. CHRISTOPHER, I., MARTIN, D., GRAHAM, D. and DAMO, S. Computational Modeling of the S100A12-RAGE Complex. Department of Life and Physical Sciences, Fisk University, Nashville, TN.**

The receptor for advanced glycation end products (RAGE) is a critical cell surface pattern recognition receptor that is involved in the inflammatory response. Misregulation of RAGE expression is connected to tumor outgrowths, diabetic complications, and neurodegenerative disorders, which are increasing worldwide concerns. Hence, RAGE is a potential target for therapeutic intervention. Understanding the molecular mechanisms and interactions that induce the activation of RAGE will allow for the rational design of small molecule inhibitors to dissect the RAGE signaling axis and potentially treat disease. To this end, we used a computational docking approach to determine the structure of the receptor-ligand complex of RAGE and S100A12 and compared this to previously determined experimental structures of homologous proteins. Interestingly, the RAGE-ligand interaction surface is highly conserved and is comprised of both a basic and nonpolar surface. Arginine 104 (R104) is a critical component of the RAGE ligand recognition motif, as well as residues Q47, Q46, P66, G69, G70, and P71 play an important role in the receptor-ligand binding complex of RAGE. Together, these data establish a computational model for understanding RAGE-ligand interactions that can be validated using biophysical experimental approaches.

#### **7. CORONA, C. and ONG, H.C. Microbial Survey of Photosynthetic Life at Steele Creek Park Lake. Department of Biology, King University, Bristol TN**

Scientists estimate there are 10 million species on Earth, of which only 2 million have been discovered. Of these two million, 99% are plant and animal species. This remaining fraction is made up of smaller organisms such as photosynthetic microbes, which are predicted to make up the bulk of the undiscovered species. Ecogenomics, or molecular ecology, is the process of isolating DNA sequences from environmental samples that can be analyzed to identify the presence of individual species. The data is quantitative; scientists no longer have to catalog organisms based on their morphology alone. This has had a tremendous impact on our ability to catalog the missing 8 million species. With modern techniques, multiple organisms can be cataloged in a short amount of time and also used to compare biodiversity in other habitats. Steele Creek Park houses a 54 acre man-made lake that serves as an ideal habitat for photosynthetic microbes. We collected water samples from various spots and depths and then cultured the microbes in the lab. DNA was isolated from growing colonies and subjected to Polymerase Chain Reaction amplification. The project is ongoing and will add to the growing database of freshwater bacterial species.

#### **8. DE CARDENAS, G. A Review of Mathematical Modeling Studies to Identify Challenges and Understand the Impact of Interventions on College Alcohol Drinking Dynamics. Arizona State University, Tempe, AZ.**

Alcohol abuse has been a problem for universities and colleges around the country. Literature suggests different social and environmental mechanisms that may have influence on college alcohol drinking patterns. I have revived the role of various dynamical mathematical models and the college data needed to parameterize and to

perform sensitivity analysis. The goal of my current research is to review and develop a simple modeling framework to identify critical environmental mechanisms that could alter current college drinking patterns. The model captures the dynamics of alcohol drinking using multiple environmental factors. With preliminary results that the environment of a student's social circle affects the drinking habits more than any other social interaction, I have concluded that in order to reduce drinking behaviors on campuses, policies will need to be implemented in order to incentive a non-drinking culture.

**9. DESHPANDE, R. Mathematical Modeling of Chronic Wound Healing with Optimal Control Theory. Western Kentucky University, Bowling Green, KY.**

Damaged skin undergoes an intricate healing process. However, the progression of healing may be interrupted by external factors. An acute injury that does not heal within a reasonable amount of time is known as a chronic wound—chronic wounds remain in an inflammatory state for a prolonged period of time due to several underlying factors, including excess bacterial growth in the wound. Neutrophils are unable to produce a sufficient amount of reactive oxygen species to counteract bacterial growth, so topical oxygen therapy has been proposed to supplement wound healing. Optimal control theory (OCT) was used to analyze this treatment strategy. In OCT, a control variable, the topical oxygen, is selected to minimize objective functionals. In this case, chosen objective functionals minimize bacterial levels as well as supplemental oxygen. The equations are numerically solved using a forward-backward sweep algorithm in Matlab and the differential equations are solved using ode15s. The numerical results are compared to a model that uses no supplemental oxygen to determine the effect the application of topical oxygen had on bacteria levels. Results show that, with suitable initial conditions, supplemental oxygen has a beneficial effect on wound healing by driving bacteria levels in the wound to zero.

**10. DRAPER, M., PEPE, M. and WILHELM, D. Mathematical Modeling of the James Spiny mussel. James Madison University, Harrisonburg, VA.**

The James Spiny mussel (*Pleurobema collina*) is endangered and at the top of Virginia's conservation list. This species plays a critical role in the environment by filtering and cleaning water while providing shelter and food for macroinvertebrates. However, conservation efforts are complicated by the mussels' burrowing behavior, camouflage, and complex life cycle. The goal of this research was to estimate detection probabilities that could be used to determine whether the species is present in an area and to track individually marked mussels to test for source-sink dynamics. Using existing literature and mark-recapture field data, these goals were accomplished by evaluating dispersion type, clustering trends, odds of detection based on environmental factors, substrate preferences, and matrix population models. These analyses serve as the foundation of mathematical models used to aid in the recovery of the James Spiny mussel.

**11. EASTMAN, J. and SASS, J. Inducing Alternans in Cardiac Models using Delay Differential Equations. University of Maryland, Baltimore, MD**

Cardiac electrical alternans is a period-2 dynamical behavior with alternating long and short action potential durations (APD) that often precedes dangerous arrhythmias associated with cardiac arrest. Despite the importance of alternans, many current ordinary differential equations models of cardiac electrophysiology do not produce alternans, thereby limiting the use of models to study the mechanisms that underlie this conditions. Because delay differential equations (DDEs) commonly induce complex dynamics in other systems, we investigate whether incorporating DDEs can lead to alternans development in cardiac models. We use the Fox et al. canine ventricular action potential model, which produces alternans as published. After suppressing the alternans in the original model, we restore alternans by introducing DDEs and quantitatively compare the DDE-induced alternans with the alternans present in the original model. We analyze the gating variables of the model to study the effects of implementing DDEs and to determine how alternans is restored, and we discuss the mathematical and physiological implications of our findings. In the future, we aim to extend our approach to induce alternans in models that do not naturally produce such dynamics.

**12. ENGEN, L., GIERKE, L., KOTWITZ, B. and WILLIAMS, J. A Mathematical Model for Nutrient Interactions of Deep Phytoplankton Biomass Layers in Lake Michigan. Division of Biological Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.**

Primary producers in aquatic ecosystems live in a complex environment. This environment is dependent on a consistent supply of light and nutrients. These factors are not evenly distributed in a water column. Instead they form layers of varying compositions. Due to these layers and availability of light and nutrients, phytoplankton have different rates of production and consumption. Primary producer's abundance, composition and production has experienced considerable changes in the past decade. This has been in large part modulated by the dreissenid invasions which has resulted in a disruption in the layers of the lake ecosystem. As the life cycle of dreissenid reaches an end, the lake ecosystem is further perturbed by their presence. The decomposition of their bodies releases a nutrient source of ammonium that Lake Michigan was formerly deprived of. We hypothesize that ammonium, which is scarce in Lake Michigan, is preferred and more energetically efficient in comparison to nitrate which is in excess. To demonstrate this we prepared a series of nutrient spike experiments using water obtained from distinct layers in the lake. We intend to use current models and literature to develop and expand the models to describe these new dynamics.

**13. FARHAT, A. Model Analysis of Prostate Cancer Metastasis into the Bone Microenvironment. University of Michigan, Ann Arbor, MI.**

Although localized prostate cancer (PC) is easily treatable, metastasis to the bone presents an enormous threat to those who have the disease. Several positive feedback loops in metastasis have been observed, particularly hijacking of the canonical WNT-Frizzled pathway and the PTH-RANK-RANKL axis. This hijacking causes high rates of bone turnover and remodeling with eventual net bone growth, releasing growth factors that support cancer proliferation throughout the body. We refine the computational model produced by Pivonka, et. al. and Wang, et. al., in order to both incorporate calcium as a limiting factor in bone growth and account for mesenchymal cell production of Dickkopf-related protein 1 (DKK1). This model simulates prostate cancer numerically, progressing from normal bone and hormone levels to clear diseased states. The simulations clearly demonstrated phenomena similar to those found clinically in prostate cancer patients. In addition, a novel effect emerged in this model: in particular, an unstable steady state presented itself between the final disease state and the undiseased state, which appears to be the result of DKK1 significantly inhibiting WNT. Several potential therapeutic options were explored in the model, with some potential drug targets showing more promise than others: in particular, completely blocking WNT and greatly increasing DKK1 had significant positive effects, while, in agreement with clinical studies, blocking RANKL did not improve the outcome of the simulation.

**14. FENNELL, C. The Prevalence and Risk Factors of Oral Human Papillomavirus within ALIVE Study Cohort. Spelman College, Atlanta, GA.**

The purpose of this study was to determine the prevalence and risk factors associated with the oral Human Papillomavirus (HPV). Participants consisted of 199 individuals selected from the AIDS Linked to the Intra Venous Experience (ALIVE) study. Oral-rinse samples were collected and the subjects surveyed. This cohort included heterosexual men (66.3%) and women (22.1%), and HIV negative (67.8%) and HIV positive (32.2%) individuals. All subjects had a past or current history of injecting drugs. Univariate and multivariate analysis were conducted. Oral HPV DNA was common among subjects (28.6%), including 26 subjects with oncogenic oral HPV (13.1%). There was a significantly higher prevalence of oncogenic oral HPV amongst HIV positive than HIV negative individuals (23.4% vs 8.2%,  $p < 0.01$ , Table 2). Nadir CD4, HIV/CD4, and sexual orientation were associated with increased odds of oral HPV. In multivariable analysis, sexual orientation and HIV/CD4 count remained significant predictors of oral HPV infection. There was a higher prevalence of oral HPV amongst HIV positive individuals than HIV negative subjects. Bi/Lesbian subjects had notably higher odds of oral HPV. Future studies with larger cohorts should be conducted to determine the consistency of these results.

**15. HARTLEY, C., MESTRE, LUIS., CISNEROS, JORGE., MASTEN, E., ROBERTS, N., and STURMAN, L. Analysis of a Metapopulation Model with an Allee Effect. University of Nebraska-Lincoln, Lincoln, NE.**

A metapopulation is a collection of subpopulations of the same species living in separated habitats (called patches) coupled by migration. We will consider a metapopulation for which each subpopulation has a carrying capacity and an Allee threshold. An Allee threshold for a patch is a population under which the species is not viable in the patch. Other parameters needed for the model are migration probability and migration survival. We develop a model for such a metapopulation in an arbitrary number of patches, and study the dynamics in two patches in detail. We are especially interested in conservation, so we study which combination of parameters and initial populations lead to persistence of the population. Using detailed simulations in MATLAB, Python, and Sage, we describe the basin of attraction for the zero population, that is, the range of initial conditions for which the population goes extinct; these are the initial conditions we want to avoid, and if there are too many of them, the population is more likely to go extinct.

**16. HOUSER, J., ESKANDAR, G., PROCHASKA, E., WOJTKIEWICZ, J., LEBAIR, T., PEERCY, B. E., WATTS, M., and SHERMAN, A. Modeling the Effect of Calcium Diffusion on Metabolic Oscillations and the Synchronization of Beta Cells. University of Maryland, Baltimore County, Baltimore, MD, East Tennessee State University, Johnson City, TN, Creighton University, Omaha, NE, Louisiana State University, Baton Rouge, LA, National Institutes of Health, Bethesda, MD.**

In order to further understand diabetes mellitus, a disease characterized by elevated concentrations of blood glucose due to irregular insulin production, it is necessary to investigate the dynamics of insulin secretion in the bloodstream. Clusters of beta cells, found in islets of Langerhans, are responsible for the production and regulation of insulin based on changes in glucose levels. A mathematical model, the Dual Oscillator Model (DOM), has been previously developed that captures the full dynamics of insulin secretion including the fast- and slow-bursting behavior from electrical and glycolytic oscillations, respectively. Using the DOM, we examined how calcium handling within individual pancreatic beta cells affects the synchronization of metabolic oscillations within electrically coupled islets. Calcium permeability was implemented into the DOM, and numerical solutions of the system were obtained via Matlab using modified memory techniques and automatic differentiation on a high performance computer (<http://hpcf.umbc.edu>). A synchronization index has been developed to quantitatively describe the synchronization of variables between nearest neighboring cells and throughout the islet as a whole. Our research shows that calcium diffusion between heterogeneous cells enhances metabolic oscillations for low voltage coupling and is overshadowed by the voltage coupling for high voltage coupling.

**17. JACKSON, D. and HOTA, S. Drug Dosage – Ensuring a Level of Effectiveness, While Not Being Harmful., Department of Mathematics and Computer Science, Fisk University, Nashville, TN**

The medical field is quickly expanding. As people push the assumed boundaries of life longevity, medical research continues to find new treatments for diseases which are only valuable when dosage research is conducted alongside it. In this study a pharmacokinetic mathematical model was developed to determine the dosing regimen of a drug administered multiple times trying to maximize the therapeutic effect of the drug while maintaining a safe concentration in the blood stream. Pharmaceutically-relevant parameters for drugs were determined through experimentally established data. Computations were performed using Mathematica. The study shows that a drug administered multiple times leaves residual amounts in the blood stream. Long intervals between doses make the residual quantity seem almost absent. On the other hand, if the interval between two consecutive doses is too short there is significant residual drug build up leading to toxic level in blood stream. In attempts to make these models more practical we begin to consider immune resistance to drugs and how they can affect results thus manipulating our models to represent such situations. In the future, these models will be able to better predict immunity by eliminating some of our broad assumptions by statistical data.

**18. JOHLIE, C. and MILLER, A. Mathematical Modeling the ANWR Ecosystem. Sam Houston State**

**University, Huntsville, TX.**

We are investigating the Aransas National Wildlife Reserve (ANWR) in order to effectively model the ecosystem in the area. We are specifically concerned with the ecosystem and habitat of the endangered species *Grus americana* (whooping crane). In order to effectively model the ecosystem of ANWR we must accurately model the hydrology, and the blue crab population within the region. The cranes winter in the estuarine ecosystems in ANWR where nutrient transport is very important to the health of the region.

**19. MUSICK, M., ROBINSON, C. and VAUGHAN, L.K. Data Mining and SNP Identification: A Bioinformatics Exercise. Department of Biology, King University, Bristol TN.**

Bioinformatics is not a very well-known field to many people but it provides information to a researcher that is useful to everyone. The Bioinformatics field is a compilation of several different areas of study, including Biology, Math, Computer Science, and more. Each of these disciplines work together to help the other interpret data and report their results. Using data mining we were able to find information on an unknown SNP that we were given as a final project in our Bioinformatics course. The information we found about its function and where it was located helped us to use the techniques we learned in the course. Once the name of the gene that was associated with the SNP was found, we were able to find what phenotypes were expressed by the gene and what systems in the body it affects. In the research that we did on this project we barely scratched the surface on what information can be discovered using Bioinformatics. This project is a good illustration on how Bioinformatics techniques can be used to introduce students to the importance of interdisciplinary research.

**20. O'CONNOR, B., ZIMMER, J., HALMO, K., XIONG, A., CUHEL, R., AGUILAR, C., LAUKO, I., PINTER, G., Bacteria Nitrification and Nitrosification Rates in a Fluidized Sand Biofilter. School of Freshwater Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.**

Aquaculture, or aqua-farming, refers to the artificial cultivation of aquatic organisms. Aquaculture could conceivably replace fisheries--which rely on natural fish populations--as a food source. This practice has the potential to alleviate the stress currently induced by over-harvesting and damming, which reduce wild fish populations. The recirculating aquaculture system we studied at the UW-Milwaukee School of Freshwater Sciences consists of three main chambers. The primary tank contains a population of yellow perch that produce ammonia as a toxic waste product. This ammonia is filtered and recycled by chemolithotrophic bacteria present in the system's two biofilters. The first filter, containing beads, is responsible for solid waste removal. Ammonia and nitrite, which can reach relative toxicity levels, leave this filter and are further neutralized into nitrate by two types of bacteria in the biofilter. Since nitrate is not toxic to fish at relatively high levels, this water is then pumped back into the initial holding tank. The mathematical model we are developing is designed to simulate the nitrogen limitations in a mature recirculating biofilter, which is the main site of nitrogen fixation. Parameters in the model were determined using a combination of roller bottle experiments and real-time spikes of the RAS.

**21. PARKMAN, V., DANTZLER, A., HUJOEL, M., WILD, A., LENHART, S., LEVY, B., and WILKES, R. Canine Distemper Outbreak Modeled in an Animal Shelter. National Institute for Mathematical and Biological Synthesis, University of Tennessee, Knoxville, TN; University of Tennessee, Knoxville, TN; University of Tennessee, Chattanooga, TN; Harvey Mudd College, Claremont, CA; Tennessee State University, Nashville, TN; University of Tennessee College of Veterinary Medicine, Knoxville, TN.**

Canine distemper virus (CDV) is a highly contagious virus that can cause outbreaks, specifically in crowding situations, such as an animal shelter, in which a large number of susceptible dogs are brought together. Introduction of this virus into a shelter can have devastating effects, potentially resulting in shelter canine depopulation. Motivated by recent outbreaks in Tennessee, a mathematical model was constructed to find relevant factors that could assist in preventing or reducing outbreaks. A system of ordinary differential equations (ODEs) was derived to represent the spread of CDV through S (susceptible), E (exposed), I (infected), and R (recovered) classes as well as a vaccinated and two different infectious classes. Our model was adapted to represent a local Knoxville shelter. The effect of various control methods, both preventative and corrective, on

disease spread was investigated.

**22. PRASAD, A. A Mathematical Model for the Interactions of Matrix Metalloproteinase and Their Inhibitors in a Wound. Western Kentucky University, Gatton Academy, Bowling Green, KY.**

The medical treatment of diabetic foot ulcers remains a challenge for clinicians. A quantitative approach using patient data and mathematical modeling can help researchers better understand the physiology of the wounds. In this work, we analyze a previously developed mathematical model describing the interactions among matrix metalloproteinase, their inhibitors, extracellular matrix, and fibroblasts (Krishna et al., submitted). In the previous work, the parameters were estimated using least squares from average patient data in Muller et al. (2008) for the system of four differential equations. However, the system can be reduced to three differential equations since a closed-form solution exists for the fibroblast equation. We numerically analyze and compare differences in the curve fits of the non-autonomous three-equation system to the original four-variable autonomous system.

**23. PTASZNIK, A. A Comparison of Blue Vane and Pan Traps for Determining Bee Diversity. University of Colorado at Boulder, Boulder, CO.**

Bees (family: Apidae) are important ecologically and economically as primary pollinators of many natural and agricultural systems. Given current concerns about declining numbers of bees, many survey-oriented studies are being conducted to understand factors that contribute to the loss of bees and to direct conservation efforts. For these studies to be informative, however, researchers must be aware of biases associated with different sampling methods. We investigated sampling biases associated with blue vane traps versus the more commonly used pan traps at two different high elevation sites in the Front Range of Northern Colorado. At each site, (1) sampling efficiency (number of species and abundance of bees associated with each method) were compared and (2) the overlap in species sampled by each method determined. We also examined the degree to which potential biases in the bees sampled by each method was associated with life history characteristics of the bees (level of sociality, floral specialization, nesting habits, and body size). Individual-based rarefaction curves, a calculation of species richness per individual sampled, showed that for an equal number of individuals sampled by both methods, pan traps would sample more species despite having caught less specimens. This finding was supported further by the use of mathematical estimating tools, a method rarely used in similar studies. Differences in species associated with each trap type were not caused by bee sociality, floral specialization, nesting habits, or body size. Given the differences in sampling efficiency and the low overlap of species captured by the two sampling methods, caution is suggested when comparing studies that employed only one of these methods. Rather, the use of both methods is suggested to better represent the species present within a given area.

**24. ROHLY, M., JOHNSON, T., KHANAL, J., SIREK, N., DAY, J., LEGRAND, E., and PANTHA, B. Exploring Host-Pathogen Interactions with Agent-Based Models in NetLogo. National Institute for Mathematical and Biological Synthesis, Knoxville, TN; Columbus State University, Columbus, GA. Morehouse College, Atlanta, GA; Southeastern Louisiana University, Hammond, LA; L&N STEM Academy, Knoxville, TN; The University of Tennessee, Knoxville, TN.**

Previous work has shown agent-based models (ABM) effectively represent host-pathogen interactions. The purpose of this research is to further model the interactions that take place between host cells and pathogens, while including other parameters, such as specialized cells, inflammation radius, pathogen distribution, viral infections, and barriers around key host cells. We utilize the ABM modeling software NetLogo to observe these intricate processes. The proximity of the pathogen to key host cells and fever presence are vital factors in host survival.

**25. SCHLAGENHAUFF, E. and SATKAUSKAS, M. A Host-Parasite-Commensal Ecological Model Based on Field Studies in the Great Plains. Creighton University, Omaha, NE.**

Although mathematical models for ecosystem dynamics exist, most do not consider commensal relationships

found in the niche. We offer a model for a freshwater snail-trematode-*Chaetogaster* ecosystem found at the Pine Ridge Indian Reservation. Trematodes infect the snails, while the *Chaetogasters* both prey on the trematode and have a commensal relationship with the snail. We analyze populations in terms of a nonlinear host-parasite-commensal ecosystem model using the Hartman-Grobman Theorem to find stable equilibria, and for more involved eigenvalue computations, we give intervals that guarantee asymptotic stability via the Routh-Hurwitz Theorem.

Additionally, we plot the percent of snails (in- and out-of-transect) infected with *Chaetogasters* against the observed trematode infections, and a linear regression shows *Chaetogaster* prevalence correlates negatively with trematode prevalence.

**26. SHETH, P., JOYCE, T., SCHUGART, R. Analyzing a Mathematical Model of Bacteria-Neutrophil Interactions in a Chronic Wound. Department of Mathematics, Western Kentucky University, Bowling Green, KY.**

An estimated 5-10 billion dollars are spent each year in the United States on the treatment of chronic wounds. A chronic wound is classified as such if it takes more than 30 days to heal. One reason for a wound to enter a chronic state is if the body fails to remove bacteria from the wound area, prolonging the inflammatory phase of the wound healing process. Neutrophils are one of the major body cell types involved in removing bacteria from the body during inflammation. Using a number of assumptions regarding bacteria and neutrophil behavior, a mathematical model based on partial differential-equations was successfully developed in order to model the interactions of bacteria and neutrophils during the wound healing process. Both analytical and numerical methods were used to analyze the model. When the model was analyzed in a three-variable system, oxygen being the additional variable, several new steady states were determined. The end goal of this project is to gain a better understanding of the wound healing process that may eventually lead to improved treatment strategies using oxygen therapy and increased ability to interpret and predict the behavior of chronic wounds.

**27. KOBLER, D.M. and SIPES, K.M. Analysis of habitat use for the endangered James Spiny mussel (*Pleurobema collina*) to assist in long term community stability. James Madison University, Harrisonburg, VA.**

Freshwater mussels are keystone species in their ecosystems, and their filter feeding ameliorates water quality in downstream areas. Over 70% of freshwater mussel species worldwide are listed as vulnerable or more greatly threatened. The James Spiny mussel (*Pleurobema collina*) is a species of top priority for conservation in Virginia. Due to limited research, cryptic appearance and behavior, and small population sizes, freshwater mussel conservation efforts have been hindered. A mark and recapture study has tracked approximately 20 James Spiny mussels and 60 Notched Rainbow (*Villosa constricta*) mussels marked with Passive Integrated Transponder (PIT) tags at Swift Run in the summer of 2014. Multiple mussel recapture histories provide data about habitat use, stream-bed surface expression, and inform source-sink models. This integrated approach aims to further our understanding of rare cryptic organisms.

**28. STEWART, M. The Interaction of Chemotherapy with Cancer and Normal Cells: A Quantitative Study. Fisk University, Nashville, TN**

Cancer occurs when certain cells in the body divide and form more cells without the ability to stop the process. There are many treatment types for cancer that come with different results. The most common treatment used by oncologists is chemotherapy which refers to drugs used for treating cancer. These drugs, after being administered into the body, interact with both normal and cancer cells. As a result the normal cells are damaged along with cancer cells and this causes many side effects. The main objective of this project was to perform a quantitative analysis of the interaction effect of chemotherapy drugs with cancer and normal cells. A logistic mathematical model was developed using a system of ordinary differential equations (ODE) involving cancer cells, normal cells, and chemotherapy drugs. The effects of the drugs on the cells were investigated by performing the stability analysis of the ODE system at equilibria with and without chemotherapy. Numerical simulations were carried out using Mathematica to explore various cases during chemotherapy treatment. The



parameter values used in the model were obtained either from references in the literature or from previous studies on this topic published in the journals. The results showed that both normal and cancer cells were affected by the drug at different intensities and the interaction varies with the environment and the aggression of the cells. Conditions for cancer-free state and intermediate state in terms of relevant model parameters were derived and numerical results were illustrated.

**29. WHITE, I.M. Race, Place, Politics, and Needles: Social Determinants Which Impact DTaP Vaccination Health Disparities in the United States, 2013. Spelman College, Atlanta, GA.**

Vaccinations are extremely important to the health of a child, as well as all those with whom they come in contact. Vaccinations are administered by physicians and nurses on a schedule set forth by the Advisory Committee for Immunization Practices (ACIP). There are health disparities for various demographic subgroups. Social determinants of health may be related to these differences in vaccination coverage among children in the United States.

**30. WILLIAMS-HAMILTON, T. Functional Studies of Missense Mutation in MSH2 Gene. Spelman College, Atlanta, GA.**

Hereditary Non-polyposis Colorectal Cancer is linked mutations in MSH2, a gene that is involved in DNA mismatch repair mechanism. In this study, human pathogenic mutations were reconstructed in cognate sites in the *Saccharomyces cerevisiae* (yeast) MSH2. URA-3, a genetic marker found in yeast, will indicate DNA transformation in an FOA assay, which will suggest mutation rates when MSH2 is nonfunctional and produce colonies. The formation of colonies suggest that the mutation is detrimental and would be an indicator of a potential HNPCC diagnosis. To further investigate the pathogenicity of the mutation, flow cytometry revealed the DNA content within the yeast cells. A missense mutation G693D in MSH2 found to decrease the repairing activity of MSH2.

**31. ZUMA, B. Roles of Invertase Inhibitors during Early Seed Development in Arabidopsis. Spelman College, Atlanta, GA.**

In plants, carbohydrates are transported as sucrose through the phloem from photosynthetic tissues to non-photosynthetic tissues. At the destination, sucrose is cleaved to its hexoses before non-photosynthetic tissues, such as fruits and roots, can utilize it. One of the enzymes that facilitate this cleaving process is invertase. In Arabidopsis, embryo growth accelerates after endosperm cellularization, suggesting that invertase activity is up-regulated to support the increase in growth rate. This hypothesis is supported by our preliminary data that two invertase inhibitors are down-regulated after endosperm cellularization. We have generated transgenic Arabidopsis plants to ectopically express invertase inhibitors after endosperm cellularization, which exhibited delayed embryo growth. This data further supported our hypothesis that invertase inhibitors control embryo growth by suppressing the function of invertase. Understanding how embryo development is regulated can be useful in improving certain agronomic traits, such as seed size and yield.

**ORAL PRESENTATION ABSTRACTS (Alphabetical)**

**BYERLY, A., KHAN, T., VALDEZ-LOPEZ, J., HOFFMAN, K., KANG, H.W., and ROBINSON, P. Experiments and Simulations of Heterologously Expressed Mouse Melanopsin. Department of Mathematical and Statistical Sciences, Department of Biological Sciences, University of Maryland Baltimore County, MD.**

G protein-coupled receptors (GPCRs), the largest family of eukaryote transmembrane receptors, respond to extracellular stimuli and trigger an intracellular response. Opsins are specialized GPCRs that are involved in the conversion of light into a biological signal. Melanopsin, an opsin found in intrinsically photosensitive retinal ganglion cells (ipRGCs) in the mammalian retina, regulates non-image forming vision functions such as

circadian photoentrainment and pupillary constriction. While much of the phototransduction pathway activated by melanopsin has not been fully elucidated, we hypothesize that melanopsin is internalized after light-activation and deactivation the phosphorylation of its carboxy tail and the binding of  $\beta$ -arrestin. To test this hypothesis, we appended on to the mouse melanopsin gene the reporter green fluorescent protein (GFP). This gene was cloned into a mammalian expression vector, and expressed in Human Embryonic Kidney (HEK) cells. We then assayed the localization of melanopsin within the cell using confocal microscopy. Preliminary results from confocal imaging confirms internalization of the melanopsin constructs in HEK cells. The phenomenon of internalization was incorporated into a mathematical model of the phototransduction pathway of melanopsin by adjusting the model parameters to account for the delay in reactivation. Internalization has been implicated as a mechanism for receptor adaptation.

**FALK, W. and WILLIAMS, J. Modeling Ebola Using an SEIR Network. University of Wisconsin, Milwaukee, WI.**

First confirmed in March 2014, the ongoing Ebola epidemic in West Africa, is by far the largest and most complex outbreak to date. According to World Health Organization data, there have been more cases and deaths in this outbreak than all others combined. We propose a differential equations model describing the 2013-2015 outbreak in the three most effected countries: Guinea, Liberia, and Sierra Leone. This model describes the dynamic relations between the susceptible, exposed, infected, dead, and recovered populations across a network of the most populated areas of these three countries. This being a more spatial model, we can look at how the progression of the disease influences the migration of exposed individuals. We describe how existing WHO data is used to parameterize the model and discuss so key differences between this and other existing Ebola models. In addition, simulations under varying parameter values corresponding to different migration conditions are investigated. This data is then used to determine possible control measures and prevention strategies.

**FELTS, H. and STILTNER, A. Effects of Proprioception on Balance and Ankle Injuries in Athletes at King University. Department of Biology, King University Bristol, TN.**

Proprioception, or the ability to sense the position of joints in space, is an important part of our daily lives. This may be especially important for athletes, since the lack of proprioception could increase susceptibility to injury. However, there are little studies that directly address this question. To address this question, we designed a study to test the proprioception of athletes. Baseline proprioception was tested using the Romberg's test, which is a series of four tests with progressive balance challenges. Athletes from various sports at King University voluntarily participated in the study. Initial analysis of the data focused on the ability of athletes to pass the series of balance tests. Comparisons across sports and between males and females were also conducted. Although the study is still underway, preliminary results indicate that there is some difference in proprioception between sports and between genders within sports. Future analysis will include injury data to test if lack of proprioception is associated with increased ankle injury. Results of this study will provide better information on the prevention and treatment of ankle injuries pertaining to balance training. Research funded by ACA Ledford Scholarship (HDF).

**FRYE, R. and VAUGHAN, L.K. From the Laptop to the Bench Top: A Bioinformatics Approach to the Identification of Parkinson's Disease Gene Candidates Department of Biology, King University, Bristol, TN.**

With the advent of sequencing technology and the advent of public access databases, bioinformatics has opened opportunities for a paradigm shift. Preliminary studies of complex, non-Mendelian human diseases and those with complex environmental factors can now be done prior to a scientist setting foot into a wet laboratory. Parkinson's Disease (PD), characterized by neurodegeneration, is one such complex disease hypothesized to have a genetic and environmental component. Using a bioinformatics data-mining approach, gene candidates for Parkinson's Disease were identified through the use of public access genetic databases. Orthologs of the candidate genes were identified in the model organism *Caenorhabditis elegans*. From this list, the most

prominent candidate genes were identified for study of the environmental effects of pesticide on PD gene candidates in the *C. elegans* toxicology lab of Dr. Vanessa Fitsanakis. This approach to gene identification and subsequent wet laboratory testing is an innovation in that few bioinformatics results have yet to be confirmed by wet laboratory data.

**GALLOWAY, I. and ALLEE, C.T. The Effects of Mutation Levels on the Evolution of Cooperation. University of North Carolina, Greensboro, NC.**

Although cooperation can be advantageous for individuals within groups, such systems are traditionally vulnerable to exploitation of defectors. Even without that risk, however, the ability of cooperative groups to organize initially amid non-cooperative individuals remains an open problem. We establish a dynamic model of two behavioral morphs within a population and examine how the behavioral mutation of offspring can transition a population from a "selfish" state to a "cooperative" one. Small mutation levels produce coexistence states at a mutation-selection balance point; however, an asymmetric response at intermediate mutation rates transforms the population into one dominated by cooperators. This dynamic switch is dependent on the resource availability, and cooperators achieve critical mass with lower mutation levels in areas of high resources.

**IRELAND, T. and MILLER NEILAN, R. An Agent-Based Model of Interacting Feral Cat Colonies and Analysis of Spatial Population Control Strategies. Department of Mathematics and Computer Science, Duquesne University, Pittsburgh PA.**

Free-roaming feral cat populations are common in nearly all areas of concentrated human habitation, and can pose considerable threats of nuisance and damage to native ecosystems. Trap-neuter-return (TNR) and trap-vasectomy-hysterectomy-return (TVHR) are two humane methods for the reproductive control of feral cat populations. We built a stochastic agent-based computational model in NetLogo for simulating the behavior and growth of interacting feral cat colonies and the use of TNR and TVHR to limit population size and nuisance behavior. The model implements a novel movement algorithm that calculates the daily probability of individual cat migration between colonies based on the social structure of the cat's colony, distance to neighboring colonies, and a parameter indicating the connectedness of the colonies. Spatially targeted TNR and TVHR policies are evaluated using two management goals: (1) reduce total population size and (2) reduce nuisance behaviors of feral cats. Results yield insight into the most effective strategies for applying reproductive control to feral cat colonies with various spatial configurations and environmental parameters.

**LAGERGREN, J. Mathematical Demographic Analysis of Enrollment Trends at a Regional University. Department of Mathematics and Statistics, East Tennessee State University, Johnson City, TN.**

A matrix model is used to explore longitudinal trends of enrollment in a regional university, with student population of 14000. Least square methods are applied to several matrix models, together with observations from East Tennessee State University annual enrollment reports. Genetic algorithms are implemented to minimize a residual sum of squares functional. Additionally, model selection by means Akaike Information Criterion is employed to rank mathematical models. Residual analysis is carried out to verify assumptions on observation error structure. Standard errors in the parameters of the best ranked model are calculated with bootstrap sampling on residuals with appropriate error structure. Ultimately, model parameter estimates are utilized to estimate student life tables.

**LAMP, C. and GARCIA, D. Atherosclerosis and Social Influences. Shippensburg University, Shippensburg, PA.**

Heart disease is the leading cause of death in the United States. Atherosclerosis is a condition associated with many types of heart disease. Atherosclerosis is the accumulation of plaques, mainly consisting of fats and cholesterol, in arteries. Smoking and obesity can lead to Atherosclerosis. In this presentation, we develop a preliminary mathematical model which views smoking and obesity as epidemics that can be spread through social influence. We discuss and present some results.

**LAWHORN, M. and SCHOMAKER, R. Comparative Analysis of Transcriptomic Data: Modeling Gene Overlap Using Gene Flexibility. Department of Mathematics, Winthrop University, Rock Hill, SC; Department of Biology, Florida Southern College, Lakeland, FL.**

Comparative transcriptomic data, or gene expression profiles, is used to examine similarities and differences in the gene expression of organisms, allowing scientists to conclude whether similar gene expression from two different experiments share a biological cause, which can be beneficial when developing treatments for cancer or mental health diseases. Typically, two independent experiments are performed that identify differences in gene expression between two experimental conditions or organisms. The differences are compared between experiments to test for significant overlap in differentially expressed genes. Traditionally, the fact that the quantity of transcription factor binding sites on a gene varies is not taken into consideration. Thus, conclusions from these analyses could be considered more significant than they actually are. In this study, a computer simulation was created that produced significance values when the number of transcription factor binding sites per gene varied. The simulations generated a null expectation of transcriptome overlap for genes with different genetic architectures. When these distributions were compared to empirical data, results suggested traditional methods for measuring gene overlap may need to be reevaluated and more stringent criteria need to be applied. Past overlap may have been systematically overestimated due to inherent differences in gene expression flexibility among genes.

**MCCARTT, P. and WHITE, R. Development of a PBPK Model to Study the Effects of BMI on Effectiveness of an Antibiotic. Department of Mathematics and Statistics, East Tennessee State University, Johnson City, TN.**

In this talk, a physiologically-based pharmacokinetic (PBPK) model is developed which can be used to analyze the absorption, distribution, and elimination of an antibiotic under varying body mass index values. We estimate parameters in the model for a specific antibiotic using a least squares formulation and data found in the literature. We then perform a sensitivity analysis to determine the effect of small changes in the parameter values on variables in the model. Finally, we use the model to examine the effects of varying BMI on the absorption of antibiotics. This information could potentially be used to help determine proper dosing for individuals based on their BMI.

**MONTGOMERY, K.M., BURCHFIELD, S.L., BAILEY, A.C., WIDNER, B., BAILEY, D.C., TOLDT, C.E. and FITSANAKIS, V.A. Transport of Glyphosate in *Caenorhabditis elegans* is Not Mediated via Presynaptic Dopaminergic Transporters. Department of Biology, King University, Bristol, TN.**

Parkinson's disease is a neurodegenerative disorder, sometimes linked to environmental toxicants like pesticides and herbicides. *Caenorhabditis elegans* are often used as model organisms because their nervous system is homologous to humans. Previous work in *C. elegans* when treated with the glyphosate-containing herbicide TouchDown (TD) showed evidence of neurodegeneration. The purpose of these studies was to determine if TD is transported into neurons via pre-synaptic neurotransmitter transporters. *C. elegans* were pre-treated with antagonists for dopamine (DAT), serotonin (SERT), or GABA (GAT) transporters to determine if this ameliorated TD-induced neurodegeneration. Following incubation with the respective antagonist, worm strains were exposed to various concentrations of TD for 30 min (acute) or 24 h (chronic). In the acute paradigm, there was no neuroprotection seen. In the chronic paradigm, neuroprotection was seen only in the GAT group. Protection may be observed in the GABA group because glyphosate and GABA have similar structures, making it possible for the neuron to recognize glyphosate. Funded by NIEHS R15ESO15628-01A1 and ESO15628-01A2 (VAF).

**MOODY, K. Impact of Community Retention Programs on Gang Activity. Virginia Tech, Blacksburg, VA.**

Communities have been ravaged by the anti-social lifestyle and harmful environment presented by gangs for decades. The focus of this project was to analyze why individuals join gangs and how that information could be used to reduce gang activity. Through the use of compartmental modeling, several factors in gang dynamics

were identified. The convenience and quickness at which scenarios can be constructed then visualized is one of the many benefits of compartmental modeling. Much of the analysis is tied in and related to the reproductive number. The reproductive number is a threshold value at which an outbreak can occur. It represents the average number of new gang members caused by a gang member in a completely susceptible population for the duration of gang membership. This is an important quantity as all the parameters' effectiveness is measured by how much they affect the reproductive number. The sensitivity of each parameter is obtained through sensitivity analysis. The results of the project determined that community retention programs are effective in reducing gang activity and an overall increase in gang organization can increase the gang population. Concluding prevention is the best strategy and organized gangs present a greater risk to communities.

**PATRICK, A., and AMANDA, L. Mathematical Model of Recycling. The University of Texas at Arlington, Arlington, TX.**

As epidemic-type mathematical models have been previously used to study diseases, rumors and behaviors, their application will be further applied to study recycling influence. The types of influences taken into account were recyclers influencing non-recyclers to recycle, recyclers influencing other recyclers to quit recycling (recycling discouragement), and advertisements influencing non-recyclers to recycle. Generally, autonomous differential equations can be analyzed by calculating the equilibrium solutions and finding the eigenvalues to determine stability. The recycling population at UTA was modeled for constant and changing population. The average population increase and decrease were calculated for the system with constant population to calculate stability, and for a more accurate representation, a linear equation was calculated for changing population. Surveys were used to calculate parameters for advertisement influence and social influence between recyclers and non-recyclers. The parameters were manipulated, and each system was solved for number of recyclers and non-recyclers throughout time. The results showed a decline in recyclers with lower recycling discouragement as opposed to when it was zero even with advertisement influence parameter doubled. Additionally, a lower value for the parameter regarding recyclers influence on non-recyclers and a higher value for recycling discouragement caused non-recyclers to become the larger subpopulation as time increased.

**PULIDO, S., GOFF, W., and MURPHY, C. Evaluating Mechanisms For The Spread of Ebola. Middle Tennessee State University, Murfreesboro, TN.**

The 2014 Ebola epidemic is the largest Ebola outbreak on record. Data generated through this epidemic have evidenced an inability of previous models to predict the course of the epidemic. In this research we investigate the potential of basic SEIR models to describe an Ebola epidemic by studying the initial outbreak, in Meliandou, Guinea, which developed with limited external intervention and within a small village of about 500 individuals. Specifically, we compare the accuracy of various SEIR-type models in order to select the most accurate models of transmission and disease-induced responses. Interestingly, we find that, although frequency-dependent transmission is standard for modeling Ebola, models with density-dependent transmission are better able to describe the Ebola epidemic in Meliandou. In addition, models that include mortality-induced behavioral changes are more able to describe this epidemic than those that include infection-induced behavioral changes or emigration.

**SWALLOW, E. and BRUNKEN, W.J. Astrocyte Maturation and Microglial Association: Implications for Arterial-Venous Specification. SURF Program, SUNY Upstate Medical University, Syracuse, NY; Department of Biology, King University, Bristol, TN.**

Angiogenesis is an important process in the development of the retina, with blood vessels forming from pre-existing vasculature. Retinal arteries and veins differentiate from blood vessels in the eye by the process of vascular remodeling, however this process is not well understood. On a cellular level, astrocytes are vital to the vascular development since astrocytes lay out the template for blood vessels to progress and migrate throughout the retina. Alternatively, microglia influence in vascular branching of the retina. We hypothesize that arterial and venous specification is dependent upon the interactions between key retinal cell types: vascular endothelial cells, microglia, and astrocytes. Astrocyte maturation and microglial association along the arteries and veins

were studied to determine if there was a correlation with arterial-venous specification. Images of mouse retinas stained biomarkers of key cell types were analyzed to provide a baseline for the remodeling phase. Here we show a preferential astrocyte localization and microglial activation along the retinal veins, suggesting that they are related to the venous specification in the retina. Vascular abnormalities within the retina are one of the leading causes of blindness among adults and infants, thus the important implication of this research. Funding provided by NIH-NEI R01 Ey12676 (WJB).

**VO, A. Numerical Methods for an Auditory PDE. Creighton University, Omaha, NE.**

Peripheral auditory neurons are interesting both biologically and mathematically. Auditory neuron cells has smaller sizes, thus have fewer membrane channels, which transports ions and compounds in and out the cells. Because of its interesting behaviour, biologists and mathematicians are interested in modeling the timing of action potential and property of auditory neuron system.

In this research, we work with a PDE model [Gasper, 2013]. We find numerical solutions to the partial differential equation using three methods: (1) Finite Difference (explicit), (2) Finite Volume-Complete Flux (implicit), and (3) Finite Volume (explicit, with two choice flux limiters). These results can be used in direct comparison with clinical testing results, and lead to improvements in cochlear implants.

**WEI, J., MUMMAH, R., SASHIDHAR, D., RICE, H., PARKER, L., MAREK, A., EDA, S., GANUSOV, V.V. Discriminating between alternative mechanisms of in vitro mycobacterial granuloma formation in Johne's disease. National Institute for Mathematical and Biological Synthesis, Knoxville, TN; University of Minnesota, Twin Cities, MN; The Pennsylvania State University, University Park, PA; North Carolina State University, Raleigh, NC; University of Tennessee, Knoxville, TN.**

Johne's disease is a costly chronic enteric disease which affects ruminants worldwide. Caused by *Mycobacterium avium* subspecies paratuberculosis. Johne's disease forms iconic granulomatous structures in the intestinal tract. Using experimental data, with deterministic and stochastic simulations of two models based on ordinary differential equations, we examine alternative mechanisms of granuloma formation. Through image analysis, granuloma areas measured. The experimental granuloma size distributions best resemble lognormal distributions, with the mean numbers of granuloma cells increases linearly over time at a rate of 2.2 cells per day. From the first model, the accumulation of infected macrophages is not the primary mechanisms driving granuloma formation. Rather, as seen in the deterministic component of Model II, there are other factors involved that are instrumental to granuloma growth such as migration of macrophages to the granulomatous structure. Model II demonstrated similar increases in average size and lognormal distributions, but failed to generate the increase in variability found in the data. In contrast, the stochastic component of Model II displays the linear increases in average size and variability, but not distributions of the data. Thus, further studies include honing the model so that encompasses both parametric variability as well as stochasticity.

**WHITE, Z. The Effects of Government Intervention and Rehabilitation on Prostitution. Israel Charles Norcom High School, Portsmouth, VA; Virginia Tech, Blacksburg, VA.**

Prostitution has impacted society to be regarded as the oldest profession. In 2009, over 70,000 prostitutes were arrested in the United States. Rehabilitation programs, such as Project ROSE, have been put in place to intervene the need to prostitute by providing resources that can help prostitutes to become self-sustaining financially and emotionally. A Sitr compartmental model was constructed to examine the dynamics of prostitute interactions and the impact of rehabilitation programs on prostitution. Using the Next Generation Operator (NGO), prostitute generation number ( $R_0$ ) was determined. Typically,  $R_0 < 1$  indicates a prostitution-free population, while  $R_0 > 1$  indicates an existence of prostitution endemic state in a population. Stability of prostitution-free and prostitution-present equilibria were established. Parameter values were chosen to describe these dynamics. As a result, simulations were produced to examine a prostitution-free society and prostitution-induced society. The simulations concluded analogous to the sensitivity analysis of  $R_0$ . The simulations also revealed that prevention is more effective than any effort in reducing  $R_0$ . Furthermore, government intervention and successful rehabilitation hold significant roles in the reduction of  $R_0$ .

**WIKLE, N., YAN, R., GAULI, A., GROSS, L., SIMBERLOFF, D., CHUANG, A., AND LANDERER, C. Projecting Terrestrial Species Invasion Spread Using Commodity Flow Pathways. National Institute for Mathematical and Biological Synthesis, Knoxville, TN; Truman State University, Kirksville, MO; College of William and Mary, Williamsburg, VA; Fisk University, Nashville, TN; University of Tennessee, Knoxville, TN.**

Models to create projections of invasive species spread are critical in identifying high priority shipping centers and pathways of bioinvasion, essential information in the prevention of environmental and economic harm caused by invasive species. Research into the development of models of biological invasion across broad spatial regions have been targeted towards network models of international shipping pathways. The majority of models for terrestrial invasions have been confined to basic diffusive spread. Nevertheless, many species of harmful pests are known to travel long distances, in part due to transport through commodity shipments. For example, *Solenopsis invicta*, the red imported fire ant, can travel via turf shipments within the United States. The availability of commodity flow data suggests that a model utilizing domestic freight as the dominant vector of dispersal may be a promising, yet unexplored, avenue of research in invasive species ecology. To this end, we utilize data from the Freight Analysis Framework (FAF) to create projections of invasive species spread. The FAF data provides tonnage information on commodities shipped within the United States at state level resolution. Weight values from four sets of data are used in a resampling method to generate the transition matrix at the core of a stochastic matrix model used to create projections of terrestrial invasive species spread. Additionally, we incorporate elements of environmental difference and logistic growth in our projections to achieve greater biological soundness in the results. Furthermore, we introduce ComFlo, an interactive web-based tool designed to aid in the visualization of commodity shipments within the United States.