Fifth Annual

Undergraduate Research Conference at the Interface of Biology and Mathematics

November 16-17, 2013

University of Tennessee Conference Center

Knoxville, TN

CONFERENCE OVERVIEW

Welcome! This conference is hosted by the National Institute for Mathematical and Biological Synthesis (NIMBioS), housed on the campus of the University of Tennessee-Knoxville. Undergraduate students conducting research in mathematics and biology will present over 60 oral and poster presentations. A keynote by Dr. Mariel Vazquez and featured talk by Dr. Andrew Liebhold 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 7, oral presentation abstracts start on page 17.

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 sixth 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 7.

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 2013

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.

Join our groups to connect to colleagues, friends, and new contacts in advance of the conference and start making plans for Knoxville!

KEYNOTE LECTURE

Dr. Mariel Vazquez
Associate Professor of Mathematics
San Francisco State University

DNA Unlinking by Xer Recombination

Newly replicated circular chromosomes are topologically linked. Controlling these topological changes, and returning the chromosomes to an unlinked monomeric state is essential to cell survival. XerCD-dif-FtsK recombination acts in the replication termination region of the Escherichia coli chromosome to remove links introduced during replication. We use topological methods to show definitively that there is a unique shortest pathway of unlinking by XerCD-dif-FtsK that strictly reduces the complexity of the links at every step. We delineate the mechanism of action of the enzymes at each step along this pathway and provide a 3D interpretation of the results.

FEATURED SPEAKER

Dr. Andrew Liebhold
Research Entomologist
USDA Forest Service

Forest Insect Outbreaks: A Never-Ending Puzzle

Most forest insect species are relatively rare and are seldom noticed. However, a handful of species exhibit episodic eruptions from relatively low to extremely high densities. During these episodes, very high population densities may cause total defoliation of host trees or extensive mortality to host trees. Many insect species exhibit periodic oscillations such that outbreaks are recurrent at relatively constant intervals. Identification of the mechanisms responsible for these population cycles has received considerable attention, but despite the intense work of many scientists, the causes of these cycles are not clear. Interactions between plant-feeding

insects and host trees as well as interactions with predators, parasites and pathogens appear to be the main causes of these cycles but these mechanisms are complex and difficult to understand. Mechanistic mathematical models have been extremely useful for the exploration of hypotheses explaining population cycles. Most forest insect outbreaks also tend to occur synchronously over large regions spanning several hundred kilometers. Again, several hypotheses have been advanced to explain this synchrony. It is well-known that variability in weather conditions tends to be synchronous and this could synchronize insect populations as well. However synchrony can also be caused by large-scale movement of these plant-feeding insects as well as their predators. Unfortunately, both mechanisms are capable of producing nearly identical patterns of synchrony and it is very difficult to differentiate between these two effects. Again, mathematical models have proven to be extremely useful tools for exploring hypotheses regarding synchrony in insect outbreaks.

SCHEDULE

Saturday, November 16: 413AB (Except where noted)

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

1:10-2:10 Keynote Lecture:
Mariel Vazquez, Associate Professor of Mathematics, San Francisco State University
DNA Unlinking by Xer Recombination

2:20-2:35

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

406: Conrad Beckmann and Jacob Lambert: *Social Structure and Rank Predict Fitness in Spotted Hyenas*

413AB: Ethan Levien: *Effects of Network Topology on Pattern Formation in Systems of Coupled Phase Oscillators*

2:40-2:55

403: Aileen Toja, Ashley Carter, Joanna Gonzalez, Omomayowa Olawoyin: *A Theoretical Model of Coinfection Dynamics: Modeling Competition Dynamics Between* Borrelia burgdorferi *and* Anaplasma phagocytophilum *Within a Human Host*

406: Joseph Phillips: *Increasing complexity decreases the effects of energy flux on food web stability*

413AB: Saba Nafees: *Modeling Positions coupled to F508, site of Chief CF Causing Mutation*

3:00-3:15

403: Tyler George, John Aaron Gowins, Jake Weismann: *A Dynamical Model Examining the Effects of NFkB and HIF1 Pathways in Aspergillus fumigatus Infected Airway Epithelial Cells*

406: Laura Asaro: *Asymmetric Intraguild Predation Between Protoperidinium and Heterocapsa in the Presence of a Mutual Predator*

413AB: Zeyad Boodoo and Pamela Guerron: *Applications of Graph Connectivity Indices in DNA Data Analysis*

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 Featured Speaker:
Andrew Liebhold, Research Entomologist, USDA Forest Service
Forest Insect Outbreaks: A Never-Ending Puzzle

5:05-6:00 Career Panel (Moderator: Suzanne Lenhart, Associate Director at NIMBioS)
Dr. Andrew Liebhold
Dr. Mariel Vazquez
Dr. Talitha Washington, Associate Professor of Mathematics, Howard University

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 17: Rooms 403, Auditorium 406, 413AB, 413C

8:00 Continental Breakfast

8:30-8:45

403: Kristen Bales and Ty Frazier: *Spatio-Temporal Model for Burglary Reports in Tennessee*

406: Jeffrey Kopsick: *The Exploration of 3D Printed Environments for* Caenorhabditis elegans

413AB: Wendy K. Caldwell, Benjamin Freedman, Michael M. Thomas and Luke Settles: *Substance Abuse via Legally Prescribed Drugs: The Case of Vicodin in the United States*

8:50-9:05

403: Nicole Bender, Christian Mason and Sunil Shahi: *Automatic detection of rare bird species*

406: Cecilia Dorado and Zach Helbert: *A Demographic Population Dynamics Approach to Student Enrollment*

413AB: Yesenia Cruz Pascual and Jennifer Houser: *Sensitivity Analysis of Hepatitis C Virus Dynamics*

9:10-9:25

403: Benjamin Manifold: *Automated Tracking of Small Objects in Video Recordings*

406: Dylan Hardwick and Liv Heidenreich*: Estimation of Growth Rates of* Dreissena bugensis *in Lake Michigan*

413AB: Nejc Zupan, Tom Madsen: *Seasonal Fluctuation in Tsetse Fly Populations and Human African Trypanosomiasis: a Mathematical Model*

9:30-9:45

403: Kiersten Utsey: Mathematical Modeling of Fetal Electrocardiograms

406: Alicia Weeks and Rebecca Peot: Assessing the Parasite Manipulation Hypothesis in an Invasive Host (*Bithynia tentaculata*)

413AB: Jackie Chism: *Mathematical Modeling of Action Potential in Cell Processes*

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

403: Emily Ziegler: *Maximizing Reproduction in* Bithynia tentaculata *with a Parasite Infection*

406: Caitlin Ross and Dominick Defelice: *An Investigation of Genome Features and Their Effect on Meiotic Recombination Rates in* Apis mellifera

413AB: David Sykes: *Kleptoparasitic Interactions and Internal States*

1:20-1:35

403: Audrey Utkus: *The impact of individual-level heterogeneities on infectious disease dynamics and control*

406: Robert Stolz: *Mapping Recombination Pathways in Circular DNA*

413AB: Alex John Quijano: *Expansion of a Stochastic Model for* Anelosimus studiosus *Movement during Prey Capture*

1:40-1:55

403: Kathryn Schaber and Brittany Hale: *Modeling Feline Infectious Peritonitis in a Cattery*

406: Andrea Ekey: *Protein-Protein Interaction Detection Using Mixed Models*

413AB: Ryan DeMuse: *A Modified Goodwin Model of Biological Oscillators*

2:00-2:15

403: Brad Hart and Harvir Grewal: *Estimating Body Fat Content in Ctenosaura similis using Body Condition Indices*

406: Miranda Henderson: The Dynamics for Frameworks for Two Boolean Models for Gene Regulatory Networks

413AB: Matt Cattivera: *A perturbation approach to approximate extinction time in ecological systems due to harsh conditions*

2:20-2:40: Break and Snacks

2:45-3:00

403: Jiyoon Park: *Mutation of the MDS-1 and EVI-1 complex locus causes kyphosis by affecting embryo development*

406: Sarah Kramer: *Analyzing the Impact of Individual- and Network-Level Behavioral Factors on HIV Spread among Women in Washington, DC*

413AB: Weifan Liu: *Modeling Calcium Dynamics and Muscle Mechanism*

3:05-3:20

403: Andrea Thompson: *The Molecular Phylogeny of tropical lichenized fungi genus Phaeographis*

406: Jocelyn Keung: *Agent-based model to investigate seasonality in Escherichia coli O157 transmission between pastoral beef cattle*

413AB: Akira Horiguchi: *No-Analog Communities in Space and Time*

3:25-3:35

406: Closing Remarks

3:40 Adjourn

POSTER ABSTRACTS BY SEQUENCE

1. BROWN, C., and A. KISER. An Analysis of Tiger Salamander (*Ambystoma tigrinum nebulosum*) Survival Based on Body Size and Other Covariates. Departments of Biological Sciences and Mathematics & Statistics, Murray State University, Murray, KY.

Survival is an important aspect of fitness in the natural world and depends on a number of factors. We are investigating the survival of tiger salamanders, Ambystoma tigrinum nebulosum based on covariates such as morph, sex, and body size. We have collected data from the Mexican Cut nature preserve in the Gunnison National Forest on thousands of tiger salamanders spanning the years 2005-2013. We utilized individuals implanted with passive integrated transponders (PITs) whose capture histories were recorded in a long-term database. We used capture-recapture models via MARK as well as life tables to analyze salamander survivorship based on sex and morph. A. t. nebulosum adults exist in two different forms referred to as metamorphs and paedomorphs; moreover, this analysis enabled us to see if one morph has an advantage over the other. Furthermore, we used a multistate capture-recapture model to examine survival as it pertains to body size in this natural population. The results of our analyses will be discussed.

2. CARBAJAL, E., THOMASON, C., PEDERSEN, A., FENTON A., and A. GRAHAM. Modeling Sin Nombre Virus in Wild Co-Infected Peromyscus. Ecology and Evolutionary Biology, Princeton University, Princeton, NJ.

Sin Nombre Virus (SNV) is responsible for hantavirus pulmonary syndrome (HPS), a fatal respiratory infection in humans. While hantaviruses cause a lifelong and asymptomatic infection in naturally infected hosts, human infection occurs most commonly through the inhalation of contaminated aerosols of rodent urine, feces, or saliva. To address a gap in our understanding of how SNV interacts within parasite communities, we sampled 800 deer mice (Peromyscus maniculatus) and white-footed mice (Peromyscus leucopus)—the reservoir hosts of SNV—at Mountain Lake Biological Station (VA) using a mark-recapture procedure and an SNV-specific ELISA IgG at Princeton University to test whether the seropositivity for hantavirus is affected by the presence of helminths. In order to discern the spatiotemporal dynamics of co-infection, we analyzed SNV seropositivity and helminth abundance in relation to mouse age, sex, and condition. Current literature shows that SNV seropositivity will be higher in hosts with a higher helminth burden on the basis that (1) SNV goes viral during the first 20 days or so of infection when neutralizing antibodies are not available and (2) helminth infection delays neutralizing antibodies, further enhancing transmission. Although still in process, we have found SNV seroprevalence to be about 10% in the population.

3. CLAUSE, N. Numerically Solving A Linear Optimal Control Problem in Wound Healing. Western Kentucky University, Bowling Green, KY.

For this research, the goal is to optimize the treatment strategies for chronic wounds using oxygen therapy. The state equations in the mathematical model relate the levels of bacteria, oxygen, and neutrophils in a chronic wound. Working with these equations, we use optimal control theory to try to find the optimal control, which in our case is the input of oxygen to the wound. The optimal control is linear, which gives a bang-bang result, and this discontinuous function is approximated with a smooth function. Numerically, we attempt to solve the problem using the steepest descent algorithm combined with the sweep method, which solves the state equations forward in time and the adjoint equations backwards in time. The equations are solved iteratively until the convergence criteria have been met. The method has been successfully applied to a test problem and will be implemented for the large-scale problem.

4. CUNNINGHAM, C., and W. MARZLUFF. Forming an Ectopic Histone Locus Body in Human Cells with a Mouse Histone Gene Cluster. Department of Biology, Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill, NC.

Because of their role in DNA packaging, most histone genes are replication dependent; expressionof these

histone genes occurs exclusively during the S-phase of the cell cycle when DNA is replicated and their mRNAs are rapidly degraded at the end of S-phase. The rapid synthesis of histone mRNA occurs at clustersof histone genes which are regulated by protein complexes called Histone Locus Bodies (HLBs). In *M. musculus*, a long, non-coding RNA (lncRNA) has been identified by deep sequencing in between a highly conserved pair of duplicated histone H2a and H3 genes at the mouse histone 2 locus. My experiments are designed to examine the role of this lncRNA on HLB formation and histone gene expressionat mouse histone locus 2. I have created several transgenic lines of HeLa cells by transfecting human cell lines with a copy of the entire mouse histone locus 2 on a 187 kb BAC. These cells express the mouse histone genes present in histone locus 2. In future experiments, I plan to knockdown the lncRNA and/or mutate the lncRNA promoter region on the BAC and observe the effect on mouse histone gene expression and HLB formation in human cell lines.

5. DEHANEY, R. The Algebraic Connectivity of Laplacian Matrices: Fielder's Theorems and Applications to Bioinformatics. Department of Mathematics, Morgan State University, Baltimore, MD.
A Laplacian Matrix is a matrix in graph theory. Laplacian matrices have several important properties derived from its second eigenvalue which is defined as the algebraic connectivity. The notion of algebraic connectivity is part of a bioinformatics algorithm called RNAmute. In this poster we present theorems of Miroslav Fielder that are used to prove properties of the matrices. We then apply RNAmute to HIV-1 RNA sequences to predict possible mutations in the sequences.

6. DISHUCK, P. Regulation of Estradiol-Induced Prolactin Surges. Department of Biology, Washington & Lee University, Lexington, VA.
The surge of prolactin that occurs during proestrus, preceding ovulation, is of primary reproductive importance. Rhythms of prolactin that occur during other reproductive paradigms, pregnancy and lactation, have been well characterized and explained, but the presumably estradiol-induced proestrus surge of prolactin remains a relative mystery. The primary motivation of this research is to further the understanding of this surge's regulation to inform future reproductive medicine. We are using computational modeling of hormone systems along with experimental work in ovariectomized and estradiol-supplemented rats (*Rattus norvegicus*) to test regulatory hypotheses. We have shown *in silico* that a prevalent theory of prolactin regulation, a short-feedback loop of dopamine inhibition of prolactin and prolactin stimulation of dopamine secretion, is incompatible with experimental data for estradiol-induced prolactin surges. Additional models demonstrate the necessity of additional stimulatory factors, inhibitory factors, and/or circadian regulation of neural responses to explain the experimental data. We are currently testing these hypotheses in ovariectomized rats with and without estradiol replacement via immunocyctochemistry for circadian variation in receptor expression and neuroendocrine dopaminergic neuron activation. Multiple circadian inputs to the hypothalamus are likely required to induce and time estradiol-induced prolactin surges.

7. DOHERTY, R., EDGREN, J., IGEL, D. and A. WATSON. Modeling HPV Spread Among Students at Washington and Lee University, and the Effects of Potential Countermeasures. Washington and Lee University, Lexington, VA.
Because HPV infections are a significant and widespread problem on college campuses and are the cause of numerous downstream health hazards, it is in the interest of a university to develop a model to chart the progression of the disease on campus. Furthermore, being able to model an outbreak can allow a university to analyze the effects of potential schemes to reduce spread. We present a model of the spread of HPV on the campus of Washington and Lee University, created from a combination of national and school-specific survey data concerning rates and types of sexual activity. The model is altered to reflect a variety of attempts to reduce the spread of the disease on campus, including an increase in vaccination rates, and an increased use of barrier protection. We also compared these preventative measures to a model with heavily reduced promiscuity. We present an analysis of the different efficacies of each approach, both singly and in combination, with the conclusion that an increased rate of vaccination, especially among males, is the most efficacious and easily accomplished means of reducing HPV spread on a college campus.

8. DUNGEE, N. The Effects of Temperature and Water Type on Seed Germination in *Asclepias incarnata*. North Carolina A&T University.

9. EHNIS, K. and S. PHILIP. Sonification of EEGs. Texas Tech University, Lubbock, TX.
Ten patient Electroencephalogram (EEG) recordings were selected from a study conducted at a Lubbock hospital. These recordings include 8 normal and 2 abnormal EEGs, which were stripped of personal identifying information. Recent publications indicate that sonification (converting data to sound) allows the human ear to analyze series data and detect irregularities that might otherwise go unnoticed. Since brain rhythms are typically lower than the human hearing range, signal-processing techniques, including but not limited to modulation, Fourier transforms, wavelet analysis, and digital filtering, will be applied to convert EEGs to sound. Our objective is to demonstrate that in addition to traditional visual analysis, auditory acuity may be useful in the analysis of EEGs and aid in the early detection of abnormal EEG activity. The project will be a success if an algorithmic approach to sonification leads to the identification of important features of the EEGs by listening to the transformed signals

10. FRICKLE, S., LE, M., SUMDANI, H., and M. TRAN. Protist and Bacteria in an Aquatic Environment: A Predator-Prey Model. University of Texas at Arlington, Arlington, TX.
The purpose of this study is to represent the dynamical patterns of a protist preying on living and deceased bacteria, using a mathematical model. Three differential equations are used to represent the numbers of protists, living bacteria, and deceased bacteria in the system. The model takes into account parameters that affect both the rate at which bacteria and dead bacteria are consumed and how this consumed material aids in the protist's growth. Parameters in this model include an encounter rate between the prey and predator and the rate of consumption of the prey by the predator. Another important parameter in this model is the conversion constant which describes how much a protist can reproduce with each bacterium ingested. The results show that changing the different parameters can lead to different, biologically-meaningful scenarios such as an overall decrease in the protist population despite a high consumption rate. The different scenarios that this model can predict show that it is an effective predator/prey model for microbial systems. The simplicity of the model makes it a valid starting point for more complicated predator prey systems.

11. GHENT, C. A Mathematical Model of Flavor-Calorie Associations and their Effects on Hunger. North Carolina A&T State University, Greensboro, NC.
The purpose of this study is to model the relationship between flavor-calorie associations in the brain and how they affect weight. Flavor calorie learning is an example of classical conditioning. To understand weight fluctuations it is not enough to look at food intake and energy expenditure. A pure set-point model of weight control implies that obese people should never be hungry. Roberts (unpublished) hypothesized that stronger flavor-calorie associations raise the set point, allowing hunger to be expressed and weight to rise. Roberts also hypothesized that in the absence of environmental input, the set point steadily decreases. Using a set of differential equations we will parameterize Robert's model and test our results using data from The Minnesota Semi-Starvation Study.

12. GODDARD, D. ATP Receptor Desensitization Kinetics In Human Bronchial Epithelial Cells. North Carolina A&T State University, Greensboro, NC.
Cystic fibrosis is an inherited disease characterized by abnormal regulation of the airway surface liquid. In cystic fibrosis, ion transport is disrupted due to mutations in the chloride ion transport protein cystic fibrosis transmembrane regulator. These mutations result in a reduced ability of cells to secrete chloride and water onto the airway surface. ATP-signaled increase in chloride secretion via an alternative chloride channel is a possible therapeutic avenue but is brief due to what we hypothesize is the quick desensitization of ATP receptors on the cell surface. In order to characterize the response and desensitization of ATP receptors in airways, a series of ATP dosing experiments were conducted in Ussing Chambers in human bronchial epithelial cells from patients

with cystic fibrosis. These recordings were performed in 2005 and were submitted as part of a PhD. We used the software program GraphClick to digitize Ussing chamber signals from the ATP dosing experiments in the thesis and transferred the results to Microsoft Excel. The signals were analyzed for the duration of the dose response, the maximum height of the current response, the area under the current versus time response. For both sodium and chloride currents, there was an increase in the maximum height of the current response and the area under the curve as the concentration of ATP increased. The duration of the chloride current from start to end was less as compared to sodium for equivalent concentrations of ATP. These results and the future analysis of the cumulative ATP-current dose-response experiments will be used to test possible dosing regimens of ATP analogs as therapy for individuals with cystic fibrosis.

13. GREENWOOD, A.S., UNTHANK, J., and ARCIERO, J. Collateral Circulation Following Acute Arterial Occlusion: A Model of Compensatory Vasculature Distal to Occlusion in the Lower Extremities. Department of Mathematics, Indiana University-Purdue University Indianapolis, Indianapolis, IN.

Peripheral arterial disease encompasses many different clinical manifestations of arteriosclerosis in the peripheral vascular system, including claudication, rest pain, and critical limb ischemia. In different experimental and clinical studies, varying degrees of restored blood flow have been observed distal to sites of complete and partial occlusion. This flow restoration has been shown to be the result of dilation and development in collateral vasculature, arterioles, and capillaries. However, some debate still exists about which vascular segments contribute most to restoring blood flow to distal tissues following major arterial occlusion. This study presents a predictive model that identifies the primary sites of resistance, pressure changes, and blood flow following complete femoral artery occlusion to determine the vascular segments that provide the most blood flow restoration. This was achieved through a two-fold investigation. First, different published experiments in Rats, Dogs and Humans that measure pressure, flow and resistances for the different vascular segments in the lower extremities were reviewed to obtain relevant data. Second, using MatLab ® software an outline of the relationships between hemodynamic factors was used to create a theoretical model to determine which vascular segments best compensate for blood flow following acute, complete occlusion of the femoral artery. Results indicate following occlusion the primary site of vascular resistance is shifted from the arterioles to the collateral vessels, that dilation of the collateral arteries is the primary mechanism through which blood flow to the distal tissues is restored, and that synergistic dilation of both the collateral arteries and distal microvasculature is required for complete restoration of blood flow to distal tissues following acute occlusion of the femoral artery.

14. GUSMAN, A. and J. LOWENGRUB. A Mathematical and Computational Model of Cell Lineages: The Effect of Branching and Feedback. Vanguard University of Southern California, Mesa, CA and University of California, Irvine, CA.

Previous studies using the mammalian olfactory epithelium (OE) have increased our understanding of the growth dynamics of cell lineages. Yet the current models have focused on simple lineages, which do not take into account the branched structure of the OE lineage where the stem cells may have produced two types of differentiated daughter cells. When these models are manipulated to remove certain negative regulatory factors on stem cells, the number of committed progenitor and terminally differentiated cells increases exponentially, contrary to biological observations. Using ordinary differential equations and computational simulations of cellular growth dynamics, we present a mathematical model of the steady-states, their stability, and the dynamics of branched lineages that incorporates positive and negative feedback factors. This model better accounts for all the known biological observations of the OE.

15. HUTCHINSON, S. Testing the Life History Theory Predictions of Trade-offs Between Reproductive Rate and Life Span in Yeast. North Carolina A&T State University, Greensboro, NC.

A major goal in biology is to understand why organisms live as long as they do. Mutations that increase life span are often found in genetic screens, so the question is: If there is a possibility for evolution to result in an extended lifespan; then why don’t organisms live longer? Previous life history theory research has shown that

lifespan increasing mutations reduces reproduction rates because both traits are controlled by the same genes. This trade-off between life-span and reproductive rate as function of the same gene(s) is known as antagonistic pleiotropy. An antagonistic pleiotropic trait in saccharomyces cerevisae affects chronological aging and reproduction causing the unicellular organism to have a trade-off. In this study we attempted to determine if a pleiotropic trade-off between reproductive rate and senescence exists in the yeast Saccharomyces cerevisae. We hypothesized that any single mutation that increased the rate of reproduction should reduce life span. We created a collection of yeast strains where each mutant had a higher rate of cellular proliferation (B454) under exposure to the antifungal drug; Fluconazole. After validating the Mendelian inheritance of each mutation in the collection, we quantified changes in reproduction rate and chronological lifespan. This research will help identify the molecular genetic mechanisms for the trade-off between reproduction and life span in yeast.

16. JACKSON, A., ORTEGA J., ROBINSON, P., and HOFFMAN, K. A Mathematical Model of Melanopsin Adaptation. Department of Biological Sciences, UMBC, Baltimore, MD and Department of Mathematics and Statistics, UMBC, Baltimore, MD.

Melanopsin is a recently discovered photopigment found in intrinsically photosensitive retinal ganglion cells (ipRGCs). It is involved in non-image forming vision, such as circadian rhythm entrainment and the pupillary light reflex. It is also involved in light-related disorders, such as seasonal affective disorder. When light activates the photopigment, a phototransduction cascade commences, which produces an electrical signal that is sent to the brain.

Light adaptation is the visual system's ability to adjust its performance to the ambient level of illumination. The three hallmarks of this process are a reduction in sensitivity of the ipRGCs, an acceleration of response kinetics, and an extension of the operating range. To describe melanopsin's phototransduction and adaptation pathways, a mathematical model was developed using the law of mass action to convert the chemical equations to a series of differential equations to be solved with Matlab. Model parameters of the activation and deactivation were determined by fitting the model results to experimental calcium imaging data collected from transfected human embryonic kidney cells expressing the melanopsin gene as well as electrophysiology data collected from ipRGCs. Mathematical simulations of flash-response light adaptation produce similar results to those seen in the experimental data.

17. JACKSON, D., HOWARD, W., and S. HOTA. Drug Dosage – Ensuring 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 attempt to push the assumed boundaries of life longevity, medical research continues to find new cures for once incurable diseases. These cures are only valuable when dosage research is conducted alongside it. In this research study a pharmacokinetic mathematical model was developed to determine the dosing regimen of a drug that will be administered multiple times with the goal of maximizing the therapeutic effect of the drug while maintaining a safe drug concentration level in the blood stream. Pharmaceutically-relevant parameters for the drug were determined from the experimentally established data of the drug. Computation and simulation was performed using Mathematica. The study shows that for a drug which is administered multiple times, residual amount in the blood stream during a particular dose is higher than that of the previous one. When the interval between two consecutive doses is quite long, residual quantity is almost absent and each dose administration are almost independent of each other. 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.

18. JASTREBSKI, M., PONCE, J. ET AL. Ticks, Deer, Mice, and a Touch of Sensitivity: A Recipe for Controlling Lyme Disease. Northeastern Illinois University, Chicago, IL.

Borrelia burgdorferi sensu stricto is a bacterial spirochete prevalent in the Northeastern United States that causes Lyme disease. Lyme disease is the most common arthropod-borne disease in the United States; affecting mice, deer, humans and other mammals. The disease is spread by Ixodes Scapularis, a species of tick whose primary food source are deer and mice. Reducing the population of ticks feeding on both large and small mam-

mals below some critical threshold can decrease the prevalence of Lyme disease among humans. A simplified, six-dimensional Susceptible-Infected, SI, model is used to capture the mice-deer-tick dynamics while considering the impact of varying population-specific death rates on infected population size. We analyzed the stability of the models two equi-libria, the unstable disease free equilibrium and the endemic equilibrium. Static forward sensitivity analysis is conducted on the basic reproduction number and the endemic equi-librium. A dynamic approach was explored to observe change in the sensitivity of the death rates over time. These analyses were conducted to determine the efficacy of chang-ing death rates in order to reduce prevalence of Lyme disease.

19. KHAN, M., TOWERS, S., MUBAYI, A., ET AL. Climate Change and Influenza: The likelihood of early and severe influenza seasons following warmer than average winters. Northeastern Illinois University, Chicago, IL.

Influenza is a viral infection that is seasonal in temperate climates, normally peaking in the months of winter. Occasionally influenza epidemics may appear earlier than normal and with this comes a significant increase of incidences during the autumn months. During the winter of 2011-2012, the influenza season was abnormally late and mild, which could be because of it being the fourth warmest winter recorded in the United States according to the National Oceanic and Atmospheric Administration. However, the 2012-2013 flu season has begun abnormally early and severe for both strains A and B even though the autumn temperature was as usual. Our research goal was to investigate if the mild influenza seasons during warmer winters will result in a severe epidemic in the following year. We used laboratory confirmed incidences data, obtained from the CDC, recorded across ten US regions between 1997-1998 to 2012-2013 influenza seasons. The demographical and geospatial data were obtained from the US Census Bureau. After analyzing population weighted average temperatures for winter and autumn from the years 1997 to 2012, we found that the early winter of 2012 has been warmer than the average temperature even though the temperature of autumn stayed consistent with the average. The measure of epidemic severity can be determined through the growth rate of the epidemic. Using a mathematical model, we analyzed the growth rate and peak timing of the epidemic as a function of the growth rate and average temperature of the previous season. In order to determine the exponential growth rate, parameter estimation methods was used to fit an exponential curve to the epidemic data. When a mild winter occurred, we found that on average 72% of the time the following outbreak was more severe than normal, with epidemic growth rate higher than average by 40%, and a peak timing occurring earlier than usual by eleven days. Furthermore, the relative probability of the following epidemic peaking before January was over 80% higher. The findings of this research showed a high correlation between warmer winters and severe epidemics due to the fact that a large susceptible population is going into the subsequent season. Our study of this climate pattern can aid with timely manufacturing and distributing of influenza vaccination to offset the severity of imminent epidemics.

20. KNIGHT, K.N. and F.B. AUGUSTO. Mathematical model of community-acquired and hospital-acquired methicillin-resistant *staphylococcus aureus* transmission in hospital and community settings. Department of Mathematics and Statistics, Austin Peay State University, Clarksville TN.

Mathematical models are often used to study infectious diseases and antibiotic resistance. Current research utilizes deterministic models to quantify the behavior of methicillin-resistant *staphylococcus* aureus (MRSA) in the hospital setting only. Recent outbreaks of MRSA have been found to circulate in the community. We propose two deterministic models for MRSA which analyze the behavior of the bacteria in both the hospital and community settings. Also unique to our model is the incorporation of environmental contaminants and isolation of colonized and infected patients for the hospital community. The reproduction numbers were obtained for both models; in addition, the impact of control measures, such as hand-washing and isolation, in the hospital and community settings were determined.

21. MASSARO, M. Equine Gait Analysis with PEGASYS. State University of New York at Geneseo, NY.

The diagnostic force plate system, PEGASYS (“Portable Equine Gait Analysis SYStem”), is a 3-axis equine

force plate developed to measure the hoof-ground reaction forces produced by an equine subject. The system is composed of a stainless steel plate encased in a rectangular aluminum housing containing 10 force sensors. These sensors are capable of measuring forces up to 1,000lbs in the vertical, forward, and lateral directions. Through additional analysis, hoof torque, impulse, center of force, resultant force magnitudes, and angles of impact are calculated. A healthy horse and an injured horse distribute their weight across their legs differently, causing their gaits to differ in force and magnitude. After establishing a healthy gait pattern, any deviations from the normal calculations are evaluated and can potentially be used as evidence of an injury. The data acquired by the force plate system will be useful to equestrians and veterinarians in determining lameness and evaluating an animal's progress through medical treatment and recovery.

22. MILLER, P. and A.W. PARK. The Perfect Storm: Factors that Lead to Increased Transmission and Resistance Emergence of Heartworm in the United States. Gustavus Adolphus College, St. Peter, MN.
Heartworm disease has been observed all over the world but is distributed heterogeneously where hotspots are thought to be promoted by factors such as climate, pet and owner demographics, and percent of canid population given medication. Recent concerning evidence has suggested the establishment of drug resistant worms in some areas of the United States. Because only one class of drugs exists to treat heartworm, resistance presents a large problem. Two of the first models for heartworm disease dynamics and drug resistance emergence, one deterministic and one stochastic, were developed in order to identify factors that could lead to higher rates of transmission or faster rates of resistant allele increases. Factors analyzed included vector abundance, treatment coverage, and fitness benefit of mutation. It was found that areas with high mosquito abundance and low treatment coverage are more likely to suffer from higher worm burdens in general. Speed of resistance emergence and probability of resistant worm invasion depend on the fitness cost of mutation in heartworms and founding size of resistant worm population. Collectively, these models help to identify key factors and regions that are associated with successful and rapid establishment of drug resistant heartworm populations.

23. NOLEN, S. and S. HOTA. A Mathematical Model of HIV/AIDS Epidemic with Stability Analysis. Fisk University, Nashville, TN.
HIV/AIDS has become the biggest epidemic since the Black Plague over five hundred years ago. Within about thirty years into the HIV/AIDS epidemic, close to forty million people have been affected worldwide and the number is alarmingly large within the African American population in the United States. The goal for this research is to analyze mathematically the progression and transmission dynamics of the HIV epidemic and to perform stability analysis for the epidemic. A simple compartmental model of HIV/AIDS is developed based on the SIR epidemic model with the assumption that the rate of becoming susceptible is proportional to the size of the susceptible population. The equilibrium points were found and the asymptotic stability of equilibrium points was determined. Numerical simulations are performed to illustrate the analytical results. This study shows that if the number of people developing AIDS is higher than the number of people infected by HIV then the infection will persist whereas the epidemic will eventually die out if the number of people becoming infected by HIV is higher than the number of people developing AIDS.

24. POPPENWIMER, T. Modeling the Evolution of Pollination Syndromes in Angiosperms. Biology and Mathematics Department, The College of Wooster, Wooster, OH.
An ongoing debate in evolutionary ecology centers on the outcomes of angiosperm evolution; a generalist or specialist pollination syndrome. Generalists attract and utilize many moderately efficient pollinators while specialists attract and utilize few highly efficient pollinators. Numerous hypotheses suggest that certain variables have an effect on the fitness of a plant which in turn affect the outcomes. Recent studies show that the synergistic effects of multiple variables can be large and need to be considered. A model, currently being developed, uses a combination of variables and examines their synergistic effects. This model will utilize Markov chains and agent based modelling to simulate a patch of angiosperms and their pollinators. The fitness of each plant will be determined by: pollinator populations, interactions, and efficiency, spatial arrangement of

plants, flower morphology, nectar quality, and pollen quality. Evolution will be incorporated through "seasonal turnovers" where individual flowers survive or die. A death leaves an empty space where a new plant will sprout, which has a probability of displaying a new phenotype. It is hoped that this model will provide an accurate simulation of the outcomes through its incorporation of the synergistic effects of multiple variables and the unique method of including evolution.

25. RAPHAEL, T., RAFA TODD, C., BATE, T., and BERGES, J. Agent-Based Modeling of Phytoplankton Cell Death: Responses to Abiotic Factors in a Small Urban Pond. University of Wisconsin-Milwaukee, Milwaukee, WI.

Natural phytoplankton populations are affected by factors that control growth (e.g. temperature, nutrients, light) and mortality (e.g. grazing). One cause of mortality described in laboratory cultures is programmed cell death; its significance in nature is poorly understood. The goals of this project were to examine phytoplankton mortality in a small freshwater urban pond and to create an agent-based model incorporating abiotic factors. Phytoplankton populations were examined using flow cytometry and mortal staining to enumerate live versus dead cells. Temperature and irradiance were measured using data loggers and nutrient concentrations were analyzed in discrete water samples. Flow cytometry identified several discrete phytoplankton populations. Overall, dead cells constituted about 25% of the total. From July through September, temperature and irradiance decreased while nutrients were consistently low. We constructed an agent-based model of phytoplankton cell death. In the model, growth was a function of temperature, irradiance, and a limiting nutrient (using published models and parameters). Death occurred stochastically when one of the abiotic factors fell below a critical minimum and was modeled as either a strict threshold or in proportion to the severity of limitation. We plan to use this predictive model to generate hypotheses that relate cell death to abiotic factors.

26. RODRIGUEZ, J., LEUNG, M-Y and J. ZHANG. Protein-Protein Interaction of HSP70 and HSP60 with Other Cancer-related Proteins. The University of Texas at El Paso, TX.

The purpose of this project is to use Protein-Protein Interaction (PPI) Networks to help elucidate the roles of HSP70 and HSP60 in cancer. Since different proteins often interact with one another to perform a biological function, it is important to find other cancer-related proteins that interact with HSP70 and HSP60. PPI Networks require the use of in-silico methods to find other cancer-related proteins, called interactors, which interact with the target proteins. Examples include the interaction retrieval, protein-protein docking, and visualization methods used in the software packages like HPRD, DECOMP, GRAMM, Chimera, PISA, and Python Molecule Viewer. Eighty-eight cancer-related proteins that interact with the HSP60 were found in the Human Protein Reference Database, of which 28 were expressed in cancer. Thirty-one interactors were found for HSP70 in the same database, of which 9 were expressed in cancer. These interactors need to be further analyzed in terms of their 3-dimensional structures to see exactly how they interact with the target proteins and whether they can be used as biomarkers for cancer detection. The computational analysis results can be used as a guide to help design wet-lab experiments to study HSP70 and HSP60 and is expected to save valuable time and lab resources.

27. SIEGLER, K., MYERS, N., ZELLMER, J., MILLER, T., LAUKO, I., PINTER, G., Numerical Simulation of Nutrient Dependent Competitive Algal Growth in a Eutrophic Environment, University of Wisconsin Milwaukee, Milwaukee, WI.

Microcystis has been gaining recognition for contributing to harmful algal blooms due to its negative effect on recreational and potable water. Literature suggests that in a eutrophic environment, water column mixing, light intensity, and nutrient conditions are all influential factors in microcystis growth. Since other species' growth depends on these factors, we consider a competition model which incorporates the interaction of microcystis and other phytoplankton. In this work, we build our mathematical model as a system of nonlinear integro-partial differential equations including convective and diffusive terms and non-local light-limited nutrient dependent growth. We simulate the changes in species biomass through the water column incorporating different buoyancy characteristics. In particular, we study the various environmental effects on the formation and persistence of microcystis blooms. Through the analysis of the dynamical behavior of the system, we aim to

forecast the onset of harmful algal blooms under a variety of environmental conditions.

28. STRINGFIELD, K., and V. DARLING. Mathematical Model of the Effects of Time and Temperature on Tropical Termite Nest Growth and Decline Patterns. Departments of Biological Sciences and Mathematics & Statistics, Murray State University, Murray, KY.
Termites act as ecosystem engineers, capable of maintaining the flow of resources in an ecosystem by recycling dead organic materials. This characteristic may be especially important on St. John, USVI, where the arboreal nesting termite, Nasutitermes acajutlae is the major invertebrate degrader. Our goal is to investigate nest growth and longevity patterns of these termites in five tropical habitat types (dry forest, mangroves, moist forest, sparse vegetation, and woodlands) on St. John via mathematical modeling. We have collected data on >200 N. acajutlae nests from these habitats spanning the years 1998-2013. Using nest volume data, we expanded a logistic model capable of describing nest growth annually by adding the effect of external temperature in each habitat. We found that external temperature is inversely proportional to growth rate, meaning as the ambient temperature increases the nest growth rates declines. This relationship is expected in each habitat, but each habitat seems to have its own pattern of growth rate and decline. Due to this, we assumed that each habitat would share a similar relationship between temperature and growth rate. Modeling the dry and mangrove habitats in St. John verified the relationship and we expect the other habitats will also follow this trend.

29. SUIZA, G. The Impact of Climatic Factors on Incidence of Visceral Leishmaniasis in Bihar, India. Northeastern Illinois University, Chicago, IL.
Visceral Leishmaniasis (VL) is a vector-borne disease caused by a protozoan parasite that is deadly if not treated. VL is transmitted between humans through the bite of the vector, sandflies. The patterns and distributions of disease outbreak are based on vector abundance and their survival, primarily affected by environmental conditions. The objective of the study is to improve VL surveillance system by assessing modeling methods to predict the incidence of VL, months before the start of its outbreak. The goal can be achieved by identifying critical climatic factors that can predict incidence of VL. Incidence and climatic data from 2000 to 2007 from Bihar, India are used in the analysis. Dynamic linear regression and a time series model are constructed to understand the impact of climatic factors on the incidence. The results suggest that a lag of 1-3 months in average precipitation alone can best explain VL incidence in Bihar, India. Furthermore, temperature may be significantly affecting forecasting of VL incidence as compared to the humidity. The methodology and results used have direct public health implications in helping the prediction of VL. Also, implementation of timely and efficient prevention programs especially in resource limited countries like India.

30. TALBOT, O. Dynamics and Control of Invasive Species: The Case Of The Rasberry “Crazy” Ant Colonies. Morehouse College, Atlanta, GA.
This project is motivated by the costs related with the documented risks of the introduction of non-native invasive species of plants, animals, or pathogens associated with travel and international trade. Such invasive species often have no natural enemies in their new regions. The spatiotemporal dynamics related to the invasion/spread of Nylanderia fulva, commonly known as the Rasberry crazy ant, are explored via the use of models that focus on the reproduction of ant colonies. A Cellular Automaton (CA) simulates the spatially explicit spread of ants on a grid. The impact of local spatial correlations on the dynamics of invasion is investigated numerically and analytically with the aid of a Mean Field (MF) model and a Pair Approximation (PA) model, the latter of which accounts for adjacent cell level effects. The PA model approach considers the limited mobility range of N. fulva, that is, the grid cell dynamics are not strongly influenced by non-adjacent cells. The model determines the rate of growth of colonies of N. fulva under distinct cell spatial architecture. Numerical results and qualitative conclusions on the spread and control of this invasive ant species are discussed.

31. THOMAS, M., DAVTYAN, A. and G. PAPOIAN. Developing a Coarse-Grained Model of Protein, DNA, and Ions. Department of Chemistry and Biochemistry, University of Maryland, College Park, MD.

Molecular modeling of protein-DNA complexes is a valuable tool for investigating many biological phenomena. Although atomistic simulations are well developed and capture many details, they are too computationally expensive for most practical applications. To study DNA packaging, for example, a large system must be observed over a long period of time. One approach to obtaining coarse-grained protein-DNA interaction potentials is simply knowledge-based. For these statistical potentials, the critical assumption is that favorable contacts will occur at a greater frequency relative to their statistical probability than unfavorable contacts in a native complex. A non-redundant database of sufficiently resolved native DNA-protein interfaces was compiled from the PDIdb (Norambuena, 2010). Then ten-thousand decoys were generated for each interface using sequence permutation. The statistically-adjusted frequencies at which each type of contact was observed in the native and decoy interfaces were used to calculate the strength of the interaction potentials. The final potential defines 240 interaction strengths between four nucleotides and twenty amino acids in each of three interaction types (direct, polymer-mediated, and water-mediated). By combining this potential with previously developed intra-molecular and ionic force fields, this model will be capable of simulating the dynamics of systems containing DNA, peptides, and ions with all the computational power that coarse-graining provides.

32. WEBER, H. Incorporating Macrophage Dynamics into a Mathematical Model of a Bacterial Infection in Wound Healing. Western Kentucky University, Bowling Green, KY.

Chronic wounds are categorized by their prolonged state of inflammation in the wound-healing process. In the Unites States alone, it is estimated that $5-10 billion are spent annually treating these wounds so a more thorough understanding of them is vital. In the inflammation stage, macrophages play a key role in helping to cleanse the wound, forming granulation tissue, and other activities which promote new growth. Therefore, my work involves incorporating that macrophage element into a differential-equation model of a bacterial infection through wound-healing. In this model, there are currently three variables accounted for, including neutrophils (n), bacteria (b), and oxygen (w). Through the addition of macrophages to the model, a more realistic model can be created. This increased understanding will allow for more effective treatment methods using oxygen therapy and will ultimately result in a better system.

33. WILSON, L. and ZHAO, S. Exploration of Various Operator Splitting Schemes for Solving the Nonlinear Poisson-Boltzmann Equation, Department of Mathematics, University of Alabama, Tuscaloosa, AL.

The Poisson-Boltzmann (PB) model is a widespread and effective approach for electrostatics analysis of biomolecules. However, the nonlinearity associated with the PB equation introduces major difficulties when solving the equation numerically. This work explores the viability of various operator-splitting methods for solving a nonlinear PB equation in a pseudo-transient continuation approach. Within this framework, analytical integration of the nonlinear term in the PB equation was employed to suppress the nonlinear instability. To verify our schemes, a simple spherical-case analytical solution to the PB equation was employed. In our numerical benchmarks using this case, the steady state solutions of these operator-splitting schemes using a range of different initial values all converge to the time invariant analytical solution, suggesting a high degree of stability, particularly over existing explicit Euler schemes whose stability is highly dependent on initial values. When applied to actual biomolecules, the schemes maintained stability for even very large time increments. One particular multiplicative operator splitting scheme displayed higher accuracy than the other schemes. To further refine this method, Richardson extrapolation was applied, producing a highly stable, efficient, and relatively accurate method for biomolecular simulation in the PB framework.

34. WURM, A., YAZDI, S. AGUILAR, C., POLANCO, G., LEUNG, M-Y., ALMEIDA, I.C.Using Bioinformatics to Determine which Proteolytic Enzymes cut GPI-Anchored Proteins into Peptides of Ideal Length for Mass Spectrometry Analysis. Border Biomedical Research Center, Dept. of Biological Sciences; Bioinformatics Program, Dept. of Mathematical Sciences; and Computational Science Program, The University of Texas at El Paso, TX and the National Institute for Mathematical and

Biological Synthesis, University of Tennessee, Knoxville, TN.
The focus of this project is to determine which enzymes cut proteins into peptide sequences of ideal lengths for mass spectrometry (MS) analysis in order to better identify biomarkers for cancer detection. Glycosylphosphatidylinositol (GPI) is a universal posttranslational modification of proteins. GPI-anchored proteins (GPI-APs) can possibly be used to identify biomarkers for prostate cancer, a leading cause of cancer deaths in men. Studies have shown that GPI-transamidase (TA), the enzyme that attaches the GPI anchor to the protein, is overexpressed in prostate cancer tissue. To prepare GPI-APs for MS, three enzymes –Asp-N endopeptidase, Lys-C lysyl endopeptidase, and trypsin– were chosen to virtually cleave the GPI-APs. Each enzyme follows a specific set of rules on where to cut a protein. We have written a series of Perl scripts that use the rules of each enzyme to virtually cut protein sequences into theoretical peptides to identify which enzyme, or combination thereof, will provide the greatest number of ideal length peptides. The ideal peptide length for detection by MS falls between six and twenty amino acids. We are further exploring the effect that the small probability to miss a cut at each possible site has on the choice of enzymes.

ORAL PRESENTATION ABSTRACTS (Alphabetical)

ASARO, L., MYERS, J., VERA RECIO, C., WIRKUS-CAMACHO, A., MANNING, M., ZHENG, Y. and B. SONG. Asymmetric Intraguild Predation Between Protoperidinium and Heterocapsa in the Presence of a Mutual Predator. Mathematical and Theoretical Biology Institute, Arizona State University, Tempe, AZ.
The azaspiracid toxin contaminated the harvest of the mussel, *Mytilus edulis*, off the coast of Ireland in 1995. Investigation showed that the genus *Protoperidinium*, previously thought to be harmless, was to blame for a new condition brought about by the azaspiracid toxin. To address this concern, we use nonlinear ordinary differential equations to study the dynamics of two dinoflagellate species, as well as their common predator. An asymmetric intraguild predation model with a mutual predator is introduced, in which the toxin producing Protoperidinium preys on the non-toxic Heterocapsa, while both ingest the nutrients available in the system and are preyed upon by a higher predator. The equilibria were found and global and local stability was determined. We then found the mode of coexistence of the system in an equilibrium. After the initial analysis, we considered interventions, such as modifying nutrient flow, to reduce the levels of the azaspiracid toxin and observe their effect on the persistence of the system.

BALES, K. and FRAZIER, W.T. Spatio-Temporal Model for Burglary Reports in Tennessee. Department of Mathematics and Statistics, East Tennessee State University, Johnson City, TN.
We consider the dispersal of crime waves in a similar manner as to how epidemics spread in time and space. Longitudinal datasets, for household burglaries, corresponding to ninety-five counties of Tennessee are employed here. Geographical distance among counties is incorporated into a force of infection that depends on time and space. These prevalence-like datasets are fitted to an epidemiological model, formulated by a system of nonlinear ordinary different equations, by means of an ordinary least squares procedure. We discuss the effects of underreporting.

BECKMANN, C., BLOOM, J., LAMBERT, J., WARD, R., ILANY, A. and J. JIANG. Social Structure and rank predict fitness in spotted hyenas. National Institute for Mathematical and Biological Synthesis, Knoxville, TN; University of Vermont, Burlington, VT; Eastern Connecticut State University, Willimantec, CT; University of Tennessee, Knoxville, TN; Rhodes College, Memphis, TN..
Social networks are effective tools for analyzing relationships within populations. Higher connectivity between actors in the network can lead to individual benefits, such as information exchange, higher social rank, and access to resources. Spotted hyenas (Crocuta crocuta) live in large clans and maintain a complex social structure, making them an ideal study population when analyzing social networks. They have well-defined social ranks determined by maternal kinship. Cubs inherit social rank from their mothers, resulting in subgroups

of female descendants with the same social rank, called matrilines. We examined the Talek clan in Kenya's Maasai Mara National Reserve using observational data collected over a 22 year study. Our study focuses on adult female hyenas because of their dominant role in the social hierarchy. Modeling the hyena population as a social network allows us to show relationships between the connectivity, social rank, and reproductive fitness of matrilines. Previous studies indicate that social rank influences fitness, but chance also plays a significant role in the success of low-ranking matrilines. Our results indicate that a model including social interactions between matrilines and within matrilines predict fitness more accurately than a model involving rank alone. Future studies might test such a model on similarly structured species.

BENDER, N., MASON, C., SHAHI, S., KERSHENBAUM A., and D. BUEHLER. Automatic detection of rare bird species. National Institute for Mathematical and Biological Synthesis, Knoxville, TN, Marist College, Poughkeepsie, NY, Harvey Mudd College, Claremont, CA, Southeastern Louisiana University, Hammond, LA, University of Tennessee, Knoxville, TN.
Wildlife Conservations are constantly searching for new ways to aid in the development of management tactics for endangered species. Many species of the animal kingdom make use of their vocalization abilities to communicate with others. Researchers have begun developing ways to monitor population dynamics of endangered species by taking advantage of this natural sound source. The prairie warbler, native to the Eastern United States, has been placed on the Audubon Conservation WatchList as a result of a decline in their natural habitats due to anthropogenic causes. The goal of this project was to create a working algorithm for detecting prairie warblers within unattended sound files. This process was broken up into four separate components: 1) collection of raw data from multiple methods, 2) preprocessing of the data for input into a neural network, 3) training of the chosen neural network using large data sets, and 4) testing the performance of the algorithm on two realistic data sets obtained both by ground-based and balloon recordings. The tests on the first data set led to a 91.7% detection rate of prairie warbler calls, with only 9 false positive classifications. There was a 100% detection rate of prairie warbler calls for the second data set, with 15 false positives.

BOODOO, Z. and P. GUERRON. Applications of Graph Connectivity Indices in DNA Data Analysis. Montclair State University, Montclair, NJ.
Using graph index techniques to analyze DNA data has become a new method in recent years. Our research applies the Randić Connectivity Index, together with various generalized forms of it, to analyze DNA sequence data of Chagas disease obtained from biology research. It aims to better understand the evolutionary relationships of the insect vectors. We apply the graph index method on converted DNA line graphs, perform normalization and principle component analysis on them, and build phylogenetic trees from the data in order to answer scientific questions about the disease. In this presentation we will report the results from this on-going research. This research is funded by NSA (grant H98230-13-1-0270) and NSF (grant DMS-1156582) through MAA NREUP.

CALDWELL, W. K., FREEDMAN, B., THOMAS, M. M., and L. SETTLES. Substance Abuse via Legally Prescribed Drugs: The Case of Vicodin in the United States. University of Tennessee, Knoxville, TN, Bucknell University, Lewisburg, PA, and Kennesaw State University, Kennesaw, GA.
Vicodin is the most commonly prescribed pain reliever in the United States. Research indicates that there are two million people who are currently abusing Vicodin, and the majority of those who abuse Vicodin were initially exposed to it via prescription. Our goal is to determine the most effective strategies for reducing the overall population of Vicodin abusers. More specifically, we focus on whether prevention methods aimed at educating doctors and patients on the potential for drug abuse or treatment methods implemented after a person abuses Vicodin will have a greater overall impact. We consider one linear and two non-linear compartmental models in which medical users of Vicodin can transition into the abuser compartment or leave the population by no longer taking the drug. Once Vicodin abusers, people can transition into a treatment compartment, with the possibility of leaving the population through successful completion of treatment or of relapsing and re-entering the abusive compartment. The linear model assumes no social interaction, while both non-linear models

consider interaction. One considers interaction with abusers affecting the relapse rate, while the other assumes both this and an additional interaction between the number of abusers and the number of new prescriptions. Sensitivity analyses are conducted varying the rates of success of these intervention methods measured by the parameters to determine which strategy has the greatest impact on controlling the population of Vicodin abusers. These results give insight into the most effective method of reducing the number of people who abuse Vicodin. From these models, we determine that manipulating parameters tied to prevention measures has a greater impact on reducing the population of abusers than manipulating parameters associated with treatment. We also note that increasing the rate at which abusers seek treatment affects the population of abusers more than the success rate of treatment itself.

CATTIVERA, M., HANEY, S., and A. SIEPIELSKI. A Perturbation Approach to Approximate Extinction Time in Ecological Systems Due to Harsh Conditions. University of San Diego, San Diego, CA.
Changes in the environment can have an effect on the stability of ecological communities. Further, harsh environmental conditions can prompt the extinction of vulnerable species. How can we determine how long it takes for a species to go extinct given harsh environmental conditions? Here, we use the classic Lotka-Voltera competition model to study this problem. The Lotka-Volterra model is an unsolvable ODE system; however, in the particular case of ecological equivalence (where competing species have equal competition coefficients and growth rates) it is only the sum of the species that is regulated and the system can be solved exactly when no environmental fluctuations are present. Under the assumption that the environment has a small effect on the dynamics of the species, we use a perturbation method to approximate analytical solutions to extinction time given harsh or favorable environmental conditions.

CHISM, J. Mathematical Modeling of Action Potential in Cell Processes. Tennessee State University, Nashville, TN.
The purpose of this project is to analyze and understand three different models for action potential cell processes in computational cell biology. The three models were: Hodgkin-Huxley, FitzHugh-Nagumo, and Morris-Lecar. Using differential equations, linear algebra, and computer assisted simulations in the computer program MatLab, we were able to approximate numerical solutions and do phase portrait analysis and bifurcation analysis for each of the three models. We also came up with a modified form of the FitzHugh-Nagumo model using a Sine Function.

CRUZ, Y. and J. HOUSER. Sensitivity Analysis of Hepatitis C Virus Dynamics. Department of Mathematics and Statistics, East Tennessee State University, Johnson City, TN.
Basic deterministic models are used to describe the interactions between Hepatitis C virus, immune responses (antibodies and CTL's), and target cells. We employ an application called "plot digitizer" to digitize scanned graphs of longitudinal data. In this way we generate several datasets that are employed in model calibration. We compute numerical solutions of relative sensitivity equations to determine which model parameters are most influential and in what time intervals they provide most information. In light of parameter sensitivity information we outline how to formulate an optimal control problem.

DEMUSE, R. and S. HANEY. A Modified Goodwin Model of Biological Oscillators. University of San Diego, San Diego, CA.
Biological oscillators control many things including sleep cycles, neural activity, and the heartbeat. Here, we create a model of two coupled biological oscillators whose coupling strength depends on an environmental variable. We use this model to analyze dynamic switching between different oscillatory modes and determine what biological impacts this switching may have. We examine two specific scenarios; namely, the phase resetting in the circadian rhythm that occurs during periods of jet lag, and in general, inducible switching between synchronous and asynchronous behavior in a system of two genetic oscillators being influenced by an

environmental force. By determining the properties of this dynamic switching we hope to elucidate mechanisms of complex biological behavior.

DORADO, C.A. and Z. HELBERT. A Demographic Population Dynamics Approach to Student Enrollment. Department of Mathematics and Statistics, East Tennessee State University, Johnson City, TN.
Mathematical models with demographic effects, such as emigration, immigration, births, deaths, are explored. In particular, Leslie models with discrete group or stage structure are implemented. The relation between dominant eigenvalue elasticity and orbits (time solutions) is addressed by numerical means. Demographic datasets, obtained from the US Census Bureau and the US Department of Education, are incorporated with some of the models. Particular consideration is given to modeling student enrollments.

EKEY, A. Protein-Protein Interaction Detection Using Mixed Models. Howard University, Washington, DC.
Membrane protein-protein interactions (PPI) play an important role in biological processes; however, knowledge about membrane proteins is limited. In order to study membrane protein interactions, the mating-based split-ubiquitin system (mbSUS), which utilizes yeast as a heterologous system, is used. The resultant fluorescence is an indicator of PPIs, so the fluorescence scores are a focal point of this study. The observed scores may be affected by various fixed and random effects such as overall mean fluorescence, test versus positive control groups, plate effect, and PPI effect. We propose a statistical model of these effects, a mixed model, and apply it to a simulated data set. From this, we develop a methodology for analyzing the PPI data and determining significant PPIs. The results of the simulation study suggest that the mixed model may be a good fit for the real data.

GEORGE, T. GOWINS, A. and J. WEISSMAN. A Dynamical Model Examining the Effects of NFkB and HIF1 Pathways in Aspergillus fumigatus Infected Airway Epithelial Cells. Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA.
The ubiquitous fungus, Aspergillus fumigatus, is responsible for an increasing number of deaths each year from airway complications and diseases. In immunocompromised persons, A. fumigatus acts as an opportunistic pathogen, causing potentially fatal infections in the respiratory tract with symptoms including necrosis of the endothelial tissue and extensive inflammation. Evidence is growing indicating that bronchial epithelial cells not only provide a physical barrier of defense to pathogens such as A. fumigatus, but also actively participate in the immune response through a variety of pathways. We present a discrete mathematical model in the form of a polynomial dynamical system representing a snapshot of the transcriptional response of the host to fungal infection, based on RNA-seq data and published literature. This network links A. fumigatus infection to iron import in epithelial cells via a range of fungal recognition and immune response pathways. Iron is an essential nutrient for both humans and fungi, and by examining iron regulation in epithelial cells under stress due to fungal interaction, it is possible to better understand the dynamics of the host and thus identify future targets for research into treatments for invasive pulmonary aspergillosis and other Aspergillus-related diseases.

HALE, B., HOANG, K., SCHABER, K., RICE, H., LENHART, S.L., EDA, S. and M. KENNEDY. Modeling feline infectious peritonitis in a cattery. National Institute for Mathematical and Biological Synthesis, Knoxville, TN; University of Tennessee, Knoxville, TN; Emory University, Atlanta, GA; University of Dayton, Dayton, OH.
Feline Coronavirus (FCoV) is an RNA virus that infects cats and appears in two forms: Feline Enteric Coronavirus (FECV) and Feline Infectious Peritonitis Virus (FIPV). FECV, the more common form, is widely spread throughout feline populations and infects feline intestines but is non-fatal. FIPV, a mutated form of FECV, leaves the intestines by infecting neighboring macrophages and spreads throughout the body. Feline Infectious Peritonitis (FIP) is a fatal immune-mediated disease resulting from FIPV infection, and no cure has yet been found. With the long term goal of controlling the spread of this disease, we present a mathematical

model for the epidemiology of FIP in cattery. Our age-structured, differential equations model focuses on tracking the development of FIP from FECV in felines in catteries. The condition for the existence of a disease free equilibrium is found, and our model without disease is approximately at equilibrium. With a basic reproduction number greater than one, FCoV is expected to spread throughout the cattery population. Latin Hypercube Sampling and Partial Rank Correlation Coefficient (LHS/PRCC) sensitivity analysis shows key parameters that have a strong effect on the FIP-affected population.

HART, B. and GREWAL, H. Estimating Body Fat Content in Ctenosaura similis using Body Condition Indices. Division of Mathematical Biology, Truman State University, Kirksville, MO.
Fitness of organisms is important to biologists because individuals with greater fitness are more likely to survive and reproduce. Organisms with greater energy reserves are more likely to survive and reproduce, so body fat content can be used as a lethal instantaneous indicator of fitness. However, when conducting population studies or working with species of conservation concern a nonlethal indicator is needed. Body condition index (BCI) is a nonlethal estimate of relative health and body fat content based on the relationship between mass and length. However, BCIs have not been validated in lizards. We validated BCI as a predictor of energy reserves in Ctenosaura similis, the black spiny-tailed iguana. We used Ctenosaura similis because it is readily available, not of conservation concern, and closely related to species of conservation concern. We calculated BCIs based on the relationship of mass to length. In allometric studies there is debate over the form of linear regression to use. We used ordinary least squares, major axis and reduced major axis regression. We determined the model that best fit our data as the best predictor of body fat. If valid, BCI can be applied to populations of related species that are of conservation concern.

HEIDENREICH, L., HARDWICK, D., AGUILAR, C., CUHEL, R., LAUKO, I., PINTER, G., Estimation of Growth Rates of *Dreissena bugensis* in Lake Michigan, University of Wisconsin Milwaukee, Milwaukee, WI
With the colonization of Lake Michigan by quagga mussels (*Dreissena bugensis)* in 2003, significant changes in the Lake's physical characteristics and biological community were observed shortly thereafter. Termed "ecosystem engineers", these benthic filter feeders have undergone seemingly exponential growth in the specific conditions of the lake. Despite their impact, the reproductive characteristics of quagga mussels in Lake Michigan have not been quantified.
Samples of the mussel population have been obtained from consistent locations over the past decade and lengths of the shells have been measured to create size frequency distributions. Although the sampling methods are imprecise and mussel density can vary over fine spatial scales, we propose that the distributions are accurate reflections of the local population structure and can be used to determine growth rates.
To validate our approach, we implemented an individual based stochastic growth model in MATLAB which simulated growing cohorts of quagga mussels. We then reconstructed our predefined growth curve using Bhattacharya's method in UN fisheries software FiSAT II.
These techniques were applied to actual data sets from historically sampled locations to estimate growth rates and gain insight on life cycle characteristics of quagga mussels based on time series of size distributions.

HENDERSON, M. The Dynamics for Frameworks for Two Boolean Models for Gene Regulatory Networks. Benedictine University, Lisle, IL.
We consider the synchronous and asynchronous updating Boolean frameworks for gene regulatory networks. We determine how the presence of one gene that is affected by two genes and two feedback circuits affect the dynamics of the state-transition graph of the networks. We are particularly interested in the effects of the logical gate and signs of the feedback circuits on the dynamics. We investigate how the characteristics of these networks relate to the dynamics in the state-transition graph for a network.

HORIGUCHI, A., BEWICK, S., YANG, V., CANTRELL, R. S., COSNER, C., FAGAN, W. F. No-Analog Communities in Space and Time. Department of Mathematics, University of Maryland, College Park, MD.
Climate change is shifting species ranges and species phenologies worldwide. However, the magnitudes of the induced changes appear to vary across species. While range and phenology shifts are weakening certain species interactions, they are strengthening others, ultimately leading to novel systems that have been termed 'no-analog' communities. We consider the consequences of no-analog communities from the perspective of a consumer-resource system. Specifically, we study a three-species community comprising a consumer, its native host plant and a substitute host plant that was not historically available, either because it emerged at a different time of the year or else because it occurred at a different location in space. Using a spatially and temporally explicit model, we predict the long-term consequences of shifts in the spatial and temporal overlap between the consumer and the two resource species. Our model suggests that, in certain cases, the appearance of the substitute plant will save the consumer from extinction. In other cases, however, the appearance of the substitute plant will have the opposite effect and will drive the consumer to extinction. Our model thus helps to determine whether and when novel species interactions are likely to help or harm existing consumer-resource systems.

KEUNG, J., NAPOLES, M., VELLA, M., LANZAS, C. and S. CHEN. Agent-Based Model to Investigate Seasonality in *Escherichia coli* O157 Transmission Between Pastoral Beef Cattle. National Institute for Mathematical and Biological Synthesis, Knoxville, TN; University of North Carolina, Chapel Hill, NC; Humboldt State University, Arcata, CA; University of Notre Dame, South Bend, IN; University of Tennessee, Knoxville, TN.
Cattle serve as asymptomatic reservoirs for Escherichia coli O157. Transport of contaminated fecal matter beyond the pasture and consumption of contaminated beef are common pathways of E. coli O157 to humans. Greater summer incidence of E. coli O157 infections in humans and cattle has been observed despite decreased pathogen survival in higher temperatures. The drivers of this seasonal phenomenon are disputed. The objective of this study was to 1) accurately depict behavior of grazing cattle; 2) quantify seasonal differences in pathogen prevalence on the pasture; and 3) form a hypothesis to explain these differences. An agent-based model was developed which incorporates time of day, temperature, cattle behavior, and E. coli O157 dynamics in the environment. We simulate a herd of 25 cattle grazing during April and July for the years of 2003 to 2012. We establish a significant difference in mean total infections in April versus July of 1.213 cows (95% CI 1.102-1.323). These values correspond to 8.56% prevalence in April and 13.4% prevalence in July. We hypothesize that the reason for this prevalence trend is temperature-dependent cattle behavior. Results of this study can inform policymakers to minimize E. coli O157 transmission at the farm level.

KOPSICK, J. The Exploration of 3D Printed Environments for *Caenorhabditis elegans*. James Madison University, Harrisonburg, VA.
Using the 3D printers in the JMU Maker Lab, we have developed a protocol for printing 3D environments for the study of C. elegans swimming in different geometries and fluids of different viscosities. C. elegans offers an unprecedented middle ground between the macro and microscopic. This project involves experimental and theoretical components as well as techniques in image segmentation and processing. From these techniques, we aim to quantify how significant the role of environment is to the swimming gait of nematodes. If we can quantify a significant difference between an isolated droplet and a droplet within our environment, we will begin to model the worm's fluid mechanics.

KRAMER, S. and S. BANSAL. Analyzing the Impact of Individual- and Network-Level Behavioral Factors on HIV Spread among Women in Washington, DC. Georgetown University, Washington, DC.
HIV prevalence rates in Washington, DC, are among the highest in the nation, and rival rates in some parts of Sub-Saharan Africa. Among heterosexual individuals, women are infected at rates almost three times higher than those among men. Although several measures can be taken by the individual to prevent infection, prior

research has repeatedly shown that individual risk factors alone cannot account for differences in HIV prevalence between groups, and that network factors, such as assortativity and concurrency, must also play a role. Using data from the Women's Interagency HIV Study, an ongoing cohort study started in 1993, we will use statistical analyses to quantify heterogeneity in risk and treatment behaviors, both among individuals over time and among the population as a whole. Based on our calculations, we will develop mathematical models in order to observe the effects of altering behavior at the population level. We hypothesize that populations with realistic levels of behavioral heterogeneity will experience larger and more concentrated epidemics than populations homogenous for behavioral factors, and that increasing levels of concurrency and assortativity will intensify this effect. Based on our results, public health interventions on both the individual- and population-levels will be suggested.

LEVIEN, E. Effects of Network Topology on Pattern Formation in Systems of Coupled Phase Oscillators. Wheaton College, Wheaton, IL.
Certain biological systems can be modeled as spatially discrete networks of temporally continuous dynamical systems. When these systems are exhibiting persistent oscillatory behavior it is possible to gain qualitative insight into their dynamics by studying a simpler system of coupled phase oscillators. A network of oscillators is in a phase locked state when each oscillator's phase has the same constant velocity. Of particular interest are the asynchronous phase locked states, or patterns. Previous studies have been devoted to understanding the stability and basin of attraction of synchrony, as well as patterns in highly symmetric networks. We study the more general problem of determining a relationship between the topology of a network, its tendency to obtain patterns, and the structure of typical patterns. An r-regular networks is a network for which every node has r neighbors. By solving the phase oscillator system numerically on random r-regular networks a relationship between network connectivity and the basins of attraction for patterns can be observed. It is also observed that typical patterns have an underlying rotating wave structure given by restrictions on the number of times the phases of neighboring oscillators wind around the unit circle relative to each other.

LIU, W. Modeling Calcium Dynamics and Muscle Mechanism. Worcester Polytechnic Institute, Worcester, MA.
Currently, most models on muscle contraction do not account for the effect of calcium concentration on a microscopic level, which could significantly affect the cross-bridge attachment and thus the force. We investigate the role of calcium dynamics on muscle contraction by proposing a simplified two-compartment calcium movement model for skeletal muscle of frog. To capture the muscle contraction mechanism driven by calcium dynamics, we coupled the system of ODEs for the Distribution Moment Model to the calcium concentration and Hodgkin-Huxley equation. Additionally, we accounted for the effect of calcium inactivation mechanism, which enabled us to produce a more authentic cytosolic calcium concentration. We modified the velocity of muscle contraction to be a variant using a damped spring mass system, as opposed to the constant velocity used in previous models. With this coupled model, we are able to investigate the role of accounting for a time dependent calcium concentration on force generation of frog. Simulation results will be presented to show how the proposed model is an accurate and efficient model that captures the muscle contraction mechanism and calcium-force relationship observed in experiments.

MADSEN, T., WALLACE, D., and N. ZUPAN. Seasonal Fluctuation in Tsetse Fly Populations and Human African Trypanosomiasis: a Mathematical Model. Department of Mathematics, Dartmouth College, Hanover, NH.
Human African trypanosomiasis, commonly known as sleeping sickness, is a vector- borne disease endemic to Sub-Saharan Africa. An estimated 55 million people are at risk, and the World Health Organization classifies it as one of the world's neglected tropical diseases. We develop a model of the dynamics of one species of vector, Glossina tachinoides, which incorporates the impact of seasonal temperature fluctuation on the life cycle of the disease vector. We examine the effect of three vector control strategies and develop an interactive tool for local governments to estimate the cost-effectiveness of their implementation.

MANIFOLD, B., PARRISH, T., PAULI, S., and M. KALCOUNIS-REUPPELL. Automated Tracking of Small Objects in Video Recordings. University of North Carolina Greensboro, NC.

The automated analysis of videos has many applications, such as video surveillance of traffic or people. It can also be used to process video recordings of animals in the wild. One of the fundamental methods of video analysis is the the tracking of moving objects. Automated video tracking methods involve the processes of isolating foreground information, identifying individual foreground components, and tracking these components over time. We will investigate each process from an algorithmic perspective, and cover both simple and advanced foreground isolation methods, object identification by connected component contour tracing, and naive object tracking. As a specific example, we discuss the application of these methods to infrared video recordings of free living mice, which we used to extract and analyze behavioral information from remotely recorded video. In this specific application we had to overcome some challenges: 1) The video was recorded with an infrared camera which yields greyscale output with no absolute temperature calibration; 2) The camera was suspended 10 m over the ground which makes mice very small objects. From the tracking data we extracted the average speed and the total distance traveled as measures of mice activity and found that the average speed is predicted by moonlight and wind speed.

NAFEES,S. Modeling Positions coupled to F508, site of Chief CF Causing Mutation. TTU/Howard Hughes Medical Institute, Center for Integration of Science Education & Research, Texas Tech University, Lubbock, TX.

Cystic Fibrosis is a genetic disease that arises due to misfolding of the protein CF Transmembrane Conductance Regulator, CFTR, and is predominantly caused by deletion of a single amino acid, Phe508, along with many other mutations. Although our understanding of Cystic Fibrosis has increased dramatically over the last few decades, currently there are no known mechanisms that explain how common mutations act and interact to inhibit CFTR protein folding. It is known that multiple mutations join to have a coupling effect on the CFTR protein folding machinery, impacting both its processing and folding. Proper and deep analyses of the mutation coupling data could illuminate the way the various mutations act independently or dependently to produce disease. This information could provide insight into CFTR protein folding mechanics and enable us to pharmacologically target the protein folding process to ensure better treatment for CF patients. Modeling this coupling effect to uncover its impact on the whole system is a profound mechanistic problem. Studying interactions between different mutations requires fitting nonlinear functions to the data. A typical way to do this would be to use multivariate polynomial regression. However, in standard polynomial regression, the coefficients of each term are a function of the degree of the polynomial that we choose to fit. This is because the different terms (first order, second order, etc.) are not independent of one another. Therefore, the coefficients do not have independent biological meaning, and it is impossible to use polynomial curve fitting and obtain a function that precisely reveals the properties of the ambiguous data set. We thus must identify functions that are independent of each other and can be analyzed separately to give meaning to the coefficients. This is the purpose of Orthogonal Polynomials and, for multivariate data, the use of dual basis. The observed distribution of mutations defines a covariant basis and a contravariant basis. Projecting different phenotypic responses, such as protein folding and processing, into these and taking the covariance would yield their interrelation. With regards to CF, our goal is to build functions that capture the intrinsic properties of the chief mutations of CFTR so that we can assess each mutation's coupling interaction with other mutation(s). We can define a basis per mutation and their covariance will indicate their interaction. This will provide insight into the mechanism of the mutation-caused misfolding problem. In general, the orthogonal polynomial and dual spaces approach conserves intrinsic biological properties of any phenomenon being tested while simultaneously capturing its quantitative properties. This approach also allows one to work with nearly any kind of data (univariate, multivariate, continuous, discrete, etc.). This means that the models can be expanded to include all types of causal factors, both genetic and environmental. We aim to illuminate the interactions between not only different variables in genetic diseases, but to a wide variety of biological phenomena, including but not limited to, interactions of different cancer drugs and parent/offspring phenotype relationships.

PARK, J. Mutation of the MDS-1 and EVI-1 Complex Locus Causes Kyphosis by Affecting Embryo Development. University of Rochester, NY.
The MECOM locus is composed of two genes: EVI-1 and MDS-1. EVI-1 was first discovered as a proto-oncogene, where its overexpression was connected to myeloid tumors. In embryogenesis, we have a limited knowledge of the role EVI-1 and MDS-1 plays due to the lethality it causes when underexpressed. When a homozygous deletion occurs in the MECOM locus, it causes kyphosis in adult mice. However, it has been previously found that adult mice do not express either gene in the spine. This leads to the hypothesis that the locus is involved in the development of the vertebrae, but its phenotype is not seen until the mouse is a complete adult. To test this hypothesis, the gene expressions of EVI-1 and MDS-1 were traced separately at different stages of the embryo. Results showed that both genes start expressing around 8.5 dpc in similar patterns. This makes sense because the genes are part of the same locus, but is also a surprising find as the two genes are 0.5 Mb apart. Furthermore, the expression of both genes was observed in the primordial cartilage of the vertebrae which supports our hypothesis that the MECOM locus causing kyphosis in adult mice through embryonic development

PENNINGTON, H. and N. KRISHNA. A Mathematical Model for the Interaction of the Proteins MMP-1, TIMP-1, and ECM in a Wound. Western Kentucky University, Bowling Green, KY.
In this talk, we will discuss 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 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. MATLAB’s GlobalSearch and fmincon routines were used to estimate parameter values by minimizing the least-squares residual between collected data and model output. A steady-state analysis identified which end-states the proteins tended to as time approached infinity. Sensitivity analyses numerically measured to what degree the model was affected by slight changes in one or several parameter values. A classical sensitivity analysis followed by an SVD-QR subset selection and a Latin-Hypercube Method sensitivity analysis identified insensitive parameters, or parameters whose changes had negligible effects on the model. The developed model has the potential for application in clinical studies, such as identifying treatment regimens for an individual patient not included in the modeling process.

PHILLIPS, J.S. and J.P. GIBERT. Increasing Complexity Decreases the Effects of Energy Flux on Food Web Stability. School of Biological Sciences, University of Nebraska-Lincoln, NE.
Characterizing the factors that determine food web stability is a major goal in ecology. Previous theory suggests that greater energy flux should destabilize food webs by increasing pair-wise interactions strengths. However, the link between energy flux and interaction strengths is not fully understood, limiting our understanding of how energy flux affects stability. In this study, we investigated the effect of energy flux on the stability of a set of increasingly complex food web modules. We used generalized dynamical models that allowed us to draw explicit connections between energy flux, interaction strengths, and stability for a wide range of specific models. We ran 5000 simulations for each module and calculated how the fraction of stable cases changed with energy flux to each species. Our results show that increased energy flux to primary producers has a positive effect on stability, while increased energy flux to consumers generallyhas a negative effect on stability. Most importantly, the overall effect of energy flux declines with increasing complexity, suggesting that it has little or no role to play in determining the stability of large, complex food webs.

QUIJANO, A. Expansion of a Stochastic Model for Anelosimus Studiosus Movement during Prey Capture. Department of Mathematics and Statistics, East Tennessee State University, Johnson City, TN.
In this talk, we discuss how we update an earlier version of a model, which simulated the movement of Anelosimus Studiosus during prey capture. The previous model was made to successfully match the data for movement of the spider taken from three video feedings. However, when the model was tested against a new set

of data for the same spider species, the model did not match well. During the interaction between the spider and prey, the spider tends to have an error in direction, together with varying velocities and a varying number of pauses (with different durations). We suspect that the error in direction might have been the cause of the discrepancy between the data and simulations of the model. Since the previous model did not fully incorporate the velocities and pauses, we analyzed the new data more closely and develop an expanded model merging the velocities and pauses to simulate the movement more precisely. It is observed that this sub-social species spaces out on their web during certain times of the day. The improved model can be used to answer the question of whether the sub-social spider species spaces out optimally to cooperate during prey capture.

ROSS, C., DEFELICE, D. and O. RUEPPELL. An Investigation of Genome Features and Their Effect on Meiotic Recombination Rates in *Apis mellifera*. University of North Carolina Greensboro, NC.
Recombination is important for ensuring chromosomes segregate properly during meiosis, but it also increases genetic variance. The honey bee, Apis mellifera, has been observed to have higher recombination rates than many other species, and the higher recombination rates are found genome-wide in A. mellifera. Proper chromosome segregation does not seem to explain this excess recombination, so recombination rates in the honey bee must be influenced by other factors. In our study, we have collected information on a variety of genomic features in 100KB windows throughout the honey bee genome to investigate their correlation with recombination rates. We used eight genetic maps along with a physical map to determine the average recombination rates for each 100KB window. We collected data about occurrences of various sequence motifs, di-, tri-, and quad-nucleotide sequences, low complexity sequences, and microsatellites comprised of dinucleotide repeats from the latest assembly (Amel_4.5) of the A. mellifera genome sequence. We also used available gene data to determine the number and average sizes of genes, introns, and exons and the average distance between genes for each window. Correlations between these genome features and the average recombination rate and its variance will be used to test alternative hypotheses that may explain the evolution of recombination in general.

STOLZ, R. Mapping Recombination Pathways in Circular DNA. San Francisco State University, San Francisco, CA.
Polygons in the simple cubic lattice have been demonstrated to be useful for modeling enzyme driven topological changes on circular DNA. Currently, our research in this area is motivated by a desire to understand the process of DNA unlinking by the XerC/D proteins. In Escherichia coli the process of DNA unlinking has been attributed to topo IV, a type II topoisomerase. In the last decade the Sherratt lab has shown that in the absence of topoIV, the site-specific recombinases XerC/D allow E. coli cells to simplify the topologically complicated DNA links that come about naturally during DNA replication. We aim to understand the unlinking pathways followed by the enzymes. We simulate this recombination process on knotted and linked conformations in the cubic lattice. By perturbing these conformations between recombination attempts using the BFACF algorithm and a Monte Carlo process, we are able to approximate and model XerC/D driven recombination. Our goal in performing these simulations is to determine the transition probabilities associated with each topological state change. By mapping these probabilities, we may also be able to establish a mathematical basis, rooted in knot theory, for why certain transition pathways are favored over others. In service of this goal, we have developed a Composite Markov Process (CMP), which will enable us to construct a knot conformation library to allow more efficient sampling of rare and otherwise difficult to sample conformations that more closely model circular DNA, such as unknots with a highly negative writhe. The conformation database will eventually be accessible via the internet and have additional applications in the wider scientific community.

SYKES, D., BROOM, M. and J. RYCHTAR. Kleptoparasitic Interactions and Internal States. University of North Carolina Greensboro, NC.
A kleptoparasitic interaction occurs when one individual (a kleptoparasite) attempts to take resources from another individual. Some animals exhibit different behavior in similar interactions, and we would like to

understand why they may have evolved to do so. Internal states, such as health, age, or hunger, can affect what behavioral strategies yield optimal gains. To study this effect, we have created a mathematical model that describes the outcomes of these interactions in terms of the value of contested resources, the cost of a fight (or a similar conflict), and the internal states of individuals involved. Changing the degree to which internal states affect an individual's appraisal of resources changes optimal behavior, as indicated by our model. When this degree is high, it can happen that individuals should forgo stealing from weaker individuals, and this does not happen when the degree is low. This degree can also be set so that the constant strategy of always stealing is optimal behavior; however, for most parameter settings, optimal behavior is not a constant strategy (i.e. a strategy of always making the same decision). Optimal behavior should, in most cases, be adaptive to changes in resource value, cost of conflict and internal health.

THOMPSON, A., KRAICHAK, E., Sittiporn Parnmen, Robert Lücking, Thorsten Lumbsch. Molecular Phylogeny of tropical lichenized fungi genus Phaeographis. Science and Education, The Field Museum of Natural History, Chicago, IL.

Lichens genus Phaeographis belong to the largest family of tropical lichens called Graphidaceae. A recent phylogenetic study reveals that the genus Phaeographis, as currently described, might be polyphyletic. However, this conclusion is based on limited sampling of taxa and loci. The current study attempts to generate more molecular data in order to better study phylogenetic relationships among Phaeographis species, as well as their position within the family. Two ribosomal RNA regions (mtSSU and nuLSU) and two protein-coding regions (RPB1 and RPB2) were amplified from DNA extracts and used for this phylogenetic study. A total of 159 sequences were generated, doubling the number of currently available sequences on GenBank for this genus. A preliminary analysis provides evidence for polyphyletic nature of the genus. Further studies on morphological and chemical characters will be needed for a revision of this genus.

TOJA, A., CARTER, A., GONZALEZ, J., OLAWOYIN, O., GROVER, J., KOJOUHAROV, H., and C. KRIBS-ZALETA. A Theoretical Model of Coinfection Dynamics: Modeling Competition Dynamics Between *Borrelia burgdorferi* and *Anaplasma phagocytophilum* within a Human Host. University of Texas at Arlington, TX.

Though many mathematical models have been used in the field of epidemiology, few models aim to predict the outcome of competitive coinfection dynamics within humans. This study used a theoretical model to analyze the competition between two infectious bacteria, such as Borrelia burgdorferi and Anaplasma phagocytophilum, which often coinfect human hosts. Interactions between coinfecting species in the human body are complex, since both microorganisms are competing for the same resource, which in this study is iron, and elicit different rates of innate immune responses from neutrophils and macrophages. The goal of this study was to identify whether resource limitation or immune responses are more efficient in clearing a coinfection. Literature values were used to parameterize the interactions for numerical simulations. Results showed that a 10% decrease in iron availability below baseline parameters would clear the coinfection, while an 8% increase in neutrophils would produce the same results. Through these simulations it was concluded that both, decreasing the iron availability and increasing the neutrophil concentration in this system, were equally efficient at clearing the coinfection. The results showed that these changes have the potential to be artificially induced in humans as an alternative treatment method for coinfections.

UTKUS, A. The impact of individual-level heterogeneities on infectious disease dynamics and control. Department of Biology, Georgetown University, Washington, DC.

Infectious disease is one of the leading causes of human death in the world and accounts for nearly half of non-predator livestock deaths. Contact networks models provide an individual-level description of epidemiologically-relevant patterns of infectious disease epidemics, and can elucidate infectious dynamics to answer key public health questions. The transmission of infectious agents within host populations is influenced by many different sources of heterogeneity ranging from behavioral heterogeniety to immunological and genetic heterogeneity. A consequence of such heterogeneity is the commonly observed aggregated distributions

of infection in which a few hosts are rapidly, frequently, or heavily infected, while the majority either evade infection or suffer infrequent or light infections. We consider three types of heterogeneity through the presence of superspreaders, supershedders and supergetters in host populations, and the implications of each of these sources of heterogeneity on disease dynamics. Our preliminary results show that the presence of super shedders results in a large epidemic sizes while the presence of "supergetters" results in a high probability of an epidemic occurring. The results of our study will have consequences for the success of intervention strategies in human and livestock populations in which these heterogeneities are present.

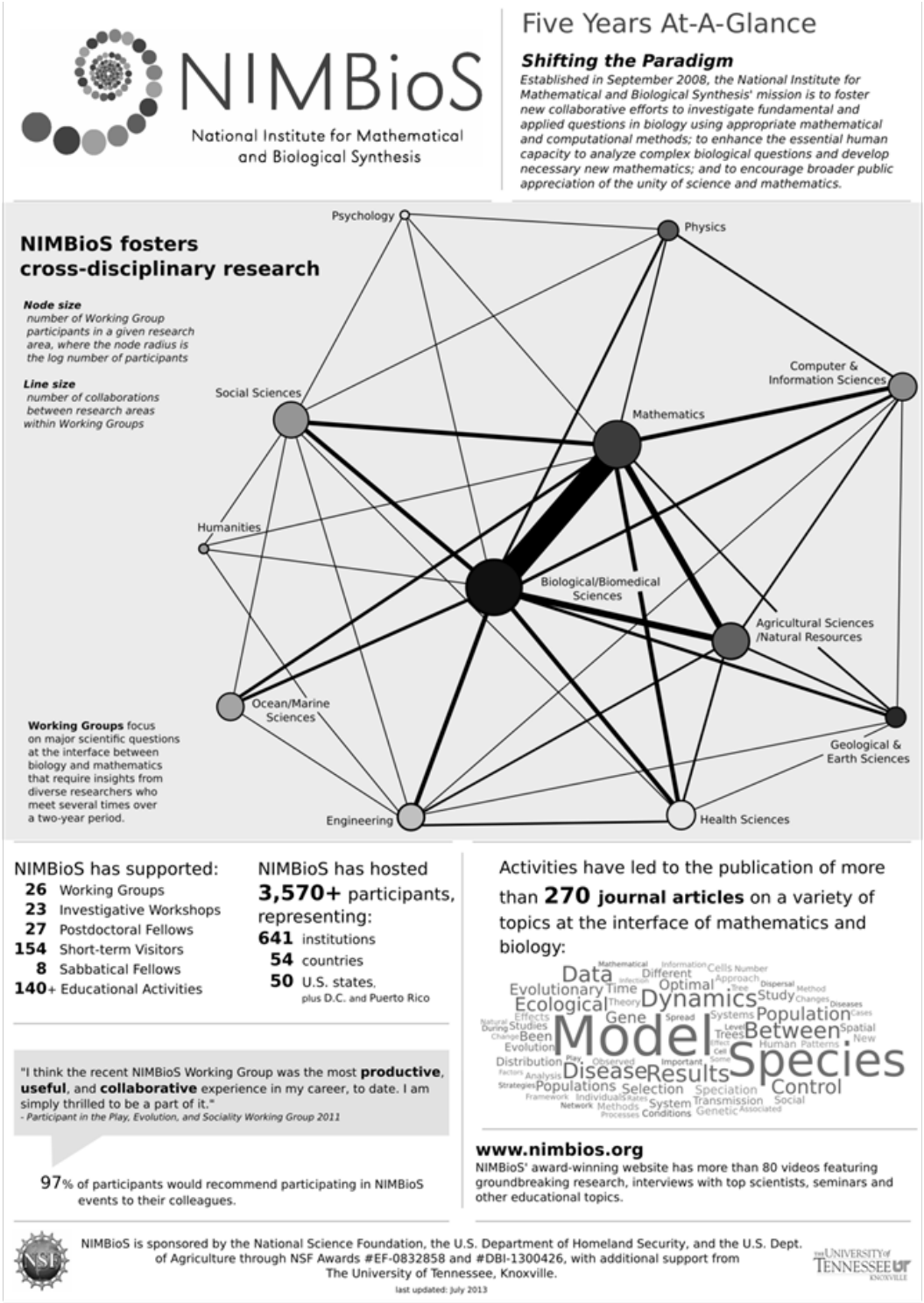
UTSEY, K., ESTES, S., KALOBWE, E., FINOTTI, H., and X. ZHAO. Mathematical Modeling of Fetal Electrocardiograms. Carroll College, Helena, MT, University of Tennessee, Knoxville, TN, LeMoyne-Owen College, Memphis, TN, National Institute for Mathematical and Biological Synthesis, Knoxville, TN.

Some of the most common and fatal birth defects are related to the heart. In adults, possible heart conditions are often identified through the use of an electrocardiogram (ECG). However, due to the presence of other signals and noise in the recording, fetal electrocardiography has not yet proven effective in diagnosing these defects. This paper develops a mathematical model of three-dimensional heart vector trajectories, which we use to generate synthetic maternal and fetal ECG signals. This dipole vector model simulates the electrical activity of the heart as a single time-varying vector originating at the center of the body. We use a system of ordinary differential equations and two sets of parameters to simulate maternal and fetal cardiac activity. Various physiological factors, including heart rate variability and baseline wander, are also simulated. These cardiac dipole vectors are then projected onto three dimensional unit vectors to simulate fetal electrocardiogram (fECG) data collection. White noise and power line noise are added to the projections. Using this model, we have built a database of realistic, synthetic fECG signals using different parameter values and noise levels. This database can be used in effectiveness testing of fetal signal extraction algorithms.

WEEKS, A. and R. PEOT. Assessing the Parasite Manipulation Hypothesis in an Invasive Host (*Bithynia tentaculata*).

Bithynia tentaculata is an invasive freshwater snail that was first detected in the upper Mississippi River (UMR)- in 2002. The snail harbors trematode parasites, including Sphaeridiotremapseudoglobulus,- that have been associated with large-scale waterfowl die offs in the region. Mortality occurs after birds feed on snails infected with these parasites. Unfortunately, little is known about the factors facilitating transmission of these parasites between snails and waterfowl. We conducted complementary field and laboratory experiments to explore the idea that S. pseudoglobulus may be enhancing its own transmission to waterfowl by modifying the behaviors of B. tentaculata. Results from our field work show that Sphaeridiotrema infections interact with host gender to predict where snails are found on rocky substrates (top vs. bottom). A follow-up laboratory experiment was then performed to assess whether snails experimentally infected with S. pseudoglobulus responded differently to light/dark exposures. Results from this study showed no significant influence of either infection or gender on the time snails spent in the lit vs the dark portion of experimental arenas. Together these results suggest that infection may differentially influence the distributions of male and female snails; however, future work is required to more thoroughly understand the behavioral mechanisms underlying these patterns.

ZIEGLER, E., KERSWILL, S., BENNIE B., HARO, R., PEIRCE, J., and SANDLAND, G. Maximizing Reproduction in *Bithynia tentaculata* with a Parasite Infection. Departments of Mathematics and Biology, University of Wisconsin- La Crosse, La Crosse, WI.

Mathematical models can be utilized to understand complex biological systems including those involving hosts and their parasites. *Bithynia tentaculata* is an invasive aquatic snail that was recently discovered in the Upper Mississippi River (UMR). Along with disrupting the local benthos, *B. tentaculata* also harbors a number of flatworm parasites that cause thousands of waterfowl deaths when birds consume infected snails. To better understand how the parasite affects *B. tentaculata*, we developed an optimization problem that encompasses the energetic responses of snails to infection and, more specifically, maximizes host reproduction. To do this we

performed laboratory-based respiration experiments and incorporated the results into a system of differential equations representing rates of energy allocation to various host energy sinks, such as growth. Using a survival probability that includes recent energy investment into maintenance, we numerically solved the optimization problem. In this talk we will present our model and outline preliminary life-history solutions for varying parasite doses.