



2010

## **2010 Conference Abstracts: Annual Undergraduate Research Conference at the Interface of Biology and Mathematics**

National Institute for Mathematical and Biological Synthesis (NIMBioS)

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*Second Annual*

**Undergraduate Research Conference**

**at the Interface of**

**Biology and Mathematics**

*November 19-20, 2010*

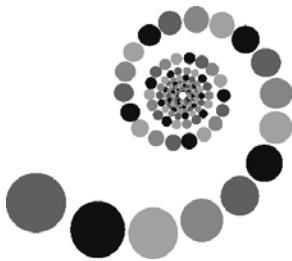
**University of Tennessee Conference Center**

**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 almost 60 oral and poster presentations. A keynote by Dr. Abdul-Aziz Yakubu will take place Friday afternoon and a panel discussion on career opportunities will be featured on Saturday morning. Poster abstracts start on page 4, oral presentation abstracts start on page 16.

## **NIMBioS**



So what is NIMBioS? Pronounced NIM-bus, the National Institute for Mathematical and Biological Synthesis is a center that brings together talented researchers in the fields of math and biology from all over the world. At NIMBioS, researchers work to cross the boundaries of their disciplines and address the many questions and challenges of 21<sup>st</sup> century biology. Currently in its third 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 and veterinary students program and workshops for math and biology faculty. For more information on NIMBioS and its research and educational opportunities please visit [www.nimbios.org](http://www.nimbios.org).

## **UNIVERSITY OF TENNESSEE & KNOXVILLE**

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



Knoxville is the oldest and third-largest city in Tennessee. The prominent Sunsphere west of the conference center is a remnant of the 1982 world's fair themed on energy, due to Knoxville's close connections to the Tennessee Valley Authority and Oak Ridge National Laboratory. Also nearby is a revitalized portion of downtown known as Market Square: a pedestrian mall with restaurants and shops.

## **INFORMATION FOR HANGING POSTERS**

The poster session will be immediately following dinner on Friday, from 7:15-8:45 pm. Please hang up your poster prior to that time. 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 4.

## **INFORMATION FOR ORAL PRESENTERS**

Refer to the schedule to find your presentation time and room number. You will have 15 minutes to speak followed by 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 Moran) to have your talk loaded onto the appropriate computer in advance.

## **SCHEDULE**

### **Friday, November 19: Auditorium Room 406**

1:30-1:40 Welcome: Louis Gross, Director of NIMBioS

1:40-2:40 Plenary Speaker: Abdul-Aziz Yakubu, Howard University Fish Population Dynamics and Constant or Periodic Proportion Harvesting Policies

2:55-3:10 Garrett Graham: *Goldbeter-Koshland switch as a stochastic sensor*

3:15-3:30 Tyler Massaro and Guang Yang: *Using a system of difference equations to examine the relative effectiveness of a test and cull management strategy with the new EVELISA testing versus commercial ELISA testing*

3:35-3:50 Snack break

3:55-4:20 Kelly Moran, Education and Outreach Coordinator NIMBioS

4:20-4:50 Jory Weintraub, Assistant Director Education and Outreach at NESCent: *Opportunities for Involvement and Support at the National Evolutionary Synthesis Center*

5:00-5:15 Reka Kelemen: *Effect of cymene on distribution of germination and growth of Beauveria bassiana*

5:20-5:35 Curtis Atkisson: *Inferences regarding population density in pre-Columbian Amazonia using phylogenetic modeling.*

5:40-6:00 Sekeenia Hayes and Harry Richards: Unique Graduate Program Opportunities: PEER and Scale-It

6:00-7:15: Buffet Dinner

7:15-8:45 Poster Session and Desserts

## **KEYNOTE**

**Dr. Abdul-Aziz Yakubu**  
**Professor and Chairman, Department of Mathematics**  
**Howard University**

### **Fish Population Dynamics and Constant or Periodic Proportion Harvesting Policies**

Overfishing, pollution and other environmental factors have greatly reduced commercially valuable stocks of fish. In a 2006 Science article, a group of ecologists and economists warned that the world may run out of seafood from natural stocks if overfishing continues at current rates. We will explore the interaction between harvest policies and recruitment dynamics. In case studies, we analyze periodic proportion policies (PPPs) and constant proportion policies (CPPs) as they might be applied to Gulf of Alaska Pacific halibut fishery and the Georges Bank Atlantic cod fishery based on harvest rates from 1975 to 2007. We will show that PPPs and CPPs at the recent harvest rates can be effective at preventing collapse in the halibut fishery but these same policies at the recent harvest rates may fail to prevent a collapse in the cod fishery. The likelihood of collapse in both fisheries increases with increased weather variability.

## **Saturday, November 20, Morning: Room 406**

8:00 Breakfast

8:40-8:55 Kelly Geyer, David Bulger and Jillian Trask: *Biodiversity in the Great Smoky Mountains National Park: Past and Present Measurements.*

9:00-9:15 John Feldmann and Mayra Yanez: *Analysis of gene expression in Bordetella avium using microarrays*

9:20-9:35 Sepideh Khavari: *Modeling the Regulation of Gene Expression in the Presence of Selenite in E. coli.*

9:40-9:55 Robert Parise: *Patterns of Chitin Synthase Gene Expression in the Thermally Dimorphic Fungal Pathogen Penicillium marneffeii.*

10:00-10:20 Break

10:30-noon Career Panel, Rene Salinas, Appalachian State University, Moderator:  
Virginia Dale, Group Leader, Oak Ridge National Laboratory Landscape Ecology & Regional Analysis Group  
Tim Elston, Professor, University of North Carolina and Director, Graduate Program in Bioinformatics and Computational Biology  
Louis Gross, Professor, University of Tennessee Ecology & Evolutionary Biology & Mathematics and Director of NIMBioS  
Abdul-Aziz Yakubu, Professor and Chairman, Department of Mathematics, Howard University

12:00-1:15 Lunch

## **Saturday Afternoon: Rooms 406 and 400A**

1:20-1:35

406: David Schuchart: *Measuring Behaviors of Peromyscus Mice Using a Blob Tracking Algorithm Analysis of Remote Thermal Video*

400A: Samantha Erwin and Aron Huckaba: *Using matrix analysis to model the spread of an invasive plant, Alternanthera philoxeroides. BioMaPS*

1:40-1:55

406: Lauren Jeffers, Elizabeth Moses, Drew Neavin and Kyle Strand: *Stage-Structured Disease Model*

400A: Ashley Hughes and Charlie Murphy: *Gene Regulatory Networks of Rainbow Trout Enlightened by Modularity*

2:00-2:15

406: Herman Pittman and Nneka Richards: *Stability analysis and Threshold phenomena in the SIR model with the inclusion of mortality.*

400A: Kyla Lutz: *Protein Structural Alignment*

2:20-2:35

406: Lisa Curll and Lindsay Blazsek: *Mathematical Modeling of Stochastic Riparian Ecosystems.*

400A: Audrey Bechette, Tom Stojisavljevic and Maxx Tessmer: *Dynamic modeling of aquatic viruses with an internal phosphorous quota*

2:40-3:00 Snacks

3:00-3:15

406: Audrey Gonzalez, Ahn Tuan Nguyen, and Sara Wilder: *A Modeling of the Glassy-winged Sharpshooter in Texas Vineyards.*

400A: Timothy Crisci, Kevin Chodnicki, James Tanner and Brendan Wray: *Analyzing the Movement of Infants at Risk for Autism Spectrum Disorders*

3:20-3:35

406: Boryana Koseva and Stephen Quinn: *Energy Allocation in Nerodia Sipedon*

400A: Sara Brnich and Julia Filiberti: *Mathematical and Computational Techniques for Microarray Data Analysis.*

3:40-3:55

406: John Collins and Ngoc Thai: *Ant foraging behavior in the presence of climate change*

400A: Bryan Conner and Michael Grant: *Using Cluster Analysis to Examine the Genetic Network in a Human Leukemia Cell Line.*

4:00-4:10 Closing Remarks

4:10 Adjourn

## **POSTER ABSTRACTS BY SEQUENCE**

### **1. HARE, A. and R. SCHUGART. Simulating Dermal-Epidermal Interactions in Wound Healing.**

**Department of Mathematics, University of Kentucky, Lexington, KY, and Department of Mathematics and Computer Science, Western Kentucky University, Bowling Green, KY.**

Dermal and epidermal interactions play a significant role in the wound-healing process. Mathematical models have yet to be formulated to study their interactions. The purpose of this work is to analyze a model created by Dr. Richard Schugart for the purpose of determining its value as a predictive tool for wound healing. The key components in the model are fibroblasts and extracellular matrix (ECM), which are found in the dermal layer, keratinocytes, which are cells found in the epidermal layer, and their interaction through the production of matrix metalloproteinases (MMPs) and tissue inhibitors of matrix metalloproteinases (TIMPs), which are produced by both fibroblasts and keratinocytes. A steady-state analysis was conducted, where a steady state is a point where the levels of the proteins and cells will not change over time. In our work, we found steady-state values that correspond to both healed and unhealed wounds.

### **2. HOWARD, B., and SCHUGART. R. Using a Mathematical Model to Analyze the Treatment of a Wound Infection with Oxygen Therapy. Department of Mathematics and Computer Science, Western Kentucky University, Bowling Green, KY.**

A mathematical model was developed focusing on using oxygen therapy to fight bacterial infection in chronic wounds. The model is a set of ordinary differential equations, which describes the relationship among neutrophils, bacteria, oxygen, inflammatory cytokines, and reactive oxygen species (ROS). A quasi-steady-state assumption was made for the inflammatory cytokines and ROS by setting the derivative equal to zero for all time. This reduces the model to a system of three equations - neutrophils, bacteria, and

oxygen. Two steady-state analyses were conducted - first on the neutrophil/bacteria subsystem, and then on the three-equation system – to evaluate what happens when time goes to infinity. Model parameters were estimated from both values found in the literature and the steady-state analyses. Model simulations were conducted using Mathematica for different oxygen concentrations in the wound. The results from the steady-state analyses and computer simulations will be presented.

**3. RINDFLEISCH, J. and W. KHANTUWAN. Dividing Embryonic Epithelia: Centroidal Voronoi Analysis of Multiple Divisions. Beloit College, Beloit, WI.**

How do embryos grow? First, both invertebrate and vertebrate organisms begin as a single fertilized cell. This cell divides into two cells, these in turn divide again into four cells, etc. through many iterations until a complete embryo is formed. As they divide and grow, cells assume different polygonal shapes. We have observed cells that have from 3 sides to 11 sides. We are trying to understand the causes of these shapes and to test models of such causes in a quantitative fashion. Does each daughter cell occupy half as much area as its parent? Is the area of a cell proportional to its number of sides? Are the membranes of the cells on the equidistant borders between adjacent nuclei? Are the observed tessellation patterns somehow minimizing surface tension on the embryo? Do cell shapes become more uniform over time?

The data that we primarily analyzed are the mitotic cell divisions of the common fruit fly embryo (which were collected by Thomas Gregor at Princeton University and are available from his video titled “Early mitotic divisions in a *Drosophila* embryo” [<http://www.youtube.com/watch?v=XSKh-GLQn4E>]). These data allowed a big breakthrough compared to previous studies [Ankit B. Patel, William T. Gibson, Matthew C. Gibson, Radhika Nagpal. (2009). Modeling and Inferring Cleavage Patterns in Proliferating Epithelia. Public Library of Science Computational Biology 5(6): e1000412.] because the biological data was collected over time instead as single images of data. In the video, the number of cells within the viewing area increases over time, thereby causing cells to become compacted. Using data from the first five mitotic divisions, we tested two hypotheses [Cleavage Plane Regulation Model and Lewis’s Law] in the literature and an additional one of our own [Gravitational Center of Mass Model] by using a new biological image analysis package (Ka-Me’) with built in functions for computational geometry and graph theory.

Hexagonal patterns were most common in our sample; they may be the most preferred shape that cells in a tissue can acquire under the stress of surface tension. But that does not explain the observed frequency distribution of diversity in the number of sides. Statistical data involving the Pitteway criterion, area vs. sides, area vs. perimeter, and spatial dispersion (random, aggregated, dispersive, uniform) will be used to support our conclusion that a centroidal Voronoi tessellation best fits our data. Features in the Ka-Me’ program such as the spatial indices of dispersion, Delaunay Triangulation, Voronoi Diagram, Gabriel graph, Relative nearest neighbor graph, Ulam tree, Convex Hull, and Circumcircle will be defined and shown how they correlate to the data. We conclude that nuclei move from random locations within the interior of a cell to the centers of mass of cells under surface tension and that this movement results in the observed Voronoi tessellation whereby the perimeters of cells are equidistant between two adjacent cell nuclei and accounts for the observed distribution of different sided-polygons.

**4. WRIGHT, J. and R. SCHUGART. The Mathematical Modeling of Inflammation in Diabetic Wounds Becomes More Accurate upon Considering the Latent Forms of TGF- $\beta$ . Department of Mathematics and Computer Science, Western Kentucky University, Bowling Green, KY.**

In patients with diabetes, a prolonged inflammatory phase can delay the repair response of a wound. In an attempt to describe this process, mathematical models can become very complex. The model on which we are basing our research was created by Waugh and Sherratt and involves three differential equations, where each equation models the rate of change in the population of a certain macrophage or growth factor. After analyzing this model and the steady states it creates, we modified the equation for transforming growth factor- $\beta$  (TGF- $\beta$ ) to include only the active forms, since the latent forms do not aid in attracting more monocytes—which can differentiate into inflammatory macrophages—to the wound. We found that the two

stable steady states created in the original model—one which mimics the biological response in a normal wound environment; the other which mimics that in a diabetic wound environment—were successfully recreated in our modified model, but the transition now occurred at a higher ratio of inflammatory macrophages to repair macrophages. This result confirms the hypothesis that more inflammatory macrophages must exist initially if less are created at the wound site over time. Thus, the ratio of inflammatory macrophages to repair macrophages in a diabetic wound must be higher than initially expected by Waugh and Sherratt, since proteins *in vivo* exist in latent and active forms. A ratio above the bifurcation point in our model is a more accurate proposition for creating the persistent inflammation stage that is characteristic of diabetic wounds.

**5. MARCUS, A. A Comparison of Growth into Poroviscous Versus Poroelastic Tissues. Department of Mathematics, North Carolina State University, Raleigh, NC.**

Growth into tissues is an important process that occurs in developmental biology. The ability to accurately model this process is imperative to knowing how organs such as lungs grow in the fetal stage. The growth rates of these tissues are dependent on the structural properties of the cells of the tissue and those of the surrounding medium. Many models currently only model these tissues as having poroviscous properties. However, modeling them as both poroviscous and poroelastic gives way to a more precise representation of the tissues that experimentalists see in the lab. These models allow us to have an accurate idea about how the growth of different types of living cells is affected. The existence of a capsule around the growing cells and how fast the cells are growing into this medium are important pieces of information to biologists and are part of the main results of this study.

**6. MIKE, J. and Z. KALIK. Modeling Arrhythmia Vulnerability: Right Ventricular Sex and Regional Differences in Calcium Current Levels. Departments of Biologic Sciences and Mathematics and Statistics at Youngstown State University, Youngstown, OH.**

Sex and apex-base differences in cardiac L-type calcium current ( $I_{Ca-L}$ ) levels were previously found to affect susceptibility to arrhythmogenic early afterdepolarizations (EADs), in adult rabbit left ventricular cardiac myocytes. We have now investigated the role of  $I_{Ca-L}$  in EAD formation in right ventricular myocytes using the patch clamp technique to ascertain apex-base distribution and properties of the L-type calcium current in adult male and female rabbits.  $I_{Ca-L}$  density measured at 0mV was 84.6% higher in female ( $7.2 \pm 0.83$  pA/pF,  $n=8$ ) than male base myocytes ( $3.9 \pm 0.38$ ,  $n=12$ ,  $p < 0.001$ ). Regionally, the female right ventricle demonstrated 56.5% higher  $I_{Ca-L}$  density at the base ( $7.2 \pm 0.83$  pA/pF,  $n=8$ ) than apex ( $4.56 \pm 0.45$  pA/pF,  $n=9$ ,  $p < 0.02$ ). No gender differences in  $I_{Ca-L}$  density were seen in male-female apex myocytes. In addition, we found no gender or regional differences in the voltage dependence of  $I_{Ca-L}$  activation and inactivation. Utilizing this data, we performed numerical simulations with a modified version of the Luo Rudy mathematical model of cardiac action potentials (APs). With 50% suppression of the rapidly inactivating delayed rectifier potassium current to model Long QT Syndrome Type 2 (LQTS2), female base myocyte simulations exhibited longer AP duration and increased EAD vulnerability as compared to male base myocytes. In general, higher levels of  $I_{Ca-L}$  were predicted to cause longer AP durations. The biophysical data and mathematical simulations together support the hypothesis that higher levels of  $I_{Ca-L}$  contribute to EAD genesis. Other studies have found that beta-adrenergic stimulation enhances  $I_{Ca-L}$  and the slowly inactivating delayed rectifier potassium current ( $I_{Ks}$ ) and that recovery from beta-adrenergic stimulation is associated with an increased likelihood of arrhythmia. We hypothesize that  $I_{Ks}$  may recover from beta-adrenergic stimulation more rapidly than  $I_{Ca-L}$ , which could increase arrhythmia propensity and possibly aggravate the male-female difference in EAD vulnerability. We are testing this hypothesis in model simulations of male and female base and apical myocytes.



7. **EURY, A., DUNCAN, I., WASSERBERG, G. and C. SMYTH. The effect of vector-host coupling on the dynamics of vector borne diseases Department of Mathematics and Statistics and Department of Biology, The University of North Carolina at Greensboro, Greensboro, NC.**

The role of the host is often ignored when modeling the dynamics of Vector-borne diseases. In this project, we investigated the effect of the dependence of the vector on the host (hereafter, vector-host coupling) on disease dynamics. Specifically, we examined how disease prevalence in the host population changes with host or vector abundance. We used an object-oriented-programming approach to simulate three vector-host coupling scenarios: un-coupled, using random movement of the vector, semi-coupled where vectors seek hosts only for blood-meals (e.g., mosquitoes), and totally-coupled where the vector requires contact with the host throughout its life-cycle (e.g., ticks). In all scenarios, decrease in prevalence with host abundance was observed. This is an expected outcome resulting from decrease in the vector-to-host ratio. In the uncoupled scenario, these relations occurred throughout the host abundance range. In contrast, the totally-coupled scenario prevalence first increases and only later decreases. In the semi-coupled scenario prevalence remain constant in low host abundance and then decreases. These relations result from the vector's host-seeking behavior which results in increase in the connectivity of the host population at low densities and thus buffers the decrease in the vector-to-host ratio. Meta-analysis of the literature shows that studies of the relation of abundance in vectors and hosts are a based largely on observations and indirect associations that do not measure the degree of vector-host coupling. From the limited articles focusing on the effects of vector-host population densities, only 5% of papers actively controlled and compared vector and host abundance levels on the prevalence of disease. The remaining 95% of relevant vector-host coupling papers observed results where only the vector's or host's density fluctuated and used these results to make indirect and theoretical associations based on observations of temporal and spatial variation. Results of this work highlights the importance of incorporating biological information on the degree of vector-host coupling to better predict and control vector-borne disease outbreaks.

8. **KEENEY, E., WILSON, C. and T. DERTING. Adaptive Immunity is Not Energetically Costly. Department of Biological Sciences, Murray State University, Murray, KY.**

The immune system is critical to survival and subsequent reproductive success of organisms. Many researchers have suggested that some components of the immune system, especially adaptive immunity, are energetically expensive. Our goal was to quantify the cost of the immune system to determine whether trade-offs in energy use occur between branches of the immune system and between the immune system and other physiological processes during an immune response. We tested the null hypothesis that an ongoing humoral immune response has no effect on the development of a cell-mediated immune response. Using adult male old-field mice, *Peromyscus polionotus*, cell-mediated responses were induced in cell-mediated/humoral (CH; n=10) and cell-mediated (Cm; n=10) adult male mice using dinitrofluorobenzene. A humoral response was induced using sheep red blood cells. Results were compared with a control group (Ct; n=10). We measured the energetic cost and strength of the immune responses through analysis of daily metabolic rate, resting metabolic rate, red and white blood cell counts, pinnae measurements, and hemagglutination assays. Metabolic rates of the CH and Cm mice did not differ significantly from those of Ct mice, despite significantly smaller masses of immune and vital organs in the latter group. In addition, we failed to find any significant difference between the Cm and CH groups in any measured parameter. Thus, our work showed no significant trade-offs between the humoral and cell-mediated immune systems. Importantly, our results also did not support the widely-used assumption of a high energetic cost of adaptive immunity.

9. **ABDELMAGEED, S., LOWDEN, J. and L. TANNENBAUM. Vancomycin-Resistant Enterococci Colonization-Infection Model: Simulation, Analysis and Basic Reproduction Number. Ursinus College Collegeville, PA.**

Vancomycin-Resistant Enterococci (VRE) infections have been linked to increased mortality and ICU costs.

We developed and analyzed a new model of a VRE infested intensive care unit (ICU) based on transitions between five classes of patients: susceptible, colonized without special preventive care, colonized under special preventative care, infected undergoing VRE treatment and infected without VRE treatment. We investigated the dynamics of the corresponding system of non-linear differential equations, as well as the interplay and impacts of nineteen independent parameters involved in the transitions. We created computer simulations of VRE dynamics, and mathematically visualized and measured the impacts of the parameters on the spread of VRE infection. We conducted disease free analysis, and computed the basic reproduction number and its bifurcation diagrams. We pinpointed good strategies to efficiently adjust adequate parameters for controlling VRE infection and preventing outbreaks, without the risk involved in clinical testing, including the parameters with the largest impact and the values that minimize outbreak risks. For example, it was shown that in certain ICUs, the outbreak risk can be the lowest by requiring only 60% of newly colonized patients to be under special preventive care. In the future we hope to expand the work on this model to include a stochastic approach to account for uncertainties and to use optimal control theory to refine our prevention protocol.

**10. PARKINSON, G. Malaria Control in Haiti. Howard University, Washington D.C.**

Early January, Haiti was struck by a massive earthquake which devastated the country. This earthquake, which was the largest to hit the Americas in over two centuries, cost 200,000 citizens their lives and left 300,000 people severely injured. It also displaced 2 million residents from their homes. Malaria is widespread throughout Haiti, particularly during the rainy season, and these current outdoor living conditions (tents and temporary shelters) have only made the population more vulnerable to malaria outbreaks. Currently, the WHO and the Centre for Disease Control (CDC) are performing a series of worldwide controlling and eradication procedures to reduce the health burden of malaria. Through vector elimination by DDT spraying, distribution of antimalarial drugs, effective surveillance systems and overall improvements of living standards in communities there is a firm goal to eliminate malaria in impoverished countries. The success of Haiti in these programs depend on many factors including urbanization, agricultural practices, water resources, health and sanitation status, and epidemiological aspects such as local malaria and vector species, and patterns of malaria transmission. This project investigates through modeling how likely, in this post earthquake situation, Haiti is to control this disease or better yet eradicate it with these current programs.

**11. CHODNICKI, K., CRISCI, T., TANNER, J., WRAY, B., CHAI, E., CHAVIS, J., DESTLER, N., GRAHAM, D., JORDAN, K., LANDA, R., MERKLE, C., PARK, S., PAXTON, C., and R. SOOD. Analyzing the Movement of Infants at Risk for Autism Spectrum Disorders. Gemstone Program, University of Maryland, College Park, MD.**

Current research suggests that autism spectrum disorders (ASD) negatively affect motor development. Among experts, it is widely accepted that early intervention is the most effective method for improving quality of life for individuals with ASD. This study aims to determine whether or not the effect of ASD on motor development can be used as an early indicator for identifying infants displaying characteristics of ASD. Using motion capture technology, the movements of infants at high risk of ASD will be compared to the movements of those at low risk. Specific movements of interest include head lag, as demonstrated in a pull-to-sit task, and arm trajectory exhibited in reaching for an object. In analyzing the collected data, it is expected that a discernible difference in movement will be detected. If results are as expected, this study will lay the foundation for the creation of a developmental benchmark intended to identify infants displaying early indicators of ASD.

**12. DRENDEL, J., JEFFERS, L., MOSES, E., NEAVIN, D., STRAND, K., CHASE, L., COSTAIN, E., ECHLIN, M., HOPKINS, D., MIKUCKI, M., PARKS, S., THORNTON, R., WOOTEN, L., ANTOLIN, M., FIELD, S., HAMILTION, S. and S. TAVENER. Stage-Structured Disease Model. Department of Mathematics, Colorado State University, Fort Collins, CO.**

Flour beetles of the genus *Tribolium* have been the subject of a long series of experiments on nonlinear population dynamics. Adults and larvae cannibalize eggs, and adults cannibalize pupae. These interactions are a source of nonlinearity and are captured in a six-class (uninfected larvae, uninfected pupae, uninfected adults, infected larvae, infected pupae, and infected adults) model. Given a 4-dimensional population array, which contains the number of individuals in each class and genotype ( $X(t)$ ), it is possible to construct a nonlinear projection function which represents the difference equations that govern the population dynamics of the system.  $X(t)$  is the population during time step  $t$ . One time step in the model represents 2 weeks. (One time step in the LPA model developed by Dennis et al. represents 2 weeks. The LPA model has had considerable success. For this reason, this well-validated model is taken as part of the evolutionary model.) The basic iterative procedure:

$$X(t + 1) = S(t)X(t) + N(S(t)X(t)),$$

where  $S$  and  $N$  are nonlinear functions.

- 13. BRNICH, S., FILIBERTI, J., CONNER, B., GRANT, M., BITTNER, D., COX, C., HASSINGER, J., KUNKLE, A., MANNING, K., WOOD, K., FORRESTER, J., and M. ROBERTS. Re-programming Human Leukemia Cells : Changes in Gene Expression During Leukemia Cell Differentiation. Departments of Biology, and Mathematics/Computer Science, Dickinson College, Carlisle, PA.**  
 HL-60 cells represent an established line of human acute myeloid leukemia cells that can be induced to differentiate along several different myeloid lineages. Phorbol esters activate the protein kinase C (PKC) signaling pathway which causes the leukemia cells to differentiate into macrophage-like cells. As the leukemia genetic program is converted to the macrophage program, the cells exit the cell cycle, undergo morphological changes and become adherent, exhibit other macrophage properties, and ultimately initiate apoptosis. Because of the inherent complexity of the genetic network, an understanding of the regulatory mechanisms in the cells requires a variety of mathematical techniques. Using DNA microarray analyses, real-time PCR, immunofluorescence microscopy and the electrophoretic mobility shift assay (EMSA) we have explored changes in gene expression at the mRNA and protein levels in an effort to understand how continuously dividing cancer cells reprogram to become "normal" differentiated myeloid cells. In this poster, we present evidence that implicates specific genes in the processes of cell cycle egress, differentiation, and apoptosis.
- 14. ALBANESE, A., BAIG, N. and R. NGUYEN. Mathematical Modeling of the BMP4 and FGF Signaling Pathways during Neural and Epidermal Development in *Xenopus*. University of Houston – Downtown, Houston, TX.**  
 During embryonic development, ectodermal cell fate in *Xenopus laevis* is determined by the mitogen-activated protein (MAP) kinase and bone morphogenetic protein-4 (BMP-4) signaling pathways. In an attempt to further understand the interactions between these two pathways, a mathematical model consisting of coupled, nonlinear ordinary differential equations has been developed. Linear stability analysis and bifurcation theory are used to describe the properties of this model. Numerical computations, including bifurcation studies have been carried out to elucidate the interaction between the two signaling pathways.
- 15. GIUFFRE, C. Motility of the ciliate paramecium in a non-uniform chemical landscape. University of Wisconsin-Milwaukee, Milwaukee, WI.**  
 We study the chemotactic behavior of the unicellular eukaryotic organism *Paramecium tetraurelia* using a newly developed microfluidic assay. These microfluidic devices provide cheap and quick quantitative analysis of the motility of the protzoan *Paramecium tetraurelia*, and can be used to study other aquatic chemosensitive organisms as well. It is important to understand how microorganisms sense their surroundings, as this may provide better diagnostic devices for environmental pollutants at the bottom of the food chain. Spatial statistics can be utilized to describe the behavior of single-celled organisms on a landscape of attracting or repelling chemicals in microfluidic devices, which are immune to the large systematic biases due to gravitation and fluid flow. We utilized spatial Poisson processes, and showed that a

motion towards an attracting source occurs faster than the dispersion of the individuals in a flat chemical landscape that would be attributed to random motion alone.

Additionally, modeling observed behavioral patterns could result in predictive models which can be comparatively analyzed after the experimental data has been collected. We present a model that simulates the chemotactic behavior of *Paramecium tetraurelia*, and can serve as a platform for an agent-based simulation exercise.

**16. CALLAWAY, D., RUSHING, S., CROWE, M. and J. RYCHTAR. Using biological data to modify a model of kleptoparasitic behavior in dung beetles. Hendrix College, Conway, AR and Department of Biology, Office of Undergraduate Research, Department of Mathematics and Statistics, The University of North Carolina at Greensboro, Greensboro, NC.**

*Onthophagus taurus* is a dung beetle that exhibits kleptoparasitism. Females build brood balls to lay their eggs in which can then be stolen by other females. Data from experiments showed that female beetles will often build multiple brood balls within close proximity to each other. With this supporting data, we worked on modifying our original game theory model so that beetles would be able to guard and build brood balls at the same time. The goal of this modification was to see if this behavior would increase the beetle's fitness. We also modified the model to analyze a guarding effectiveness model and to do so we needed a rate of kleptoparasitism. We gave beetles multiple brood balls to steal and observed how many they would steal over a fixed period of time. Using this rate, we completely analyzed the guarding effectiveness modification.

**17. CANTRELL, J., MARLAND, E., MARLAND, G., and K. SHIRLEY. The Cost of Carbon: Watch your Tail. Department of Mathematical Sciences, Appalachian State University, Boone, NC.**

To model sequestration and release from carbon containing products, a probability distribution model can be used to simulate the changes that occur as a function of time. This approach is different from previous models that viewed the decay of carbon stocks as functions of the size of the carbon stock. Among other benefits, such as increased accuracy, the new model has advantages in understanding the valuation of carbon if its release to the atmosphere incurs some cost. This valuation can then be described in terms of contracts and payment plans. In this research we look at the implications of error on the valuation of carbon release and its effects on contracts and payment plans. Economic forecasting, pricing of carbon release, and the release of carbon into the atmosphere are the three significant sources of error encountered when using this method for the valuation of carbon. A sensitivity analysis was conducted on the distribution parameters to determine the effects of the error on pricing. The results from this analysis led to a discussion of implications for short and long term contracts and directions for further research on the effects of error in carbon valuation.

**18. WHITAKER, J. and M. GEILE. From Field to Lab: An Overview of Salamander Population Studies and Genetic Analysis. Murray State University, Murray, KY.**

Phenotypic plasticity is a phenomenon that affects many organisms. To explore the costs and benefits of such plasticity, we examined facultative paedomorphosis in salamanders, in which individuals can exhibit one of two distinct adult morphs as a result of environmental and genetic cues. Facultative paedomorphosis is exemplified by the species used in this study, *Ambystoma tigrinum nebulosum* (tiger salamanders) and *Ambystoma talpoideum* (mole salamander). Both metamorphic (terrestrial) and paedomorphic (gilled/aquatic) adult forms occur within the populations found around our study areas Land Between the Lakes and the Mexican Cut, CO. To study the interactions of salamanders adapting to their environment, ecological data has been collected in the field and genetic analysis has occurred in the laboratory. Morphological and life history measurements of salamanders were recorded, and a separate study was conducted to examine the effects of body size on behavioral thermoregulation in one species. Our laboratory work was designed to determine the fitness consequences of facultative paedomorphosis. Microsatellite markers are being developed to assign parentage in order to better understand the costs and benefits of

paedomorphosis. In optimizing 8 different primers, we found that microsatellite loci were polymorphic, producing 2-9 alleles. We are continuing to evaluate the variability of different primers for parentage assignment, in order to determine the number and types of progeny the different morphs produce. The results of this study will be used to better understand both the ecology of these two species, and the evolutionary costs and benefits of phenotypic plasticity.

**19. CHAVEZ, R. On the Use of Stable Isotope Analysis in Mammalian Ecology. Mathematical Biology, New Mexico State University, Las Cruces, NM.**

Stable isotope analysis is a powerful tool that ecologists use to explore food web structure, predator prey dynamics, resource composition, and trace nutrient movement in ecosystems. Mixing models are often used to estimate the contribution of carbon and nitrogen from multiple sources to tissues of an animal from stable isotope data. A fundamental assumption for construction of a mixing model is that carbon and nitrogen isotopes are independent of one another; that is, they do not covary. In order to test the primary hypothesis of independence, I conducted a meta-data analysis from data collected in a review of mammalian stable isotope ecological literature published over the last 26 years. Additional hypotheses tested were the effect of ecosystem type and trophic position on carbon and nitrogen isotopic ratios. I also evaluated the distribution of mammalian orders represented in the literature. Results indicate that carbon and nitrogen stable isotopes significantly covary within mammalian muscle tissue. There are significant differences between ecosystem type and trophic position within mammals. This study also reveals the need for broader coverage across mammalian taxa in ecological isotopic experimentation. In conclusion, I present empirical evidence that critical assumptions of carbon and nitrogen stable isotope independence are violated, calling into question the usefulness of mixing models to analyze stable isotope data.

**20. RUSHING, S., CALLAWAY, D., CROWE, M. and J. RYCHTAR. Field experiments to determine the time interval in which dung beetles could kleptoparasitize. Department of Biology, Office of Undergraduate Research, Department of Mathematics and Statistics, The University of North Carolina at Greensboro, Greensboro, NC, and Hendrix College, Conway, AR.**

The overall question we are interested in answering is when the dung beetle, *Onthophagus taurus*, will kleptoparasitize versus create its own brood ball. Kleptoparasitism occurs when a female *O. taurus* steals a brood ball made by another, rids it of the existing egg, and either replaces it with her own egg or uses the brood ball as food source. We need an understanding of the dung beetles' behavior within a cow pat. To determine how our beetles use the dung pats, we set up field experiments to monitor when the beetles enter, where they spend their time, and when they leave a pat. Our results show that female beetles arrive to the dung pat within 12 hrs of creation; the majority are found between 5 and 10 cm below the surface, and often stay within a cow pat for at least 4.5 days which leaves plenty of time for them to create a brood ball. Although we found many pieces of buried dung, we found very few brood balls. This result might be explained by a field experiment in which we found that the probability a brood ball is destroyed by close to 60%.

**21. SMART-DUMOUCHEL II, T. Mathematical Modeling of Recirculating Aquaculture System. University of Wisconsin-Milwaukee, Milwaukee, WI.**

As fish stocks decline from overfishing, reduced water systems, and taxing chemicals, there has been a socio-economic push for efficient fish farming aquacultures. A Recirculating Aquaculture System (RAS) is a closed system of a culture tank and filters that recycle water. Ammonia and nitrite are two compounds of high importance in a RAS since at high concentrations ammonia and nitrite can be poisonous to fish. Biofilters in the system contain bacteria that convert ammonia to nitrite and nitrite to nitrate, which is safe at moderate concentrations. Mathematical modeling, in particular coupled systems of ordinary differential equations, allow for representations and predictions of the RAS dynamics. Through systematic testing of parameters and optimization, questions can be answered about the oxidation of the nitrogen cycle.

Furthermore, the model can be used to identify safe loading for and influence the design of RASs for optimal performance and give further insight to the biofiltration process. These results will help countries' urban agricultures in implementation and efficient operation of Recirculating Aquaculture Systems.

**22. BOECKMANN, E. Geometrical Modeling of Aggregatory Behavior in *Dreissena bugensis* Under Flow Conditions. University of Wisconsin-Milwaukee, Milwaukee, WI.**

Mussel behavior is commonly studied in terms of single individuals or large groups. This study focuses on organizational behaviors of Quagga mussels (*Dreissena bugensis*) within aggregations and how differing flow rates and intermittent predation affect colony growth. Each potential location within a clump has distinct biological advantages and disadvantages; by interpreting the natural arrangements of mussels using spatial modeling these biological mechanisms may be better understood. Using simulations we aim to predict the effect of flow variations allowing for periods of predation, and therefore removal of individuals, on Quagga mussel community growth, using a two-dimensional flow dependent dynamical model. Biological fouling by *Dreissena bugensis* in conditions such as power plant intake pipes could be predicted, and possibly prevented or passively managed by utilizing scheduled low-flow periods when predators (such as the Round Goby, *Neogobius melanostomus*) could remove or maintain low *Dreissena* populations.

**23. BLAZSEK, L. and L. CURLL. Statistically Categorizing Landform Distribution in an Eastern Riparian Ecosystem. Department of Biological Sciences and Department of Mathematics & Statistics, Youngstown State University, Youngstown, OH.**

Zoar Valley, in New York State, is a natural riparian ecosystem, mostly isolated from human disturbance. It is one of the last Old-Growth forests in the northeastern United States. Selected landforms in Zoar Valley were categorized using recorded data of the types, numbers, ages and sizes of trees present. Based on quantities recorded from trees such as basal area, shade tolerance, and age, the landforms can be grouped into four categories: Stand Initiation, Stem Exclusion, Understory Re-initiation, and Old Growth. Given that landforms in Zoar Valley are periodically created and destroyed due to changing river courses, typical of a riparian ecosystem, all four categories can be observed. Data was analyzed from nineteen landforms and compared using Multi-Dimensional Scaling Analysis to represent the defined groups of forest succession in Zoar Valley. Data variables that displayed high loading factors represented important distinguishing characteristics between classes. These results directed the synthesis of categories for a differential equation model of the successional development of landforms over time, including a stochastic flood term. This research was funded by NSF grant DBI-0827205.

**24. JACKSON, A. Ant Foraging and Climate Change. National Institute for Mathematical and Biological Synthesis, Knoxville, TN and North Carolina Agricultural & Technical University, Greensboro, NC.**

For abstract, see Collins et al. oral presentation.

**25. THOMPSON, H. Patch Models of an Insect Predator-Prey System. Colorado College, Colorado Springs, CO.**

I present patch models of an insect predator prey system of ladybugs (*Coccinella septempunctata*, *Hyppodamia convergens*) and aphids (*Aphis yuccae*) on yucca plants (*Yucca glauca*). Spatially implicit two patch and spatially explicit 107 patch models, which include the conspecific attraction of ladybugs, replicate some key characteristics of field data. The models are parameterized by field and lab experiments, and bifurcation diagrams are used to illustrate parameter sensitivity in the two patch model.

**26. GONZALEZ, A. and G. ABARCA. Non-metric Multidimensional Scaling Analysis for Bacterial Endophyte Communities in Texas Grapevines. Interdisciplinary Training for Undergraduates in Biological and Mathematical Sciences, University of Houston-Downtown, Houston, TX.**

Pierce's disease (PD) of grapevines is caused by *Xylella fastidiosa* (*Xf*), a bacterial plant pathogen. PD has had devastating effects in the growing Texas grape industry and in the estimated \$60 billion grape industry

of California. Recently, there has been great interest in the role of microbial endophyte communities on disease resistance. European, hybrid and wild grapevines differ in their resistance to PD. Therefore, we hypothesized that differential resistance among varieties may result from distinct endophyte communities. Endophyte species were identified within eight replicates of a hybrid grape variety (Blanc du Bois) and a European grape variety (Merlot). Samples were collected monthly from April to July and 736 bacterial species identified through 454 Pyrosequencing. Total microbial numbers by species were analyzed using Non-metric Multidimensional Scaling (NMS) PC-ORD, which measures dissimilarities and similarities of biological communities within a data set. NMS iteratively searches for possible solutions and iterations to determine the best statistical model of the community. NMS ordination graphs of our data showed two distinct communities for the first month of April, while in May the microbial endophyte communities merged. For the June and July sampling months, distinct communities were observed again. This is the first time that distinct microbial communities have been demonstrated for different grapevine varieties growing in the same vineyard. The distinct communities (or the plant conditions which result in these communities) may be responsible for variable resistance to PD. August and September samples will also be analyzed to obtain a better understanding of the temporal differences between endophyte communities for these hybrid and European varieties.

**27. KEMFORT, T., OSWALD, S.A. and J.M. ARNOLD. Modeling the effects of investigator disturbance on ring-billed gulls *Larus delawarensis* using a multi-state mark-recapture analysis. Division of Science, Pennsylvania State University, Reading PA.**

Development of management protocols that minimize adverse effects of research while maximizing data collection requires knowledge of the impacts of investigator disturbance. Studies of the impacts of disturbance on waterbirds have had mixed results. This study was designed to dissociate impacts of disturbance intensity and measurement frequency on productivity and data quality. Data were collected in the field during the summer of 2008 at Presqu'ile Provincial Park in Brighton, Ontario. The study design used six plots that were visited with differing regularity (daily, weekly, biweekly) but were not all sampled on every visit. For example, some plots were visited daily but sampled weekly or biweekly. Chicks were color banded and capture histories were compiled for each chick with the goal of determining survival rates for chicks in each treatment group. This data set presented unique challenges since histories reflected near-daily, weekly, or biweekly recapture, and recoveries were included. Fledging also posed a challenge since it was necessary to differentiate between disappearance due to death or fledging. A multi state live-dead model was used because it allowed movement of birds to a fledgling state where recapture probabilities and survival rates are expected to be statistically different. Goodness-of-fit testing showed that model assumptions were sufficiently supported. A full model structure was determined based on *a priori* knowledge and models are currently being reduced using Program MARK. Model selection will be used to determine the separate effects of differing levels of investigator disturbance and monitoring intensity on chick survival and overall productivity.

**28. ALCOCER, A., IPPOLITO, D. and K. ST.JOHN. The Space of Phylogenetic Networks. Department of Mathematics and Computer Science, City University of New York, Lehman College, Bronx, NY.**

Phylogenies, or evolutionary histories, play a central role in modern biology, illustrating the interrelationships between species, and also aiding the prediction of structural, physiological, and biochemical properties. Trees are often used to represent these phylogenies. But in many cases, such as hybridization and lateral gene transfer, a better model of evolution is a phylogenetic network, a tree with extra edges representing alternative evolutionary scenarios. We limit our networks to those where internal nodes have at most two in-edges. Our goal in this project is to understand the space of phylogenetic networks under the Robinson-Foulds network.

**29. CACERES, A.J. and D. MOORE. Visualizing Landscapes of Phylogenetic Treespace. Lehman College, City University of New York, Bronx, NY**

Evolutionary histories, or phylogenies, provide a central role in biology. They are used to illustrate evolutionary mechanisms, to design new drugs, and to trace the spread of disease. Finding the optimal phylogeny for a set of species is NP-hard under the popular Maximum Parsimony and Maximum Likelihood optimization criteria. The problem is further complicated when different genes evolve differently. We have developed a visualization of the space of all trees with 7 leaves that shows not only the optimal trees for each gene but the entire landscape of all trees and their scores. This visualization illustrates the interplay between tree topologies and optimal trees under differing genes.

**30. DEJESUS, J. and L. LI. Neighborhoods in Phylogenetic Treespace. Lehman College-- City University of New York, Bronx, NY.**

Phylogenetic trees show the evolutionary relationships among various biological species that are known to have a common ancestor. A tree space is a graph containing all phylogenetic trees for a given number of species using a chosen metric. Each n-species tree space is composed and organized into groups called neighborhoods and the root tree. The number of neighborhoods and their respective sizes are determined by the shape of the root tree and the chosen metric (specifically the Nearest Neighbor Interchange metric). Currently, there is no accurate determination of how large these neighborhoods are nor the exact quantity of neighborhoods within each n-species tree space. We have discovered an expression for determining the number of 2<sup>nd</sup> neighbors in n-species tree space when the root tree is a caterpillar tree. Our objective is to develop formulas that determine the number the size of each neighborhood in any n-species tree space.

**31. HINTZ, M. and O. MENDEZ. Estimating NNI Distance with RF Distance. Division of Mathematics and Computer Science, City University of New York, Lehman College, Bronx, NY.**

A tree is a connected graph with no cycles. A phylogenetic tree is a diagram that displays the evolutionary relationships among various biological species or other entities based upon similarities and differences in their physical and/or genetic characteristics. There are different ways of comparing trees (i.e. metrics) and each metric produces different treespaces, which is the space of all trees with x number of leaves, where x is the number of species. One metric, the nearest neighborhood interchange (NNI), exchanges subtrees to obtain a new tree. The NNI distance between two trees is the minimal number of moves needed to transform one to the other. However this distance is computationally expensive. An alternative distance is Robinson Foulds (RF), it is defined as  $(A + B)$  where A is the number of species contained in the first tree but not the second tree and B is the number of species contained in the second tree but not the first tree. Computing RF distance is extremely efficient, thus, our goal is to determine how closely related RF distance and NNI distance are.

**32. HELLWIG, E. Phylogenetic Tree Construction Using STR Data: The Importance of Data Truncation. Colorado College, Colorado Springs, CO.**

**33. OGUNJOBI, B. and L. QIAN. Using a Workflow Management System to Process Bioinformatics Data. Department of Computer Science, Fisk University, Nashville, TN.**

Advances in modern day medical research make it easier to collect large quantities of biological data which may prove difficult to manage and analyze. To ensure proper data analysis and control of data, several Workflow Management Systems (WMSs) have been proposed. In this project, we use Kepler, a free WMS, to retrieve and analyze data from The Cancer Genome Atlas (TCGA). TCGA studies and generates information about the molecular anatomy of normal, pre-cancer and cancer cells using high-throughput genome analysis techniques. The raw data can then be analyzed to ensure improved diagnosis and treatment for patients. For optimal results, the data is organized into workflows and then analyzed. Kepler was chosen because of its ease of use and support of hierarchy in workflows. Kepler also allows for workflows to be shared via a web portal and web service interface. Using Kepler, we can utilize web services of the TCGA Data Portal, the Cancer Molecular Analysis Portal and MSKCC CancerGenomics Analysis. This



project presents the implementation of a workflow system that can process data gotten from bioinformatics research and it shows how this analysis method makes a large volume of data easier to analyze.

**34. MURPHY, C. and A. HUGHES. Gene Regulatory Networks of Rainbow Trout Enlightened by Modularity. Great Lakes WATER Institute and University of Wisconsin at Milwaukee, Milwaukee, WI.**

RNA-microarrays provide a high-throughput method that enables glimpses into a genome's expression patterns. Microarray experiments are accumulated for an increasing number of species, and this cumulative data carries an abundance of information about the genome's pathways, interactions and regulations networks. Our goal is to reveal the structure of such gene regulatory networks and to identify important functional connections by analyzing cumulative public data with statistical and algorithmic tools. In our project we combined whole-genome microarray data from 17 different experimental series focused on Rainbow Trout (*Oncorhynchus mykiss*). The data were obtained from the National Center for Biotechnology Information (NCBI). Based on the combined data, we computed correlations involving all genes and applied an optimal modularity algorithm to detect gene communities with high level of interdependence. Our next step is to investigate the efficacy of the algorithm by finding experimentally confirmed, functionally connected gene groups. The implementation of the segmentation algorithm poses a considerable computational challenge and requires a computational platform for computation with sparse matrices. We plan to develop a visualization software tool to efficiently navigate the identified gene community structure.

**35. BENNETT, C. Competitive game theory across various disciplines - economics, biology, political science, sociology, and mathematics. North Carolina A&T State University, Greensboro, NC.**

We have developed theorems for common conditions in chomp so that the player can manipulate the game. These theorems can be applied to several disciplines including economics, biology, political science, sociology, and mathematics. The objective of this project is to design and implement a winning strategy for chomp grid with up to three pieces in the 3rd row. The take-away game Chomp is played on a rectangular grid with  $m$  number of rows and  $n$  number of columns. The grid is divided into squares. Two players alternate removing pieces from the grid. The lower right hand piece is poison and the player who removes this piece loses. By expanding the standard version of Chomp of 2 rows and 5 columns to 3 rows and infinitely many columns, we would like to investigate if we can come up with a way to find all the losing positions of a chomp grid when there are 3 rows and 0, 1, 2, or 3 pieces in the top row. Losing positions are members of the set  $L$ . All other positions are considered winning and a member of the set  $W$ . If a player can force the game to alternate from a position in  $W$  to a position in  $L$  and back to a position in  $W$  making the game go "W, L, W, L", the other player will lose.

**36. FASSINO, S. Structure and Evolution of a Mathematical Collaboration Network. University of Tennessee, Knoxville, TN.**

We investigate the collaboration network of mathematicians taken from Mathematical Reviews between 1985 and 2007. We use several tools common to social network analysis to explore this network and compare it to other real-world networks. We track changes in the structure of this network over time using sliding windows. We investigate effects on this network by external factors such as programs hosted by an NSF mathematics institute.

## **ORAL PRESENTATION ABSTRACTS (Alphabetical)**

### **ATKISSON, C. and R. WALKER. Inferences regarding population density in pre-Columbian Amazonia using phylogenetic modeling. Department of Anthropology, University of Missouri, Columbia, MO.**

Population density in pre-Columbian Amazonia (before the arrival of Europeans) is a contested topic in the anthropological literature. Recent archaeological findings indicate that population density was higher in tribal areas than it is now. Some have argued against those findings, claiming that the Amazonian rainforest is a “green desert”. This research makes inferences regarding the pre-Columbian population density, and we find that the density was likely much higher than it is now. Using the most comprehensive database in existence of cultural features of extant Tupi-speaking groups, we perform phylogenetic analysis to determine the prototypical cultural features of the ancestor group of the Tupi linguistic family. This process is performed by taking the most recently published sets of the relationship of Tupi speaking groups and mapping cultural characteristics to those linguistic relationships. We then use the process of maximum parsimony, the base condition that requires the least changes from the data, to arrive at a proto-Tupi condition. We find the proto-Tupi group to be more complex than the extant groups. Integrating this with existing literature on population density and cultural complexity, we come to the conclusion that population density was higher in pre-Columbian Amazonia than it is now. A discussion of phylogenetic methods along with ethnographic examples highlights how mathematics allows us to explore interesting ideas of human cultural evolution, and make contributions to existing debates.

### **BECHETTE, A., STOJSAVLJEVIC, T.G. and M.H. TESSMER. Dynamic Modeling of Aquatic Viruses with an Internal Phosphorous Quota. Department of Biological and Mathematical Sciences, University of Wisconsin – Milwaukee, Milwaukee, WI.**

Recent studies indicate that viruses are ubiquitous in aquatic ecosystems and may play critical roles in nutrient cycling. Nitrogen and phosphorus released by viral lysis are essential nutrients limiting in many freshwater environments. Previous mathematical models have examined population dynamics of bacterial and viral communities, but have limited experimental background, limited testing and have not addressed nutrient recycling. Since nutrients inside the cell affect growth, Fuhrman (2008) took a novel approach by introducing an internal quota,  $Q$  (the nutrient inside the cell), into her model. Our goal was to test the validity of the model and determine the importance of incorporating  $Q$ . Using natural planktonic communities from Lake Michigan and the eutrophic Estabrook Pond, we compared 20L samples left untreated with 20L samples enriched with nutrients ( $6\mu\text{M}$  phosphate for both communities, plus  $128\mu\text{M}$  nitrate for Estabrook community) over a two week period in summer 2010. Time series of bacterial and viral abundance, total phosphorous, phosphate and nitrate were collected. We compared this experimental data to the predictions of Fuhrman’s model. In testing the validity of the model, we examined key parameters such as burst size, contact rate, free virus death rate, and the lytic time period.

### **BULGER, D.<sup>b,g</sup>, GEYER, K.<sup>c,g</sup>, TRASK, J.<sup>d,g</sup>, ADHIKARI, S.<sup>a,g</sup>, ARMSWORTH, P.<sup>e</sup>, and W. GODSOE<sup>f</sup>. Biodiversity in the Great Smoky Mountains National Park: Past and Present Measures. <sup>a</sup>Mount Holyoke College, South Hadley, MA, <sup>b</sup>Oral Roberts University, Tulsa, OK, <sup>c</sup>Virginia Tech, Blacksburg, VA <sup>d</sup>University of Tennessee, Knoxville, TN, <sup>e</sup>University of Tennessee, Department of Evolutionary Biology and Ecology, Knoxville, TN, <sup>f</sup>National Institute for Mathematical and Biological Synthesis, Knoxville, TN, <sup>g</sup>Listed Alphabetically**

Biodiversity is of great interest to ecologists for many reasons, one of which is its importance in maintaining stable ecosystems (1). This study evaluates and compares biodiversity levels at eleven sites in the Great Smoky Mountains National Park (GSMNP) using data obtained through the All Taxa Biodiversity Inventory (ATBI). We use alpha, beta, and gamma diversities, as well as the Shannon-Weiner index, Simpson’s index, and Fisher’s Log Series Distribution to describe the diversities of, between, and among these sites. In addition, we compare the distributions of families as suggested by the ATBI Pilot Study data to those concluded by Whittaker in 1952 (2) through the use of more modern

inferential statistical methodologies. Here we show that the ATBI Pilot Study data suggests that biodiversity is striking in the GSMNP and that revisiting Whittaker's conclusions is worthwhile.

#### References

- [1] Science Clarified, Biodiversity (2010). URL <http://www.scienceclarified.com/As-Bi/Biodiversity.html>
- [2] R. H. Whittaker, A study of summer foliage insect communities in the great smoky mountains, Ecological Monographs 22 (1952) 1–44. Preprint

**BRNICH, S., FILIBERTI, J., BITTNER, D., CONNER, B., COX, C., GRANT, M., FORRESTER, J. and M. ROBERTS. Mathematical and Computational Techniques for Microarray Data Analysis. Departments of Biology, and Mathematics/Computer Science, Dickinson College, Carlisle, PA.**

The HL-60 human leukemia cell line can be induced in culture by a variety of compounds to differentiate toward several different cell types of the myeloid lineage. The observed phenotypic changes are caused by the differential expression of a large number of genes. Determining a comprehensive list of the genes showing significant changes in expression during this process represents the first step in elucidating the genetic network controlling the leukemia cell. DNA microarrays provide a platform for simultaneously assaying the expression of thousands of genes in a single experiment. The complexities of the resulting data sets require advanced mathematical and computational tools for their analysis. In this talk, we discuss several mathematical and statistical methods used to analyze these large data sets and determine which of the genes in the leukemia cell have changed in a statistically significant way at various time points after induction of differentiation.

**CHODNICKI, K., CRISCI, T., TANNER, J., WRAY, B., CHAI, E., CHAVIS, J., DESTLER, N., GRAHAM, D., JORDAN, K., LANDA, R., MERKLE, C., PARK, S., PAXTON, C., and R. SOOD. Analyzing the Movement of Infants at Risk for Autism Spectrum Disorders. Gemstone Program, University of Maryland, College Park, MD.**

Current research suggests that autism spectrum disorders (ASD) negatively affect motor development. Among experts, it is widely accepted that early intervention is the most effective method for improving quality of life for individuals with ASD. This study aims to determine whether or not the effect of ASD on motor development can be used as an early indicator for identifying infants displaying characteristics of ASD. Using motion capture technology, the movements of infants at high risk of ASD will be compared to the movements of those at low risk. Specific movements of interest include head lag, as demonstrated in a pull-to-sit task, and arm trajectory exhibited in reaching for an object. In analyzing the collected data, it is expected that a discernible difference in movement will be detected. If results are as expected, this study will lay the foundation for the creation of a developmental benchmark intended to identify infants displaying early indicators of ASD.

**COLLINS, J., THAI, N. and A. JACKSON. Two Ant Species Competition and Climate Change. REU Project at NIMBIOS, University of Tennessee, Knoxville, TN.**

Ants are often described as indicator species, because these short-lived social insects are highly sensitive to variations in the environment, such as those due to climate change. Ants also are a keystone species; sudden drastic changes in their populations could have a devastating impact on other species in the ecosystem. For instance, certain ants fill a crucial roll in the seed dispersal of some plants. To understand the impact of climate change in a competition between two ant species, we constructed a two-scale model of ant foraging and colony dynamics for hot-tolerant and cold-tolerant ants. The two-scale approach used in this model examined ant populations on both an individual level (small-scale) and an aggregate level (large-scale). The small-scale model used a stochastic, agent-based approach to simulate two species of ants foraging for the same food resources on a daily basis. Many runs were conducted with the small-scale model over a range of parameters. Functions were then fitted to the averaged daily food intake for the respective species. These deterministic 'haul functions' provided the link between the small and large-scale models. Since the haul functions are analytic expressions, the overall simulation time for the aggregate model was much lower compared with the situation where the stochastic foraging process was simulated on a daily basis. The large-scale model was

comprised of difference equations for the food controlled by each species and the two ant populations and tracked food and population dynamics on a monthly basis. The large-scale model was utilized to predict the population dynamics over a time scale of years based on foraging behaviors (rules) that could be affected by the average daily temperature. Climate change was incorporated into both of these models. We used average monthly high temperatures from the Smoky Mountains National Park and considered various climate change scenarios. In the small-scale model, three different levels of temperature (hot, medium, and cold) were used to dictate ants' foraging movements. In the large-scale model, temperature conditions determined foraging seasons and overall metabolic rates for foraging and reproduction, along with foraging success through the haul functions derived from the small scale model. Our results showed the possibility of a switch in numerical dominance from cold-tolerant ants, which prefer to forage in colder temperatures, to hot-tolerant ants, which have a higher temperature threshold for foraging. In particular, if temperatures rose to a new equilibrated yearly average (a saturation point) that was not too extreme, then a new equilibrium could be attained in the ant populations where the once minority hot-tolerant ants were now the majority. However, if the average yearly temperature rose too high then we saw both species crash. We also modeled the scenario of temperature rising, then falling back to current levels, and observed that natural equilibriums could in some cases be restored, but only if neither of the populations were wiped out during temperature rise.

**CHODNICKI, K., CRISCI, T., TANNER, J., WRAY, B., CHAI, E., CHAVIS, J., DESTLER, N., GRAHAM, D., JORDAN, K., LANDA, R., MERKLE, C., PARK, S., PAXTON, C., and R. SOOD. Analyzing the Movement of Infants at Risk for Autism Spectrum Disorders. Gemstone Program, University of Maryland, College Park, MD.**

For abstract, see poster #11.

**CONNER, B., GRANT, M., BITTNER, D., BRNICH, S., FILIBERTI, J., COX, C., FORRESTER, J. and M. ROBERTS. Using Cluster Analysis to Examine the Genetic Network in a Human Leukemia Cell Line. Departments of Biology, and Mathematics/Computer Science, Dickinson College, Carlisle, PA.**

The HL-60 human leukemia cell line can be induced in culture by a variety of compounds to differentiate toward several different cell types of the myeloid lineage. Using DNA microarrays, our group has identified thousands of genes that are differentially expressed at various times after the induction of differentiation by the phorbol ester PMA. Organizing these genes into regulatory groupings is an important step in analyzing the structure of the genetic network in these cells. We have used cluster analysis to organize differentially expressed the genes by their pattern of expression. In this talk, we provide an overview of cluster analysis and introduce various metrics and linkage methods used in cluster formation. Finally, we will discuss the use of graphical techniques for examining the structure of the genetic network of the leukemia cell.

**CURLL, L. and L. BLAZSEK. Mathematical Modeling of Stochastic Riparian Ecosystems. Department of Mathematics & Statistics and Department of Biological Sciences, Youngstown State University, Youngstown, OH.**

Zoar Valley, in New York State, has been isolated from logging and other human disturbance even throughout early European colonization, and contains one of the last Old-Growth riparian forests in the northeastern United States. The valley is subject to diverse river conditions which create and erode portions of the valley floor and change the characteristics of riparian environments. From 2002 to 2010, tree species in 19 riparian landforms were cataloged and characterized into early- or late- successional classes based on a number of identifying variables like shade tolerance and basal area, and were further labeled juvenile or mature based on size. A system of differential equations predicts the successional development of new landforms over time based on data from over 30 sample sites. Given an approximate age of a landform and values for variables such as mortality rate and competition, the model predicts the number of trees present in each of the four categories and estimates future steady-states. The model also includes variables for irregular and random flood events, based on USGS flood data from the past 80 years. This research was funded by NSF grant DBI-0827205.

**ERWIN, S., HE, K., HUCKABA, A. and M. McCARTHY. Using matrix analysis to model the spread of an invasive plant, *Alternanthera philoxeroides*. BioMaPS, Murray State University, Murray, KY.**

*Alternanthera philoxeroides*, more commonly known as alligator weed is an invasive species indigenous to South America. With its alarming invasion of south east United States water ways, understanding its invasiveness of this plant species is both important and imperative. Utilizing experimental growth data obtained over the summer of 2010 matrix analysis is used to precisely model the growth of alligator weed. These matrices are population projection models whose eigenvalues represent the growth rate of alligator weed in its different stages of the life cycle. A high growth rate is a key feature of successful invaders. Residuals and sensitivity analysis are being performed to test the accuracy and importance of the models.

**FELDMANN, J. and M. YANEZ. Analysis of gene expression in *Bordetella avium* using microarrays. James Madison University, Harrisonburg, VA.**

**GRAHAM, G., and O. LIPAN. Goldbeter-Koshland switch as a stochastic sensor. Department of Physics, University of Richmond, Richmond, VA.**

Cell signaling pathways consist of multiple connections of different type of gene, mRNA and protein networks. It is not a trivial task to follow the signals flowing through these networks. The difficulty comes from considering the entire biological structure as a single network without breaking it in connected modules. The study of these networks simplifies if the complex system is reduced to a hierarchy of interconnected modules. A salient feature of biological signals is that they are stochastic. No molecular reaction is guaranteed to interact with every signal flow. Thus, each reaction is instead associated with a probability of being involved in the signal flow. The interconnection of stochastic modules is a useful approach to understand signaling pathways. Out of many potential modules, a specific one, namely the Goldbeter-Koshland switch, was specifically encountered by the authors during their study of the Mammalian Heat Shock Response Network (MHSRN) where the switch acts as the sole or primary stress sensor. Usually, only the steady state behavior of the switch is studied in which the phosphorylated protein given as a function of the enzyme concentration. Experimental results show that the heat shock response is still present 20 hours after the temperature stress had ended. Thus, it is useful to consider a switch that couples the environment to the MHSRN using time-dependent transitory signals and not just sudden jumps between steady-states. Also, the coupling should be stochastic not only because fundamental principles require it, but because experimental results do also. Our aim is to present the method by which the switch may be stochastically coupled to its environment or to another network and by which the resulting transitory signaling process may be studied.

**JEFFERS, L., MOSES, E., NEAVIN, D., STRAND, K., CHASE, L., COSTAIN, E., DRENDEL, J., ECHLIN, M., HOPKINS, D., MIKUCKI, M., PARKS, S., THORNTON, R., WOOTEN, L., ANTOLIN, M., FIELD, S., HAMILTION, S. and S. TAVENER. Stage-Structured Disease Model. Department of Mathematics, Colorado State University, Fort Collins, CO.**

Using the well-characterized population dynamics of *Tribolium Castaneum* beetles infected by the sporozoa *Nosema Whitei*, a stage-structured disease model was built and modified to incorporate resistance evolution.

This non-linear iterated map incorporates single-locus, single-allele resistance, and has been modified to demonstrate the behavior of completely dominant, heterozygote advantage, and completely recessive modes of gene action. Starting with an infected, non-resistant population at equilibrium, a mutant individual is introduced carrying a resistant allele, and the evolution of resistance is modeled under each mode of gene action. Then, starting with an abnormally high level of infectivity and cost of infection such that the initial non-resistant population is doomed to extinction, resistant individuals are introduced to determine what minimum initial prevalence of the resistant allele will save the population from extinction.

**KELEMEN, R., GWINN, K.D., JOO, J., NGUYEN, L. and D. BODIROGA. Modeling the effects of cymene on the distribution of germination and growth of *Beauveria bassiana*. Iowa State University, Ames, IA and National Institute for Mathematical and Biological Synthesis, University of Tennessee,**

**Knoxville, TN.**

Essential oils have antifungal and antipathogenic effects and therefore are targets in plant pathology research for their potential uses as natural substitutes for inorganic plant pesticides. *Beauveria bassiana*, an entomopathogenic fungus, can endophytically colonize a vast number of plant species and trigger induced systemic resistance against plant pathogens. Spore germination is the most vulnerable in the fungal life cycle and is therefore a good candidate for monitoring the effect of essential oils on the growth of *B. bassiana*. Percentage germination of fungal spores and lengths of germination tubes were recorded from experiments. Proposed mathematical model was able to capture the effects of cymene, an essential oil produced by *Monarda*, on the germination and growth of the beneficial fungus, *B. bassiana*. This is the first report of a model for the impact of essential oils on *B. bassiana* spore germination.

**KHAVARI, S and B. BELCIK. Modeling the Regulation of Gene Expression in the Presence of Selenite in E.coli. Department of Mathematics and Statistics and Department of Biological Sciences, Youngstown State University, Youngstown, OH.**

The regulation of gene expressions for a wild-type selenite-resistant strain and a mutant of *Escherichia coli* is investigated. The two target genes, Glutathione Reductase (Gor) and Arsenic Resistance (Ars), are expected to be expressed during different phases of the growth cycle in the bacteria. QPCR (quantitative Polymerase Chain Reaction) experiments were performed on the wild-type and the mutant with both genes to determine the relative expression of each of the target genes during various growth phases. A system of differential equations is developed to model the expression of Gor and Ars in the presence of toxic selenite. The mathematical model predicts the steady states for the variables with any given initial condition. Furthermore, stability of the steady states in this system is examined. The system of differential equations can also be solved numerically to give the gene expression as a function of time. This helps to identify the phases of growth when specific target genes are expressed in the presence of selenite.

**KOSEVA, B. and S. QUINN. Energy Allocation in a Generalist Predator, *Nerodia Sipedon*. Truman State University, Kirksville, MO.**

The energy available to an organism to do work is allocated to competing physiological functions based on the organism's life history and its environment. The successful allocation of energy determines the lifetime reproductive success of an organism (i.e. its fitness). We studied the Northern Watersnake (*Nerodia sipedon*) in order to understand how energy budgets work and incorporated our results in a modeling framework to predict effect on lifetime fitness.

**LUTZ, K., SHIBBERU, Y. and A. HOLDER. Protein Structural Alignment. Department of Mathematics, Rose-Hulman Institute of Technology, Terre Haute, IN.**

Protein structure is important in determining its function in an organism. Being able to compare a protein with a known function to another protein with an unclear function allows scientists to conduct experiments from a more accurate starting point. More focused comparisons can be made *in silico* and experimentally with other proteins with similar structure and function. We developed a method to compare two proteins *in silico* by using the distances from each residue to every other residue within each protein. This method uses matrices representing the distances for each protein's residues and uses linear transformations so that an approximate alignment is obtained. We use a heuristic in combination with a polynomial time algorithm to obtain this alignment.

**MASSARO, T. and G. YANG. Using a system of difference equations to examine the relative effectiveness of a test and cull management strategy with the new EVELISA testing versus commercial ELISA testing. State University of New York at Geneseo, Geneseo, NY, Appalachian State University, Boone, NC, and the National Institute for Mathematical and Biological Synthesis, Knoxville, TN.**

Johne's disease, also known as paratuberculosis, is a chronic and progressive inflammatory gastrointestinal disease primarily affecting ruminants, especially dairy cattle. According to a 2007 USDA study, the primary

causative agent of Johne's disease, *Mycobacterium avium* subsp. *paratuberculosis* (MAP), is present in a minimum of 68% of US dairy herds. The widespread prevalence of Johne's disease is economically significant, with an estimated cost to US dairy producers amounting to greater than \$200 million per year due to reduced milk production, premature culling, and decreased slaughter value. In recent years, the most inexpensive method for detection of the disease has been the commercially available enzyme-linked immunosorbent assay (ELISA) test. However, the ELISA test provides at best a 30% sensitivity. Speer and Eda et al., researchers from the University of Tennessee, have developed their own detection method which is not only cheaper, but more sensitive: the ethanol vortex ELISA (EVELISA) test. Using a nine-compartment system of difference equations modeling the spread of Johne's disease through a typical dairy herd, we establish that the newly created EVELISA test, along with a test and cull management strategy, provides farmers with the most cost effective method for handling their herd.

**MURPHY, C. and A. HUGHES. Gene Regulatory Networks of Rainbow Trout Enlightened by Modularity. Great Lakes WATER Institute and University of Wisconsin at Milwaukee, Milwaukee, WI.**  
See poster abstract #34

**PARISE, R, YAZVAC, R., COOPER, C. and G. YATES. Patterns of chitin synthase gene expression in the thermally dimorphic fungal pathogen *Penicillium marneffeii*. Department of Biological Sciences and Department of Mathematics, Youngstown State University, Youngstown, OH.**  
*Penicillium marneffeii* is the only member of the *Penicillium* that is known to be thermally dimorphic and capable of causing disease, and *P. marneffeii* infection is a potentially lethal AIDS-defining illness. The fungus grows as a saprophytic mold at room temperature (25°C) and as fission yeast at human body temperature (37°C). The dynamic nature of the structure of the fungal cell wall is a key factor in this dimorphism. Chitin is the most important structural polymer in the fungal cell wall, and differential expression of chitin synthase (the enzyme responsible for chitin synthesis) may be an essential step in the dimorphic switch. There are seven chitin synthase isoenzymes in the *P. marneffeii* genome: each isoenzyme produces chitin, but they differ in localization and temporal activity. Using qPCR, we characterized the expression patterns of three of these isoenzymes at 25°C and 37°C through a five day growth cycle. We used a simple Boolean network to explore the gene regulation of the chitin synthases. This network allowed us to examine gene regulation, and allowed us to predict stable states of gene expression at both temperatures. This research was funded by NSF grant DBI-0827205.

**PITTMAN, H., RICHARDS, N. and S. HOTA. Stability Analysis and Threshold Phenomena in the SIR Model with the Inclusion of Mortality. School of Natural Science and Mathematics, Fisk University, Nashville, TN.**

This project studies the SIR epidemic model taking into consideration the mortality factor. We performed the stability analysis of equilibria and determined the conditions for disease free state and the occurrence of the epidemic. Using Mathematica, some examples are explored and numerical simulations were performed to obtain the orbit graphs.

**SCHUCHART, D.<sup>2</sup>, PAULI, S.<sup>3</sup>, SUTHAHARAN, S.<sup>2</sup>, and M.C. KALCOUNIS-RUEPPELL<sup>1</sup>. Measuring Behaviors of *Peromyscus* Mice Using a Blob Tracking Algorithm Analysis of Remote Thermal Video. Departments of Biology<sup>1</sup>, Computer Science<sup>2</sup>, and Mathematics<sup>3</sup>, University of North Carolina at Greensboro, Greensboro, NC.**

Measuring behaviors of free-living, wild animals is difficult because the presence of an observer can impact the behaviors being measured. Additionally, measuring behavior of nocturnal animals is difficult because traditional methods of recording behaviors such as filming or observing from behind a blind are not possible in the dark. One solution that mitigates both of these difficulties is to use remote thermal (IR) video to record behaviors of free-living animals. Remote thermal video recording eliminates observer bias and allows for the study of animals in the dark. However, remote thermal video recording introduces a new problem in that it can generate

massive amounts of image data, especially if recording is done continuously in real time, which takes a significant time investment to process by hand. We show that using modern video and signal processing techniques, it is possible to measure behaviors directly from video data in an automated way. The species we used in our analysis were two species of *Peromyscus* mice, *P. californicus* and *P. boylii*. Over 131 nights in 2008 and 2009, continuous thermal video of free-living wild mice was recorded as part of a study to examine the behavioral context of ultrasound production by these two species. We analyzed terabytes of video to quantify behaviors associated with locomotion. As our first variable, we examined running speed. We used a C++ library called OpenCV to apply Gaussian and median filters in order to isolate the mice from the background of the video. Once the mice were isolated, we used a blob-tracking algorithm (cvBlob), which recognizes “blobs” of similar pixels as foreground, to write the location of the mice to a data file. The data file containing the location information was analyzed against time in order to generate speed data. We examined running speed in relation to species and abiotic conditions. Our speed results will be presented. Ours is the first study to quantify running speed of free living nocturnal rodents and relate these speeds to biotic and abiotic factors. Further, our study provides a method for measuring other behaviors recorded remotely from thermal video recording. Our study demonstrates that is possible to remotely record and measure behaviors from free-living mammals using blob tracking algorithms in conjunction with other modern video processing techniques.

**WILDER, S., NGUYEN, A. and A. GONZALEZ. A Modeling of the Glassy-winged Sharpshooter in Texas Vineyards. Interdisciplinary Training for Undergraduates in Biological and Mathematical Sciences, University of Houston-Downtown, Houston, TX.**

*Xylella fastidiosa* is the bacterium which causes Pierce’s disease, a grapevine disease which is vectored by the Glassy-winged Sharpshooter insect. The disease has routinely been a problem for many Texas vineyards and costs millions of dollars per year in damage. In order to understand how the disease spreads, we must have a better understanding of the temporal and spatial abundances of the Glassy-winged Sharpshooter. A database of thousands of insects was created from 50 vineyards during 2003-2008 by Dr. Forest Mitchell in Texas AgriLife Research. It was our goal to model the changes in abundance data from one region in Texas (the Texas Hill Country) over a five year period. A delay logistic differential equation was used to represent the oscillatory behavior represented by the experimental data. Simulations run in the software program MATLAB were used to determine parameter values which would fit the theoretical model to the histogram. Local behaviors were studied analytically, using the linearized model near the carrying capacity. Further modifications of the model will focus on the decaying phenomena of the solution; considerations will include environmental factors like insecticides, weed control, etc.