



2011

## **2011 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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***Third Annual***  
**Undergraduate Research Conference**  
**at the Interface of**  
**Biology and Mathematics**

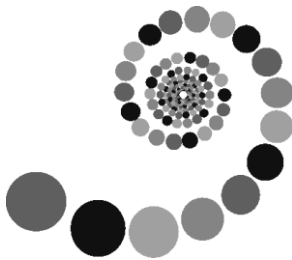
***October 21-22, 2011***

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

**CONFERENCE OVERVIEW**

Welcome! This conference is hosted by the National Institute for Mathematical and Biological Synthesis (NIMBioS), housed on the campus of the University of Tennessee-Knoxville. Undergraduate students conducting research in mathematics and biology will present 50 oral and poster presentations. A keynote by Dr. Carl Panetta will take place Friday afternoon and a panel discussion on career opportunities will be featured on Friday evening. Poster abstracts start on page 5, oral presentation abstracts start on page 11.

## **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 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 program and workshops for math and biology faculty. For more information on NIMBioS and its research and educational opportunities please visit [www.nimbios.org](http://www.nimbios.org).

## **UNIVERSITY OF TENNESSEE & KNOXVILLE**

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

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



## **INFORMATION FOR HANGING POSTERS**

There will be two poster sessions. The first will immediately follow dinner on Friday, from 7:30-8:30 pm. Presenters whose posters are assigned odd numbers will present at this time. The second will precede lunch on Saturday, 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 5.

## **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 Sturmer) to have your talk loaded onto the appropriate computer in advance.

## **SCHEDULE**

### **Friday, October 21: Conference Room 413BC**

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

1:40-2:40 Plenary Speaker: Carl Panetta

2:45-3:30 Networking Activity and Snack Break

3:35-3:45 NIMBioS Outreach: Kelly Sturner

3:45-4:30 Featured Speaker: John Jungck

4:40-4:55 Aurrielle Eberhardy, Moksha Shah, Daniel Monge: Modeling the Effects of Quagga Mussels on Cladophora Growth in near-shore Lake Michigan

5:00-5:15 Jordan Angel: Game theoretical analysis of vaccination coverage in voluntary vaccination populations with epidemic modeling

5:20-6:20 Career Panel (Moderator: Suzanne Lenhart, Mathematics, UTK)

Mitchell H. Goldman, Medicine, UTK

Michele Lynn Joyner, Mathematics, ETSU

Cynthia Peterson, Biochemistry, UTK

6:30-7:30 Buffet Dinner in 404AB

7:00 Turn in SET game sheets to Sturner or Lenhart at dinner

7:30-8:30 Poster Session I: Odd numbered posters presented (and desserts)

## **KEYNOTE LECTURE**

Dr. Carl Panetta

Department of Pharmaceutical Sciences

St. Jude Children's Research Hospital

### **Selected Examples of Mathematical Models in Cancer Treatment**

A variety of mathematical modeling methods are currently used to describe the complex effects of chemotherapy. Not only do these models help us understand the dynamics of the agents, but they provide an efficient method to explore multiple doses and treatment schedules which would be clinically impractical. Three examples of agents that have been modeled include Methotrexate and Asparaginase which are used in the treatment of childhood acute lymphoblastic leukemia (ALL) and Topotecan which is used in the treatment of pediatric neuroblastoma. In each case mathematical models are developed to describe the disposition and the mechanism of action of the agent. The models are then used to help define effective doses and treatment schedules. These model predicted treatments are compared to and validated by using current and historical clinical data.

## **FEATURED SPEAKER**

**Dr. John R. Jungck**

**Mead Chair of the Sciences and Professor of Biology**

**Beloit College**

<http://bioquest.org>

### **Three Components of Undergraduate Research: Engaging Students, Faculty Mentoring, and Curriculum Reform**

Undergraduate research is at the heart of generating a cohort of curious, innovative, original, productive, ethical, and responsible scientists and mathematicians. By engaging undergraduate researchers in interesting projects that encourages them in joining the scientific community and appreciating as well as understanding its culture rather than just learning skills, this participatory experience is usually apt to sustain them and to encourage them to stay in school, complete degrees, and pursue graduate or other professional education (see Seymour *et al.* 2004). Sociologically quality undergraduate research programs engage students in problem posing, preparing a literature review, experimental design, hypothesis testing, iterative problem solving, analysis, modeling, public presentation with feedback, peer-review, and ethical conduct issues. The faculty need to interact with students not only on the everyday practices of science, but need to respect their students' career aspirations by helping them develop skills for future education and employment as well as achieving success with the project that pertain to their labs' objectives and goals. Anthropologist of Science Robin Dunbar found that the regularly most productive labs engaged student researchers with two projects: one low risk project that was very likely to lead to a peer-reviewed publication if sufficient effort were invested; and, a second higher risk project that was likely to change the direction of the lab's work if successful. So mentoring involves both logistical and strategic considerations. By engaging students in a broad spectrum of investigator roles such as publishing, presenting, peer reviewing, and editing, mentors' advising of students will not just be on the conduct of research, but also will help them better understand and appreciate scientific culture (Jungck, Harris, Mercuri, and Tusin, 2004). Furthermore, some undergraduates have won national and international awards for the research, have published autonomously in peer-reviewed journals, and have presented widely. Undergraduate research has had a significant role in the transformation of education in classrooms, laboratories, and fieldwork. New courses, new majors, new curricula, and new national initiatives have come out of the collaborations of biologists and mathematicians who co-advise undergraduates in research. These include consortia such as the BioQUEST Curriculum Consortium, CPR (Calibrated Peer Review), and CREATE (*consider, read, elucidate hypotheses, analyze and interpret the data, and think of the next experiment*).

Chapman, Orville L., and M. A. Fiore. (2000). Calibrated Peer Review™. *Journal of Interactive Instruction Development*: 11-15.

Dunbar, Robin. (1996). *The Trouble with Science*. Harvard University Press: Cambridge, Massachusetts.

Gilbert, Scott F. (2004). A Case Against Undergraduate-only Journal Publications. *CBE LifeScience Education* 3: 22-23 (Spring).

Hoskins, Sally G., Leslie M. Stevens, and Ross H. Nehm. (2007). Selective Use of the Primary Literature Transforms the Classroom Into a Virtual Laboratory (CREATE). *Genetics* 176(3): 1381-1389.

Jungck, John R., Margaret Harris, Renée Mercuri, and Joshua Tusin. (2004). Undergraduates: Do Research, Publish! *CBE LifeScience Education* 3: 23-26 (Spring).

Jungck, John R., Ethel Stanley, Sam Donovan, and Patti Soderberg. (2000). "Crossing the Chasm" of Curricular Reform: BioQUEST Curriculum Consortium Invites CAL-laboration. *CAL-laborate* 4: 10-14.

Seymour, Elaine, Anne-Barrie Hunter, Sandra L. Laursen, and Tracee Deantoni. (2004). Establishing the Benefits of Research Experiences for Undergraduates in the Sciences: First Findings from a Three-Year Study. *Science Education* 88 (4): 493-534.

Siegel, Vivian. (2004). Weighing the Pros and Cons of Undergraduate-only Journal Publications. *CBE LifeScience Education* 3: 26-27 (Spring).

## **Saturday Morning, October 22: Rooms Auditorium 406 and 400A**

8:00 Breakfast

8:00-8:30 Faculty Networking in 400A (faculty only invited, optional)

8:40-8:55

406: Christopher Biver, Morgan Schroeder, Anne Bruckner, and Daniel Uphoff: Dynamics of Bacterial Contamination on an Urban Beach at Lake Michigan

400A: James Brunner, Emily Hendryx, Andrew Reagan, Paul Vines: A Logical Model Approach to Iron Metabolism in Breast Epithelial Cells

9:00-9:15

406: Yang Yang and Tiffany Blankenship: Statistical Tracking of Fast Movements of Organelles

400A: Canaan Coppola: Quantifying Parameters for a Mathematical Model on the Interaction of Matrix Metalloproteinases and Their Inhibitors in a Wound

9:25-10:10 Graduate School Showcase in 400A

10:20-10:35

406: Ian DeTuncq, Sehar Fatima and Kolin Konjura: Effects of River Input and Hydrodynamics on Near-Shore Silicate Dynamics in Lake Michigan

400A: Jim Kotary: A Hybrid Radial Basis Function Method for Numerical Solutions of Vascular Flow

10:40-10:55

406: Samuel Pimentel: Phylo-RLQ: a three-table ordination method for microbial community data

400A: Cecilia Noecker, Krista Schaefer and Kelly Zaccheo: Theory of Early SIV Infection

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

12:05-1:05 Lunch

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

1:10-1:25

406: Rojin Chitrakar and Shreejaya Shrestha: The Effect of Borneol on the Germination and Growth of the fungus *Beauveria bassiana*

400A: Alyson Fox & Jared Catenacci: Spatial Spread of *Wolbachia*: An Attempt to Control Dengue Fever

1:30-1:45

406: Alison Feder: The likelihood ratio statistic is overly liberal for detecting natural selection in genetic time series

400A: Lindsay Lee: Modeling feral cat population dynamics in Knox County, TN.

1:50-2:05

406: Dana Botesteanu, Frances Goglio and Yicong Yong: How does the effort a mother bird expends on her offspring depend on the attractiveness of her mate?

400A: Caleb Shimberg: Analysis of Influenza-Like Illness Outbreaks at ETSU

2:10-2:25

406: Sepideh Khavari: Mathematical Modeling and Analysis of Time-to-Peak Response in Biological Systems

400A: Jessica Holt Lunsford: Prevalence of Infection in Seasonally Forced Compartmental Models

2:30-2:50: Break and Snacks

3:00-3:15

406: Steven Minich & Amanda Sherman: Life-history traits and human risk-taking behavior.

400A: Sharon Cameron: Prisoner's Dilemma Implementation on Watts-Strogatz Networks and Real Networks

3:20-3:35

406: Amanda Sherman & Steven Minich: The influence of past and present living environments on human risk-taking propensity.

400A: Jeffrey Moulton: SPASM: Stochastic Particle Approach to Simulating Morphogenesis

3:40-3:50

406: Closing Remarks

3:50 Adjourn

## **POSTER ABSTRACTS BY SEQUENCE**

### **1. ANDERSON, V., CHISLOCK, M. The effects of *Daphnia pulex* along a productivity gradient. Department of Fisheries & Allied Aquacultures, Auburn University, Auburn, AL.**

Eutrophication can pose a serious threat to the state and productivity of freshwater ecosystems. *Daphnia pulex*, a large generalist zooplankton, can consume the phytoplankton that make up these blooms, and have a substantial impact on the size and threat of harmful algal blooms. For this experiment we wanted to answer two questions: (1) how does *Daphnia* carrying capacity relate to productivity (2) how does the grazing effect of *Daphnia* scale with productivity. Using a field experiment across six ponds that vary in productivity, we show that the effect of *Daphnia pulex* increases with nutrient enrichment. These results clearly show that biomanipulation aimed at reducing algal abundance must also focus on reducing zooplanktivory.

### **2. BLAKE, K. Sensitivity Analysis of the Wnt Pathway. Wofford College, Raleigh, NC.**

Signal transduction begins with a signal binding to receptors on the membrane of the cell. This causes a cascade of protein interactions within the cell, ending in transcription of targeted genes. The Wnt pathway is a well studied protein system that plays an important role in the proliferation and adhesion of cancerous cells. When signaled, the Wnt pathway results in a buildup of Beta-catenin, which leads to transcription of certain genes. An excess of Beta-catenin can cause cells to divide unnecessarily resulting in tumors. Other factors in the pathway, such as axin and APC, help regulate Beta-catenin buildup. In order to sift through the various protein interactions to determine the most influential, we analyze the response of a state variable to a change in the parameter, also known as sensitivity functions. Solving for sensitivity functions analytically in large models such as the Wnt Pathway is not practical because it requires computing a large number of partial derivatives. In this project, we use automatic differentiation to compute the partial derivatives related to sensitivity functions. We were interested specifically in Beta-catenin and axin because of their important role in the system, but also investigated other factors. Through our sensitivity analysis of the Wnt pathway, we were able to determine the most influential protein interactions.

**3. BLALOCK, S. and FRANCISCO, L. Is There Evidence of Trade-offs in Cognitive Ability and Immunocompetence in Adult White-footed Mice (*Peromyscus leucopus*)? Murray State University, Murray, KY.**

Parasitic infection is detrimental to people worldwide, being known to occur in over two billion people worldwide. The low levels of sanitary conditions mixed with a lack of proper medical care have allowed parasites to become extremely prevalent in many of the poorer countries. Alongside the apparent physiological effects of parasitic infection, such an infection may also affect an individual's intelligence quotient (IQ). The effect on the cognitive ability of infected individuals is thought to stem from the idea that such an infection requires an energetically costly cell-mediated immune response. The energy that it takes to activate the immune system can deplete the available energy from other areas of the body, especially during energetically intense processes such as reproduction and development. The energetic cost is partially attributed to the manufacture of antibodies, causing a loss of energy and other resources normally allocated to other biological processes, including development of the nervous system.

**4. CANTER, B. Introducing a New Antibiotic to Combat Resistance in a Hospital: A Modeling Approach. Department of Mathematics and Statistics, Institute for Quantitative Biology, East Tennessee State University, Johnson City, TN.**

Within a hospital setting, antibiotic resistance plays a major role in how we treat patients who have bacterial infections. Very few new antibiotics are being developed to combat the resistance; therefore, when one is developed, it would be beneficial to know how one should best utilize the new antibiotic to provide the greatest overall benefit from the new antibiotic. We can do this by using mathematical models. In this poster, we will present two models representing different approaches in administering the new antibiotic. The mathematical models can then be used to determine the optimal treatment strategy with the newly developed drug by showing how much a new antibiotic can help reduce the total resistance depending on the method of administration.

**5. CATENACCI, C. and FOX, A. Spatial Spread of Wolbachia-Infected Mosquitoes: A Strategy to Control Dengue Fever. University of Wisconsin, Milwaukee, WI.**

**6. COPPOLA, C. and SCHUGART, R. Quantifying Parameters for a Mathematical Model on the Interaction of Matrix Metalloproteinases and Their Inhibitors in a Wound. The State University of New York at Buffalo, Buffalo, NY and Westertn Kentucky University, Bowling Green, KY.**

See Oral Presentation Abstract

**7. DEVITA, R., MCLANE, K. and SLABE, B. Mathematical Modeling and Data Analysis of the Growth and Acetone, Butanol, Ethanol (ABE) Production of *Clostridium beijerinckii*. Department of Biological Sciences and Department of Mathematics and Statistics, Youngstown State University, Youngstown, OH.**

Although fossil fuels are currently the most economically sensible source of energy, many other alternative energy sources are presently being looked at as potential replacements for fossil fuels. Currently, millions of dollars are being spent on ethanol research. However, ethanol's energy content is only two-thirds of that of gasoline. Butanol, another alternative biofuel, has similar energy content when compared to gasoline and has been gaining increased attention recently. The genus *Clostridium* is known to carry out butanol fermentation from a variety of 5 and 6 carbon sugars. A mathematical model was developed using the known metabolic pathway, as well as basic Michaelis-Menten kinematics. Due to the complexity, the parameter dependence of the equations could not be determined in the full model. However, using a simplified model, parameter dependencies and the final state of multiple products could be determined analytically. Experiments were conducted using the bacterium *Clostridium beijerinckii* in a small-scale bioreactor. Previous studies have shown that pH has a significant effect on butanol production. The goal of this research was to find the necessary conditions for optimum yields of butanol production.



**8. ESPOSITO, D., HEITSCH, C. E., POZNANOVIK, S. and SWESON, M. S. Improved RNA Secondary Structure Prediction Using Stochastic Context Free Grammars. Department of Mathematics, Georgia Institute of Technology, Atlanta, GA.**

Accurate RNA secondary structure prediction is an important problem in computational biology. The accuracy of current prediction algorithms vary widely even for RNA sequences which fold to similar structures. To understand the origins of these inaccuracies we trained a stochastic context free grammar on a hard-to-predict training set and an easy-to-predict training set which corresponds to a set of sequences with low and high prediction accuracy respectively. We found interesting statistical differences in the nucleotide composition of the sequence as well as the distribution of nucleotide base pairs between the two training sets. Stochastic context free grammars provide a means to quantify more subtle difference in the composition of native secondary structures. The discovery of these differences could potentially lead to improvements of current prediction algorithms. We are currently performing a parametric analysis of several prediction methods.

**9. GAJERA, J. What maintains rare genotypes in nature? Old Dominion University, Virginia Beach, VA.**

A complex, ecosystem-level genetic model of many lakes and river has been developed to estimate multiple types of selection and the resultant subsequent relative fitness for multiple genotypes of a polymorphic fish. The estimates of selection and survival are based upon field and laboratory research on mosquito fish. The model allows for gene flow, immigration, emigration, Founder effects and other essential changes that will be relevant to estimating genotype stability at the ecosystem level. The main focus of this model is to determine how very rare genotypes are maintained in nature, given known estimates of predation, birth rates and other relevant parameters and variables. When all relevant estimates of survival and fitness are incorporated into the simulations, we find that rare morphs are maintained in our simulations at frequencies similar to those found in nature.

**10. GEILE, M. and YOUNG, J. A mathematical approach to polyphenisms in *Ambystoma tigrinum nebulosum*. Murray State University, Murray, KY.**

Phenotypic plasticity is a phenomenon that can be found in many organisms, and modeling the life histories of these organisms helps us better understand the process. We used 22 years of data collected from a population of *Ambystoma tigrinum nebulosum* (tiger salamanders) found at the Mexican Cut, CO to look at the production and fitness of alternative morphs. Life history data of salamanders from the 1988 cohort were evaluated with a capture-recapture analysis in MARK, to obtain the necessary parameter values (probabilities of survival and recapture) for the "popbio" package in R. Within R, we will create stochastic matrix models to incorporate fecundity and evaluate population dynamics and morph fitness. Results of our analyses will be discussed.

**11. RADETIC, M., HALL, E. and SANSOM, T. Modeling the Growth of *S. maltophilia* O2 in the Presence of Selenite with a Look at Protein Expression. Youngstown State University, Youngstown, OH. Department of Biological Sciences and Department of Mathematics and Statistics, Youngstown State University, Youngstown, OH.**

*S. maltophilia*O2 is an aerobic, gram-negative bacillus that was isolated from a mercury contaminated site in Oak Ridge, TN. This strain grows in the presence of several toxic metals, including selenite, an oxyanion of the metalloid, selenium. Selenium is an essential trace element required for the growth of most organisms, but too much (10 mM) is toxic. *S. maltophilia* O2 detoxifies selenite by reducing and precipitating it as non-toxic elemental selenium. Growth of this strain was followed in the presence and absence of 10 mM selenite by measuring culture turbidity levels and through viable cell counts. Additionally, protein expression was studied via two-dimensional gel electrophoresis to determine which proteins may confer selenite resistance. The growth of the unexposed strain followed a classical growth curve with lag, log, and stationary phases. The bacterium shifted from a log phase to a stationary phase upon exposure to selenite. Three hours later it shifted back to a log phase and produced a red precipitate. Our mathematical model is based on a system of differential equations and predicts the growth and selenite metabolism of this strain over time. The results of the mathematical model

compare favorably with experimental data throughout the growth cycle.

**12. HALLAPY, J., COPPLOE, J., JACOBOWITZ, S., JALICS, J. and M. WOMBLE. Tachykinin Modulation of Prefrontal Cortex Neuron Activity. Department of Biological Sciences and Department of Mathematics and Statistics, Youngstown State University, Youngstown, OH.**

Tachykinins are neuromodulatory peptides found in the mammalian brain and high levels of tachykinin receptors are expressed on pyramidal neurons of the prefrontal cortex (PFC). The present study used the whole cell patch clamp technique and a mathematical model to investigate the ionic mechanisms underlying the responses of guinea pig PFC neurons to senktide, a tachykinin receptor agonist. Senktide (500nM) depolarized neurons, and at -70 mV in voltage-clamp, induced an inward shift of the holding current, a change that was accompanied by a decrease in membrane conductance. Current-voltage (IV) relationships showed that the senktide-sensitive current reversed at -91.6 mV, very near the calculated potassium equilibrium potential (EK) of -93 mV. Elevations of extracellular potassium shifted this reversal potential in accordance with the Nernst equation. The response to senktide was similar to the response seen with extracellular cesium (5mM) or barium (200μM), known inhibitors of the inward rectifier potassium current (IKir). Simulations using a biophysically-based neuronal model consisting of twelve differential equations showed that decreased IKir conductance yielded responses consistent with our biological data. We thus conclude that tachykinin receptor activation on PFC neurons may result in inhibition of the potassium current, IKir.

**13. KAY, S. and J. POWELL. Modeling Predator-Prey Interactions and Canid Sociability in Curlew, Valley UT. College of Natural Resources and Department of Mathematics and Statistics, Utah State University, Logan, UT.**

We explored various models to describe the oscillating behavior of coyote (*Canis latrans*) and Black-tailed Jackrabbits (*Lepus californicus*) abundances in a sagebrush-steppe community in Curlew Valley, UT over a 31-year period between 1962 and 1993. Prominent examples of predator-prey oscillations between prey-specific predators exist, but long-term data sets showing these oscillations are uncommon. Abundance indices in this study were measured for jackrabbits using flushing transects each spring and fall in a 640 square kilometer portion of the valley. Coyote indices were estimated by catch-per-unit efforts, scent station visitation, and scat deposition rates. These values were then normalized and averaged for a single density index value for coyotes each season (Knowlton and Stoddart, 1992). The coupled oscillations appear to grow larger in the mid seventies and a permanent increase in the coyote density is apparent. Social hierarchy among canid populations may affect their response to fluctuating prey densities since pack members are less likely to be prey-selective. Seasonal structure could also be a contributing factor to population dynamics since populations tend to grow in the spring/summer when new litters are born, and resources are usually not as limiting as in the winter when stress could cause coyotes to reduce pack numbers. We tested both continuous and discrete models which accounted for a variety of mechanisms to describe details of the time series including density dependence, satiable predation, hierarchal social structure, seasonal coupling, and decadal changes in critical parameters reflecting changing abiotic stresses. Cyclic patterns every ten years were evident among both species with the coyote population having a time lag approximately three years behind the jackrabbits in all models. We used Akaike Information Criterion (AIC) values, which balance model likelihood and model complexity, to compare models. Social structure and seasonality turn out to be important factors affecting population dynamics. However, other variables could be affecting the coyote population since cycles after 1975 are not as apparent and models including changing variables did not reflect possible effects due to changes in coyote harvest rates in the late seventies, or effects from a fire that occurred in the early eighties. The results also support the idea that simpler models better fit the data and are easier to use for management purposes and for others to adopt and apply in other regions.

**14. LEE, L.E., ROBL, N., BUGMAN, A., NGUYEN, A.T.N., JENNINGS, T.L., WEIMER, H., LENHART S.M. and J.C. NEW, Jr. Modeling feral cat population dynamics in Knox County, TN. National Institute for Mathematical and Biological Synthesis, Department of Mathematics, College of**

**Veterinary Medicine and Department of Statistics, Operations, and Management Science, University of Tennessee, Knoxville, TN, College of Veterinary Medicine, University of Wisconsin, Madison, WI, College of Veterinary Medicine, University of Illinois, Urbana-Champaign, IL and Companion Animal Initiative of Tennessee, Knoxville, TN.**

See oral presentation abstract.

**15. LI, W. and H. MAMIYA. Optimization of Triplex Real-Time RT-PCR for the Detection of Norovirus GI, GII, and Rotavirus. Cadham Provincial Laboratory, Department of Medical Microbiology, University of Manitoba, Winnipeg, Manitoba.**

Norovirus is the leading cause of acute gastroenteritis outbreak, and Rotavirus accounts for the majority of severe diarrhea among infants. To ease the economic and healthcare burdens, implementing a rapid and accurate method for clinical laboratory diagnosis is a high priority. The traditional methods of detection utilizing Enzyme Linked ImmunoSorbent Assay (ELISA), gel-based Polymerase Chain Reaction (PCR), and electron microscopy have several shortcomings in terms of either multi-target distinction, accuracy, labor, or the associated costs. In this research project, we optimized a triplex real-time Reverse Transcriptase PCR (rRT-PCR), a molecular assay which allows rapid and accurate detection of Norovirus genogroup GI, GII, and Rotavirus simultaneously from clinical stool specimen. The rRT-PCR is analyzed based on a Cycle Threshold (CT) value, which corresponds to the number of amplification cycles required to yield enough fluorescence given off by the probe to exceed background levels captured by the Biorad IQ5 camera. Optimization for the PCR reaction is threefold that constitutes screening for optimal reaction temperature, primer concentration, and producing a distinct sigmoid CT curve for analysis. For validation, a more sensitive duplex and singleplex rRT-PCR was used as a reference in screening 164 random stool samples suspected of Norovirus and Rotavirus respectively. The optimized triplex rRT-PCR was able to achieve sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) of respectively 89.4%, 93.5%, 84.8%, and 82.7% for Norovirus. Rotavirus validation was able to achieve sensitivity and PPV of 92.3% and 97.3%.

**16. LIANG, S.T. Three Dimensional Food Web with Mathematica: Niche Space, Trophic Levels, Interval graph and Energy Flow. Department of Biology and Mathematics, Beloit College, Beloit, WI.**

In Ecology, three of the common diagrams used to represent community structure are: (1) food webs, (2) trophic levels, and (3) energy pyramids. Each of these captures some element of biomass productivity or energy flux between trophic levels. However, it is challenging to precisely and scientifically display the complexity of relationships among species such as: what is the niche space of each species, how much do predators compete for particular prey, and how much impact would be experienced by the removal of a species in a food web or energy pyramid? Mathematically, visualizing the relationship of predators and prey by using graph theory is capable of insight into these ecological communities. By utilizing JavaFoodWeb, the predator-prey matrix is transformed into a symmetrical predator-predator matrix and then by applying the theory of partially ordered sets, the predator-predator matrix is transformed into a “Shkurba format” in order to produce an interval graph wherein each interval is a maximal clique that identifies a “niche space.” We imported the biomass data following the structure of the niche space and trophic levels into Mathematica to re-represent the food web with a three-dimensional BarChart. We also employed Biographer to recognize the maximal cliques in a predator-predator matrix in two different ways: Circular-arc Model and Spring Model, and compute the diameter and the clustering coefficient of the graph. Furthermore, we plotted the histogram of the degree of each vertex in these graphs. With these computational properties, we verified that the linear order found in the interval graph of maximal cliques was well matched with the niche spaces, trophic levels, and energy usage. We believe that by applying fundamental graph theoretic algorithms, data visualization, and measurement of graph properties, these three-dimensional food web histograms enable a fuller comprehension of complex ecological communities.

**17. MATTHEWS, L. Effects of Multiple Past Population Bottlenecks when Inferring Population History. Departments of Anthropology and Ecology & Evolutionary Biology, Tulane University, New Orleans, LA.**

Many different researchers have searched for clues to explain the demographic history of the Peopling of the Americas several thousand years ago. Evidence has ranged from archaeology, anatomical comparison and most lately population genetics to estimate the timing and size of the population bottleneck assumed to be associated with the colonization and expansion into the New World by PaleoIndian populations. However, current studies neglect the much more recent population bottleneck associated with the European colonization of the New World in interpretations of more ancient population history. Here I run ms, a program developed by Hudson (2002) to simulate population genetics, with parameters that describe the demographic history of Native American populations. I examine the effect of one versus two past population bottlenecks on the genetic diversity to investigate the sensitivity to the estimation of recent and ancient changes in population size. Hudson, R. R. 2002. Generating samples under a Wright-Fisher neutral model of genetic variation. *Bioinformatics* 18: 337-338.

**18. NANNEY, S. Analyzing Optimality Criterion for RNA Secondary Structures Prediction. Western Carolina University, Hickory, NC.**

We describe a method of analyzing functions that score RNA secondary structures. Given a linear scoring function with unspecified coefficients, we construct polytopes that assist us in choosing a set of coefficients for which the structure with an optimal score is similar to the native structure. This was done with functions that are based on the nearest neighbor thermodynamic model (NNTM). The new sequences of various types. The accuracy of the predictions was close to the accuracy of the NNTM and exceeded the accuracy of the NNTM for certain sets of RNA sequences.

**19. NOLEN, S., ACROBETU, R., and PAUL, O. Highly Communicable Disease on an Isolated Population. Fisk University, Nashville, TN.**

This research project is based on a mathematical treatment of the epidemiology of a highly communicable disease on a small isolated population. The transmission dynamics of the disease is studied through a logistic model and the parameters critical in determining the spread of disease were found through data simulation. This model allowed for a quantitative method to predict the number of people who will be infected at a particular time and the kind of treatment plan be adopted in order to control the spread.

**20. PETERS, SAMUEL. Game Theory Analysis of Vaccination Coverage with Epidemic Modeling. Department of Mathematics and Statistics, Institute for Quantitative Biology, East Tennessee State University, Johnson City, TN.**

We consider vaccination within a population, using game theoretical modeling. Special emphasis is placed on epidemic modeling and the inherent conflict between individual interest and group interest. Our results are subjected to sensitivity analysis using Monte Carlo sampling and are summarized in histograms detailing the difference in coverage and increased mortality. Additionally, the role of perceived risk in changing the population's vaccine uptake level is graphically and analytically explored.

**21. PIMENTEL, S. Phylo-RLQ: a three-table ordination method for microbial community data. Stanford University, Stanford, CA.**

See oral presentation abstract.

**22. POSNER, J. and YANG, Y. Voronoi Diagrams Applied to *Radiolaria* Skeletons and *Drosophila* Embryos. Beloit College, Beloit, WI.**

**23. ROLAND, B. Analysis of Influenza-Like Illness Outbreaks at ETSU. Department of Mathematics and Statistics, Institute for Quantitative Biology, East Tennessee State University, Johnson City, TN.**

During the course of seven months, data was collected from the student health clinic located on the East Tennessee State University campus. The clinic reported the number of patients with influenza-like illness seen by each nurse in the facility. A model for the spread of this influenza-like illness was created using a basic single outbreak SIR model. The differential equations defining the SIR model were solved numerically using a built-in MATLAB function called ode45 (based off an explicit Runge-Kutta(4,5) integration method). In this system of equations a fourth was created to report the incidence rate of the influenza-like illness.

This incidence rate is what we are going to fit to our data in order to determine transmission rates, reproductive rates, and recovery rates. In this there are two models, one with constant parameters and another with a time-dependent transmission rate. In the second model, we used another MATLAB function called Pchip (Piecewise Cubic Hermite Interpolating Polynomial) to interpolate the values of transmission rate over the time of the data. This interpolation allows us to vary the number of interpolating values of transmission and to explore subintervals for major shifts.

**24. SHAH, M., MONGE, D. and EBERHARDY, A. Modeling the Effects of Quagga Mussels on *Cladophora* Growth in Near-shore Lake Michigan. University of Wisconsin, Milwaukee, WI.**

See oral presentation abstract.

**25. SMITH, K. Modeling the Effect of Diversity in Host Plant-Herbivore-Predator Interactions. Ursinus College, Collegeville, PA.**

**26. WURM, A., SINGH, K., AGUILAR, C., MARQUES, A., LEUNG, M-Y., ALMEIDA, I.C. Using Bioinformatics to Efficiently Organize and Analyze Significant Immunogenic Epitope Sequences in Various Stages of *Trypanosoma cruzi*. Border Biomedical Research Center, Dept. of Biological Sciences, Bioinformatics Program, Dept. of Mathematical Sciences and the Computational Science Program, The University of Texas, El Paso, TX.**

The identification of suitable epitope sequences could contribute to finding the right immunogenic element that can offer protection against Chagas disease caused by *Trypanosoma Cruzi* (*T. cruzi*), a protozoan parasite. Due to the complexity of the parasite surface, no vaccine for Chagas disease has been discovered to date. There is an urgent need of an efficient process to identify the most probable surface protein sequences capable of eliciting an immunogenic response. The aim of this project is to use existing bioinformatics tools to filter protein sequences from the *T. cruzi* parasite and to construct a Perl script to automate the process. Through mass spectrometry experiments, *T. cruzi* protein sequences were obtained. The epitope prediction software in IEDB (Immune Epitope Database) is one of the primary tools we utilize to filter the sequences and distinguish epitope sequences within the protein. Three different prediction methods, based on artificial neural networks, stabilized matrices, and average relative binding, are used to generate 3 lists of epitope candidates. We will perform a consensus analysis among these 3 lists to further improve the confidence level of the predictions. The most likely epitope candidates can then be tested in vitro for immunogenic properties.

**27. ZHENG, J., BRIMKOV, B., KOTARTY, J. and LIU, X. Optimizing the Performance of a Hybrid Method for Numerically Solving and Visualizing Vascular Flows. State University of New York, Buffalo, NY.**

The human vasculature sometimes exhibits defects such as bifurcations, stenoses, and aneurysms, which produce turbulent blood flows and can lead to medical problems. Since immediate intervention is often required to treat such problems, it is useful to have accurate models of the blood flow near the problematic areas. We employ a variety of techniques to create such models with high accuracy and speed. First, we introduce an innovative hybrid method between the high-order spectral method – which needs a strict grid restriction and is therefore used to model the smooth areas of the blood vessel – and the radial basis function method, which does not require a strict grid and is used to model the irregular parts of the blood vessel. Hence, we adopt a complex geometry while maintaining high-order accuracy. We also use the Python programming language coupled with Nvidia's CUDA parallel computation application, which lets us employ a Graphics Processing Unit (GPU).

GPUs are very efficient at manipulating computer graphics, and their highly parallel structure makes them more adept than general-purpose CPUs for algorithms where processing of large blocks of data is done in parallel. Thus, this will enable us to keep the processing times to a minimum.

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

**ANGEL, J. Game theoretical analysis of vaccination coverage in voluntary vaccination populations with epidemic modeling. Department of Mathematics and Statistics, Institute for Quantitative Biology, East Tennessee State University, Johnson City, TN.**

In populations with voluntary vaccination policies, it is possible that the vaccination coverage achieved is not the coverage level that would be optimal for the population. We use a game theory model in combination with epi-demic modeling to analyze what differences exist in vaccination uptake when individuals act in self-interest compared to the coverage that is best for the group. We define player strategies that reflect individuals acting in self-interest as opposed to the group's interest. Our results characterize the difference in vaccination uptake and the increased cost to a population due to suboptimal coverage. Additionally, we will investigate a model when individuals vaccinate based on perceived risk of vaccination versus a perceived risk of infection.

**BLANKENSHIP, T., TISDALE, C. and Y. YANG. Statistical Tracking of Fast Movements of Organelles. National Institute of Mathematical and Biological Synthesis, University of Tennessee, Knoxville, TN, University of Texas-El Paso, El Paso, TX, Auburn University, Auburn, AL, and Beloit University, Beloit, WI.**

Since the late 18th century, scientists have struggled to explain the seemingly random movement of organelles within the cell. Employing modern fluorescence microscopy, it has been revealed that organelles are moving relatively quickly along actin filaments using myosin motors. However, the direction of these movements remains unknown and a mathematical method for predicting their simultaneous movement has yet to be discovered. By taking advantage of the celebrated Kalman filter and incorporating the recorded movements of organelles via automated time-lapse imaging, an appropriate algorithm for tracking simultaneously the fast movements of these organelles is constructed. This algorithm is the first step of creating a set of robust computational mechanisms which will enable cell biologists to address further questions on organelles' movements in a quantitative fashion.

**BOTESTEANU, D., GOGLIO, F., YONG.Y, GILMAN, T., JHWUENG, T. How does the effort a mother bird expends on her offspring depend on the attractiveness of her mate? National Institute of Mathematical and Biological Synthesis, University of Tennessee, Knoxville, TN, Department of Mathematics, Mount Holyoke College, South Hadley, MA, Department of Biology, University of Wisconsin at Madison, Madison, WI and Department of Mathematics and Statistics, University of Florida, Gainesville, FL.**

The Differential Allocation Hypothesis (DAH) proposes that selection would favor individuals in a population that invest more resources in their current reproductive attempt when paired with a high-quality mate, at the expense of future reproductive attempts. Additionally, it is argued that differential allocation should take place to a greater extent in polygamous species than in those that are strictly monogamous, since these species are more likely to engage in extra-pair copulations or mate switching. In this study, a two-fold approach was used to investigate the circumstances in which DAH would occur: firstly, a mathematical model was developed to illustrate the relationship between male attractiveness and female fitness, while taking into account viability and sexual selection, and also allowing varying levels of extra-pair paternity (EPP). The model provides a theoretical framework for determining whether DAH depends on EPP, assuming that male attractiveness only signals indirect fitness benefits. Secondly, meta-analytical techniques with correction for phylogeny were used to examine data from 31 empirical studies of 20 species of birds, using egg size and egg androgen content as response variables. A multiple regression model was formed using data collected from existing literature on

avian species to determine the correlation between the male's attractiveness and EPP in the context of DAH. The goal was to verify the predictions of the theoretical model with empirical evidence.

**BRUCKNER, A., SCHROEDER, M., BIWER, C. and UPHOFF, D. Dynamics of Bacterial Contamination at an Urban Beach on Lake Michigan. University of Wisconsin, Milwaukee, WI.**

*E. coli* and *Enterococci* are indicators of sewage pollution, and understanding their transfer and life cycle is important to maintaining a clean and healthy beach. Heavy rainfall can cause runoff and sewage overflow from urban areas, contributing to bacterial contamination on the beach and in near-shore waters. To minimize these effects, rain gardens were installed in 2008 at Bradford Beach, an urban beach on Lake Michigan. A comparison of experimental data collected on Bradford Beach from 2006 to 2010 shows a decrease in *E. coli* concentrations after the installation of the rain gardens in 2008. Creating and implementing a mathematical model will reveal the most influential parameters toward bacterial levels on the beach. The first step in modeling the bacteria levels on the beach is understanding the population dynamics of the bacteria present in the sand. Experimental data indicates that there is a dependence on moisture, temperature, and nutrients. Rainfall also causes a flushing of the bacteria through the sand, which needs to be considered. There is reason to believe bacteria is transported from the sand to the water through ground-water flow. The dynamics of the ground-water flow can be modeled through a system of partial differential equations. Coupling these partial differential equations with population growth will lead to a mathematical model that can be compared with collected data.

**BRUNNER, J., HENDRYX, E., REAGAN, A. and VINES, P. A Logical Model Approach to Iron Metabolism in Breast Epithelial Cells. University of Michigan, Ann Arbor, MI.**

Iron metabolism is a tightly regulated intracellular network consisting of numerous regulatory feedback loops. Changes in this network have been observed in connection with cancers in breast and other tissues. Because of the network's complexity and apparent importance in cancer biology, we simulated intracellular iron metabolism using a discrete logical mathematical model, from which we created a polynomial dynamical system for analysis. This model includes the main regulatory elements of the network as well as the proteins involved in heme synthesis. By adjusting the logical model, we simulated many different experiments with little extra computational effort. This use of mathematics allows us to gain insight as to which species are crucial to cancer cell survival without the expense of laboratory time and materials. The state space of the model and model perturbations successfully replicated experimental results, and simulations suggest that misregulation of the iron regulatory network is necessary to meet the increased iron demand of a neoplastic cell.

**CAMERON, S. Prisoner's Dilemma Implementation on Watts-Strogatz Networks and Real Networks. Department of Mathematics and Statistics, Institute for Quantitative Biology, East Tennessee State University, Johnson City, TN.**

Prisoner's Dilemma is a game theoretical model that considers two opposing strategies: Cooperation and Defection. Cooperators play an altruistic strategy, while defectors play a selfish strategy. In a two-player homogeneous situation, we see that defection is the best strategy because playing a selfish strategy and not helping your neighbor yields a higher payoff. However, biologically we see that this result is unrealistic as cooperation persists in small clustered communities. In order to create a more realistic situation, we limit the interactions of individuals to neighboring players in a network. We play this game on the Watts-Strogatz simulated network as well as networks created from gathering real data. Playing Prisoner's Dilemma on a network representing real data can help us understand how a seemingly unbeneficial strategy can persist throughout a network.

**CHITRAKAR, R., SHRESTHA, S., WISNIEWSKI, C., LIU, W., THIBERT-PLANTE, X., GWINN, K. and V. PROTOPODESCU. The Effect of Borneol on Spore Germination and Germ Tube Growth of the Entomopathogenic Fungus, *Beauveria bassiana*. National Institute for Mathematics and Biological Synthesis and Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN.,**

**Eastern New Mexico University, Portales, NM, Wesleyan College, Macon, GA, Southeast Missouri State University, Cape Girardeau, MO, Oak Ridge National Laboratory, Oak Ridge, TN.**

Borneol, an essential oil secreted by the monarda plant, has antifungal and antipathogenic properties, which make it a potential substitute for synthetic pesticides. The entomopathogenic fungus, *Beauveria bassiana*, has the ability to grow inside plants and induce resistance to many plant pathogens and insects. Stacking the beneficial effects of borneol and *B. bassiana* could be used as a potentially more efficient biological control mechanism. The goal of this study was to assess the effect of borneol on the germination and growth of the *B. bassiana* spores. To this end we used data from three separate trials. For each trial, we plotted (i) the percentage of germinated spores as a function of concentration and (ii) the germ tube lengths for different concentrations of borneol at four time periods, during a twenty-four hour time period. An analytical mathematical model based on gamma distribution of spore germination and growth was developed to examine the effects of the oil on the germ tube length and percent germination of *B. bassiana*. Upon more extensive study and validation, the model could be used to predict effects of borneol on *B. bassiana* at different concentrations and time periods, and harness borneol and *B. bassiana* for disease control.

**COPPOLA, C. and SCHUGART, R. Quantifying Parameters for a Mathematical Model on the Interaction of Matrix Metalloproteinases and Their Inhibitors in a Wound. The State University of New York at Buffalo, Buffalo, NY and Westertn Kentucky University, Bowling Green, KY.**

In this work, we present a mathematical model for the interactions of matrix metalloproteinases (MMPs), which degrade the extracellular matrix (ECM), and their inhibitors (TIMPs), and quantify the parameters by fitting the model to data. Measurements of the ratio of MMPs-to-TIMPs may be critical to a successful wound-healing event because an imbalance of these proteins is often found in chronic wounds. Muller et al. measure levels of MMPs and TIMPs in wound fluid. The data were divided into two subgroups – good healers and bad healers – based on healing rate, and averaged for each subgroup. The parameters in the four-equation model, consisting of MMPs, TIMPs, ECM, and fibroblasts, were fit using the commands “GlobalSearch” and “fmincon” in Matlab. Reasonable parameter values were obtained by minimizing a least-squares functional.

**DETUNCQ, I., FATIMA, S., and KONJURA, K. Effects of River Input and Hydrodynamics on Near-Shore Silicate Dynamics in Lake Michigan. University of Wisconsin, Milwaukee, WI.**

Silica plays a significant role as a nutrient in aquatic ecosystems especially by limiting the growth of certain phytoplankton, including diatoms which are important to food webs. Despite this importance, the cycling of silica in freshwater lakes is poorly understood, especially in near-shore regions. It is not known to what extent near-shore silicate concentrations are affected by benthic sources, or runoff from significant riverine sources. We explored this in near-shore Lake Michigan using flow data for the Milwaukee River during 2008-2011 and comparing with dissolved and particulate biogenic silicate data. The data indicates significant fluctuations in both near-shore (2-30  $\mu\text{M}$ ) and riverine (100-250  $\mu\text{M}$ ) dissolved silicate on a weekly time scale. By comparing the silicate concentrations in the near-shore region to silicate supplied by the river (using river flow data sets) and silicate supplied by deep water upwelling (using with the wind speed, wind direction, and temperature fluctuations) we attempted to determine the major sources of silicate. Our results did not show strong correlations between weather data and near-shore dissolved silicate. Weak relationships were found between riverine outflow and near-shore dissolved silicate. We are currently applying a hydrodynamic model (based on the Princeton Ocean Model) to integrate silicate dynamics with near-shore mixing.

**FEDER, A. and PLOTKIN, J. The likelihood ratio statistic is overly liberal for detecting natural selection in genetic time series. Department of Biology, University of Pennsylvania, Philadelphia, PA.**

A significant body of literature is devoted to detecting natural selection from genetic data sampled from a population at a single time point. Here, we investigate how to detect selection in genetic time series data, such as are increasingly available from high-throughput sequencing technologies. We appraise heuristically derived statistics by comparing simulations of Wright-Fisher populations with and without selection across population sizes and timescales. We find that most heuristic statistics lack statistical power. We then move to a maximum-



likelihood framework and investigate biases in the chi-squared likelihood ratio statistic, both through calculations using a diffusion approximation and from exact discrete Markov Chains. We find systematic overestimation of the population size by maximum-likelihood. Furthermore, when the sample size is small, the likelihood ratio statistic deviates significantly from the chi-squared distribution, such that the chi-squared assumption is overly liberal and inflates the rate of type I errors. We quantify the extent of false positives with respect to population size, sample size, number of generations, and the frequency of samples. We then propose a more conservative test that corrects the deficiencies of the chi-squared likelihood-ratio statistic.

**FOX, A. and CATENACCI, J. Spatial Spread of Wolbachia: An Attempt to Control Dengue Fever. Loyola University Maryland, Baltimore, MD, University of Wisconsin, Milwaukee, WI.**

Dengue is a disease transmitted by the mosquito species *Aedes aegypti*. Currently, strategies for controlling dengue rely upon reducing the mosquito population. An alternative method involves releasing mosquitoes infected with *Wolbachia*, a vertically transmitted bacterium that reduces a mosquitoes' ability to transmit dengue virus. The spread of *Wolbachia* is made possible by cytoplasmic incompatibility, which reduces the hatch rate of eggs laid by uninfected females that mate with *Wolbachia*-infected males. We developed a discrete time deterministic and stochastic metapopulation models to study the spread of *Wolbachia*. Using numerical simulations we studied different release strategies and the effects of fitness costs and movement rates on the speed at which *Wolbachia* spreads through populations (wave speed). In addition, we studied the effects of heterogeneous populations by varying subpopulation size. We found that simultaneously releasing *Wolbachia* into multiple, neighboring subpopulations increases the ability of *Wolbachia* to spread for a wider range of fitness and migration rates. When we allowed for heterogeneity in subpopulation size, the wave speed decreased and was more sensitive to fitness costs and movement rates. Differences in wave speed between the stochastic and deterministic models were also discovered. Which model gives a faster wave speed is dependent on the value of the fitness parameter. Overall, we found that under a variety of conditions, *Wolbachia* can spread through multiple subpopulations and *Wolbachia*-infected mosquitoes can replace an existing population.

**KHAVARI, S. Mathematical Modeling and Analysis of Time-to-Peak Response in Biological Systems. Department of Mathematics and Statistics, Youngstown State University, Youngstown, OH.**

The process of sending and receiving signals in response to environmental changes such as fluctuations in concentration of hormones, neurotransmitters, growth factors, and drugs is a part of a complex network of cellular communication in living organisms. We present a theoretical framework that first examines a simple reaction,  $AB$  with a regulating function  $f(t)$ , to establish various properties of the response variable  $B(t)$ . The qualitative properties of  $B(t)$  include its non-negativity, existence for all time, and the presence of a unique maximum. We use ordinary differential equation and analysis proofs to establish these and other properties. Furthermore, we extend this theoretical framework to incorporate more complex signaling networks including feedback and degradation. This model has applications in the pharmaceutical field for designing drugs with extended release time and chemotherapy treatments. This work is based on the recent publication by Theis et al., *Bull Math Biol* (2011) 73: 978-1003 which we extend to include nonlinear features.

**LEE, L.E., ROBL, N., BUGMAN, A., NGUYEN, A.T.N., JENNINGS, T.L., WEIMER, H., LENHART S.M. and J.C. NEW, Jr. Modeling feral cat population dynamics in Knox County, TN. National Institute for Mathematical and Biological Synthesis, Department of Mathematics, College of Veterinary Medicine and Department of Statistics, Operations, and Management Science, University of Tennessee, Knoxville, TN, College of Veterinary Medicine, University of Wisconsin, Madison, WI, College of Veterinary Medicine, University of Illinois, Urbana-Champaign, IL and Companion Animal Initiative of Tennessee, Knoxville, TN.**

Feral cats (*Felis catus*) are recognized as a problem internationally due to their negative impact on wildlife, their potential to spread infectious disease to people and other animals, and much of society's perception of them as nuisances. Trap-neuter-return (TNR) programs, a popular method employed to control feral cat populations, are currently used on a limited basis in Knox County, Tennessee. Despite the frequent use of TNR programs, their

effectiveness remains controversial. Here, we present a mathematical model to predict population shifts of feral cats in selected managed colonies under the current TNR program. We predict feral cat population changes for closed colonies over a period of five years in one month time steps for three age classes. We tested different TNR parameters to assess how targeting spay/neuter programs seasonally might better address the feral cat problem. Current TNR efforts lack specific targeting and possess limited ability to curb population growth. Seasonal targeting of TNR efforts at a 53% spay rate of all age class predicted a zero percent growth and stabilization of the feral cat population growth over a five year period compared to non-targeting which would require TNR efforts throughout the year at 60% and a higher number of total spays. Seasonal targeting at a 100% spay rate of the only adult age class showed the most dramatic population decline with the fewest total number of spays required over the five year period. Non-targeting at a 100% spay rate of only the juvenile age class throughout the year gave a decline after two years but requires a greater number of total spays. Targeting TNR intervention at adult females during the time prior to mating season (December – February) in areas highly populated by feral cat colonies may further decrease the feral cat population. These results suggest a more efficacious and economical strategy than non-targeted TNR programs, and provide a humane and cost-effective alternative to trap-euthanasia (TE).

**LEUNG, M-R., PADILLA, D., SHEMER, N., VINAGERA, J., and SONG, B. A Symmetric Intraguild Predation Model for the Invasive Lionfish and Native Grouper. Mathematical and Theoretical Biology Institute, Arizona State University, Tempe, AZ.**

Lionfish are top-level venomous predators native to the Indo-Pacific Ocean. Over the past decade, the species *Pterois volitans* and *P. miles* have become established throughout most of the western Atlantic Ocean, where they are drastically impacting coral reef communities. Overfishing of native species, such as grouper, who share their niche may be the reason for the lionfish's success; research suggests that at high density, groupers can act as a lionfish biocontrol. To determine if competition or predation is the mechanism behind lionfish suppression, we construct a symmetric intraguild predation model of lionfish, grouper, and their prey. Thus, we assume lionfish and grouper compete for prey in addition to consuming the other species. Holling type I functional responses are used to represent fecundity and predation. We conduct an equilibrium stability analysis and bifurcation analysis of the general model, and find that coexistence is feasible as a steady state or in sustainable oscillations. Simulations and a sensitivity analysis indicate that grouper mortality is more influential on the system dynamics than is lionfish mortality, suggesting that conservation of native species may be more effective than the current efforts to harvest lionfish.

**LUNSFORD, J. H. Prevalence of Infection in Seasonally Forced Compartmental Models. Department of Mathematics and Statistics, Institute for Quantitative Biology, East Tennessee State University, Johnson City, TN.**

Seasonal Infection modeling is used to describe the behavior of infection during various seasonal cycles within a fixed population. We use compartmental differential equations to achieve an understanding of the behavior of each aspect of infection and transmission that is assigned to each equation. We carry out with graphical data based upon calculated sensitivity equations that are compared over time for each of the parameters involved in the model.

**MOULTON, J. SPASM: Stochastic Particle Approach to Simulating Morphogenesis. University of Pittsburgh, Pittsburgh, PA.**

We construct a stochastic modeling tool, called SPASM, to analyze the dynamics of groups of moving cells. In our modeling framework, cells exist as groups of particles. Each particle represents a fixed volume, and particles interact through fluid and/or elastic forces. Stochastic noise represents dynamics of the cytoskeleton. Our tool includes options for a cell cortex and extracellular matrix, and allows the user to control cell stiffness and the viscosity of the environment. We ran many simulations to test our modeling framework. To analyze the biological process of cell sorting, we distributed cells of different types and varied adhesive strengths between cells. We found that a high ratio of homogeneous adhesion to heterogeneous adhesion caused some cell sorting

to occur. We placed cells above an adhesive surface, representing a plate used in experiments, to observe the change in aspect ratio (height/width) of the cells. A higher adhesive ratio caused the cells to round out slightly on top. SPASM can simulate mitosis and cell growth. Although many dynamic cell models already exist, ours is one of the first to include both fine details of individual cells and adaption to large tissues.

**MINICH, S., SHERMAN, A., LANGEN, T., SKUFCA, J. and WILKE, A. Life-history traits and human risk-taking behavior. Department of Mathematics, Clarkson University, Potsdam, NY.**

From an evolutionary perspective, human risk-taking behaviors should be viewed in relation to evolutionarily recurrent survival and reproductive problems. In response to recent calls for domain-specific measures of risk-taking, we emphasize the need of evolutionarily valid domains. We report on a recent study designed to validate a scale of risky behaviors in domains selected from research and theory in psychology and biology, which correspond to reoccurring challenges in the ancestral environment. Behaviors were framed in situations which people would have had some chance of encountering in modern times. Our domains of risk-taking included between-group competition, within-group competition, status, environmental challenges, food selection, food acquisition, parent-offspring conflict, kinship, mate attraction, and short-term and long-term mating strategies. We examine the effects of several life-history variables and early environmental factors on an individual's risk propensity.

**NOECKER, C., SCHAEFER, K., ZACCHEO, K., SMALLWOOD-SATCHELL, S., YANG, Y., DAY, J. and V.V. GANUSOV. Modeling the First 7 days of HIV Infection. National Institute for Mathematical and Biological Synthesis, the Mathematics Department and Department of Microbiology, University of Tennessee, Knoxville, TN. Department of Biology, St. Olaf College, Northfield, MN, Department of Mathematics and Computer Science, Valparaiso University, Valparaiso, IN, Department of Mathematics, University of Scranton, Scranton, PA.**

Since its first appearance in the human population, HIV has infected 1.7 million individuals in the United States. Despite this fact, HIV is a poorly transmitted virus with less than 1 out of 100 to 1000 acts of sexual intercourse resulting in virus transmission. The factors that contribute to and could potentially explain why the probability of transmission is so small are poorly understood. It is nearly impossible to study HIV replication in the first 2-3 weeks of infection because the virus is not detectable until after this time period. Simian immunodeficiency virus (SIV) in non-human primates has been used as a model for HIV infection to detect virus replication in tissues within the first 2 weeks post-infection. In this paper we use mathematical modeling to investigate which virus and host parameters greatly affect the probability of establishing an infection and the time that the infection takes to become detectable in the blood. Our model includes two types of infected cells, eclipsed cells and infected cells, varying because of the viral count in the blood, and it incorporates stochasticity and the spatial distribution of uninfected target cells. The Gillespie algorithm was used for the stochastic implementation of the model and NetLogo software was used to analyze spatial relationships between host cells and virions. We found that the probability of viral infection depends strongly on the type of infectious agent used: with one virion starting infection,  $\pi = .188$ , while when infection started with an eclipse phase and an infected cell  $\pi = .559$  and  $.642$ , respectively. The probability of infection strongly depends on the dose of the infectious agent and the mechanism that is used, and there are significant differences in times to infection between the deterministic and stochastic models. The spatial results demonstrate that local concentrations of target cells play a critical role in the probability of viral infection; in many cases, virus extinction due to depletion of uninfected target cells can lead to a very low probability of establishment of infection, which is very consistent with experimental data on HIV transmission via heterosexual route.

**PIMENTEL, S. Phylo-RLQ: a three-table ordination method for microbial community data. Stanford University, Standord, CA.**

Recent developments in sequencing technology have made it possible generate species abundance data for microbial communities within human and animal bodies. These abundance counts may exhibit dependencies on environmental factors measured at individual sites and on phylogenetic relationships between bacterial species.

These dependencies must be described and accounted for in order to appropriately analyze diversity in these datasets. Specifically, a three-table ordination method incorporating species abundances, environmental variables, and phylogenetic association is needed. A new method called phylo-RLQ is proposed, based on the RLQ method of Dolédec and Chessel (1996) which chooses axes maximizing co-inertia between two tables linked by a third. Phylogenetic dissimilarity data is adapted for use in phylo-RLQ by constructing a lag matrix, a concept from spatial statistics. Phylo-RLQ is demonstrated on simulated data and on a real data set from fecal samples of salmonella-infected mice. In these examples it selects axes that distinguish species according to the main branches of the phylogenetic tree and helps identify environmental variables of interest for further study. While the current form of phylo-RLQ makes limiting assumptions and uses potentially sub-optimal weights for phylogenetic data, it provides a starting point for exploratory diversity analysis of a microbiome.

**SHAH, M., MONGE, D. and EBERHARDY, A. Modeling the Effects of Quagga Mussels on *Cladophora* Growth in Near-shore Lake Michigan. University of Wisconsin, Milwaukee, WI.**

The invasive mussel *Quagga burgensis* was first noticed in the Great Lakes in the late 1980's. Since then its population has grown incredibly and the environment itself is impacted by their filtering behavior. Each quagga mussel filters continuously and in the course of 24 hours will have filtered ~1L of water. The clarity of Lake Michigan waters has continued to increase due to this and has led to an increase in the biomass of a green alga, *Cladophora*, as well as a decrease in phytoplankton populations. We formulated a one-dimensional model showing the phosphorous dynamics of the benthic layer, including the phytoplankton as a source of phosphorous, the excretion of soluble reactive phosphorous by the quagga, and the uptake of phosphorous by *Cladophora*. We use the model to explore scenarios under different environmental forcing conditions, such as increased temperature profiles and changes in the availability of primary producers in the benthic layer.

**SHERMAN, A., MINICH, S., LANGEN, T., SKUFCA, J. and WILKE, A. The influence of past and present living environments on human risk-taking propensity. Department of Psychology, Clarkson University, Potsdam, NY.**

Humans internalize environmental cues at an early age, which influences their subsequent risk-perception and risk-taking behavior. In the current study, we examined the effects of several life-history variables (such as age, sex, number and order of siblings, level of education) and early environmental factors (e.g. prevalence of violent and property crime), on an individual's perception of risk in past and present environments. We designed and administered an ecological survey to investigate which variables in an individual's living environment correlate to their current risk-taking behavior when going out for the night. We expected that individuals who were exposed to high-risk environments in childhood would be less inclined toward risky behaviors than individuals who grew up in less dangerous areas. Participants provided three zip code locations, enabling us to compare the actual demographics of their past and current environments with their subjective ratings of risk/danger at each location.

**SHIMBERG, C. Analysis of Influenza-Like Illness Outbreaks at ETSU. Department of Mathematics and Statistics, Institute for Quantitative Biology, East Tennessee State University, Johnson City, TN.**

During the course of seven months, data was collected from the student health clinic located on the East Tennessee State University campus. The clinic reported the number of patients with influenza-like illnesses seen by each nurse in the facility. A model for the spread of this influenza-like illness was created using a basic single outbreak SIR model. The differential equations defining the SIR model were solved numerically using a built-in MATLAB function called ode45 (based off an explicit Runge-Kutta(4,5) integration method). In this system of equations a fourth was created to report the incidence rate of the influenza-like illness. This incidence rate is what we are going to fit to our data in order to determine transmission rates, reproductive rates, and recovery rates. In this there are two models, one with constant parameters and another with a time-dependent transmission rate. In the second model, we used another MATLAB function called Pchip (Piecewise Cubic Hermite Interpolating Polynomial) to interpolate the values of transmission rate over the time of the data.

This interpolation allows us to vary the number of interpolating values of transmission and to explore subintervals for major shifts.

**SMITH, K. Modeling the Effect of Diversity in Host Plant-Herbivore-Predator Interactions. Ursinus College, Collegeville, PA.**

Predator and plant diversity can control Potato leafhopper (PLH) pest damage to the host-plant Alfalfa, used to feed cattle. New mathematical tools and computer simulations are used to construct deterministic models using systems of differential equations with particular emphasis of the damsel bug Nabid, a major predator of the PLH. The PLH damage done to alfalfa is costly, and pesticides are unsafe. Recent data and results on enemies and diversity hypotheses, in both enclosure and open-field experiments, were used to determine accurate parameter ranges and validate the models. Effects of diversity are introduced using the Shannon Index. Two models are constructed using explicit and implicit age structures, and logistic, Beverton-Holt, and Allee effect modeling approaches. Simulations are analyzed to examine the roles of the parameters in reducing the alfalfa damage. Uncertain parameters are adjusted for the models to fit the experimental data and predict outcomes for scenarios not covered by both the enclosure and open-field experiments. In conclusion, the project provides a framework for designing cost-effective and environmentally safe strategies to minimize alfalfa damage, determine critical parameters, and utilize enemies' hypothesis and polyculture diversity.

**KOTARY, J., BRIMKOV, B., LIU, X., J. and ZHENG, J. A hybrid radial basis function method for numerical solutions of vascular flows. State University of New York, Buffalo, NY.**

Detailed configuration of hemodynamics in human vasculature is a crucial part for successful surgical judgment and treatment. Vascular flows in most areas of the vasculature can be described as laminar flows, but some can be turbulent near irregular geometric areas such as bifurcations, stenoses, and aneurysms.

These turbulent flows can cause significant issues in healthy hemodynamics. Thus, obtaining accurate flow behaviors around these areas is an important task.

High-order numerical methods such as the spectral and the high-order finite difference methods can be used to capture such complex behaviors. These methods, however, need a strict grid restriction for the complex geometry. To redeem this, we develop a hybrid radial basis

function (RBF) method. The RBF method is known as a mesh-less method and yields high-order accuracy for smooth problems. Hence, with the RBF method, a complex geometry can be easily adopted and a high-order accuracy can be obtained.

We hybridize the high-order method and the RBF method. For the smooth area the spectral method is implemented with a relatively small grid resolution, while the complex geometry is efficiently covered by the RBF method. To make the hybridization function properly, we develop an efficient and stable patching algorithm.