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Fourth Annual

Undergraduate Research Conference
at the Interface of
Biology and Mathematics

November 17-18, 2012

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 60 oral and poster presentations. A keynote by Dr. Christine Heitsch and featured talk by Dr. John Glasser will take place Saturday afternoon and a panel discussion on career opportunities will be featured on Saturday evening. Graduate opportunities will be showcased on Sunday morning. Poster abstracts start on page 6, oral presentation abstracts start on page 18.

NIMBioS

So what is NIMBioS? The National Institute for Mathematical and Biological Synthesis is a center that brings together talented researchers in the fields of math and biology from all over the world. At NIMBioS, researchers work to cross the boundaries of their disciplines and address the many questions and challenges of 21st century biology. Currently in its fourth year, NIMBioS is sponsored by the National Science Foundation and the Departments of Homeland Security and Agriculture, with additional support from the University of Tennessee-Knoxville. NIMBioS also coordinates many educational programs including a summer research experience for undergraduates program and workshops for math and biology faculty. For more information on NIMBioS and its research and educational opportunities please visit www.nimbios.org.

UNIVERSITY OF TENNESSEE & KNOXVILLE

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

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

INFORMATION FOR HANGING POSTERS

There will be two poster sessions. The first will immediately follow dinner on Saturday, from 7:30-8:30 pm. Presenters whose posters are assigned odd numbers will present at this time. The second will precede lunch on Sunday, from 11 am to noon, and posters assigned even numbers will be presented. Please hang up your poster as soon as possible. Refer to the poster listing in this booklet to find your assigned number. Posters will all be hung in the hallway outside auditorium room 406. Find your assigned space and use the tacks provided to affix it to the wall or poster board. Poster abstracts and numbering start on page 6.

INFORMATION FOR ORAL PRESENTERS

Refer to the schedule to find your presentation time and room number. You will have 15 minutes to speak and including a few minutes for questions. Also, note the nearest meal or break before your presentation. At that time, please see a meeting moderator (Dr. Suzanne Lenhart or Kelly Sturner) to have your talk loaded onto the appropriate computer in advance.

Social Media at URC 2012

Have you heard? Social media is the rage for communicating science, and NIMBioS is connected to you! Get connected to the NIMBioS URC 2012 before you arrive in Knoxville.

Twitter

NIMBioS staff will be using Twitter for live updates, highlights from sessions, and more. You can follow us by visiting https://twitter.com/NIMBioS. Twitter users can just login and click "follow."

View and join in conversations about URC 2012 on Twitter by using the hashtag, #urc12. If you don't have a Twitter account, you can still view our updates and even bookmark the NIMBioS Twitter webpage.

Facebook

NIMBioS is also on Facebook: http://www.facebook.com/nimbios
Look for pictures and blog posts from the URC shared on this medium – or share your own.

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

SCHEDULE

Saturday, November 17: 413AB (Except where noted)

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

1:40-2:40 Plenary Speaker:
Christine E. Heitsch, Associate Professor of Mathematics, Georgia Institute of Technology
From Plato to Pasteur and Beyond: the Combinatorics of RNA Viruses

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

3:35-3:45 *Opportunities at NIMBioS*
Kelly Sturner, Education & Outreach Coordinator at NIMBioS

3:45-4:30 Featured Speaker:
John W. Glasser, Mathematical Epidemiologist, Centers for Disease Control and Prevention
Modeling Sexually-Transmitted Infections as Simply as Possible

4:40-4:55
406: Tara Thean: *Signature whistle models in free-ranging bottlenose dolphins,* Tursiops truncates
413AB: Sarah Bogen: *Modeling the spread of white-nose syndrome in hibernating North American Bats*

5:00-5:15
406: Karrisa Yang and Joe Strini: *Importance of spatial scale in the study of biodiversity*
413AB: Eric Jalbert: *Phase plane analysis of a double degenerate biofilm model*

5:20-6:20 Career Panel (Moderator: Suzanne Lenhart, Associate Director at NIMBioS)
Alison Buchan
John Glasser
Christine Heitsch

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

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. Christine E. Heitsch
Associate Professor of Mathematics
Georgia Institute of Technology

From Plato to Pasteur and Beyond: the Combinatorics of RNA Viruses

The interface of mathematics and biology has many facets, distinguished by both the biological applications and the mathematical motivations. We discuss here the problem of RNA folding which lies at the intersection of discrete mathematics and molecular biology. As we will illustrate, new theorems in combinatorics are helping to answer the question, "Is there a cure for the common cold?"

FEATURED SPEAKER

Dr. John W. Glasser
Mathematical Epidemiologist
Centers for Disease Control and Prevention

Modeling Sexually-Transmitted Infections as Simply as Possible*

Two approaches suitable for modeling the spread of sexually transmitted infections (STIs) in human populations have complementary strengths and weaknesses. Cross-classified population models typically require fewer, more transparently if not reliably estimated parameters than individual-based ones. And they can be analyzed, providing the generality desirable for public policymaking. As an example, we present a 2-gender, *n*-group SIRS (Susceptible, Infected, Recovered, Susceptible) model and describe its use to evaluate screening women (and men) for chlamydia, doubling the number evaluated post-treatment to ensure that they were cured and have not since been re-infected, and treating their partners. But social phenomena allegedly responsible for differences in the prevalence of sexually-transmitted diseases are more easily represented via individual-based models. Subtle differences in sexual behavior that may have consequences vis-à-vis transmission, for example, are not easily represented via differential equations. Individual-based models are complex stochastic processes that must be simulated – typically many times or in large populations with each set of control parameters (e.g., medical services to patients' partners) – because their successive realizations invariably differ. Most people have several partners during their lives, and some experiment with new relationships before terminating unsatisfactory ones. Partnerships that overlap or follow closely enough in succession for pathogens to be transmitted person-to-person are the means by which STIs spread in human populations. Most network models are descriptive (and were, until recently, static), but modeling to inform public health policymaking about the impact of possible interventions targeting influential people (i.e., those who affect pathogen diffusion disproportionately) must be mechanistic, and mechanistic network models are dynamic. We describe a dynamic sexual partnership network model whose predictions have been compared with published observations to remedy any disparities.

*JW Glasser, HW Chesson, K Owusu-Edusei, and TL Gift

Sunday Morning, November 18: Rooms Auditorium 406 and 413AB

8:00 Continental Breakfast

8:00-8:30 Faculty Networking in 413AB (faculty only invited, optional)

8:40-8:55

406: Natalie Stanley: *The role of incoherent miRNA feed-forward loops in gene regulatory network robustness*

413AB: Sara Schaal, Francis Yankey, Yang Xie, Tim Zeidler: *Analysis and development of a predictive mathematical model for light attenuation in Lake Michigan*

9:00-9:15

406: Kurtis Mann: *Creation of CellTwitch software to perform mechanical experiments on cardiac cells*

413AB: Caitlin Ross: *The impact of life history structures on the evolution of altruism*

9:25-10:10 Graduate School Showcase in 413C

10:20-10:35

406: Courtney Bruce: *Secondary aneurysm formation due to the effects of a primary aneurysm*

413AB: Nathan Kopp and Colin Teberg: *Discerning the effects of natural selection and genetic drift using a modification of Tajima's D statistic*

10:40-10:55

406: Andrew Gibson and Bryce Frazier: *Using a Glazier-Graner-Hogeweg approach to model the embryo in* Caenorhabditis elegans

413AB: Theresa Dalmut and Emily Cate: *Modeling fitness of* Onthophagus taurus: the effects of density on mating success

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

Sunday Afternoon: Rooms Auditorium 406 and 413AB

12:05-1:05 Lunch

1:10-1:25

406: Jessica Robins: *Agent-based model for Johne's disease dynamics in a dairy herd*

413AB: Michael D. Harris: *Synthesis of alpha-helical peptide (AAAAK)4AAAAY*

1:30-1:45

406: Noah Dukler: *Modeling the spread of disease on small-world networks with adaptive host behaviors*

413AB: Carol Wu: *Modeling the dynamics between yeast and bacteria*

1:50-2:05

406: Ryan Landrith, Andrea Calderon and Nhan Le: *Modeling the relationship between visceral leishmaniasis incidence and the proportion of post-kala-azar dermal leishmaniasis cases treated into remission*

413AB: Tracy Spears Gill: *Estimating risky sexual behaviors among college students using optional unrelated question RRT models*

2:10-2:25

406: Sarah Kramer: *Modeling the impact of vaccination versus antiviral treatment on influenza epidemics*

413AB: Anna Tuck: *Estimating parameters for optional unrelated-question randomized response models*

2:30-2:50: Break and Snacks

3:00-3:15

406: Eric Mooring: *Modeling the epidemiological impact of continuity in influenza vaccination*

413AB: Thomas Parrish: *Determinants of free-ranging mouse activity based on remote thermal video analyses*

3:20-3:35

406: Jessica Lunsford: *Mitochondrial iron: a mathematical model for iron regulatory disease*

413AB: Arielle Nivens: *Modeling Salmonella dynamics within a finishing pig farm: group structure effects on transmission*

3:40-3:50

406: Closing Remarks

3:50 Adjourn

POSTER ABSTRACTS BY SEQUENCE

1. ALLAN, C. and AGUSTO, F. Agent Based Avian Influenza Model with Human - Human Transmission. Department of Mathematics and Statistics, Austin Peay University, Clarksville, TN.

Reported outbreaks of the highly pathogenic H5N1 Avian Influenza virus continues to rise globally, increasing the fear of a pending pandemic influenza. These fears have been calmed by the understanding that the virus' main mode of transfer was avian origin and was only contagious among birds or from bird to mammal. Transmission of the virus from mammal to mammal had never been confirmed until recently. In September 2011 Ron Fouchier, a virologist from Earsmus MC in the Netherlands announced that he had been able to genetically modify the H5N1 virus, enabling the virus to pass among ferrets, an animal that closely mimics human reaction to the virus. In another lab, Yoshihiro Kawaoka, a virologist from the University of Wisconsin, also was able to modify the virus with similar results. News of publication of both research findings has raised concern in the areas of biosecurity and public health. These concerns raise the following questions: “What if this modified highly pathogenic virus, which is highly transmissible in humans, is unleashed into the public? At what rate would the virus transfer from human to human? Would this modified virus react the same way as if it had naturally mutated on its own? If control interventions were to be used, what would be the results of a timely intervention versus an untimely intervention?" In this project we develop an agent base model that gives insight to these questions.

2. AMORIM, A. Modeling Predator-Prey Population Cycles of the Canadian Lynx and Snowshoe Hare. Mathematics Department, Marshall University, Huntington, WV.

Alterations in predator-prey interactions can have a dramatic effect on an ecosystem; modeling this relationship can provide insight into the extent and consequences of the effect. Many models and adaptations exist to study different aspects of this relationship such as focusing on environmental factors or accounting for multiple predators. Here, the focus is on modeling the population cycles to determine the effects one has on the other. I use previous research and data to graph the population cycles and discover patterns and relationships between these two species. Using a variation of the Lotka-Volterra predator-prey model, I manipulate the capture and conversion efficiencies to analyze the population dynamics. I assume that the capture and conversion efficiencies are functions of time and determine these efficiency functions for Canadian lynx and snowshoe hare data. I analyze the resulting functions to study the effect the populations have on each other. Based on this analysis, I offer suggestions to improve my model and further my research.

3. BAUMHOFER, E., STUNTEBECK, J., MEYER, G., BARRY, K. and LAUKO, I., Patterns of emergence in a southeastern Wisconsin hibernaculum, University of Wisconsin Milwaukee, Milwaukee, WI.

The Neda Mine is one of the three largest hibernacula in Wisconsin. Bats begin emerging from hibernation in early April and emergence is complete by late May. Not much is known about environmental factors that influence bat activity when they are emerging from hibernation. Bats feed on insects and they may be triggered by similar emergence cues. Bat activity at the mine was monitored using an infra-red photo beam-break detection system that records the number of bats entering and leaving the mine on a 5-minute interval 365 days per year. Temperature data was collected using 20 battery-powered temperature dataloggers and 2 dataloggers outside. Airflow data was collected with an anemometer at the culvert of the mine. Insects were collected with a suction trap.

We modeled bat activity and insect activity in spring, to determine if bats and insects respond to similar cues. We examined the role of Julian day, temperature, airflow, and barometric pressure as drivers of daily emergence of bats. When examining bat emergence Julian day gave us the only significant relationship. When modeling insect emergence we examined the role of Julian day, pressure, temperature, and rainfall. A significant relationship was found between insects, Julian day, and temperature.

4. BECKER, C., and MAROLT, C. Validating the Use of Field Measurements for Estimating Body Fat in Lizards. Truman State University, Kirksville, MO.

The objective of this study was to test the validity of using a body condition index (BCI) as a tool in determining if fat content is an indicator of fitness in the lizard Sceloporus undulatus. Past studies have suggested that BCIs would be a valid tool in predicting fitness through body fat content. The presence and amount of body fat in an animal indicates that the animal is able to meet maintenance demands, which is evidence of fitness. Measurements of weight and snout-vent length were taken from specimens from Missouri and Colorado which were used to create a collection of viable BCIs. In determining the specimen's fat content, liver, ova, and fat bodies were dissected. No differences in BCIs were found for specimens of different sex and site. BCI was also found to be independent of water content and morphological measurements. However, it was found that reproductive state of the female could influence BCI. Overall, the BCIs were found to be a poor indicator of total body fat for small lizards, making the BCIs an invalid tool.

5. BOEDEKER, D., BURKE, J., CAMPBELL, M and BECK, J. Phylogenetic Tree Browsers in Marker-Assisted Gene Selection Studies, Departments of Agricultural Science and Computer Science, Truman State University, Kirksville, MO.
Maize is the world's most largely traded feed grain, yet the naturally occurring biodiversity of this crop is diminishing. To demonstrate the value of this diversity, Dr. Campbell and associates at the Germplasm Enhancement of Maize (GEM) project have bred a high-amylose maize line, GEMS-0067, incorporating unadapted tropical genetic material into the line with the intention of making it available for commercial use. The data collected by the Campbell laboratory is being integrated into a database for use as the basis of an interactive, computerized phylogenetic tree browser interface. Important features of this system are to allow for cross-generational comparison of data on several maize lines and to compare of data of different types, including phenotypic and genotypic data, quickly and efficiently. Principle functions of the browser will be to confirm the predictions made from the pedigree of the GEMS-0067 maize line, assist in the creation of further studies of GEMS-0067 through marker-assisted selection, and determine previously undetected patterns in the characteristics and inheritance of the high-amylose phenotype in GEMS-0067.

6. BREWER, H., BLAKE, M., LYONS, A., MUMMERT, A., and ANTONSEN, B. Biomechanical Modeling of the Praying Mantis Strike. Mathematics Department, Marshall University, Huntington, WV.
The Praying Mantis prey capture strike is a remarkably rapid movement. Resilin, a 97% effective elastic protein found in arthropods, has been studied in multiple jumping systems, where it acts as a spring storing energy to produce quick, forceful movements. The Praying Mantis strike will be investigated in terms of resilin using a multidisciplinary approach combining a gross anatomical analysis of the presence of resilin, mathematical models, and a 3-D model, which allows for simulation of the strike based on collected data. In this poster, two mathematical muscle models are compared; the first model containing two components, a series elastic component and a parallel elastic component, that have spring-like qualities, and the second model containing just one spring-like component that encompasses the components from the first model. The simulation of the strike is presented using Animatlab, a 3-D program in which both mathematical muscle models can be incorporated. These two models are compared using the data and simulation to conclude which better represents the Praying Mantis strike.

7. BRUCE, C., BELTRAN, B., BURKOW, D. and S. ERICKSON. Secondary Aneurysm Formation due to the Presence of a Primary Aneurysm. Mathematical and Theoretical Biology Institute, Arizona State University, Tempe, AZ.
Intracranial aneurysms are localized dilations of arterial vessels located around the Circle of Willis, an important network of arteries at the base of the brain. Aneurysms are at constant risk of hemorrhage; however, the number of benign cases carried by the populace, the dangers of treatment, and the risk of recurrence often null the efficacy of preventative surgery. Although the mechanisms behind the formation of individual intracranial aneurysms have been thoroughly modeled as the consequence of local hemodynamic conditions, previous simulations have concentrated on single aneurysms. Using OpenFOAM, an open source fluid dynamics toolkit, we model how changes in the hemodynamics within the Circle of Willis caused by the presence of a primary aneurysm can facilitate the formation of a secondary aneurysm. We determined the change in risk of developing a secondary aneurysm on the anterior communicating artery given a primary aneurysm at the bifurcation between the posterior communicator artery and the basilar artery. We found an average decrease in wall shear stress at the anterior communicating artery of 0-4\%. Further, the necessary theory behind modeling turbulent flows with the Reynolds-Averaged Navier-Stokes equations is exposited.

8. BURKETT, B. and MELARA, L. Mathematical modeling of Panama disease in Cavendish bananas. Shippensburg University, Shippensburg, PA.

The Cavendish banana has served global consumers for half a century and has remained unaffected by most types of Panama diseases. Currently, one type of Panama disease, fusarium oxysproum f.sp. cubense, targets the Cavendish banana. We propose a simple mathematical system of ordinary differential equations, based on an SI epidemic model, describing the interactions between susceptible, exposed and infected bananas. To lengthen survival of healthy bananas plants, infected bananas plants are removed from plantations. In our study, we consider various harvesting parameter values and present preliminary numerical results.

9. CAI, W. and MITCHELL, J. Computer-based design of de novo permutated beta sandwich. Department of Mathematics, University of Wisconsin – Madison, WI.
Investigation of structurally similar proteins is of great interest to studies in protein folding, de novo protein design, and interface recognition process. For example, we are currently interested in the protein family with immunoglobulin-like (Ig-like) fold, which consists of a beta-sandwich of seven or more strands in two sheets with a Greek-key topology. Such motifs are often involved in interactions with other proteins sharing similar Ig-like folds. However, the investigation is usually not easy since structure alignment is sequence independent. In this study, we aim to generate an algorithm that can efficiently permutate protein on the basis of 2D structure pieces, in order to search for potential proteins that are energetically favorable, with similar topology but different sequence. The de novo permutation of the protein of interest can also be applied to structure stability studies, where we hope to reveal the importance of certain 2D structure segments in protein folding.

10. DURAN, R.L. and ORTIZ, A. Developing a platform to enhance the oral bioavailability of novel pharmacophores via a protein drug delivery system for treatment of cancerous and neurodegenerative diseases. The University of Texas at El Paso, TX.
Nitrosative stress has recently been demonstrated as a crucial causal in the pathogenesis of Parkinson's and Alzheimer's diseases. Specifically, increased levels of NO disrupt the redox activity of protein-disulfide isomerase which leads to aggregation of misfolded proteins. We have demonstrated in vitro that polyphenolic phytochemicals, curcumin and 3,5-Bis(2-fluorobenzylidene)-4-piperidone (EF24), can rescue S-nitroso-PDI formation by scavenging NOx adducts. In our current research, we will explore the ligand-protein binding of 4 novel pharmacophores (pyridineamine platinum (II) complexes) which exhibit similar anti-cancerous effects. Spectrofluorimetry will determine the binding efficacy of these novel pharmacophores to β-lactoglobulin and human serum albumin. Binding of these novel pharmacophores to the milk protein and human transport protein ensures delivery to the microvilli of the intestine where it can be absorbed and transported directly into the systemic blood system. Based on a theoretical model, we propose a method for extracting the binding constants and corresponding binding site concentrations. According to this model, protein-ligand binding curves are solutions to a given linear second order partial differential equation. This method could be an alternative to the standard method of finding dissociation constants and concentrations using least squares methods. The results from this technique will allow us to guide protein-ligand docking experiments.

11. EARHART, A. and TARTER, E. Describing Tropical Termite Nest Growth and Decline Patterns Using Logistic Growth Models. Departments of Biological Sciences and Mathematics & Statistics, Murray State University, Murray, KY.
We are investigating nest growth, decline, and longevity of the termite, Nasutitermes acajutlae on St. John, USVI via mathematical models. We have collected natural history data on > 200 N. acajutlae nests from five major habitat types spanning the years 1998-2012. We developed an adaptive logistic model using nest volumes capable of describing the patterns of nest growth and decline from year to year for each habitat. We observed that growth, decline, and general nest size patterns were typically unrelated between habitats. Using this model, it is possible to estimate when nests first appeared and their likely longevity, enabling us to

effectively determine the average nest lifespan for each habitat. In the future, we will incorporate both abiotic and intrinsic biotic variables to estimate their effects on nests in each habitat. This will allow us to predict the efficacy of termite degradation in tropical ecosystems in changing environmental conditions.

12. FLYNN, J., LIBRA, G., HAMMOND, T. and MA, J. Modeling the Effect of Elevated CO2 on Phosphorus Uptake in Common Bean (Phaseolus vulgaris). Departments of Biology and Mathematics, Truman State University, Kirksville, MO.

Plant growth is dependent on below ground resources including water and mineral availability, and above ground resources of light and CO2. Among these variables, atmospheric CO2 is projected to double, although soil minerals, particularly phosphorus, are often in short supply and becoming increasingly limited. Elevated CO2 could lead to a higher rate of photosynthesis and increased plant growth. However, the long-term growth response to elevated CO2 also depends to a large extent on the availability of mineral nutrients. In this study, we investigated how the dynamics of phosphorus uptake in common bean plants was affected by CO2 supply. Plants were cultured hydroponically in two growth chambers of high (700 ppm) or low (400 ppm) CO2, and under either optimal (2 mM) or suboptimal (0.5 mM) phosphorus availability for 45 days, during which growth media were sampled every four days for phosphorus analysis. Using appropriate fitting techniques with the data, we built models that describe the temporal profile of phosphorus uptake during plant growth under varied CO2 and phosphorus conditions. Our data indicate that phosphorus uptake is faster with increased CO2, causing depletion of phosphorus earlier in the growth period before reproductive growth stage, which could lead to reduced yield.

13. FORD, E., REAL, C.C., CRESPO GARCIA, P., FITZGERALD, M., and GIORGETTI de BRITTO, L.R. Decrease of neuroinflammation markers in the beneficial effects of exercise in hemi-Parkinsonian rats. Laboratory of Cellular Neurobiology, Department of Physiology and Biophysics, University of São Paulo, São Paulo, Brazil and Laboratory of Behavioral Neuroscience, Department of Psychology, University of Tennessee, Knoxville TN.

Parkinson’s Disease (PD) involves loss of dopaminergic neurons in the substantia nigra pars compacta (SNc), which is correlated to astrocytic and microglial changes. Physical exercise protects the brain, but its relationship to astrocytic and microglial behavior is still unclear. We investigated the exercise-induced changes on those inflammatory processes in a rat model of PD induced by striatal injections of 6-hydroxy-dopamine (6-OHDA). Adult male Wistar rats were divided into two groups: (1) sedentary (S) or (2) exercised (treadmill 3 times per week for one month prior to surgery at the speed of 10 m/min for 40 min; EX). The rats were then divided into four sub-groups: (1) sedentary saline (SED+SAL), (2) sedentary 6-OHDA (SED+6-OHDA), (3) exercised saline (EX+SAL), (4) exercised 6-OHDA (EX+6-OHDA). Seven days after surgery, brains were collected for immunohistochemistry and immunoblotting for dopaminergic and glial markers into SNc and striatum (CPu). One-way ANOVA with the Tukey post hoc test ($p<0.05$) was used.

There were decreased levels of tyrosine hydroxilase in the SNc and CPu of the SED+6-OHDA group. Astrocytic activation into SNc was higher in SED+6-OHDA in relation to the other groups (ca. 100%), whereas microglia increased only in the CPu (ca. 36%). Levels of inducible nitric oxide synthase increased in SED+6-OHDA in the SNc (ca. 133%) and CPu (ca. 87%). Exercised groups exhibited reduced damage to dopaminergic cells, as demonstrated by a higher tyrosine hydroxylase expression after lesions, and reduced neuroinflammatory markers.

These results indicate that physical exercise may reduce neuroinflammation after 6-OHDA and therefore reduce its impact on dopaminergic neurons.

Supported by FAPESP, CAPES, NAPNA – USP & CNPq (Brazil) and MHIRT (USA).

14. FRAZIER, B. E., GIBSON, A. K., THATCHER, S., and WALSTON, T. Using a Glazier-Graner-Hogeweg Approach to Model the Embryo in Caenorhabditis elegans. Department of Biology and Department of Mathematics and Computer Science, Truman State University, Kirksville, MO.

Caenorhabditis elegans is a non-parasitic roundworm that is used as a model organism for embryology. It has an uncomplicated body design, short life cycle, small number of cells, and is relatively inexpensive. In this study, we are building upon an existing Glazier-Granier-Hogeweg (GGH) model of the four-cell embryo of C. elegans. The GGH model offers a flexible and easy approach for modeling cellular dynamics, such as tumor growth and cell-based morphogenesis. Our model includes cell surface area, cell volume, and cell adhesion in order to replicate the forces influencing cell movement within the embryo. Initial and target values for these parameters were obtained from videos of embryogenesis. The model aims to reproduce cell shape in the four-cell embryo by using a Genetic Algorithm that searches for optimal volume, surface area, and cell adhesion parameters. By accurately modeling the four-cell embryo, our understanding of mutations that affect cell shape and movement could be enhanced. We hope to expand our model to include centrosome movement, use additional geometric measures and eventually include cell division.

15. HARRIS JR, M.D. Synthesis of α–helical peptide (AAAAK)4AAAAY. Middle Tennessee State University, Murfreesboro, TN.

Clarification of protein structure (such as α-helix, β-sheet etc.) is important to correlate the function of a protein with its structure. X-ray crystallography is a powerful technique to elucidate the protein structure in atomic level. However, X-ray crystallography requires proteins to form a single crystal structure and lots of proteins do not meet this requirement. Therefore, the development of the novel technique which is able to address the structure of non-crystallized proteins is important. Recently, FTIR has been reported to be able to clarify the structure of a peptide with 13C isotopic labels in D2O water. On the other hand, the peptide with 25 residues (with a sequence of (AAAAK)4AAAAY) has been shown to be a model peptide of α-helix. Since α-helix is a fundamental type of protein structure, we attempted to apply the 13C labeled FTIR technique to clarify the structure of (AAAAK)4AAAAY. In this paper, (AAAAK)4AAAAY was synthesized and the success of the synthesis was confirmed by mass spectroscopy.

16. HEROLD, K., THATCHER, D., HOFFMAN, K., and ROBINSON, P. A Mathematical Model of Melanopsin Activation. Department of Biological Sciences. Department of Mathematics & Statistics. University of Maryland, Baltimore County, Baltimore, MD.

Melanopsin is a photopigment found in intrinsically photosensitive retinal ganglion cells (ipRGCs). Melanopsin is involved in many non-image forming responses, including the pupillary light reflex, circadian rhythm regulation, and light related disorders such as seasonal affective disorder. A mathematical model was developed to describe melanopsin's activation using the law of mass action to translate the chemical cascade, from G-protein activation to the opening of ion channels, into a system of differential equations to be solved using Matlab. The solution was fit to whole-cell patch-clamp recordings of ipRGCs, as well as calcium imaging readings taken from human embryonic kidney (HEK) cells. An analysis of the sets of model parameters that represent the best fit of the model to the regressions suggests that, for both the HEK cell response and the ipRGC response, the rate of melanopsin isomerization by light, the first step in the cascade, and the rate of ion channels opening, the final step, are the rate limiting steps. Additionally, a sensitivity analysis reveals that the same parameters that are most sensitive for the model in ipRGCs are most sensitive for the model in HEK cells. These results suggest that the HEK environment does not change fundamental aspects of the phototransduction cascade.

17. HEWGLEY, P. and GILCHRIST, M.A. Improving codon evolution models using complex mutation models. Department of Ecology & Evolutionary Biology, University of Tennesssee, Knoxville, TN.

We improve our Stochastic Evolutionary Model of Protein Production Rate (SEMPPR) by revising the method by which we model mutation. SEMPPR previously assumed unbiased mutation, an assumption whose inaccuracy is made clear by observed codon counts of low-expression genes, where mutation dominates. We present a new, more complex model generalized on a per-codon basis, calculated from observed codon frequencies using a maximum likelihood framework. Results obtained from SEMPPR using the codon specific mutation model proved more accurate in predicting a protein's production rate, and show that complex mechanisms govern codon mutation rates.

18. HOLZ, E. and MAKI, K.L. Settling Dynamics of a Contact Lens. Department of Biomedical Engineering and School of Mathematical Sciences, Rochester Institute of Technology, Rochester, NY.
Studying the settling dynamics of a contact lens over the surface of the eye is of great importance to manufacturers; once these dynamics are better understood, the lens can be optimized for patient comfort and ocular fit. A contact lens is subjected to forces from both the tear film in which it is immersed as well as those of an eyeblink, and in response, the lens bends and stretches. These forces allow for proper lens centration, and they create the suction pressure responsible for keeping the lens on the corneal surface. In our work, we coupled fluid and solid mechanics to determine the most prominent forces acting on the lens. The ultimate goal of the project was the formulation of a mathematical model that predicted the changes in pressure distribution and lens shape over time, allowing us to explore the role of the different forces in influencing centering and lens fit. This model's results facilitated the development of an in vitro experiment to further study the effects of contact lenses on overall ocular health. This work is in collaboration with Bausch + Lomb.

19. LIU, L. Mathematical Modeling of Human Physiology for Glycaemia Control with Applications to Diabetes: modular system design and implementation. Case Western Reserve University, Cleveland, OH.
There is large body of modeling work on physiology of glycemia and diabetes that aims to simulate itsbasic components and processes, and apply it to analysis of symptoms, diagnostics, and drugtherapies.The so-called *minimal model* of Bergman-Cobelli is widely used in diagnostics of glucose tolerance, but has limited scope and utility outside its direct task. On the opposite side arecomplex physiological models. However, they are difficult to assessdue to their complexity.
Our goal is to develop an intermediate-level "whole-body" system that could be used to explore a wide range of physiological conditions and interventions on individual and community level. As a starting point, we adopted the model and methodology proposed by T. Sorensen (1985),and its extensions.
To implement Sorensen system we adopted Wolfram Modeler tool integrated into Mathematica computational platform. We implemented and tested Sorensen model in the Wolfram Modeler setting, and conducted several numeric experiments to identify parameters of insulin sensitivity. Eventually, weplan to adopt it as part of the "agent-based methodology" for diabetes: risk analysis, prediction and control.(This research is part of an ongoing project by D. Gurarie, with S. Bolen and N. Dawson to develop an agent-based approach for type II diabetes)

20. LOMBARDI, J. Stochastic Modeling of *Wolbachia* Infected Mosquitoes. University of North Carolina, Asheville, NC.
Dengue fever, caused by a mosquito-borne virus, affects millions of humans each year, and there are numerous public health costs and concerns associated with the spread of the disease. Currently, there are no prophylactic drug treatments or vaccinations available to guard against infection, so control of the disease relies primarily on controlling the principal mosquito vector, Aedes aegypti. One proposed vector control strategy is to introduce mosquitoes infected with the bacterium Wolbachia into a native mosquito population. Mathematical modeling of mosquito population dynamics, dengue epidemiology, and Wolbachia dynamics

can help assess the feasibility of Wolbachia-based vector control methods for controlling dengue fever. We developed a stochastic model to study the spread of Wolbachia in a mosquito population and used numerical simulations and analytic approaches, when possible, to quantify whether introducing Wolbachia into a native population is a viable and effective strategy.

21. LUNSFORD, J. Mitochondrial iron: a mathematical model for iron regulatory disease. East Tennessee State University, Kingsport, TN.
Using a mathematical model that incorporates both the cytoplasm and mitochondria, we simulated the pathway of iron regulation in the cell. In particular we use seven nonlinear differential equations to model the disturbances in iron homeostasis brought about by low/ high extracellular iron levels as well as frataxin protein deficiency (which results from the genetic disease Friedreich's ataxia). Numerical and stability analysis suggests that there is a unique stable equilibrium. This is biologically significant as this robust feature is observed in the actual cell. We use sensitivity analysis to identify key processes responsible for bringing the cell to iron homeostasis. Our in-silico experiments show the importance of combined gene therapy in counteracting cell death due various iron regulatory diseases. Our mathematical findings suggest some potential treatment options.

22. MANIFOLD, S. Stability Analysis of Predator-Prey Models in Continuous Network Domains. Department of Biology, University of California, Riverside, CA.
Population ecologists use a variety of analytical and computational models to study species interactions and dynamics. Combined with field data, these models are important in making predictions about how population stability and persistence respond to perturbations of environmental conditions over a variety of spatial scales. However, there is a lack of analytically tractable models which focus on the effect of spatial heterogeneity in complicated continuous spatial domains. Existing partial differential equation (PDE) models which consider a continuous spatial domain are usually restricted to simple geometries such as the interval or disk. Other models which consider more complicated geometries usually do so by parsing space into discrete patches or nodes. Using Quantum Graphs, a modeling structure that has been largely restricted to quantum chemistry and physics, it is possible to use the machinery of PDEs on a continuous network domain to more accurately reflect how barriers of movement and intricate geometries can affect population dynamics. I construct a nonlinear reaction-diffusion system on a continuous network and present methods for analyzing stability properties of predator-prey systems. In particular, I examine ways in which graph structure influences the onset of Turing Instability. Particular attention has been paid to the case of Star and Tree graphs, though general trends and areas of further inquiry are noted.

23. MILES, C., PETTY E., HINKELMANN F., BRANDON M., and LAUBENBACHER R. Sensitivity Analysis of Discrete Biological Models Using Polynomial Dynamical Systems. Lafayette College, Easton, PA, SUNY Geneseo, Geneseo, NY, Mathematical Biosciences Institute, The Ohio State University, Columbus, OH, Virginia Bioinformatics Institute, Virginina Tech, Blacksburg, VA.
Discrete biological models are often intuitive to construct and able to reveal the qualitative dynamics of a complex system. Sensitivity analysis, which provides insight toward the effect of perturbations and uncertainty in a system, is typically regarded as essential in the modeling process. While methods for performing sensitivity analysis of continuous models have been studied extensively, far fewer analogous methods exist for discrete models. In this presentation, a novel method is proposed for performing sensitivity analysis on discrete models based on analogous continuous model techniques. The method of quantifying sensitivity is based on artificially introducing unknown parameters to the model and comparing the resulting dynamics to the original model. A mathematical framework, namely polynomial dynamical systems, is used to algebraically compute the dynamics of models with unknown parameters, a computation that might otherwise be

computationally infeasible without the developed theory. An implementation of the algorithm is publicly available as a Macaulay2 package and was applied to published gene regulatory networks to provide a benchmark for the sensitivity of discrete biological models.

24. PELLOCK, S. and THOMPSON, A. Testing Darwin's Naturalization Hypothesis Using Generalized Linear Models. Departments of Biological Sciences and Mathematics & Statistics, Murray State University, Murray, KY.
Naturalization is the process of introduction and establishment of an exotic or nonnative species in a novel environment. Darwin's naturalization hypothesis states that if a nonnative plant species is introduced into an environment with few native congeners, the nonnative species will have greater chance of being naturalized. To test this hypothesis we used approximately 800 plant species of Kentucky and selected particular traits of the plants, such as growth form, life span, flower and fruit type, native origin, habitat type, etc. to determine what type of traits or factors affect the probability of successful naturalization. We used generalized linear models to investigate the success or failure of naturalization of nonnative plants with various combinations of variables. Results of our analyses will be discussed.

25. PENNINGTON, H. and KRISHNA, N. Quantifying Parameters for a Mathematical Model on the Interaction of Matrix Metalloproteinases and Their Inhibitors in a Wound. Western Kentucky University, Bowling, KY.
For this research, we aim to quantify parameters for a mathematical model describing interactions among matrix metalloproteinases (MMPs), their inhibitors (TIMPs), the extracellular matrix (ECM), and fibroblasts in a diabetic wound. By comparing the data taken from Muller et al., we created a functional which minimizes the sum of the squares of the error. Using MatLab's "globalsearch" and "fmincon" functions, we minimized the functional by selecting an initial set of parameter values and having MatLab identify the local minimum value. MatLab's "globalsearch" algorithmically selected additional parameter values and either identified a local minimum for the selection or tested another set of parameter values if the results were not improved with the selection. The smallest of the local minimum values was used to identify the optimal parameter values. We extended the model by including a variable for the TGF-β, which better coupled the equations. A parameter sensitivity analysis is to be conducted.

26. PEREZ, A., DILLON, J., LI, W., GILCHRIST, M., and CHAI, J.J.. Modeling Protein Genome Evolution. National Institute for Mathematical and Biological Synthesis, Knoxville, TN, University of Texas, El Paso, TX, University of Scranton, Scranton, PA, Luther College, Decorah, IA, University of Tennessee, Knoxville, TN.
We have observed a specific tendency in the genetic code. On amino acids with multiple synonymous codons, we see redundancy in using specific codons over the others. This selection referred to as codon usage bias remains unexplained. Basing our model in our theory that codon usage bias is driven by effective ribosome use makes sense considering that some codons stall the ribosome more than others and these faster translating codons are the ones we are seeing to be favored by this bias. When applying our model to a whole genome S. cerevisiae after getting the MAP values against some empirically measured protein production rates (phi values) we observe a correlation of 0.67. Since there is some kind of experimental error in these measured values we can never achieve a 1 to 1 correlation. However, since our model is based solely on population genetics and probabilities greater accuracy can be achieved if we take into consideration more biological phenomena and add that information to our model. More importantly we now can leap from a genotype, mutation bias, and elongation times to predict protein production rates in genomes where production rates haven't been empirically measured.

27. PROVENCHER LANGLOIS, G. Mathematical Optimization of Timed Thrombopoietin Therapy for Cyclical Thrombocytopenia. McGill University, Montreal, QC.

Patients with cyclical thrombocytopenia, a rare blood platelet disorder, demonstrate abnormally large periodic fluctuations in their platelet count over time. Such individuals are at risk of bleeding or forming blood clots as their platelet count vary from near-zero to extremely high levels. Little is known about the causes of the disorder, and standard treatments of platelet diseases with thrombopoietin, the main protein which regulates platelet production, are usually very ineffective. The relative timing of thrombopoietin treatment with respect to circulating levels of platelets and thrombopoietin is critical for a positive clinical response.

We have developed a mathematical model of platelet regulation to investigate the possible pathways to cyclical thrombocytopenia, and compared our theoretical results with clinical data. Using our results, we simulated different intravenous and subcutaneous thrombopoietin administration protocols and studied the response of platelet growth to both thrombopoietin dose and timing with respect to platelet count in the blood.

Our findings identified key physiological parameters associated with the onset of oscillations in platelets. The timing of thrombopoietin administration with respect to the fluctuating platelet levels is crucial in obtaining a positive response. These findings demonstrate the necessity for clinicians to design intelligent thrombopoietin administration protocol to treat cyclical thrombocytopenia.

28. ROCHE, K., GRIMES, L., HALL, W., DHILLON A. GROVER J., KOJOUHAROV, K. Staphylococcus aureus and its Small Colony Variant. Department of Biology and Department of Mathematics, University of Texas at Arlington, Arlington, TX.

Staphylococcus aureus, known as golden staph, is a Gram-positive bacterium that exists in two forms: a wild type and a Small-Colony Variant (SCV). S. aureus is a very prevalent bacterium in the human body, as is another species, Pseudomonas aeruginosa, which produces a signal molecule that causes S. aureus to transition from wild type to SCV. The SCV phenotype is resistant to standard antibiotics, therefore likely to cause recurring infection, as seen in cystic fibrosis patients. A mathematical model is presented for the transition between the wild type and SCV S. aureus in a chemostat culture with a nutrient medium that provides S. aureus with the signal molecule. The corresponding system of differential equations represents the population dynamics of these two variants. Analysis of this system yields three equilibria, one of which is the trivial- a condition in which neither population persists. The stability of the equilibria varies, depending on the supply of the critical nutrient, iron, and the dilution rate of the chemostat. When either nontrivial equilibria represents a meaningful (positive) population, the populations each persist at this equilibrium. When neither are positive, the populations do not persist. All theoretical results are supported by a set of numerical simulations.

29. RUSSELL, B. Using Partial Differential Equations to Model and Analyze the Treatment of a Chronic Wound with Oxygen Therapy. Department of Mathematics, Western Kentucky University, Bowling Green, KY.

Chronic wounds plague approximately 1.3-3 million Americans. The treatment of these wounds requires knowledge of the complex healing process of typical wounds. With a system of partial differential equations, this project attempts to model the intricate biological process and to describe neutrophil concentrations, oxygen levels, and other biological parameters with respect to time and space. Solutions for this model will be sought in the form of travelling wave solutions. To do so, the system is first reduced to two ordinary differential equations, on which we perform both a linear stability analysis without the diffusion of neutrophils and then a perturbation analysis with very little diffusion of the neutrophils. The system of equations will be numerically solved using Matlab. Future work on the system includes modifying both the model and the solutions in order to provide further insight about current oxygen therapy techniques and specifically how they affect the chronic wound site.

30. SANTANA, L., CAMERON, J., GRANERA, L.D., JAWORSKI, P. and ANGELOS, J. Discrete Models with Proportional Harvesting. Skidmore College, Saratoga Springs, NY, University of Texas, Austin, TX, Yale University, New Haven, CT, Central Michigan University, Mt. Pleasant, MI.

Difference equations used to model populations are analyzed. We show how to control stability and induce chaos using proportional harvesting. In particular, we use the Beverton-Holt and Ricker models with proportional harvesting to demonstrate that a harvested system can be more stable than its unharvested counterpart.

31. SCHAAL, S., XIE, Y., YANKEY, F., ZEIDLER, T., AGUILAR, C., CUHEL, R., LAUKO, I. and G. PINTER. Correlation between light attenuation and transmission in Lake Michigan and the impact of Dreissena bugensis. Department of Mathematical Sciences, School of Freshwater Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.

The non-indigenous species Dreissena bugensis (quagga mussel) recently became the dominant benthic species of Lake Michigan. Its rapid proliferation and extreme filtering activity across the region is re-engineering the biological processes of the lake on the ecosystem scale by altering the lake's physical and biogeochemical processes. This study concentrated on the impact of quagga mussel filtering on optical properties of the water column. Visible light characteristics of the water column were computed based on CTD data collected from 1993 to the present. Using Matlab software, extinction coefficients were calculated for the water column on a given day (sample range from 0.02582/m to 0.2311/m) and depths of 1% light were calculated for pre-quagga (average: 29.79m, maximum: 46.13m) and post-quagga periods (average: 36.98m, maximum: 55.63m). We also investigated seasonal variation in depth of 1% light. Analyses indicated significant changes at the deep mid-lake station, and less pronounced changes at inshore stations. Our study suggests that there is a correlation between percent transmission and extinction coefficient values, and that comparative analysis of perturbations in both measurements may detect thin layers in the water column.

32. SIGNORIELLO, A. and FIORENTINO, N. Stochastic Models of an Antibiotic-Resistant Nosocomial Infection. Ursinus College, Collegeville, PA.

Approximately 10% of U.S. hospital patients acquire a clinically significant nosocomial infection. These infections have been linked to increased mortality (about 100,000 deaths per year) and increased costs. About one-third of infections contracted in intensive care units (ICU) are caused by Vancomycin-resistant enterococci (VRE). This project emphasizes the use and comparison of stochastic modeling approaches to derive and analyze models for VRE infections in an intensive care unit. Stochastic models are derived from a deterministic model that incorporates the difference between colonization and infection, the role of special preventive care treatment cycles, the compliance rate, and the effect of antibiotic use. For a dynamical system with small population size, uncertainty in parameters, and variability in transitions, stochastic differential equations can produce more realistic models. Modeling procedures include using Discrete-time Markov chains, Continuous-time Markov chains, and Euler-Maruyama’s method utilizing diffusion matrices and Wiener processes. The models account for randomness and simulate transitions between the five population states in an ICU. Computer techniques created simulations to visualize and compare the models. The results were analyzed with the ultimate goals of providing an understanding of the VRE dynamic, preventing outbreaks, and determining the most efficient and economically favorable strategies to control VRE.

33. STRINI, J., YANG, K., KRUSE, H., WRIGHT, A.J. Testing the effects of spatial scale on the relationship between biodiversity-productivity in savannah ecosystems.Departments of Biological Sciences and Mathematical Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.

Biodiversity impacts ecosystem function significantly.Past research shows that productivity saturates at a small number of species compared to the overall number of species present in an ecosystem. Studies suggest that after a certain number of species, all additional species are considered functionally redundant.Evidence from highly manipulated experiments at Cedar Creek Ecosystem Science Reserve shows productivity saturating at a lower number of species in smaller plots thanin larger plots. However, they did not explicitly test for the effect of plot size. We hypothesized that as plot size increases, productivity will saturate at a higher level of biodiversity. To examine this, we used a hierarchical sampling structure in five 20x20m plots in a natural savannah in central MN. We manipulated plot size to determine whether it may limit species accumulation in experimental settings. When spatial scale was explicitly manipulated, there was not a saturating biodiversity-productivity relationship at any spatial scale – instead, biomass production increases linearly with species richness at every spatial scale. The slope of this relationship changed depending on spatial scale. We propose that the type of analysis used by ecologists to compare biodiversity-productivity relationships across spatial scales may lead to different interpretations with very different conclusions.

34. STUBBS, P.K. and CHAPPELL, M. African-American Students' Participation in STEM Majors: Factoring out Failure, Striving for Success. Mathematics Education, Middle Tennessee State, Murfreesboro, TN.
Over the years, African-American students have been identified in the education arena as an underrepresented group in STEM (science, technology, engineering, and mathematics) disciplines. Researchers and advocates have sought reasons why so few African-American students make up the STEM graduate population. Many findings suggest overwhelming disparities are attributed largely to economic factors and academic preparation. However, a need remains to understand how to increase the graduation rate for African Americans in STEM disciplines. Explored in this research proposal are different factors that contribute to the successes and challenges of African American students in STEM disciplines. Focus is given to specific factors such as: parental involvement, socioeconomic status, neighborhood context, human and material resources, academic preparation, and student self-motivation. This study aims to identify whether or not these factors actually contribute to the success or deficiency of African-American students in STEM disciplines. Findings from this study will help advance opportunities for African-American students and the STEM fields overall. Afterall, STEM fields are critical to America's future success.

35. UTSEY, K., DODSON, S., LEE, S., and LAUBENBACHER, R. RNA-Seq Analysis of Aspergillus fumigatus Infected Airway Cells: Unifying the Innate Immune Response and Iron Metabolism. Carroll College, Helena, MT, University of Massachusetts Amherst, Amherst, MA, Virginia Bioinformatics Institute, Blacksburg, VA.
Aspergillus fumigatus is an opportunistic, highly virulent fungus capable of infiltrating the human lung epithelial barrier. However, the survival of the fungus depends upon essential nutrients, including iron, and the fungus must acquire these from the host organism. A. fumigatus uses a siderophore system to sequester iron from lung epithelial cells. Iron is also essential for mechanisms including DNA synthesis, cell cycle transitions, and oxygen transport in human cells. The outcome of the fungal-host struggle for iron influences the severity of the fungal infection. To investigate the innate immune system manipulation of the iron metabolic network, a differential expression analysis of RNA-Seq data was performed on A. fumigatus infected normal human bronchial epithelial cells. RNA samples were obtained from control and infected cells at 2, 6, and 12 hours, and processed on Illumina HiSeq2000. Our data reveals significant changes in the transcriptome of infected cells over time. Several iron regulatory network genes are differentially expressed and presumably influenced by the innate immune response induced by fungal infection. Transcription factors with significant positive expression changes are involved in cell cycle progression, cytokine signaling, and apoptosis. These results provide mechanistic insight into the transcriptional response of healthy airway cells to A. fumigatus.

36. HAMMOND, M. Modeling the development of inhibitory circuitry in the prefrontal cortex (PFC) and its effects on the frequency and power of pyramidal-interneuron network gamma (PING) oscillations. University of Pittsburgh, Pittsburgh, PA.

Brain activity is characterized by neural oscillations. Synchrony in the oscillatory behavior of neuronal populations arises from the reciprocal projections between excitatory pyramidal neurons and inhibitory interneurons. Gamma waves (30-80 Hz) in particular are a pattern of oscillations believed to be a critical substrate for working memory and other cognitive functions. Electrophysiological recordings from single pyramidal neurons from the prefrontal cortex (PFC) of monkeys have shown that the kinetics of inhibitory postsynaptic responses become faster and stronger during postnatal development. We hypothesize that with these changes in inhibition come an increase in the gamma power of the cortical network. While experimental measurements of certain parameters related to gamma have been successfully investigated, they have also been constrained by the ability to only singly evaluate parameters. In this study, computational modeling is used to simultaneously manipulate and observe the influence of three parameters of interest--inhibition-to-excitation strength, decay time, and reversal potential of the inhibitory-to-excitatory synapses--on the frequency and power of the rhythm generated by a model pyramidal-interneuron network. Our simulations show how developmental changes in the properties of inhibition affect gamma power, suggesting that, with age, there is an increase in gamma, which is indicative of higher cognitive ability.

ORAL PRESENTATION ABSTRACTS (Alphabetical)

BOGEN, S., RESSLER, I., and FEDERICO, P. Modeling the spread of white-nose syndrome in hibernating North American bats. Capital University, Columbus, OH.

North American bat populations are currently being threatened by an emergent infectious fungal disease known as white-nose syndrome (WNS) which causes mass mortality in hibernating colonies. Since it was first detected in New York in 2006, WNS has spread rapidly in the United States and Canada and killed over 5.5 million bats. Control of WNS is of major concern to both the scientific and caving communities, and the disease and mechanisms of transmission are still not well understood. We developed an individual-based model at the county level to gain insight into the spatial and temporal spread of the disease. We assume the probability of infection for each county in a given year is a function of the density of caves, the cave temperature, and relative proximity to other infected counties. The model design allows for factors that may influence susceptibility and transmission not currently considered to be easily incorporated into future studies. Model parameters were estimated by means of maximum likelihood. We compared model predictions with known U.S. Fish and Wildlife infection data from 2006 until 2011. The model imitates the overall spatial and temporal patterns of the data but tends to predict infections not indicated by the data.

BRUCE, C., BELTRAN, B., BURKOW, D. and S. ERICKSON. Secondary Aneurysm Formation due to the Presence of a Primary Aneurysm. Mathematical and Theoretical Biology Institute, Arizona State University, Tempe, AZ.

See poster abstract by same name.

CATE, E. and DALMUT, T. Modeling Fitness of *Onthophagus taurus:* The Effects of Density on Mating Success. James Madison University, Harrisonburg, VA.

Male *Onthophagus taurus* dung beetles have a characteristic dimorphism that leads to differing reproductive strategies. Horned major males exhibit a guarding strategy while unhorned minor males exhibit a sneaking strategy. The success of these strategies depends on the number of other males with which an individual competes. We developed random models using Matlab and NetLogo to explore the density dependence of reproductive success. Our models showed that the sneaking strategy for minors was advantageous under lower density conditions, suggesting that the guarding strategy for majors requires high densities.

DUCKLER, N. Modeling the Spread of Disease on Small-World Networks with Adaptive Host Behaviors. SUNY Geneseo, Geneseo, NY.

Individuals exhibit the behavior best suited to preserve their well-being in a given situation. During an epidemic an individual may change their behavior to reduce the chance of infection based upon how severe they perceive the risk of infection to be. This model examines the consequences of individual's dynamic adoption of disease avoidance strategies based upon knowledge of their neighborhood's conditions. Our work suggests that behavior is important solely when hosts are highly aware and little rewiring of the network has occurred. We suggest this occurs because the rewired edges normally act as shortcuts for the disease to cross the network and under conditions of high host-sensitivity and low rewiring enough of the bridges are effectively "shut down" to return the network to a circulant-like state which is naturally unfavorable for disease transmission. This has implications for determining how strictly self-imposed disease avoidant behaviors must be adhered to in order to prevent the systemic spread of disease and in what types of communities educating individuals to encourage them to alter their behavior will ever be an effective use of resources.

FRAZIER, B. E., GIBSON, A. K., THATCHER, S., and WALSTON, T. Using a Glazier-Graner-Hogeweg Approach to Model the Embryo in Caenorhabditis elegans. Department of Biology and Department of Mathematics and Computer Science, Truman State University, Kirksville, MO.

See poster abstract by same name.

HARRIS JR, M.D. Synthesis of α–helical peptide (AAAAK)4AAAAY. Middle Tennessee State University, Murfreesboro, TN.

See poster abstract by same name.

JALBERT, E. Phase plane analysis of double degenerate biofilm model. University of Guelph, Guelph, ON.

A biofilm is a system of many micro-organisms surrounded in a polymer matrix that grows on most surfaces. The use of biofilms in the modern world has a great impact on many technologies and issues that affect everyone. Since they are so influential, it is imperative that we understand how biofilms perform their functions. One important aspect of biofilms that needs further study is modeling the growth and propagation of biofilms. A simplified biofilm model is changed into a system of two ordinary differential equations and investigated by use of phase plane analysis. The equation is unique in that it is a doubly degenerate reaction-diffusion equation with two singularities. These singularities come from the density-dependent diffusion coefficient, which degenerates at two points. This system is analyzed for a traveling wave solution. A traveling wave solution is a wave solution that keeps its shape as it travels at constant speed. Two traveling wave solutions are found, one is a twice differentiable traveling wave solution, and the other is only piece-wise twice differentiable.

KOPP, N. and TEBERG, C. Separating the Effects of Genetic Drift and Selection Using a Modification of Tajima's D Statistic. Departments of Biology and Mathematics, Truman State University, Kirksville, MO.

Many statistical tests have been devised to infer selective processes and demographic structure from the patterns of nucleotide variation within a population. However, interpretation of the results is complicated by the fact that a wide range of population-level processes can yield similar patterns within the data. Here we propose and evaluate a partitioning approach that separately analyzes synonymous and nonsynonymous variation. Using modified versions of Tajimas D statistic, we demonstrate that this approach successfully distinguishes data sets simulated under a neutral evolutionary model from those simulated under purifying selection, diversifying selection, and population subdivision. These last three models are also rejected in an analysis of actual genetic sequences from the V3 loop of HIV. However, population bottlenecks could not be resolved from the neutral model. Power analyses confirm that data partitioning approaches have promise but require further refinements to increase their statistical power.

KRAMER, S. and BANSAL, S. Modeling the Impact of Vaccination versus Antiviral Treatment on Influenza Epidemics. Department of Biology, Georgetown University, Washington, DC.
Influenza causes annual epidemics, and is responsible for high levels of complications and mortality in very young children and the elderly. Currently, vaccination is the most effective influenza control strategy, but influenza vaccines suffer from several drawbacks. Treatment with antiviral drugs, which makes infected individuals less likely to transmit influenza to others, may be an attractive alternative to vaccination. To test this possibility, contact network modeling was used to compare the impact of vaccination and antiviral treatment in populations experiencing influenza epidemics. Specifically, an urban network with age structure was used. Preliminary results indicate that, when control strategies are implemented randomly, treating 20-40% of infected individuals with antivirals reduces mean epidemic size by more than does vaccination. Thus, the idea that antivirals can be used as an alternative to vaccines is so far supported. Further research is being conducted in order to compare vaccination and antiviral treatment in cases where vaccine efficacy differs by age group, and where control strategies are targeted toward specific age groups. It is hypothesized that control strategies that specifically target children will be most effective in reducing epidemic size and probability, and that, in these scenarios, antiviral treatment will be the more effective control strategy.

LANDRITH, R., CALDERON, A., LE, N., and KRIBS ZALETA, C. Modeling the Relationship Between Visceral Leishmaniasis Incidence and the Proportion of Post-Kala-Azar Dermal Leishmaniasis Cases Treated into Remission. Department of Biology and Department of Mathematics, University of Texas at Arlington, Arlington, TX.
Visceral Leishmaniasis (VL) is a fatal disease caused by species of the Leishmania protozoan parasite. VL infection results in the death of thousands and illness of hundreds of thousands every year in countries including India and Sudan. Post-kala-azar Dermal Leishmaniasis (PKDL) is a cutaneous manifestation of Leishmaniasis following the treatment of VL and serves as reservoir for the transmission of VL. This study focuses on the relationship between VL incidence during a given period and the proportion of PKDL cases treated into remission during the same period using a dynamical system to model VL and PKDL infection dynamics over a fixed period of time under the assumption that the infection has reached an endemic state.Here the proportion of PKDL cases treated is defined as the ratio of cummulative number of PKDL cases treated to the incidences of PKDL over the time period. This study indicates that with the current treatments available and considering achievable levels of treatment the impact of treating new PKDL cases on incidences of Visceral Leishmaniasis cases does not diminish at higher proportions of new cases treated, however the ability to treat new cases is precipitously inhibited at high proportions.

LUNSFORD, J. Mitochondrial iron: a mathematical model for iron regulatory disease. East Tennessee State University, Kingsport, TN.
See poster abstract by same name.

MANN, K. and CAMPBELL, S. Creation of CellTwitch Software to Perform Mechanical Experiments on Cardiac Cells. Department of Physiology, University of Kentucky, Lexington, KY.
One of the research projects in the Campbell Muscle Lab at the University of Kentucky takes live rat cardiac muscle tissue, dissolves it into individual live cardiac cells, and analyzes the mechanical properties of said cell. To perform these experiments, software was written in Matlab to communicate with and control a variety of instruments. Object oriented programming is the focus of this software and the functionality created by this

program includes movement of the stage of the microscope, movement of two manipulator 'arms', streaming an image from a camera as well as capturing live video and snapshots, controlling temperature of the experiment environment, and collecting data.

MOORING, E. and BANSAL, S. Modeling the Epidemiological Impact of Continuity in Influenza Vaccination. Department of Biology, Georgetown University, Washington, DC.

Mathematical models can help epidemiologists design effective vaccination strategies. Modeling two influenza epidemics in succession allows us to test the epidemiological relevance of the degree to which the subpopulation vaccinated in one season overlaps with the subpopulation vaccinated in the subsequent season. Contact network models are used to simulate two successive influenza seasons and test the effect of different levels of overlap in vaccination on epidemic size. Preliminary results suggest that, on heterogeneous contact network structures, more overlap leads to smaller epidemics, all else being equal. Current research focuses on developing and testing additional models to more rigorously describe and explain this pattern. It is hypothesized that level of overlap is especially relevant in heterogeneous networks because when individuals with a comparatively large number of contacts are vaccinated in the first season but are not revaccinated, herd immunity is reduced more than in a homogeneous network, where all individuals have more similar numbers of contacts. This hypothesis is being tested with models that measure herd immunity and models that preferentially revaccinate individuals with certain numbers of contacts. This research has the potential to identify novel strategies to use vaccine more effectively.

NIVENS, A., CROSLEY, E., RUBIN, I., LANZAS, C., PHAN, T., LELU, M., and S. LENHART. Modeling Salmonella dynamics within a finishing pig farm: group structure effects on transmission. National Institute for Mathematical and Biological Synthesis, Knoxville, TN, Maryville College, Maryville, TN, Bowdoin College, Brunswick, ME, Cornell University, Ithaca, NY, University of Tennessee, Knoxville, TN.

The spatial structure of farming houses may influence the spread of diseases. There is a general trend in modern, large-scale pig farming towards housing animals in larger pens, and larger grower houses. To understand the implications of this trend in the dynamics of foodborne pathogens in swine populations, we developed a spatially explicit model of Salmonella transmission of a grower house in an intensive, all-in-all-out system. The model is an ordinary differential equation system with four classes of individuals: susceptible, clinically infectious, subclinically infectious, and carrier. The population is divided into a discrete pen structure. Infectious pigs can transmit the infection to neighboring pens through direct contact, and to all pens through indirect transmission. Several pen configurations and sizes were evaluated through simulation. The basic reproduction number was derived for different pen configurations. Pen density and total population in the house had a larger effect on Salmonella prevalence than pen configuration. However, the configuration of the pens in the grower house had also significant impact on the infection prevalence. Moving the pen configuration away from a square structure and towards more linear configurations (e.g. 8 X 2 from 16 X 1) decreases the spread of Salmonella in the facility. The general trend of larger houses and larger pens facilitates the transmission of Salmonella. The physical structure of the farming facilities should not be ignored when modeling within farm transmission of foodborne pathogens.

PARRISH, T., PAULI, S. and KALKOUNIS-RUEPPEL, M. Determinants of Free-ranging Mouse Activity Based on Analysis of Remote Thermal Video. Department of Mathematics and Statistics, Department of Biology, University of North Carolina at Greensboro.

Because of their nocturnal and secretive nature, the study of rodents in their natural habitat is difficult. Due to this difficulty, environmental queues that mediate behavior have not been fully examined. As a means to study behavior, remote sensing thermal video was recorded, dusk to dawn, over 131 nights at the Hastings Natural History Reserve, in upper Carmel Valley, CA. At this site, two species of mice, Peromyscus californicus and Peromyscus boylii coexist in the same habitat.

To determine environmental factors that influence mouse behaviors, we developed a method for tracking small objects in our thermal video. Objects were classified into categories according to their size and speed. From the tracking data, average traveling speed and total distance traveled by mice per night were computed as measures of mouse activity. We determined how speed and distance were influenced by biotic and environmental factors.

These factors included average nightly temperature, soil temperature, wind speed, and humidity, and moonlight, as well as number of ultrasonic vocalizations, mice observed, and predator presence. No factors influenced distance traveled however speed was influenced by an interaction of moonlight and wind speed. On moonlight nights with low wind, mice were fast whereas with high wind, mice were slow. This interaction is likely due to conflicts associated with increased predation pressure in high light and the need to process increased olfactory cues in high wind.

ROBINS, J., BOGEN, S., FRANCIS, A., WESTHOEK, A., EDA, S., LENHART, S., and A. KANAREK. Agent-based model for Johne's disease dynamics in a dairy herd. National Institute for Mathematical and Biological Synthesis, Knoxville, TN, University of Tennessee Knoxville, TN, Capital University, Columbus, OH, University of Wisconsin, Madison, WI, Wageningen University, The Netherlands.

Johne's disease is an infectious gastrointestinal disease in ruminants caused by Mycobacterium avium ssp. paratuberculosis that causes diarrhea, emaciation, decreased milk production and eventually death. The disease is transmitted in utero and via milk and colostrum to calves, and fecal-orally to all age classes. Financial losses due to the disease are estimated to be over $200 million in the US dairy industry. The goal of this study was to identify the primary transmission pathways driving disease dynamics, and determine which management strategies and diagnostic tests are most effective in decreasing the prevalence of Johne's disease in dairy herds, in an economically viable way.

An agent-based, discrete time model was developed to simulate Johne's disease dynamics in a US dairy herd. Spatial aspects of disease transmission were taken into account by using six spatial compartments: five separate barns and a pasture. The effects on disease prevalence and economics were studied for different scenarios: three colostrum management strategies, five levels of assumed fecal-oral transmission, with and without fecal-oral transmission in the pasture, and culling and colostrum management decisions based on ELISA or EVELISA diagnostic tests.

The disease prevalence is highly dependent on the maximum probability of infection through the fecal-oral route, for which there is no widely accepted estimate. Assuming no fecal-oral transmission on the pasture markedly decreased total disease prevalence. Additionally, with more opportunities for calves to drink potentially contaminated colostrum, the disease prevalence increases. Culling and colostrum management based on both ELISA and EVELISA testing resulted in lower disease prevalence compared to the no-testing scenario, especially at low values of fecal-oral transmission. However, the disease prevalence does not decrease over time. Our model implies that testing and culling alone is not enough to control Johne's disease, but more accurate parameter estimation is needed to justify conclusions from the model. Results of the economic analysis of using the ELISA and EVELISA tests were inconclusive, but could be an area of further study.

ROSS, C., JACKSON, K., RUEPPELL, O., RYCHTAR, J., The Impact of Life History Structures on the Evolution of Altruism. Department of Mathematics and Statistics, Department of Biology, University of North Carolina at Greensboro, NC.

The evolution of altruistic behavior is intriguing because selfish actions often seem to benefit the individual. Game theorists often model this predicament by using the Prisoner's Dilemma. Two players simultaneously decide on a strategy, and though a defector whose partner cooperates will benefit most, mutual defection yields the worst consequences for both players. When using this game to study the evolution of cooperation, it has been shown that spatial structure favors altruistic behavior. We study how life stages affect the evolution of cooperation in a spatially structured, aging population. The spatial structure of the model allows for the evolution of cooperation in otherwise inherently selfish populations. We examine how changing the existence and length of pre-reproductive, reproductive, and post-reproductive stages of life affects the evolution of altruism. Using computer simulation, we show that in general, a proportionally long reproductive stage allows cooperators to thrive best. The existence of any non-reproductive stage suppresses cooperation—post-reproductive more substantially than pre-reproductive. Therefore, our study suggests that cooperation evolves most likely in populations with simple life history, at least when interactions between different life stages are symmetrical.

SCHAAL, S., XIE, Y., YANKEY, F., ZEIDLER, T., AGUILAR, C., CUHEL, R., LAUKO, I. and G. PINTER. Analysis and Development of a Predictive Mathematical Model for Light Attenuation in Lake Michigan. Department of Mathematical Sciences, School of Freshwater Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.
As light enters a body of water, it is reflected, scattered, and absorbed as a result of particulate matter and biological organisms suspended in the water column. These properties determine the rate of light extinction in the water column, and allow researchers to estimate the depth at which incident light decreases to 1% of its surface value (1% depth). Typically, 1% depth, the maximum depth at which photosynthesis and net growth occurs, is calculated by extrapolating the surface extinction coefficient to the entire water column. However, this does not take into account variations in extinction coefficients throughout the column. We attempted to incorporate these variations through several iterations of data analysis and refinement. These included performing a piecewise regression of linearized light decay data, calculating running average slopes, smoothing the base light data via five point running averages, and calculating running average slopes of unprocessed data. During our data analysis, we observed a correlation between change in percent transmission and change in extinction coefficient in the water column. This correlation suggests that a mathematical model can be developed to predict extinction coefficients from transmission profiles, regardless of light conditions.

SPEARS, T., TUCK, A., CROWE, M., GUPTA, S. Estimating Risky Sexual Behaviors Among College Students Using Optional Unrelated Question RRT ModelsDepartment of Mathematics and Statistics, Department of Biology, University of North Carolina at Greensboro, NC.
Subjects often provide untruthful responses when asked sensitive or incriminating questions. This response bias leads to inaccurate estimation of population parameters such as mean. Randomized Response Technique (RRT) has been shown to decrease response bias in surveys of sensitive information (Warner, 1965; Greenberg et al., 1969). One variation of RRT, the Optional Unrelated-Question RRT model, may be used to simultaneously estimate the mean of the sensitive behavior, as well as the proportion of subjects that would not be comfortable answering the question directly (Sensitivity Level).
This model has been shown to provide good estimates of mean and Sensitivity Level (Gupta et al., 2002), but has not previously been applied to studies of human subjects. We test this model through surveys administered to undergraduate college students about sensitive behaviors. We ask one question that requires a quantitative response, one that requires a binary response, and collect basic demographic information. The same survey questions are administered using three different methods. One method is face-to-face direct question method, which has a very high response rate but also high response bias. Another method, anonymous surveys, has a low response bias but a low response rate. We hypothesize that response bias will be improved with the proposed method as compared to face-to-face direct questioning, and that response rate will be improved over the anonymous survey method. This method also provides an estimate of Sensitivity Level, which other methods do not. Knowledge of the Sensitivity level is important because it allows

researchers to assign better-trained interviewers for surveys involving highly sensitive questions.

STANLEY, N., KIRKHAM, M., BROWN, M., MURRUGARRA, D., LAUBENBACHER, R. The Role of Incoherent miRNA Feed-Forward Loops in Gene Regulatory Network Robustness. Dickinson College, Carlisle, PA, Virginia Bioinformatics Institute, Blacksburg, PA, North Andover, MA, Merrimack College, North Andover, MA, Winston Salem State University, Winston-Salem, NC, Georgia Institute of Technology, Atlanta, GA, Virginia Tech, Blacksburg, VA.
Incoherent micro RNA feed-forward loops (miRNA FFLs) are recurring motifs in gene regulatory networks that link a transcription factor, a micro-RNA and a target gene. These FFLs have been shown to contribute to network stability. Specifically, miRNA FFLs assist in the maintenance of optimal protein levels in the cellular environment of an organism by providing a buffer against extrinsic and intrinsic noise. The stability of a gene network is correlated with a relatively larger number of initial conditions leading to a steady state or a limit cycle (basins of attraction). It can be shown that the addition of miRNA FFLs also increases the maximum basin of attraction size and therefore indicates stability. In this study, we examined how miRNA FFLs contributed to gene regulatory network stability, using a discrete framework. Finally, a numerical simulation was performed on the sensory organ precursor network in drosophila to justify the stabilizing effect of the microRNA, miR-7 in a biologically relevant context. This work was completed at Virginia Bioinformatics Institute in the 2012 Modeling and Simulation in Systems Biology REU Program.

STRINI, J., YANG, K., KRUSE, H., WRIGHT, A.J. The importance of spatial scale in the study of biodiversity.Departments of Biological Sciences and Mathematical Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.
Past research in small highly manipulated experimental settings have shown a positive saturating relationship between plant diversity and ecosystem productivity. Comparisons of long-term data from biodiversity experiments demonstrate that the shape of this positive relationship may change depending on the size of experimental plots - in smaller plots productivity saturated at a lower number of species than in larger plots. We hypothesized that as area increases, the relationship between biodiversity and productivity increases linearly. To test this hypothesis, we used a hierarchical sampling structure in five large randomly chosen plots at Cedar Creek Ecosystem Science Reserve (CCESR) that were sampled at different spatial scales. Plant biomass samples were systematically taken in mid-July using clip strips. Plot size was manipulated during data analysis to determine whether scale-of-measurement limits species accumulation in observational settings. We found that the relationship between diversity and biomass production is not saturating at any spatial scale in an observational diversity gradient; in our results the pattern was linear at all spatial scales. However, the slope of the diversity-productivity line differed across spatial scales. We propose that this is related to well-known ecological principles, such as species area curves and the “productivity area” curve.

THEAN, T., V. JANIK, R. WELLS, and L. SAYIGH. Signature Whistle Models in Bottlenose Dolphins, *Tursiopstruncatus.* Princeton University, Princeton, NJ.
Bottlenose dolphins (*Tursiopstruncatus*) develop signature whistles to convey identity information and maintain group cohesion. Bottlenose dolphin calves are thought to incorporate whistle modulation patterns from other members of the population into their own. It is unclear which of those members young dolphinsuse as whistle models, however. Using a dataset of 70 calves recorded during brief capture-release projects in Florida between 1984 and 2012, we sought to identify a relationship between the strength of a calf’s association with other dolphins during the first year of its life, and the similarity of their whistles. We did not find a relationship between association and whistle similarity, though both seemed distributed around the lower ends of their respective scales. However,a greater percentage of mother- calf pairs showed high whistle similarities than did non-mother-calf pairs. Further, a greater percentage of males than females had signature

whistles very similar as well as very different from those of their mothers. Limitations to the data set include varying and sometimes limited amounts of association data during the calves' first year of life and difficulties quantifying large numbers of visual comparisons of whistle similarity. Further analyses will investigate other possible influences on the vocal development process.

TUCK, A., SPEARS, T., CROWE, M., and GUPTA, S. Estimating Parameters for Optional Unrelated-Question Randomized Response Models. Department of Mathematics and Statistics, Department of Biology, University of North Carolina at Greensboro, NC.

Obtaining accurate information is essential in all surveys, but can be problematic when subjects face sensitive or incriminating questions. Despite assurances of anonymity, subjects often give untruthful responses, leading to serious response bias. One method of reducing this bias is the Unrelated Question Randomized Response Technique (RRT), in which a predetermined proportion of subjects are randomized to answer an innocuous unrelated question with known prevalence (Greenberg et al., 1969). Subjects are provided a higher level of anonymity because the researcher does not know which question (sensitive or innocuous) any individual answered, although the mean of the sensitive question can be estimated at the aggregate level.

We propose a generalization of the Unrelated Question RRT model, to be used with a quantitative response question, which takes into account the fact that a question may be very sensitive for one person, but not at all sensitive for another (Gupta et al., 2002). Each subject is presented the option of omitting the randomization step if the question is deemed non-sensitive. We simultaneously estimate the Mean Prevalence of a sensitive behavior, as well as the Sensitivity Level of the underlying question (proportion of subjects who consider the question sensitive). We also show that both estimators are asymptotically normal and unbiased. Computer simulations are used to validate these theoretical results.

WU, C., and ROE-DALE, R. Modeling the Dynamics between Yeast and Bacteria. Department of Mathematics and Computer Science, Skidmore College, Saratoga Springs, NY.

Oral Candidiasis, or thrush, is a common yeast infection that may occur in infants, diabetics, and immune-compromised patients, especially following prolonged antibiotic therapy. When antibiotics kill off bacteria that normally compete with yeast cells for nutrients, the yeast cells function as opportunistic pathogens and rapidly multiply, thus leading to infection. We model the population dynamics between bacteria and yeast using a system of differential equations. In particular we analyze the stability of these growth models and discuss the basins of attraction for the set of fixed points in the absence of antibiotic treatment. We then simulate treatment using a pulse-condition model, which kills a certain percentage of each population, and we investigate how this treatment alters the behavior and dynamics of the model.