NIMBioS

National Institute for Mathematical and Biological Synthesis

Eighth Annual

Undergraduate Research Conference at the Interface of Biology and Mathematics

October 8-9, 2016

University of Tennessee Conference Center

Knoxville, TN

CONFERENCE OVERVIEW

Welcome! This conference is hosted by the National Institute for Mathematical and Biological Synthesis (NIMBioS), housed on the campus of the University of Tennessee-Knoxville. Undergraduate students conducting research in mathematics and biology will present over 60 oral and poster presentations. A keynote by Dr. Jorge X. Velasco Hernández and featured talk by Dr. Judy Day 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 15.

NSF

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 eighth year, NIMBioS is sponsored by the National Science Foundation and the Departments of Homeland Security and Agriculture, with additional support from the University of Tennessee-Knoxville. NIMBioS also coordinates many educational programs including a summer research experience for undergraduates program and workshops for math and biology faculty. For more information on NIMBioS and its research and educational opportunities please visit www.nimbios.org.

UNIVERSITY OF TENNESSEE & KNOXVILLE

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

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

INFORMATION FOR HANGING POSTERS

There will be two poster sessions. The first will immediately follow dinner on Saturday, from 7:00-8:00 pm. Presenters whose posters are assigned odd numbers will present at this time. The second will precede lunch on Sunday, from 11 am to noon, when posters assigned even numbers will be presented. Please hang your poster as soon as possible and leave it up for the duration of the conference. Refer to the poster listing in this booklet to find your assigned number. Posters will all be hung in the hallway areas outside auditorium room 406. Find your assigned space and use the tacks provided to affix it to the wall or poster board. Poster abstracts and numbering start on page 6.

INFORMATION FOR ORAL PRESENTERS

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

Social Media at URC 2016

Twitter

Check Twitter for live updates, highlights from sessions, and more. Follow us by visiting https://twitter.com/NIMBioS. Twitter users -- just login and click "follow."

View and join in conversations about URC 2015 on Twitter by using the hashtag, #nimbiosURC. If you don't have a Twitter account, you can still view our updates or bookmark the NIMBioS Twitter webpage.

Facebook

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

KEYNOTE LECTURE

Dr. Jorge X. Velasco Hernández
Instituto de Mathemáticas
Universidad Nacional Autónoma de México

The Gene, the Pattern, the Virus and the Idea: A Personal View of the Applications of Mathematics to Biology

The talk will visit several areas of Biology where Mathematics has made an impact, from powerful methods, to simple explanations and new insight. Mathematics is like a methodological microscope that allows the researcher to see beyond the apparent complexities of biological processes and this talk will illustrate this claim with several examples and from a very personal view point.

FEATURED SPEAKER

Dr. Judy Day
Department of Mathematics
University of Tennessee, Knoxville

Working @ the Interface: The Challenges and Opportunities of Mathematical Biology

The questions that drive Mathematical Biology research and the quest for their answers make working at the interface of mathematics and biology interesting and exciting. However, it is also a place of great challenge and struggle where two very different fields are being melded together to synergistically create something greater than the sum of the parts. The amount of time that must be spent in the great "in-between" of the interface is often taken for granted; yet, it is here where skill, logical thinking, and creativity (not to mention patience!) are greatly required. Using examples from immunology, I will illustrate some of the challenges and opportunities that may be encountered when working at the interface.

SCHEDULE

Saturday, October 8: 413AB (Except where noted)

1:00-1:10 Welcome: Dr. Suzanne Lenhart, Associate Director of NIMBioS

1:10-2:10 Keynote Lecture:

Dr. Jorge X. Velasco Hernández, Instituto de Mathemáticas,
Universidad Nacional Autónoma de México

The gene, the pattern, the virus and the idea: a personal view of the applications of mathematics to biology

2:20-2:35

400A: Elizabeth Stephenson – *A Mathematical Model of Skeletal Muscle Regeneration*

406: Kelly Reagan – *A Mathematical Model of Dengue Fever Incorporating Human Travel*

413AB: Sharee Brewer and Taylor Swett – *A Predator-Prey Model on a Food Web in a Lake*

2:40-2:55

400A: Cody Rogers **–** *Data Mining of Genes Correlated with Nicotine Addiction & Metabolism*

406: Kelly Buch – *Mathematical Model of Swimmer's Itch with Praziquantel Treatment.*

413AB: Gregory Javens – *Chemotactic Models for Banding and the Volcano Effect*

3:00-3:15

400A: Joshua Darville and Omar Nasir – *Decoding Allostery by Mathematical Analysis of Molecular Dynamics Simulations*

406: Rebekah Wagner – *A Deterministic Model of Methicillin-resistant Staphylococcus Aureus Aransmission Among Injection Drug Users.*

413AB: Claudia Kassouf and Abigail Rich – *Mathematical and Biological Analysis of the MAPK Pathway in Starfish Oocytes.*

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

Kelly Sturner, Education & Outreach Coordinator at NIMBioS

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

4:10-4:55 Featured Speaker:

Dr. Judy Day, Department of Mathematics, University of Tennessee, Knoxville

Working @ the Interface: the Challenges and Opportunities of Mathematical Biology

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

Dr. Jorge X. Velasco Hernández
Dr. Judy Day
Dr. Albrecht von Arnim, Professor of Biochemistry & Cellular and Molecular Biology, UTK
Dr. Christina Edholm, Postdoctoral Fellow, Mathematics, UTK

6:00-7:00 Buffet Dinner in 404A

6:30 Turn in SET game sheets to Sturner or Lenhart at dinner

7:00-8:00 Poster Session I: Odd numbered posters presented (and desserts)

Sunday Morning, October 9: Auditorium 400A, 406, 413AB, 413C

8:00 Continental Breakfast

8:30-8:45

406: Jacquelyn Lane - *Cannabinoid Pharmacokinetic Modeling*

413AB: Alana Cooper, Kelly Reagan, and Emily Horton - *Modeling of Human Emotions*

8:50-9:05

406: Stefano Chiaradonna – *The Dynamics of an Epidemiological Model for HPV with Partial Vaccination with a Heterogeneous Population*

413AB: Patrick McKenzie – *Quantifying Uncertainty in the Outputs of a Forest Landscape Model*

9:15-9:30

406: Luojun Yang – *An Age-structured Model for Assessing Unintended Fitness Consequences of Aquaculture on Wild Populations*

413AB: William Wang – *The Interaction of Calcium and Metabolic Oscillations in Pancreatic Beta-cells*

9:35-9:50

406: Marianne Hull – *Synthesis of Poly(silylether)s by Dehydrogenative Coupling of 1,4:3,6-Dianhydrohexitols and Hydrosilanes with Salen-Mn Complex*

413AB: Jonathan Stetler – *Are Zooplankton as Patchy as Phytoplankton?*

9:55-10:50

413C: Graduate School Opportunities & More Showcase

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

12:05-12:55 Lunch

1:00-1:15

406: Tequania Lake – *Doping Level Dependence and Cleaving Atmosphere Correlation of Topological Insulator Bismuth Selenide*

413AB: Myson Burch and Elizabeth Franko – *Theoretical Model of Flow Compensation following Vascular Occlusion*

1:20-1:35

406: Josias Gomez – *Diagonal Ramsey Numbers for Trees with 9 Vertices*

413AB: Elizabeth Rodriguez – *Agent-based Model for Integrated Pest Management with Periodic Control Strategies*

1:40-1:55

406: Alanna Gary, Vera Liu and Penny Wu – *Developing a Particle Filtering Algorithm to Track Organelle Movements in Plant Cells*

413AB: Christina Mortensen and Diane Sanborne – *Adapting Cyclical Management for Information Poor Fisheries – A Case Study from the Gulf of California*

2:00-2:15

406: Kirill Shmilovich – *Simulations and Force Clamp Spectroscopy of Protein Hydrogels*

413AB: Emily Meyer and Erin Stafford – *Modeling the 2014-2015 Chickungunya Outbreak*

2:20-2:35

406: Howsikan Kugathasan - *Developing Video Games for Inquiry-Based Elementary and Middle School Mathematics and Biology Education*

413AB: Morganne Igoe and Theresa Sheets - *A Discrete Age Structured Model of Hantavirus Among Rodents in Paraguay*

2:40-2:55

406: Austin Ryan Lawson - *Basins of Attraction for a Predator-Prey Model with Intraspecific Competition*

413AB: Nirja Dave and Andre Lesartre - *Control of Cardiac Tissue Using Feedback-Based Synchronization*

3:00-3:15

406: Demisha Porter – *Better targeting, Better Efficiency of Adeno-associated Virus Gene Transfer in the Central Nervous System for Expression of Retromer Proteins*

413AB: Ziaqueria Short and Christopher Pritchard – *Optimal Vaccination Strategies for Cholera*

3:20-3:35

406: Miranda Goodman – *Differential Expression Analysis of Serotonin Transporter Knockout and M172 Transgenic Mice and the Impact on Neuronal Pathways in the Midbrain*

413AB: Ayush Prasad - *Using Individual Patient Data to Quantify a Mathematical Model for the Interactions of Matrix Metalloproteinases and Their Inhibitors in a Wound*

3:40-3:50

413AB: Closing Remarks

3:50 Adjourn

POSTER ABSTRACTS BY SEQUENCE

1. ARCHIBALD, A. A Mathematical Investigation of Vaccination Strategies in An Heterogeneous Population to Prevent Epidemics. North Carolina A&T State University, Greensboro, NC.
This presentation focuses on an investigation of vaccination strategies to prevent measles epidemics. An SVIR model was created to investigate the process of how an epidemic of measles can spread within a heterogeneous population where a portion of each sub-population has been vaccinated. Included in the SVIR model is a contact matrix, which represents the level of interaction between the sub-populations and within each sub-population itself. This project considers an overall population that is divided into nine sub-populations. Simulations from the model are used to determine how the disease spreads based on from where the outbreak originates. Simulations will also be used to investigate the effect of pockets of low vaccination on the overall population. Results from different scenarios will be presented.

2. BOGGESS, E., JANN, T. and P. VERA-LICONA. Reverse Engineering Functional Brain Networks from fMRI Data Using Probabilistic Boolean Networks. Center for Quantitative Medicine, University of Connecticut Health Center, Farmington, CT.
The brain functions by communicating information across multiple regions, and neurological diseases can alter the way these brain regions communicate. To characterize brain disorders and eventually propose systematic approaches to diagnosis, we should study the brain as a whole and consider both its structure and dynamics. The objective of this project is to develop and validate a pipeline to infer the static and dynamic mathematical models of the brain from fMRI data. Using probabilistic Boolean networks (PBNs) as our mathematical framework, the pipeline we propose consists of iteratively applying the following steps: (1) Inference of static functional brain network from fMRI data, (2) Binary discretization of fMRI data and, (3) Inference of deterministic Boolean network using as input the outcome of steps (1) and (2). To infer a PBN, we segment both our original and discretized time series into overlapping windows and generate a Boolean network from each window. We then combine these networks to generate a PBN. We studied the different steps of our proposed pipeline using in silico networks to generate in silico fMRI data. Each step had non-trivial aspects to resolve and we successfully validated steps (1) and (2) of the pipeline. For step (1), the inference of static networks, we used 44 different reverse engineering methods and identified the top-performing methods for which we proposed a way to combine them such that the result, a consensus network, outperformed any method individually. In step (2) we used 11 different discretization methods and proposed a novel method to benchmark and rank them. Finally, we were able to do some preliminary studies to construct deterministic Boolean network and PBNs. We found that creating consensus networks from combining the top performing network inference methods proved effective. Our proposed benchmarking discretization metric was helpful in identifying appropriate discretization methods for our fMRI data. The fMRI data discretized using our identified top performing discretization method, BiK-means, yielded the most promising results when inferring the dynamic deterministic and probabilistic Boolean models. For the last step of our pipeline, the inference of the dynamic models, we only had the opportunity for preliminary studies and future work should be focused on the validation of inferred dynamic models.

3. BRITTAIN, K., SEIPELT-THEIMANN, R. L. and E. MCCLELLAND. Transcriptome Analysis of Clinical *C. neoformans* Strains. Department of Biology, Middle Tennessee State University, Murfreesboro, TN.
Cryptococcus neoformans (*Cn*) is a fungal pathogen and leading cause of cryptococcal meningitis worldwide. It is fatal to immunocompromised patients and is a major cause of death for those patients. The aim of this project was to identify differences in gene expression among seven clinical strains of *Cn* isolated from patients in Botswana, Africa. Clinical strain gene expression was compared to that of a wildtype strain using RNA sequencing technologies. From strains grown under conditions mimicking that of the central nervous system, RNA was extracted and used to create cDNA libraries, which were sequenced. The results were quality checked

and analyzed using bioinformatics tools. As expected, many gene expression differences (≥2 fold) were observed. Over 1700 upregulation gene expression differences and more than 2300 downregulation gene expression differences were found among any of the clinical strains compared with the wildtype. Additionally, more than 6200 upregulation gene expression differences and more than 7500 downregulation gene expression differences were detected among the clinical strains alone. Currently, the study is focused on finding patterns of differential gene expression that correlate with the patient clinical data, as well as determining which biological processes and molecular functions are represented in up and down regulated genes.

4. BURCH, M. and E. FRANKO. Theoretical Model of Flow Compensation following Vascular Occlusion. Indiana University – Purdue University Indianapolis, Indianapolis, IN. University of Scranton, Scranton, PA.

Peripheral arterial disease (PAD) is a major health problem in which arteries within the systemic vasculature become partially or fully blocked, often due to atherosclerosis, leading to a significant reduction in blood flow to tissue. Patients often require surgical bypass grafts to restore flow to their tissue; in extreme cases, amputation is required. The absence of data regarding the relative importance of adaptations in collateral arteries, arterioles, and capillaries to compensation after arterial occlusion is a major roadblock for the development of successful and noninvasive therapies for PAD patients. The objective of this project is to integrate experimental and theoretical techniques to assess the significance of changes in vascular segments at rest and during exercise subsequent to a major arterial occlusion on an acute and chronic time frame. Model-predicted values of vascular resistance are compared with experimental studies to validate the model. The model is extended to predict changes in vessel diameter according to mechanistic responses to pressure, shear stress, and metabolism following an occlusion. Theoretical results suggest that therapies that increase collateral diameter in combination with distal microcirculation adaptations provide the maximum benefit to patients with PAD. Ultimately this project offers a first step in optimizing experimental design and diagnostic criteria to focus on the most relevant vascular segments in studies of vascular compensation in health and disease.

5. CARRILLO, D. and J. DURAN. Identification of Cell Cycle Proteins in G. lambila using HITUHMM (Homolog Identification Tool Using Hidden Markov Modeling). University of Texas El Paso, El Paso, TX.

The purpose of this project is to develop a bioinformatics pipeline to identify proteins important for cell division across distantly related phyla. To date, much of the existing knowledge about cell division is derived from model organisms within the eukaryotic domain, such as yeast, fruit fly, and mouse. This work focuses on the early divergent protist Giardia lamblia, which is the most common intestinal parasite worldwide, causing over 280 million cases of Giardiasis annually. Identifying cell division proteins is an important step towards understanding the cell cycle pathways in G. lamblia, which can lead to finding possible drug targets to treat Giardiasis.

Protein sequences from model organisms responsible for cell division were selected using GO: annotation to be used to search for homologs in G. lamblia. We approach this by identifying homologs from varying taxonomic groups using BLAST (Basic Local Alignment Search Tool), aligning them with MUSCLE (Multiple Sequence Comparison by Log Expectation) to locate conserved regions, and generating a hidden Markov model for each conserved region using HMMER (Hidden Markov Model Based Sequence Alignment Tool). Then, the model was used to search against G. lamblia sequences available in public databases such as GiardiaDB to identify probable homologs.

6. CATES, L., RAHMAN M. and N.K. VAIDYA Mathematical Modeling of the Zika Virus in French Polynesia. Department of Mathematics & Statistics, University of Missouri – Kansas City, Kansas City, MO.

The first reported outbreak of the Zika virus (ZIKV) occurred in French Polynesia between October 2013 and April 2014. The recent devastating spread of ZIKV in the Americas poses a major global public health emergency and prompts our attention. ZIKV, a member of the Flavivirade family, is primarily vector-borne, with some reported cases of sexual or blood-fusion transmission. This arbovirus is spread by the *Aedes* genus of

mosquito and is linked to neurological disorders such as *Gullian-Barre Syndrome* and microencephaly in infants. Using a mathematical model of vector-borne infection, we have modeled the transmission dynamics of ZIKV on six islands in French Polynesia during the 2013-2014 outbreak. This study estimates a key epidemiological parameter, known as basic reproduction number, which is defined as the average number of secondary cases generated by a typical infectious individual in a fully susceptible population. Our study reports the reproduction number in French Polynesia to range from 2.18 to 3.77 suggesting an epidemic is likely to continue. Our estimates may be incorporated in the development of public health initiatives, such as outbreak planning or assessment of potential countermeasures. Future research will be dedicated to estimating the sizes of the infectious outbreaks and evaluating preventive measures, such as insecticides or mosquito nets.

7. COFFEY, C. Species Tree Estimation Under the Coalescent Model. Hobart and William Smith College, Geneva, NY.

Constructing gene trees from DNA data and then building the species tree from the gene trees is traditionally how species trees are estimated. Under the coalescent model we construct species trees with their branch lengths directly from the DNA data itself bypassing the step involving gene trees. Using the coalescent model we estimate distances on the species tree between two taxa and use the distances to build species trees. This distance formula we found is very similar to the popular Jukes-Cantor distance model but includes an additional constant term, which accounts for the mutation rate and effective population size. By using both formulas in the analysis of milkweed data we can compare and observe the way effective population size effects the construction of species trees.

8. DONALDSON, S., SCHUCHARD, K. and U. SICKING. Modeling relationships among growth, nutrient uptake and nitrate reductase activity in phytoplankton from a freshwater urban pond and lake. Department of Biological Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI.

Freshwater phytoplankton are typically limited by nitrogen or phosphorus. Additions of these nutrients lead to blooms, so understanding nutrient metabolism is important in predicting ecosystem responses. Nitrate metabolism was studied in an urban pond and large lake using controlled incubations of whole-water cultures. Cultures were either not enriched, or enriched with phosphate, and nitrate or ammonium and followed for two weeks, measuring nutrients, chlorophyll, particulate C and N, the activity of a key enzyme, nitrate reductase (NR), and kinetics of nitrate uptake and NR activity. Pond phytoplankton responded rapidly to enrichments; added nitrate disappeared in 5 d. Lake phytoplankton showed slower growth, with nitrate and phosphate depleted over 1-2 weeks. Only nitrate-enriched cultures had NR activity and it disappeared when nitrate was exhausted or when cells stopped growing. Nitrate uptake showed novel biphasic kinetics, first reaching a plateau, but showing with no clear saturation at higher nitrate concentrations. Half saturation constants for uptake were higher (~20µM) than for NR activity (~1 µM), suggesting internal pools of nitrate do not develop. Ongoing work includes species identification based on molecular methods, and development of an agent-based model to see if community responses to nitrate can be predicted from properties of individual species.

9. DOSKI, P., SEIPELT-THIEMANN, R.L., and E. MCCLELLAND. Host Gender's Effect on Gene Expression in Clinical Strains of*C. neoformans*. Department of Biology, Middle Tennessee State University, Murfreesboro, TN.

Cryptococcus neoformans (*Cn*) is an opportunistic yeast that is responsible for more than 600,000 deaths of immunosuppressed patients yearly. Immunosuppressed males have higher mortality due to cryptococcosis than females, despite having a higher CD4+ T lymphocyte count.There may be a genetic basis for the discrepancy between mortality rates for men and women due to selection pressures on the pathogen in the hostgender environment and/or differences in the expression of virulence genes in response to the host gender. *Cn*'s thick polysaccharide capsule, which surrounds the yeast, is an important virulence factor. The goal of this project was to investigate differences in gene expressionin strains isolated from males and females. RNA sequencing was performed on RNAs from seven strains isolated from HIV patients in Botswana, 4 male and 3 female, along with the wildtype. We identified genes that were significantly upregulated and downregulated by 2 fold between

the male and female group.Eleven genes were upregulated and four genes were downregulated by 2 fold or more. None of the total 15 genes have been previously identified in capsule production. It will be of interest to further investigate these genes and the roles they might play in pathogenesis.

10. FANG, P., and D. MURRUGARRA. Optimal Control of The Cell State in Gene Regulatory Networks. Mathematics Department, University of Kentucky, Lexington, KY.

In computational biology, one of main goals is to develop optimal control strategies to find efficient medical treatments, which change current state of cell into a desirable state. In this study, the state of a cell of gene regulatory networks are modeled as Stochastic Discrete Dynamic System (SDDS), which all components are described as discrete variables and are assigned as logical rules with inherent stochasticity. The algorithms of finding the best control policy use the theoretical results from Markov Decision Processes. Given a SDDS, a possible control policy is represented as a combination of manipulation of nodes and edges. Node manipulation requires specific technologies to completely inhibit or activate a particular gene product in a cell. Edges manipulation needs a drug or other products to inactivate an interaction between two gene components. All manipulation directly reflects a realistic control action in medical treatment. Since the algorithms of finding an optimal control is expensive, the study also develops a simulation to estimate the most likely control policy when there is a huge model, which contains plenty of components.

11. FAULKNER, K. and M. MCTAMMANY. Estimation of Daily Net Ecosystem Production Rates in the Susquehanna River Using Inverse Modeling with Dissolved Oxygen. Department of Biology, Bucknell University, Lewisburg, PA.

Ecosystem metabolism of rivers can be estimated from rate of change of dissolved oxygen in the water and was originally calculated directly from point-by-point change in dissolved oxygen concentration. New methods, termed "inverse modeling," fit observed diel dissolved oxygen concentrations to theoretical dissolved oxygen curves by finding the metabolic and reaeration rates that generate best-fitting oxygen data. Various inverse modeling methods were used to analyze dissolved oxygen data from two Susquehanna River locations near Lewisburg, PA in summer 2010. These methods use known models relating dissolved oxygen and net ecosystem production and statistical packages in R to estimate gross primary productivity and ecosystem respiration of rivers based on dissolved oxygen concentration, water temperature, barometric pressure, depth, and photosynthetically active radiation. Outputs from each method were then compared to each other and to the traditional calculation method. Inverse modeling methods produced similar results to traditional calculation, but were significantly faster and required few user decisions, thus reducing possible inconsistencies between users running the models. Inverse modeling will be used to estimate daily rates of ecosystem respiration and gross primary production of the Susquehanna River North and West Branches over 7 years.

12. FORD, D., MOORE, J., and D.A. COLEMAN. Elucidating Serine Richness in Arabidopsis Thaliana Transcript Using the Exact Distribution of Clump Statistics. Division of Natural and Physical Sciences, Philander Smith College, Little Rock, AR.

Cultivation of crops is essential for sustaining life in both humans and domesticated animals. However, crops are susceptible to fungal pathogens warranting the identification of antimicrobial proteins that function in innate immunity. A trypsin inhibitor, from the serine protease family, has been identified in Aspergillus flavus resistant corn. Thus, the analysis of Arabidopsis thaliana genome for a trypsin inhibitor with a similar sequence will suggest the same antimicrobial properties are present. Using the GenBank database provided by the NCBI's website and the Exact Distribution of Clump Statistics, the genome is analyzed to determine the abundance of the amino acid serine. This analysis is key in providing a link in the A. thaliana transcript and trypsin inhibitor. Determining the abundance of this particular amino acid suggest the presence of trypsin inhibitor in this model plant. Identifying this will lead to better molecular breeding for microbial resistance in crops. Results of our findings will be provided.

13. FUENTES, L. Using Daphnia to Monitor Water Toxicity. Division of Biological Sciences, Hawaii Pacific University, Honolulu, HI.
Contamination of agriculture's water system with organic compounds poses lethal threats to humans and aquatic organisms. In this study, Carbaryl, Chloropyrifos, Diuron, Dichlorvos Ammonia, and Microcystin-LR are used as model aquatic pollutants with a main objective to develop an effective and inexpensive way to detect water quality problems by using Daphnia magna to test for pesticides and can also be used as a low-cost preliminary screening method for insecticide pollution.

14. GARY, A., LIU, V. and P. WU. Developing a Particle Filtering Algorithm to Track Organelle Movements in Plant Cells. NIMBioS, National Institute for Mathematical and Biological Synthesis, Knoxville, TN. Rice University, Houston, TX. Houghton College, Houghton, NY. University of Chicago, Chicago, IL.
Rapid organelle movements observed in plant cells have proven necessary for healthy cell function, yet our knowledge about underlying mechanisms and function is limited. Rigorous quantitative characterization of such movements can provide valuable mechanistic insights, from which biological function may be inferred. To this end, it is vital to obtain detailed and accurate descriptions of the dynamic patterns in plant cells. Particle filtering, a novel statistical method, serves as the backbone of the robust tracking algorithm we developed to achieve this goal. We have collected data to build a suitable model for the algorithm, and synthetic data is also utilized to evaluate and improve the performance of our algorithm. With the efficiency and reproducibility provided by the tracking algorithm, more reliable track descriptions will be accessible to cell biologists to elucidate the mechanism or the biological function of fast organelle movements in plant cells.

15. HARRIS, M. Evidence of Critical Slowing Down Prior to Malaria Resurgence in Kericho, Kenya. Odum School of Ecology, University of Georgia, Athens, GA.
When the number of new infections dwindles during a disease elimination campaign, it is difficult to detect re-emergence by merely monitoring case incidence. Methods for predicting disease re-emergence are crucial in mobilizing preventative actions prior to widespread infection. Project AERO attempts to develop algorithms to detect the presence of such early warning signals in disease systems approaching critical transitions by applying methods from the Theory of Critical Slowing Down. As the system approaches the tipping point of disease re-emergence, its ability to recover from slight perturbations decreases, resulting in increases in lag-1 autocorrelation and variance. A monthly time series of malaria case incidence on a tea plantation in Kericho, Kenya from 1965 to 2002 was tested for these expected trends leading up to a 1993 malaria outbreak. Autocorrelation and variance convexity were measured across rolling windows and the strength of the trend over time of their values was quantified using the Pearson's correlation coefficient. Null models were generated by permuting the original time series and the corresponding distributions of correlation coefficients was used to evaluate the significance of the trends from the Kericho data. As predicted, autocorrelation performs poorly as an indicator, whereas the variance convexity test yields significant results.

16. HOLMAN, M., LIU, Y. and G. CHEN. Establishment of a High Performance Liquid Chromatography Method for Vitamin A. Department of Nutrition, University of Tennessee, Knoxville, TN.
Vitamin A is a lipophilic micronutrient that plays an essential role in human health, including the control of glucose and lipid metabolism. The current work is to establish the measurement of vitamin A using high performance liquid chromatography (HPLC) in the Nutrition Department. Cell and tissue samples were extracted and prepares for HPLC analysis in a C18 column linked to an Agilent 1220 Infinity LC system controlled by Chemstation software. The extracted retinoids were injected and analyzed individually and in various combinations at ultra-violet wave length 325 nano-meters. The mobile phases were 0.01M ammonium acetate (reagent A) and 100% methanol (reagent B). The A to B ratio was 5:95% respectively. The injection volume was 25 µL with retinyl acetate as loading control. A calibrated internal standard percent report was generated for each run, which includes the relative amount of each substance as a percentage of the injected

sample. The report was saved as a printout, and an electronic file. The data indicate that the method is repeatable and robust. In conclusion, we have successfully adapted a method for detection, quantification and analysis of retinoids in cellular and tissue samples, which will be used in the future to study the roles of vitamin in metabolic diseases.

17. KASSOUF, C. RICH, A., CARROLL, D. and S. KOKSAL. Mathematical and Biological Analysis of the MAPK pathway in Starfish Oocytes. Departments of Biology and Mathematics, Florida Technological University, Melbourne, FL.

The mitogen-activated protein kinase (MAPK) cascade plays a critical role in oocyte maturation and embryonic cell division. MAPKs are activated in a three-tiered cascade via phosphorylation (-pp). Several mathematical models have been developed to study the behavior of MAPK in somatic cells and in oocytes of the frog Xenopus laevis. However, there is a need for models in systems that allow for simple biological validation. The starfish may offer an advantage because of the easy availability of synchronized oocytes and the ease with which they can be matured and fertilized in vitro. Furthermore, it is possible to analyze these molecules using single oocytes. In this study, critical molecules of the MAPK pathway (MOS, MOS-pp, MEK, MEK-pp, ERK, and ERK-pp) are modeled using an initial value problem of six nonlinear ordinary differential equations with ten unknown parameters that govern the activation cascade. The numerical solutions of the system are obtained using Mathematica and compared to the collected biological data from individual oocytes of two different starfish for model validation. Sensitivity indices are calculated for each parameter with respect to the solutions and analyzed for biological significance using MATLAB. We will discuss the modeling process of the activation cascade and present the mathematical results together with biological interpretation of this novel model.

18. KIM, R. Blocking the Immune-blockers: A Mathematical Model of the Latest in Cancer Immunotherapy. Pomona College, Claremont, CA.

Cancer immunotherapy is a relatively new type of treatment that boosts the immune response against cancer cells. Dendritic cell vaccines, one form of immunotherapy, show promising results in ongoing research. A previously developed mathematical model of tumor-immune interactions simulates the current vaccine schedule for prostate cancer and reproduces experimental data showing the effectiveness of dendritic cell vaccines in stunting tumor growth. This model, a system of differential equations, could be used to compute a new vaccine schedule that optimizes treatment outcomes. Previous findings have shown that the Programmed Death-1 (PD-1) receptors on effector immune cells, when bound to PD-L1, create a pathway that suppresses effector immune cell activity and prevents autoimmunity. However, some cancer cells take advantage of this pathway by using PD-L1 to evade the immune response. Experiments using mouse models show that pathway blocker anti-PD-L1, in combination with ibrutinib (an anti-cancer drug), allows the effector immune cells to effectively combat tumor cells. We provide an extension of the initial mathematical model, adding the effects of anti-PD-L1 and ibrutinib. We fit the updated model to existing data and, in turn, use it to come up with new vaccine strategies.

19. LEE, R., MOORE, D., and D. A. COLEMAN. Using the Exact Distribution of Clump Statistics to Investigate Antimicrobial Properties Associated with Serine. Division of Natural and Physical Sciences, Philander Smith College, Little Rock, AR.

Farming provides billions of dollars in revenue for the US annual from the export of cotton fibers for textiles to seed oils used for human consumption. In rural communities farming is also important for daily nutrients and income. To improve crop yields, years of research have been focused on identifying antimicrobial proteins and peptides and increasing their expression. One family of antimicrobial proteins that has received attention is chitinases. These cysteine rich proteins are induced upon pathogen attack and other function for plant survival. Chitin is present in abundance in fungal cell walls, so the expression of plant chitinase effectively damages the major source of fungal protection, the wall. Recent methodology has been developed to compute the exact distribution of the number of occurrences and coverage of clumps of collections of strings. For this study, we examined the transcript of Arabidopsis thaliana for cysteine residue frequency using the Exact Distribution of

Clump Statistics. This work is a discussion of our findings. Increasing crop yield for rural farmers begins with improving resistance of crops to pest. To this end, analysis of cysteine residues in A. thaliana will aid in understanding the distribution of chitinases.

20. MURPHY, Q. and D. MURRUGARRA. Modeling Optimal Antibiotic Treatment Strategy Using Markov Decision Processing Techniques. University of Kentucky, Lexington, KY.
Here we study the problem of reversing drug resistance using Markov Decision Processing (MDPs) techniques. Using an optimal infinite-horizon MDPs with discounting factor for multiple treatment windows, a control policy is generated to determine the treatments for substitution paths leading from each genotype back to the wild type genotype TEM-1. Page Rank and Stationary Distribution methods were used to evaluate the effectiveness of each treatment plan. Control Policies with fixed-length duration of drug effectiveness have been obtained to evaluate its performance. Our results indicate that the duration of drug effectiveness is key in order to reverse the resistance back to the wild type genotype TEM-1.

21. OLDFIELD, S., TU, T., HAIDER, H., MORENO, R., EAGER, E., and ERICKSON, R. Demographic Modeling of an Indiana Bat Population Subject to Wind-Energy Stress. Department of Mathematics and Statistics, University of Wisconsin at La Crosse, La Crosse, WI.
Wind energy development is an increasingly prevalent source of renewable energy in the U.S. and worldwide. However, an increase in wind energy use comes at a cost. The Indiana Bat (Myotis sodalis) faces a risk of extinction due to wind energy development through collisions with wind turbines during migration. We collaborated with conservation managers at agencies such as the US Fish and Wildlife Service (USFWS) to model population trends of the M. sodalis (e.g., Thogmartin et al. 2013) and recovery efforts for future management decisions (e.g., Erickson et al. 2014).
The growth rate (λ), population inertia, extinction probability, and sensitivity and elasticity of λ with respect to each parameter were calculated using a population projection matrix adapted from Thogmartin et al. Our results will be used to assist in the recovery and conservation efforts of Indiana Bat populations. The matrix model is stage-structured and divided by reproductive status: juveniles, and adults. The survival and reproductive parameters transition between the four seasons. We found sensitive parameters for which conservation efforts should focus towards in the future for protecting bat populations.

22. RAINEY, S. Modeling the Impact of Migration on Cholera Outbreaks. Biology Department, Radford University, Radford, VA.
The effects of human migration on disease transmission are largely unquantified. Refugee camps possess high density, low resource conditions which enable infectious diseases like cholera to thrive. Cholera is a preventable disease that plagues impoverished and developing countries that are subjected to low water quality and poor sanitation. It is caused by the bacterium, *Vibrio cholerae* which can contaminate food and water sources. This study mathematically models cholera to measure the effect of migration into refugee camps on disease transmission. The dynamics of cholera outbreaks were simulated using an SIR differential equation model and parameters from prior published data. The model was run at three different migration rates and various levels of camp sizes. Model parameters were varied in order to determine under which conditions the *Vibrio cholerae* persisted in the environment after the initial outbreak.

23. RENFRO, E. and AGUSTO, F. B. Bovine Tuberculosis in African cattle and buffalo with resource competition. Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS.
Bovine TB is a contagious, slow-growing aerobic bacterium disease caused by Mycobacterium bovis. The infection commonly involves the lungs, but it may spread to other organs. It is most commonly found in cattle and other animals such as buffalo, bison, elk, and deer. More often there is close interaction between cattle and buffalo particularly during the dry seasons when resources are limited. In this study we develop a mathematical model for bovine tuberculosis transmission among cattle and buffalo and examine the impact of resource competition among the two bovine population on the disease transmission.

24. RIELAND, A., MIRANDA, D.A., ESCUSA, H., and INGRAHAM, H.A. Validation of CRISPR/CAS9 System in Mouse Liver and Primary Hepatocytes. Jackson State University, Department of Biology, Jackson, MS. University of California San Francisco, Department of Cellular and Molecular Pharmacology, San Francisco, CA

In the United States, up to a third of the population has Non-Alcoholic Fatty Liver disease (NAFLD). However, the mechanisms involved in the progression NAFLD are unknown. Recent work from the Ingraham lab indicates that acute hepatic deficiency of Liver Receptor Homolog-1 (Lrh-1) results in hepatic triglyceride accumulation independent of diet. Furthermore, IPA analysis of RNA-Seq from acute Lrh-1 knockout livers supports a role for Lrh-1 in liver lipid metabolism with the majority of down regulated genes being involved in lipid metabolism. To follow up on these studies we sought to develop a CRISPR/Cas9 system to knockout novel Lrh-1 target genes in liver. Using Lrh-1 as a proof of concept model, we cloned Lrh-1 guide sequences into the p783 lentivirus destination vector, designed by the Macmanus lab at UCSF. Lentivirus was generated in HEK293 cells and titered by RT-qPCR. To assess the quality of our lentivirus prep, we transduced primary hepatocytes and analyzed them by fluorescence microscopy for the presence of the mCherry reporter. Indeed, primary hepatocytes fluoresced red, indicative of infection. Lentivirus, along with adeno-associated virus 8 expressing Cre recombinase (AAV8-Cre), was then introduced into ROSA26-LSL-Cas9 mice via retro-orbital injection. AAV8-Cre infected ROSA26-LSL-Cas9 livers expressed Cas9 as early as two weeks post-infection as indicated by immunoblot analysis. However, hepatocytes that expressed Cas9 did not express mCherry as assessed by fluorescent microscopy analysis of liver sections. Taken together, our results indicate that we can successfully activate Cas9 and use our lentivirus to test guide sequences in-vivo. Moreover, implications of this system in the future could help understand the mechanism of fatty-acid accumulation from NAFLD.

25. ROBINSON, L and S. HOTA. A Mathematical Model For The Ebola Transmission Dynamics. Department of Mathematics and Computer Science, University of Georgia, Athens, GA.

Ebola is a deadly disease that has affected multiple countries in West Africa and still persists. This disease was discovered in 1976 and since then has had many different outbreaks in different countries. There have been 31,077 infections and 12,922 deaths to date. The 2014 outbreak severely affected 3 countries in West Africa which were Guinea, Liberia, and Sierra Leone.

In this project a SEIRQD model was developed with six nonlinear differential equations that described what happens to the population at each stage of Ebola epidemics. The system was solved using Python and plots were generated showing the profile and phases of the outbreak. Stability analysis about the equilibrium points was performed and the basic reproduction number, $R0$, was computed. The value of $R0$ obtained through the model was compared against the value obtained from 2014-outbreak data from the Centers for Disease Control and Prevention (CDC). The variation in values of $R0$ was investigated by changing different parameter values of the model. It was found that an increase in the contact rate resulted into an increase in the value of $R0$ and an overall decrease in population.

26. ROBINSON, S. Functional Data Analysis of Copy Number Alterations in Bladder Cancer Tumors. Center for Quantitative Medicine, University of Connecticut Health, Farmington, CT.

Genomic structural changes known as copy number alterations (CNAs) have a role in tumor progression. CNAs are changes in the chromosome where regions are either amplified or deleted. It is thought that bladder cancer subgroups have varying CN profiles that are similar within groups but differ across groups. We analyze array comparative genomic hybridization (aCGH) data from 93 bladder cancer patients whose profiles are in muscle invasive and non-muscle invasive subgroups. We are treating these CN profiles as functions across the entire chromosome, and using functional data analysis tools for inference. We use Bayesian, wavelet-based, functional response regression to characterize the CN profiles of muscle invasive and non-muscle invasive patients. We develop simulated aCGH profiles in order to test these methods. We find that our wavelet bases method using a fixed effects model for functional regression confirms the results of prior research about CN amplifications at 1q23.3, 1q21.2, and 11q13.2. Further, we find on chromosome 11 of our dataset that RRM1, RIN1, FG19, and

ANO1, genes which are known to be associated with bladder cancer, are altered due to the effects of muscle invasiveness within a tumor.

27. SHAHIR, J., TRUONG, K. and E.M. CHERRY. Using Delay Differential Equations to Model Intracellular Calcium Cycling. Brown University, Providence, RI, University of Maryland Baltimore County, Baltimore, MD, Rochester Institute of Technology, Rochester, NY.

Cardiac arrhythmias are irregular beatings of the heart caused by disruptions in the electrical activity that triggers contraction. One mechanism that can give rise to arrhythmias is calcium alternans, a dynamical state characterized by alternating large and small intracellular calcium concentrations in response to periodic stimuli. Despite the need to understand mechanisms for calcium-driven cardiac alternans, however, many ordinary differential equation models of intracellular calcium cycling do not produce alternans, thus restricting the scope of such models for studying alternans behavior. Delay differential equations (DDEs), which in many contexts produce complex dynamics, may be a promising tool for promoting alternans in cardiac models. We introduce DDEs in the equations for the calcium current gating variables, currents, and the release function in a model of intracellular calcium cycling. After suppressing alternans in the original model, we show that alternans can be induced by DDEs in certain compartments of the cell. We analyze the changes in the calcium concentrations, currents, and gating variables in response to these DDEs and discuss the mathematical and physiological implications of our findings.

28. TIMM, R. Analysis of Lamin A Expression & Nuclear Morphology of Cervical Cancer Cells on Turntable Nanofiber Scaffolds. Clarkson University, Potsdam, NY.

In multicellular organisms, the extracellular matrix (ECM) constitutes a complex three-dimensional microenvironment, regulating various cell functions such as proliferation, differentiation and migration. ECM composition and biophysical properties often change depending upon tissue type and developmental stage, though consequent, specific contributions in governing cell behavior are not well understood. Peptide amphiphile (PA) nanofibers offer a modular platform where these properties may be tailored through molecular design. Here, four cationic PAs of varied stiffness, surface topography, and epitope display were considered. Cervical cancer cells were plated on PA-coated substrates and studied following two days of incubation. Nuclear morphology and lamin A expression (which confers nuclear stiffness) were targeted for study, being well-known parameters determining cell migration in three-dimensions. Quantification of lamin A expression and nuclear morphology were measured from immunostained samples. Emphasis was placed on winnowing out morphological parameters and, as the data fails to meet key assumptions for common statistical analyses, development of data conditioning, transformation, and statistical testing paradigms as a framework for future analyses. These PA coating results establish a basis for ongoing studies in three-dimensional PA matrices, in which natural cell-ECM interactions may be captured more accurately.

29. TOMS, J. and B. NELMS. Investigating Dopamine Neuron Genes linked to human Disorders. Department of Biology, Fisk University, Nashville TN.

Dopamine is a neurotransmitter that controls the central nervous system. Its normal function is to control the frontal lobes of the brain. Studies prove it to have a relationship with human disorders, such as Parkinson's Disease, ADHD, Drug Addiction, Schizophrenia, and Depression. The purpose of my research is to determine the correlation between genes found in RNA-Seq to be enriched in C. elegans dopamine neurons with either predicted dopamine neuron functions and or connections to human disorders, such as Parkinson's Disease, ADHD, Schizophrenia, depression, and drug addiction. We use C. elegans as a model system because of their relative conservative genes that relate worms to humans. Genes that we find to be related to dopamine functions and human disorders will then be tested in C. elegans by comparing worms without these genes to normal worms. We have examined a list of 534 differentially expressed genes generated by comparing RNA-Seq data from isolated dopamine neurons and whole worms. We have various bioinformatics tools to find out what genes link to dopamine and human disorders. Some promising genes that we have identified include cpx-1 (Complexin 1), faah-5 (Fatty acid amide hydrolase), K03B4.4 (GTPase-activating protein SynGAP), and

C33A12.4 (Ubiquitin carboxyl-terminal hydrolase 28 isoform X12). From this research we hope to find the relationship between dopamine neuron genes that are linked to human disorders.

30. WARING, J., BENTO, A. and P. ROHANI. Epidemiological Data: Parameter Estimation and Pitfalls. Odum School of Ecology, University of Georgia, Athens, GA.

During an outbreak of an emerging infectious disease, important epidemiological parameters, such as transmission potential and mean infectious period, need to be estimated for a timely and effective public health response. The standard procedure for attaining quick estimates of these quantities is fitting transmission models to incidence data. Cumulative incidence is often used rather than raw incidence, but there is evidence to suggest that this choice of data can affect our perceptions of the variability in the parameters and hence the uncertainty in our predictions. To further elaborate on this problem, we fit deterministic and stochastic models with both raw and cumulative simulated epidemic data in order to assess the biases and errors associated with each type. Fitted simulations to the data using deterministic and stochastic methods result in comparable variances, but cumulative models under predict the true incidence. However, in stochastic parameter estimation and posterior sampling using particle Markov chain Monte Carlo (pMCMC), cumulative data produces much wider confidence intervals, and thus better quantifies uncertainty than raw models. When we consider the entire time-series of an epidemic, cumulative and raw data will both be useful in parameter estimation depending on the level of uncertainty we are willing to accept.

31. WORRELL, J. Signal Spreading and Coactivation in the Drosophila Connectome. Psychological and Brain Sciences, Indiana University, Bloomington, IN.

A growing area of inquiry in neuroscience is that of connectomics, the study of connections in the brain and how the patterns of connections influence the brain's behavior. Drosophila is a very thoroughly explored model organism, and examining it through the lens of connectomics may yield some interesting results that may be scaled or generalized to the human connectome.

The basis for this exploration of the drosophila connectome is a linear threshold model of signal spreading which has been used in previous studies of brain networks. Signal spreading is initiated by making perturbation in specific network nodes (corresponding to Drosophila brain regions, or local processing units [LPUs]). We then study how perturbations started at various LPUs spread through the Drosophila brain for varying numbers of simultaneous perturbations and varying thresholds for the linear threshold model. Specifically, results are generated primarily through examination of node-pair coactivation. For any set of initial conditions (perturbation number x threshold), we can examine how often any two nodes in the LPU network tend to adopt the signal originating from the same perturbation. This is a useful measure of communication through the network, and can reveal the role of network topology compared to other factors for information flow and signal spreading in the Drosophila connectome. The compactness of the Drosophila connectome at the LPU level allows not only a comprehensive analysis but also makes this information readily observable and computationally inexpensive to examine. _

Preliminary findings include comparison of coactivation measures against communities as assigned by a Louvain algorithm, which yielded very similar results, and construction of null models preserving everything but the matrix's topology, which didn't return anything similar to the algorithmically determined modules. Future steps for this experiment will include attempts to characterize the nature of the relation between network spreading dynamics and community structure.

ORAL PRESENTATION ABSTRACTS (Alphabetical)

BREWER, S., SWETT, T., and Q. LI. A Predator-Prey Model on a Food Web in a Lake. Division of Natural Sciences and Mathematics, Fisk University, Nashville, TN.

Acid rain decreases the pH level in a lake and the lake acidity has an effect on organisms and can reduce their body size, reproduction capacity, egg viability and mortality rate. In this paper, we developed a predator-prey model consisting of algae (cyanobacteria), Daphnia Magna (a herbivore), and a predator (Yellow Perch) and determined the coefficient functions governing dynamics of growth rate and death rate of organisms with respect to pH value in this model. Parameter values in this model are adopted from experimental data in published references.

BUCH, K. and R. HENDRIXON. Mathematical Model of Swimmer's Itch with Praziquantel Treatment. Sothern Illinois University Edwardsville, Edwardsville, IL and University of Minnesota-Twin Cities, Minneapolis, MN.
Swimmer's itch is a water-borne, emerging disease caused by parasites known as avian schistosomes. Typically, these parasites use birds as definitive hosts, but will mistakenly infect a wide-range of dead-end hosts, including humans. When parasite larvae penetrate the skin of humans they initiate an allergic reaction that causes itching and discomfort that can last for weeks to months. Previous research has shown that the Common Merganser serves as a key host for schistosomes in the Midwest, with infection rates exceeding 60% in some regions. While most efforts at schistosome control have focused on other hosts in the parasite's life cycle (snails), recent attempts have been made to target waterfowl using the anti-parasitic drug, Praziquantel. Based on this novel approach, we developed a mathematical model to explore the effects of Praziquantel dose and treatment frequency on the occurrence of swimmer's itch in a typical Midwestern lake. We modeled susceptible and infected mergansers (both juvenile and adult), and snails using first order differential equations and introduced aspects of Praziquantel treatment into the system. Results from this model help to identify treatment regimes which lower merganser infection rates and ultimately reduce the occurrence of swimmer's itch.

BURCH, M. and E. FRANKO. Theoretical Model of Flow Compensation following Vascular Occlusion. Indiana University – Purdue University Indianapolis, Indianapolis, IN. University of Scranton, Scranton, PA.
Peripheral arterial disease (PAD) is a major health problem in which arteries within the systemic vasculature become partially or fully blocked, often due to atherosclerosis, leading to a significant reduction in blood flow to tissue. Patients often require surgical bypass grafts to restore flow to their tissue; in extreme cases, amputation is required. The absence of data regarding the relative importance of adaptations in collateral arteries, arterioles, and capillaries to compensation after arterial occlusion is a major roadblock for the development of successful and noninvasive therapies for PAD patients. The objective of this project is to integrate experimental and theoretical techniques to assess the significance of changes in vascular segments at rest and during exercise subsequent to a major arterial occlusion on an acute and chronic time frame. Model-predicted values of vascular resistance are compared with experimental studies to validate the model. The model is extended to predict changes in vessel diameter according to mechanistic responses to pressure, shear stress, and metabolism following an occlusion. Theoretical results suggest that therapies that increase collateral diameter in combination with distal microcirculation adaptations provide the maximum benefit to patients with PAD. Ultimately this project offers a first step in optimizing experimental design and diagnostic criteria to focus on the most relevant vascular segments in studies of vascular compensation in health and disease.

CHIARADONNA, S. The Dynamics of an Epidemiological Model for HPV with Partial Vaccination in a Heterogeneous Population. Benedictine University, Chicago, IL.
The Human papillomavirus (HPV) is the most prevalent sexually transmitted disease in the United States. HPV-16 and HPV-18 are the primary agents of cervical cancer, and HPV-6 and HPV-11 are responsible for most genital warts and juvenile-onset recurrent respiratory papillomatosis. Highly efficacious vaccines have been developed to prevent these high-risk types of HPV, which are typically administered in three doses. We propose and analyze a mathematical model that investigates the implications of having a portion of the population not

completing the vaccine regimen. Our model also considers the impact of varied vaccination rates on subpopulations based on the number of sexual partners.

COOPER, A., REAGAN, K., and E. HORTON. Dynamic Modeling of Human Emotions. NIMBioS, National Institute for Mathematical and Biological Synthesis, Knoxville, TN. University of Tennessee, Knoxville, TN. Elon University, Elon, NC. Lynchburg College, Lynchburg, VA.
The aim of this research was to analyze emotional instability through different quantitative approaches. Participants from undergraduate introductory psychology classes recorded their own emotions while viewing video clips intended to elicit different emotions, while ten individual coders viewed recordings of the participants watching the video clips. A large database of emotional affect felt during the film clips was used in the three approaches. Primarily, data were visualized, leading to the conclusion that emotional stability did occur while the participants were watching the film. Markov chain models were created in order to model how an individual will move through affective space and to find the stability of positive, negative, neutral and ambivalent states. Another goal of the research was to find "home bases" -- or steady affective resting places-- for each of the participants. Different packages in MATLAB were used in order to find individual "home bases". Another MATLAB package was used to find agreement between the coders who analyzed facial expressions of the participants. In conclusion, mathematical and computational methods confirm that emotional instability occurs most frequently when an individual has deviated from their home base, or their most stable state.

DARVILLE, J. and O. NASIR. Decoding Allostery by Mathematical Analysis of Molecular Dynamics Simulations. Division of Natural Sciences and Mathematics, Fisk University, Nashville, TN.
Allostery in its most general form can be regarded as the molecular communication that occurs between any number of adjacent proteins. The result of this communication manifests itself as a change in the original structure or dynamics of the protein. The implication of such a change can be drastic, going so far as to dictate whether or not a gene is transcriptionally active. Due to the physiological relevance of allostery, creating drugs and treatments that exploit this regulatory mechanism have become an increasingly active area of research. However, allostery can be difficult to study using conventional experimental and computational methods. We are able to successfully examine an important class of allosteric proteins: the nuclear hormone receptor superfamily.

GARY, A, LIU, V., and P. WU. Developing a Particle Filtering Algorithm to Track Organelle Movements in Plant Cells. NIMBioS, National Institute for Mathematical and Biological Synthesis, Knoxville, TN. Rice University, Houston, TX. Houghton College, Houghton, NY. University of Chicago, Chicago, IL.
Rapid organelle movements observed in plant cells have proven necessary for healthy cell function, yet our knowledge about underlying mechanisms and function is limited. Rigorous quantitative characterization of such movements can provide valuable mechanistic insights, from which biological function may be inferred. To this end, it is vital to obtain detailed and accurate descriptions of the dynamic patterns in plant cells. Particle filtering, a novel statistical method, serves as the backbone of the robust tracking algorithm we developed to achieve this goal. We have collected data to build a suitable model for the algorithm, and synthetic data is also utilized to evaluate and improve the performance of our algorithm. With the efficiency and reproducibility provided by the tracking algorithm, more reliable track descriptions will be accessible to cell biologists to elucidate the mechanism or the biological function of fast organelle movements in plant cells.

GOMEZ, J. and B. LINDERMAN. Diagonal Ramsey Numbers for Trees with 9 Vertices. Department of Biology, King University, Bristol, TN.
The diagonal ramsey number of a graph G, denoted r(G), is the smallest integer t such that every 2-coloring (red and blue) of the edges of a complete graph Kt contains a monochromatic copy of G. There are 47 non-isomorphic trees with 9 vertices. We investigate diagonal ramsey numbers for trees with 9 vertices.

GOODMAN, M., PERLEY, D., SCHIEDEGGER, A, RODRIQUEZ, M, and L.K. HENRY. Differential Expression Analysis of Serotonin Transporter Knockout and M172 Transgenic Mice and the Impact on Neuronal Pathways in the Midbrain. Department of Biology, King University, Bristol, TN.

Serotonin (5HT) homeostasis is an important physiological process involved in embryonic development, enteric peristalsis, and psychiatric disorders. Antidepressants, such as serotonin selective reuptake inhibitors (SSRIs) alter 5HT balance by blocking reuptake of 5HT by the serotonin transporter (SERT). Recently, we engineered a mouse to express a transgenic SERT (SERT M172) that is pharmacologically insensitive to many SSRIs, providing a valuable tool for understanding the physiological impact of altered levels of synaptic 5HT. In this study, we evaluate and compare the transcriptome in the M172 transgenic (TG), wildtype (WT), and SERT knockout (KO) mice to determine the transcriptional impact of the M172 TG. RNA was purified from midbrain sections of 9 week old mice from the three groups, sequenced, computationally aligned (HISAT2), and quantified (DESeq2, DEXSeq) to examine potential epigenetic differences, differential gene expression, and differential exon usage. This study focused on neuronally defined processes and identified downregulated genes including integral membrane proteins, interferon regulatory genes, and a maternally imprinted noncoding RNA. Upregulated genes were comprised of coldinduced RNA binding paralogs and genes of unknown function. Of the differentially spliced genes, there was a preponderance of downregulated exons of unexplored genes. Significantly, the synaptic long term depression (LTD) pathway was downregulated. Whereas these data represent a vignette of 5HT homeostasis in 9 week old mice, they also provide support for the use of the TG mice in future studies on novel SSRIs.

HULL, M., VIJJAMARRI, S., G. DU. Synthesis of Poly(silylether)s by Dehydrogenative Coupling of 1,4:3,6-Dianhydrohexitols and Hydrosilanes with Salen-Mn Complex. Department of Biology, King University, Bristol, TN.

The synthesis and disposal of non-biodegradable polymers from petroleum derived compounds has a big impact in the levels of CO_2 in the atmosphere; which can result in Global Warming. The non biodegradation of materials results in its accumulation in oceans and landfills; this affects the ecosystems that surround them. Due to this situation, the search for environmentally-safe polymers is required. In the following research, poly(silylether)s were synthesized using bio derived 1,4:3,6-Dianhydrohexitols. In previous methods, non abundant and expensive catalysts containing Rhodium, Platinum and Palladium were used. For the synthesis of these polymers a Salen-Mn Complex was used with different hydrosilanes to test which one will give the polymers with the biggest molecular weights. After running the reactions under inert conditions with different hydrosilanes, it was concluded that Diphenylsilane was the most suitable for the reaction. By using C NMR, Proton NMR and IR it was able to ascertain that the poly(silylether)s were synthesized. By using a Salen-Mn complex, hydrosilanes and a bioderived substrates it was able to synthesize the polymers in an environmental friendlier manner, by eliminating HCl as a byproduct and not having to use environmental unsafe catalysts.

IGOE, M., SHEETS, T., DESALU, J., MORAN. E.J., JONSSON, C.B., LENHART, S., RÚA, M.A., and R.D. OWEN. A Discrete Age Structured Model of Hantavirus Among Rodents in Paraguay. NIMBioS, National Institute for Mathematical and Biological Synthesis. University of Minnesota Twin Cities, Twin Cities, MN. University of Maryland Baltimore County, Baltimore, MD. Rutgers University, New Brunswick, NJ. Unity College, Unity, ME.

Rodent-borne Hantaviruses are zoonotic pathogens that can cause disease in humans through inhalation of rodent excreta. Using data collected from a survey of rodents in the Mbaracayu Reserve in Paraguay to formulate and parameterize a mathematical model, we assessed the prevalence of the Jabora virus over time within its rodent reservoir by using multiple age classes and a unique infection class progression feature. This model incorporates three types of infection over the lifetime of the rodent as well as a recovered class. A new feature of the model allows transition from the latent to the persistently infected class. With a more complete age and disease structure, we are better able to identify the driving forces of epidemiology of Hantaviruses in rodent populations.

JAVENS, G. Chemotactic Models for Banding and the Volcano Effect. Indianapolis University - Purdue University Indianapolis, IN. Hunter College, New York, NY.
Chemotactic bacteria rely on chemical concentration gradients to bias their motion towards food sources or away from poisons. To describe this behavior, we propose two separate run and tumble models. In the run state, the bacterium runs in a single direction. In the tumble state, the bacterium reorients to a new direction for the next run. The amount of time spent running and the angle change during reorientation depend on the concentration gradient described as the solution to a diffusion-advection equation.
In these two models we aim to reproduce the experimentally observed Volcano Effect, wherein populations of bacteria spend most of their searching time in an annulus around the food source as opposed to directly on it. It is known that this is the result of constant overshooting. The same behavior has also been observed in marine bacteria, which we call Banding, however it's unknown whether the underlying cause is the same. Our two models account for different conceptual understandings of how bacteria achieve chemotaxis and can produce the same behavior as the result of different setups, offering a variety of possible explanations for the effects we are trying to model.

LAKE, T., DAYTON, I., GOODWIN, E., GOTTSCHALK, M., S. TESSMER. Doping Level Dependence and Cleaving Atmosphere Correlation of Topological Insulator Bismuth Selenide. Department of Biology, King University, Bristol, TN.
Topological insulators are a type of material that is insulating in the bulk, but have conducting surface states where spin and momentum are locked perpendicular to each other by spin orbit coupling. This allows small particles with charge to only move along the surface of the material. The surface states, that arises due to strong spin-orbit coupling, is composed of a pair of eigenstates on each band edge which are symmetric under time reversal. With respect to energy versus momentum diagrams, the surface states lie in the energy gap between the conduction band and valence band. These states form the Dirac cone. In this study, using Scanning Tunneling Microscopy we tested the various doping levels of bismuth selenide, to check if it will change the location of the Dirac cone. We hypothesized that the greater the doping level of the sample, the more the Dirac cone would shift in voltage. We observed that the Dirac cone did not shift in a systemic way based on the doping levels. We then tested if the atmosphere in which the samples were cleaved may be a factor in the shifting of the Dirac cone. We observed no correlation with cleaving in air, nitrogen or helium gas. At this point, the shifts in the Dirac cone with respect to voltage remains an open question.

KASSOUF, C. RICH, A., CARROLL, D. and S. KOKSAL. Mathematical and Biological Analysis of the MAPK pathway in Starfish Oocytes. Departments of Biology and Mathematics, Florida Technological University, Melbourne, FL.
The mitogen-activated protein kinase (MAPK) cascade plays a critical role in oocyte maturation and embryonic cell division. MAPKs are activated in a three-tiered cascade via phosphorylation (-pp). Several mathematical models have been developed to study the behavior of MAPK in somatic cells and in oocytes of the frog Xenopus laevis. However, there is a need for models in systems that allow for simple biological validation. The starfish may offer an advantage because of the easy availability of synchronized oocytes and the ease with which they can be matured and fertilized in vitro. Furthermore, it is possible to analyze these molecules using single oocytes. In this study, critical molecules of the MAPK pathway (MOS, MOS-pp, MEK, MEK-pp, ERK, and ERK-pp) are modeled using an initial value problem of six nonlinear ordinary differential equations with ten unknown parameters that govern the activation cascade. The numerical solutions of the system are obtained using Mathematica and compared to the collected biological data from individual oocytes of two different starfish for model validation. Sensitivity indices are calculated for each parameter with respect to the solutions and analyzed for biological significance using MATLAB. We will discuss the modeling process of the activation cascade and present the mathematical results together with biological interpretation of this novel model.

KUGATHASAN, H. Developing Video Games for Inquiry-Based Elementary and Middle School Mathematics and Biology Education. Division of Natural Sciences and Mathematics, Fisk University, Nashville, TN.
There is a rising trend among educators to apply video games as an instructional tool to utilize technology in the classroom and for more dynamic and interactive learning. These advantages of gaming coupled with the cost and resource limitations of the Biology in a Box project motivated the translation of one of the Biology in a Box' s activities to a video game format. Using the Unity 5.3.5 game engine to develop the game, with Gimp 2.8 for animation and Git/Gitlab for version control, one arcade-style video game and one simulation tool were developed. The video game meets Next Generation Science Standards and Common Core Mathematics standards while the simulation encourages visualization of difficult biological concepts. The game and simulation have met the goal of translating one part of the Biology in a Box project online, while a heuristic analysis of the impact suggests that further steps could be taken to increase the motivation of the games for students.

LANE, J. Cannabinoid Pharmacokinetic Modeling. Oklahoma State University, Stillwater, OK.
Cannabis usage has been proven to impair driving ability. No methods exist to quantify cannabis in the human body for rapid screening; urine, blood, hair follicle, and oral fluid samples are only positive/negative tests for cannabis usage. Without a way to quickly and quantitatively analyze a driver's cannabis consumption, thresholds for driving impairment cannot be set. The goal of this project is to create a mathematical model that can predict the time of last cannabis use for oral, inhalation, and IV dosage routes. We model the pharmacokinetics of delta-tetrahydrocannabinol (THC) " the primary psychoactive component in cannabis" and other cannabinoid constituents by defining a system of ordinary differential equations (ODEs), which we solve using MATLAB. Data for parameterizing the model was taken from controlled studies done at the National Institute of Drug Abuse. Several factors of cannabis intake have been explored and studied in order to determine their overall effect on cannabinoid levels in plasma. To derive a model for the inverse problem of predicting time of cannabis use given THC measurements from any of the three dosage routes, we have used our ODE model results and an existing empirical model of the inverse problem for the inhaled dosage route.

LAWSON, A.R. and S. SADHU. Basins of Attraction for a Predator-Prey Model with Intraspecific Competition. Georgia College and State University, Milledgeville, GA.
We study a three species ecological model comprising of two predators competing for their common prey. We assume that the predators follow Holling II functional response with one of the predators exhibiting a density dependent mortality rate. We explore the behavior of the system as the predating efficiency of one of the predators is varied. Interestingly, the system exhibits bistabilty in a regime, where the coexistence equilibrium state has lost its stability through a Hopf bifurcation. Depending on the initial population densities, the species may coexist in the form of small amplitude oscillation cycles or in the form of mixed-mode oscillations (MMOs), which are concatenations of small and large amplitude oscillations. We compute the basins of attraction in the bistable regime and investigate the nature of the MMOs as the bifurcating parameter is varied.

DAVE, N., and A. LESARTE. Control of Cardiac Tissue Using Feedback-Based Synchronization. Colorado School of Mines, Golden, CO.
Cardiac arrhythmias are a type of heart disease caused by the irregular propagation of electrical signals in the heart. The resultant waves can have complex patterns including one or more spiral waves. We assess the effectiveness of synchronization to control complex spiral-wave dynamics in two-dimensional cardiac tissue using three different reaction-diffusion models, each consisting of a voltage variable and a recovery variable. Our approach involves synchronizing two unidirectionally coupled systems by applying a feedback term that is proportional to the difference in the voltage variable averaged locally over uniformly spaced sensors to one of the systems, with the quality of synchronization measured in the voltage. Our study extends previous work by Berg et al. through the use of additional cardiac-specific models, a time-discrete feedback term, different initial conditions for the response system, and different model parameters for the driver and response systems. We

vary model and synchronization parameters to determine the range of conditions for which synchronization is possible. Our findings indicate that synchronization can be achieved for many cases, even with differences in the inherent dynamics of the driver and response systems.

MCKENZIE, P., THOMPSON, J., DUVENECK, M., MORREALE, L., and Y. LIANG. Quantifying uncertainties in forest landscape model outputs using a variance-based global sensitivity analysis. Harvard Forest Summer REU Program, Harvard Forest.
LANDIS-II is a popular forest landscape model that simulates tree cohort colonization, photosynthesis, and succession in response to climatic conditions. It integrates these processes with stochastic disturbances to make spatiotemporal predictions of forest biomass and composition. The new PnET-Succession extension is the most mechanistic of the LANDIS-II succession extensions; it uses equations from the PnET-II physiological model to predict changes in species biomass and spatial distribution as the result of competition for photosynthetic resources. Knowing how the new parameters influence model outputs is necessary for interpretation of model results. The Fourier Amplitude Sensitivity Test (FAST) was applied to determine which PnET-Succession parameters contribute most to variation in LANDIS-II outputs. Using indices generated by FAST, sixteen PnET-Succession input parameters were ranked by their contributions to uncertainty in LANDIS outputs. Total biomass outputs of PnET-Succession are best explained by variation in precipitation loss fraction, maintenance respiration, and climate parameters. Understanding the relative importance of these parameters in determining model outputs will improve interpretation of model outputs and prioritization of data collection. The analysis identifies a challenge in that the most influential parameters are difficult to measure empirically. Future steps involve expanding the test to include more parameters and examining interactions between parameters.

MEYER, E. and E. STAFFORD. Modeling the 2014-2015 Chikungunya Outbreak. Center of Computational Sciences, Tulane University, New Orleans, LA.
Chikungunya is a vector-borne disease transmitted by the Aedes aegypti and Aedes albopictus mosquitoes. It has been geographically isolated in parts of Africa and Asia, in the past few years it has spread quickly through the Caribbean along with parts of Central and South America. This paper focuses on modeling the spread of chikungunya using an SEIR-SEI epidemiological model. We adjust the data from Pan-American Health Organization (PAHO) in order to create a smoother curve for comparison. We work to improve upon an existing model of chikungunya created by Manore et. al. These adjustments include balancing the initial conditions for more accurate dynamics, working with the objective function used to optimize the parameters, analyzing the existence of seasonality of the mosquito population, and creating solutions for the optimizer in the cases where $R0 < 1$. With these alterations to the model, we have better short-term predictions for the number of chikungunya cases over a period of time.

MORTENSEN, C., SANBORNE, D., JOINER, E., RAHMAN, N. and HARP, M. Adapting cyclical management for information poor fisheries-A case study from the Gulf of California. Marine Conservation Lab, Arizona State University, Tempe, AZ.
Global fisheries are under increasing pressure, and our capability to effectively manage them is essential for the survival of the wildlife and the peoples reliant upon them. Citizens of developing countries are the most effected by depleting stock levels, but are also the least likely to have the governance regimes and research capabilities necessary for effective management. In such areas where the development of a research initiative may be financially infeasible, other methods of fisheries management must be developed. We present one such method for regulating the Gulf of California Sardine Fishery here. This method of management utilizes environmental cues to establish harvesting rules inspired by theory concerning the optimal management of fluctuating resources.

PORTER, DL, JACKSON, KL, DAYTON, RD, KLEIN RD. Better targeting, better efficiency of adeno-associated virus gene transfer in the central nervous system for expression of retromer proteins. Department of Biology, King University, Bristol, TN.

Researchers are using AAV gene transfer more and more in their neuroscience studies, including optogenetics, cre-lox targeting, and CRISPR gene editing. Our lab has been using the AAV9 vector serotype to express genes on a wide-scale basis throughout the central nervous system in order to study a disease that affects cells throughout the central nervous system, amyotrophic lateral sclerosis. This current project explored ways to achieve more efficient expression and in a more targeted manner than our previous work. The recently described AAV PHP.B serotype was administered to rats for the first time, and it did result in significantly more green fluorescent protein expression than did the AAV9 vector in a systematic comparison. In studies comparing the neuron-specific synapsin promoter with our previous cytomegalovirus/ chicken β-actin promoter, the latter promoter was noticeably more efficient yet the synapsin promoter did yield a transduction pattern with greater neuron-selectivity, which was the goal. We also explored intracerebroventricular injections to achieve wide-scale transduction and better avoid unwanted transduction of peripheral organs. We are combining the synapsin promoter in AAV PHP.B vectors to take advantage of these efficiency and targeting features. Our specific genes of interest that we wish to express are called the retromer proteins. Retromers make up a protein complex that is associated with the trafficking of cellular vesicles through the endosome and the trans-Golgi network. Viral constructs were made for epitope tagged versions of the retromers VPS29 and VPS35. We hypothesize that the retromers can act to prevent the formation of beta-amyloid plaques in Alzheimer's disease by altering the trafficking of amyloid precursor protein.

PRASAD, A. Using Individual Patient Data to Quantify a Mathematical Model for the Interactions of Matrix Metalloproteinases and Their Inhibitors in a Wound. Western Kentucky University, Bowling Green, KY.

Because the medical treatment of diabetic foot ulcers remains a challenge for clinicians, a quantitative approach using patient data and mathematical modeling can help researchers understand the physiology of the wounds. In this work, we extend a previously developed mathematical model describing the interactions among matrix metalloproteinases, their inhibitors, extracellular matrix, and fibroblasts (Krishna et al., 2015). In the previous work, the model was curve-fitted to the averaged data of patients with diabetic foot ulcers from Muller et al. (2008), and the model parameters were estimated using ordinary least-squares. The model and parameter values were then analyzed using global and local sensitivity analyses, which were used to describe how sensitive each parameter value of the model was to changes in the system. This work uses the individual patient data obtained from Muller for curve-fitting a modified model using similar techniques from the previous work. The goal of this work is to quantify and understand differences between patients in order to predict future responses and individualize treatment for each patient.

REAGAN, K. A Mathematical Model of Dengue Fever Incorporating Human Travel. Elon University, Elon, NC.

Dengue fever is a disease transmitted by day-biting mosquitoes in tropical, urban areas. There is currently no vaccine for dengue fever, so preventative measures are the only solution to slow the spread of the disease. In order to develop a model to simulate dengue fever spreading between two populations, an in-depth analysis was conducted on a malaria model with human traveling aspects and on a general dengue fever model. Then, parameter values relevant to dengue fever were investigated and implemented into both of the models. The results from both the malaria model and dengue fever model were regenerated. A thorough investigation of previous research in the field allowed for a combination of the malaria model and the general dengue fever model by adding the human travel aspects to the dengue model. The combination resulted in ten ordinary differential equations, which simulate humans of two different communities visiting the other community. Further simulations have been conducted on how population size differences and the length of time spent in each community affects the spread of dengue. It has been seen that the time factor does heavily impact the rate at which dengue spreads across a community.

RODRIGUEZ, E. Agent-based Model for Integrated Pest Management with Periodic Control Strategies. Benedictine University, Chicago, IL.

We consider an agent-based model (ABM) for integrated pest management (IPM). The model incorporates stage structure for both the pest species and the predator species. In this model, the two control strategies of augmentation of predator species and application of pesticide and the pest births occur periodically at possibly different frequencies. We determine conditions under which either the pest species is eradicated or both species persist. We also investigate how varying the frequency of the augmentation of the predator species and the application of pesticide with respect to the frequency of the pest births affects the amounts of augmentation and pesticide needed to obtain pest eradication and permanent solutions. We then compare the behavior of this model to an analogous model using impulsive differential equations.

ROGERS, C. and L.K. VAUGHAN. Data Mining of Genes Correlated with Nicotine Addiction & Metabolism. Department of Biology, King University, Bristol, TN.
Nicotine use and addiction are headlines in public health information due to the connection between tobacco use and cancer. Many clinical trials and genetic studies have been conducted that look at nicotine addiction and metabolism. This data is stored in public archives waiting to be mined. Data mining is an aspect of bioinformatics analysis that extracts information from large data sets and transforms it into statistical data that can be read and used. I will conduct data mining and a thorough literature review to identify all notable genes and metabolic pathways associated with nicotine metabolism and addiction. The finalized list of genes associated with nicotine metabolism will then be analyzed through a two-step process. First, I will conduct a network-based analysis to identify how they are connected. Second I will use a pathway based analysis which identifies new genes use and how they are entangled in previously discovered pathways of nicotine metabolism and addiction. The last step is relating everything together using Gene Ontology annotations. This process, of identifying known genes, using network analysis to build connections and add novel genes, and then conducting Gene Enrichment analysis to identify biological pathways will helps us to identify new genes and pathways that are associated with the addiction and metabolism of nicotine.

PRITCHARD, C., and Z. SHORT. Optimal Vaccination Strategies for Cholera. University of North Carolina Greensboro, Greensboro, NC.
Cholera is a disease that affects millions of people in the developing world each year, making it a significant public health issue. It is a waterborne disease that is transmitted through the Vibrio cholera bacterium. Here we develop a mathematical model of cholera, by adding an additional vaccinated class to an existing compartment model. Then we create a game theoretical model for cholera vaccination, in which individuals consider both the costs of vaccination as well as the costs of contracting cholera in order to decide whether or not to vaccinate themselves. From this model we determine that in a population following optimal vaccination strategies, voluntary vaccination is not sufficient to eradicate cholera. However, the optimal vaccination strategy is within 5% of the value necessary for herd immunity when the relative cost of vaccination is less than 0.00002.

SHMILOVICH, K. Simulations and Force Clamp Spectroscopy of Protein Hydrogels. Department of Physics, University of Wisconsin-Milwaukee, Milwaukee, WI.
Protein hydrogels serve as an excellent scaffold for artificial tissues and smart drug delivery systems. A protein hydrogel is a highly cross-linked network of multi-domain proteins. These proteins show a force sensitive response to folding and unfolding of their individual domains. Here, we report a dynamic model of protein hydrogel mechanics based on an empirically verified model of single molecule mechanics. Our model explains how protein orientation and domain unfolding affect the elastic behavior of protein hydrogels, such as hysteresis and stress-relaxation response. By using a custom built force clamp instrument, we can verify our model with empirical data. The model and measurements both provide a stepping stone for formulating the future of protein-based smart materials, such as those used in artificial skin and 3-D organ printing.

STEPHENSON, E. A Mathematical Skeletal Muscle Regeneration. University of Texas Arlington, Arlington, TX.

While the cellular mechanisms behind mammalian skeletal muscle regeneration have been rigorously studied in the past forty years, no mathematical models have previously been established to demonstrate the regenerative process, except in the cases of extremely specific diseases. The goal of this project is to construct a system of ordinary differential equations that effectively models the regeneration of damaged, but disease-free, mammalian skeletal muscle on a cellular level. This can aid the scientific and medical communities as they seek to more effectively heal patients with damaged muscles. A system of seven autonomous ordinary differential equations is introduced to model the interactions between classically and alternatively activated macrophages, satellite cells, myoblasts, myotubes, healthy myofibers, and damaged myofibers. The equations incorporate the sequential, overlapping stages of muscle regeneration following injury: immune response and subsequent cell proliferation, differentiation, and fusion. The system of differential equations is mathematically analyzed using Mathematica, yielding one stable equilibrium which suggests a biologically reasonable pathway to muscle recovery. A set of numerical simulations is performed using Matlab to illustrate the performance of the proposed equations and to model the effects of common treatments such as NSAIDs (nonsteroidal anti-inflammatory drugs). The ability to mathematically forecast the outcome of changes in medication could prove useful in healing damaged muscle faster and more completely. Next, we plan to implement a non-autonomous impulse, allowing us to study the impact of secondary muscle damage prior to recovery.

STETLER, J., BUELO, C., KURTZWEIL, J. and G. WILKINSON. Are Zooplankton as Patchy as Phytoplankton? Paul Smith's College, Paul Smiths, NY., University of Virginia, Charlottesville, VA., Center for Limnology, Madison, WI., Iowa State University, Ames, IA.

Phytoplankton and zooplankton form the base of most lake food webs and are the primary sources of energy for higher trophic levels. The distribution of phytoplankton and zooplankton is not constant vertically or horizontally within a lake. Recent studies have shown that the horizontal distribution of phytoplankton is not even across the surface of lakes. However, little is known about the horizontal distribution of zooplankton in the surface waters of lakes or the spatial interactions among zooplankton and phytoplankton. The aim of this study was to quantify the spatial distribution of phytoplankton and zooplankton and determine if their spatial distributions are related. We sampled zooplankton and phytoplankton at night in a 24 point grid in Paul Lake, Michigan in the late spring and early summer of 2016. Phytoplankton and zooplankton were not uniformly distributed horizontally. Instead, there were hotspots of both zooplankton and phytoplankton, and in many instances there was positive autocorrelation. Additionally, zooplankton and phytoplankton concentrations were not correlated in space indicating that grazing is likely not a driver of zooplankton or phytoplankton spatial heterogeneity.

WAGNER, R. and F.B. AGUSTO. A Deterministic Model of Methicillin-resistant Staphylococcus Aureus Aransmission Among Injection Drug Users. Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS.

In this project, we develop a deterministic model for methicillin-resistant Staphylococcus aureus (MRSA). The model incorporates transmission of the bacterial among injection drug users (IDUs). Using this model, we study the vertical relationship among non-drug users and injection drug users who are both low-and high-risk users. We also study the horizontal relation of the individuals with the bacterial with the introduction of a risk factor assigned to the injection drug user classes. We determine that there is an observable relationship between the risk factor associated with being an IDU and vertical movement to higher-risk classes, and increased MRSA colonization and infection.

WANG, W. The Interaction of Calcium and Metabolic Oscillations in Pancreatic Beta-cells. Department of Mathematics, Vanderbilt University, Nashville, TN.

Diabetes is a disease characterized by an excessive level of glucose in the bloodstream, which may be a result of improper insulin secretion. Insulin is secreted in a bursting behavior of pancreatic beta-cells in the islets of Langerhans, which is affected by oscillations of cytosolic calcium concentration. We used the Dual Oscillator Model to explore the role of calcium in calcium oscillation independent (CaI) and calcium oscillation dependent

(CaD) modes as well as the synchronization of metabolic oscillations in electrically coupled beta-cells. We also implemented a synchronization index in order to better measure the synchronization of the beta-cells within an islet. We observed that voltage or calcium coupling result in increased synchronization and are more effective in CaD modes. Furthermore, we studied heterogeneous modes of coupled beta-cells, their arrangements in the islets, and their synchronization. We saw that increasing calcium coupling or increasing voltage coupling in heterogeneous cases increases synchronization; however, in certain cases increasing both voltage and calcium coupling causes desynchronization, primarily in voltage. To better represent an entire islet, we altered previous code by further optimizing run-time and memory usage to allow for a greater number of cells to be simulated for a longer period of time.

YANG, L., BASKETT, M., and R. WAPLES. An Age-structured Model for Assessing Unintended Fitness Consequences of Aquaculture on Wild Populations. School of Life Sciences, Nanjing University, Nanjing, Jiangsu, China. Department of Environmental Science and Policy, University of California-Davis, Davis, CA. Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Seattle, WA.

The escape of farmed fish from open net-pens is to some extent inevitable. These domesticated escapees usually possess traits that are maladaptive in the wild due to artificial selection for increased productivity. By interbreeding and competition, escaped farmed fish can cause unintended fitness and demographic consequences for wild conspecifics. Current quantitative models to assess such consequences usually assume discrete, nonoverlapping generations for simplicity. However, in reality, multiple escape events with high variability in frequency and magnitude occur within a single generation. To evaluate the effects of variable escape both within and across generations, we use an age-structured model of coupled genetic and demographic dynamics for species with various life histories. As previous research suggested that constant low-level spillover has a greater impact compared with rare, large pulses of leakage, our preliminary results show that such discrepancy is lower with overlapping generations, especially for long-lived species. Additionally, earlier maturation of escapees due to accelerated growth can cause severe fitness effects on wild populations with short life expectancy. Our results indicate that taking into account the variability of spillover across time, as well as the life history characteristics of certain species is essential for effective management to minimize the unintended fitness effects.