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Baker, Quintana and Brian Linkhart, Department of Biology, Steven Janke, Department of Mathematics; Colorado College

Modeling Habitat Quality for a Breeding Population of Flammulated Owls (*Otus flammeolus*)

Distinguishing quality of avian habitats is important for appropriate monitoring and conservation efforts, but has proven difficult due to sampling limitations and variance across spatial and temporal scales. I sought to establish specific components of habitat quality for a breeding population of Flammulated Owls (*Otus flammeolus*) through the development of a territory-scale probability model. I used the model to extrapolate empirical demographic data over a period of 50 years and then tested the data for relationships with specific territory habitat parameters. I combined the most influential habitat parameters to create an index of breeding habitat quality. The optimal index of habitat quality at the territory scale included the area of ponderosa pine forest and structural parameters of large diameter trees. The index suggests that the long-term success of Flammulated Owl populations depends on the availability of mature ponderosa pine forests, and that the owls are adapted to habitats whose structure historically was maintained by frequent fires.

Branigan, John, University of Hawaii, "Modeling pattern formation in cyanobacteria."

Macroscale pattern formation in living systems is believed to stem from microscale chemical patterns, which allow modeling by systems of differential and reaction-diffusion equations. Alan Turing first suggested a reasonable activator-inhibitor based mechanism in the 1960s and these ideas have been developed extensively by Meinhardt and Greier into widely applicable devices used to study the difficult question of how most useful and wonderful large scale cell and tissue patterns emerge from seemingly homogenous arrays of cells (such as some early egg stage in higher organisms). *Anabaena,* a cyanobacterium (pond scum) provides an exceptionally simple mathematical and biological application due respectively to its peculiar filamentous nature consisting of only two cell types, and to its bacterial genome which admits the powerful techniques of modern molecular biology. My talk will survey the historical development of these ideas and continue with recent work on *Anabaena* by our NSF funded team. Our most recent work involved genetic manipulations aimed at elucidating the mechanism of formation of a gene network-induced and maintained chemical prepattern which could explain (by the Turing-Meinhardt model) the very regular cellular differentiation of *Anabaena* into the familiar chainlike pattern observed in the wild.

Bokosha, Mike, Marymount University, "What does a vaccine need to accomplish to control an epidemic? A mathematical analysis."

My research examines a simple SIR-V model that approximates the movement of a disease such as the flu through a well-mixed population. I am interested in several questions concerning the role of vaccination in controlling an outbreak. I first examine the phenomena of herd immunity in the context of this model and specifically ask what percentage of the population would need to be vaccinated to protect the entire community. I then consider a more complex question: if immunity from vaccination wanes more quickly than immunity from disease recovery, is vaccination still a good tool for mitigating the progress of an epidemic?

Burks, Jenise and Ato Wallace, FISK University, "A Mathematical Model for the determination of Optimal Thresholds for Biosurveillance."
This study is aimed at developing a mathematical model for determining the optimal time for the employment of an intervention, in light of an epidemic, to minimize the losses accrued by a business or organization. This model was developed using the SIR differential equation model for epidemic outbreak, with the integration of additional cost functions associated with the specific interventions. Then using mathematical analysis the economic impact of interventions applied to various disease epidemics was estimated. The optimal time of intervention as calculated was used to determine economically favorable detection thresholds for epidemiological biosurveillance problems.
Key words: biosurveilance, epidemic

Cameron, Sharon and Yev Lampolsky, ETSU, "A Defender-Offender Game with Defender's Learning."

Game Theory is an important concept that describes how decision making affects the fitness of an individual in frequency-dependent situations. In ecology and evolutionary biology, game theory is a useful approach to the predicting the outcomes of the competition and other interactions among species and genotypes. The goal of game theory models is usually to predict which strategies are the ESS, i.e., which become predominant when the model achieves an evolutionary equilibrium. We here consider a symmetric zero sum pure strategies version of a classic hawk-dove model with two strategies: offenders, not seeking to own a resource, but attacking resources owned by others and defenders, conditionally defending resources they own (a.k.a. bourgeoisie strategy) and resorting to offensive behavior only after failing to monopolize a resource. The chief difference from the classic implementations of the model is the ability of defenders to acquire improved defense skills when attacked often. With no such learning the model predicts an unstable equilibrium with each strategy being and ESS. With learning, however, the model predicts sets of conditions under which neither model is an ESS (stable equilibrium), or defense dominates, or offense dominates. These results can be applied to the evolution of resource monopolizing behaviors in animals, such as territoriality and monogamy.

Cool, Robert, Missouri Western University,"Suppressor Logic Toolkit and its use in Bacterial Computing."
Frameshift suppressor tRNAs have unique properties that make them useful for application in bacterial computing. They do not diffuse across cell membranes, eliminating crosstalk with other cells. Suppressor tRNAs seem to be very specific to their binding sites, though this has not been studied in depth. If combined with other cell-cell signaling pathways, such as well-studied quorum sensing pathways, a more complex bacterial computer circuit could be built. The Davidson-Missouri Western iGEM teams have designed and built several bacterial computer circuits. The latest design uses frameshift suppressor tRNAs to process extracellular signals, into the four simplest Boolean logic gates; AND,

NAND, OR, and NOR. When used in combination, these logic gates, cell signaling pathways, and time-delayed cell growth could be used to form more complex computing circuits than are currently available for living cells.

Curll, Lisa and Hillary Howard, Youngstown State University, "Analysis of Bacterial Response to Toxic Selenite in *Enterobacter* sp."
The effects of toxic selenite on bacterial growth are explored for a wild-type selenite-resistant strain of *Enterobacter* and a selenite-sensitive mutant. A system of differential equations models the coupled interaction of cell growth and selenite uptake. A comparison of the models for the two strains suggests a model for the function of the membrane pump.

Fovargue, Rachel, College of William and Mary, "The Integration of Metapopulation Dynamics into Habitat Equivalency Analysis."
When a contaminant release is linked to an anthropogenic event, an analysis, such as Habitat Equivalency Analysis, may be performed to evaluate the service losses to the local environment. I hypothesized that incorporating metapopulation dynamics into an HEA model would dramatically change the calculated losses. To test this, I created a model using Matlab that would represent a metapopulation of Carolina chickadees (*Poecile carolinensis*), then simulated the introduction of a contaminant by lowering the reproductive success and survival rates for one of the subpopulations in the model. I compared the estimated losses for both my novel method of calculation and the currently used method of calculation over a variety of parameters. I found that the novel method could provide a larger estimate of damages, indicating that metapopulation dynamics may play an important role in estimating damages from an anthropogenic event.

Hopkins, David and Moriah Echlin, Colorado State University, "Modeling of White Pine Blister Rust."
White Pine blister rust is a prevalent pathogen affecting *Pinus albicaulis,* a keystone species in sub-alpine ecosystems. Often a deterministic population projection determines the far-reaching effects of this infection and models population growth. Our research goal deviates from the constraints of this normal deterministic model, and in its place, utilizes an agent based model. We will compare and contrast the two different strategies in a system for the growth of *Pinus albicaulis* and the spread of White Pine blister rust. Both models are constructed from the same parameters in transition, survival, infection rate, and initial conditions. They also will incorporate density dependence and the effects of genetic resistance through certain alleles. With a deterministic model, every realization recreates the same projection, as it treats all individuals in a class as one. However, an Agent Based Model is a stochastic model, which predicts population dynamics with respect to individuals rather than classes. For each time step, random experiments determine the occurrence of transition, survival, infection or death for every agent. Therefore, every realization of an Agent Based Model is unique, which creates a projection sample allowing for statistical analysis. Ultimately, we expect the mean of this probability distribution to equal the outcome of the equivalent deterministic matrix model.

Hirai, Kelsi, Brown University, "One Dimensional Simulation of Cerebral

Arterial Circulation."
One-dimensional (1D) simulation of blood flow in the macrovascular cerebral network provides insight into blood flow dynamics. Low computational complexity and minimal changes required to modify the input parameters make the 1D model appealing for parametric and sensitivity studies. Stochastic unsteady flow simulations have been performed to study the effects of progressive narrowing (stenosis) in the internal carotid arteries (ICA). The uncertainty was modeled by employing the polynomial chaos and Monte Carlo methods and setting the radii of the ICA as a stochastic variable. Presented here are the sensitivities of the flow patterns in the entire macrovascular intracranial network due to the ICA stenosis and a comparison of the efficiency of the polynomial chaos and Monte Carlo methods.

Knighten, Brionna and Jammal Simmons, Jackson State University, "Mathematical Modeling of HIV/AIDS Epidemic."
HIV/AIDS is an incurable virus that is mainly spread through sexual contact, the transfer of blood through transfusions, or the sharing of needles by drug users. This virus ultimately leads to AIDS which is the acronym for acquired immune deficiency syndrome. In many communities around the world, the main victims of HIV/AIDS are male homosexuals. We examined two models both consisting of systems of Differential Equations (DEs). The first model gives a more realistic view of the spread of AIDS in the homosexual community only. In the second model we examine the effect modern medicine has on the virus mathematically. From these models, we hope to get a sense of what impact this disease will have on society in the future.

Korbach, Hannah, Marymount University, "An Analysis of Several Mathematical Models for Cholera."
This presentation will focus on the change from a simple SIR (susceptible, infected, recovered) model to a more complex one. It will also address whether or not adding more details to a model really makes a difference in the outcomes. This will be done by showing comparisons of the simulations of both the original simple model and the new model.

Lau, Kin, Davidson College,"Making a transcriptional XOR logic gate using *E. coli.*"
We designed a biological XOR gate using two adjacent promoters pointing towards each other. One promoter is the commonly used pLux promoter from *V. fischeri*, while the other is pOmpC from *E. coli*, which we have isolated and characterized using synthetic biology methods. The pOmpC promoter is induced by high extra-cellular solute concentration. We characterized the activity of pOmpC in *E. coli* grown in different media that provided high solute concentration environments. We have tested the XOR gate to see if *E. coli* can be programmed to perform XOR logic. Through our project, we have learned more about how the pLux and pOmpC promoters work and have expanded our understanding of how *E. coli* could be used to perform computations and utilize logic gates.

Llera, Kristie and Jessica Gulbranson

Supervisors: S. Koksal and R. van Woesik, Florida Institute of Technology, “Estimating Vital Coral Population Parameters.”

Coral reefs support more species than any other marine ecosystem on earth. Recent and unprecented increases in ocean temperatures have had significant social, economic, and environmental impacts. Yet, we still have a poor understanding of the fundamental processes and dynamics on reefs. We mathematically defined three vital population parameters: growth, partial mortality, and total mortality to further our understanding of how these rates affect coral population dynamics.

In this presentation, two approaches are used to mathematically analyze the vital population parameters. These approaches have produced general trends for these parameters using initial colony size to define (1) relative growth rates and (2) probability density functions. Functional relationships were determined between growth rate and initial colony size using curve fitting analysis, least-squares approximation and probability functions.

Lockwood, Svetlana, Washington State University, “ Predicting Temperature Sensitive Mutations.”

Temperature-sensitive (Ts) mutants behave like wild type (WT) at the permissive temperature, but significantly drop the level of activity at the restrictive temperature. Though Ts mutants are instrumental in studying protein functions in vivo, the laborious, time-consuming random mutagenesis procedures for Ts mutant generation slow the progress of scientific discoveries. This research focuses on the development of a computational procedure for prediction of amino acid substitutions, which are most likely result in a temperature sensitive mutation. A total of 109 computable protein features (predictors) were investigated for Ts mutations. Among the top 35 predictors, 40% are features describing mutation site’s neighborhood. This discovery sheds new light into the nature of Ts mutations. Logistic regression function is chosen as a framework and results validation is performed by 10-cross validation.

Mike, Joshua, Kathryn Yazvac and Robert Parise, Youngstown State University, "The Senktide Effect on the Dynamics of Pyramidal Neurons."

Senktide is a drug that increases firing activity in prefrontal cortex layer V pyramidal neurons. In order to investigate this response, we developed a biophysically based model incorporating the multiple currents affecting the firing activity of these neurons. This model was compared to our experimental data, obtained from whole cell patch recordings of the neurons in vitro, in order to determine the currents sensitive to senktide. Additionally, the model was analyzed using dynamical systems techniques to determine the mechanisms of the senktide response.

Niccum , Brittany *[1,2], Marisa Rivera*[2], Jewgeni H. Dshalalow[1], Richard R. Sinden[2]
[1]Department of Mathematical Sciences, [2]Department of Biological Sciences, Florida Institute of Technology, 150 W. University Blvd.

Melbourne, Florida 32901 Genome instability associated with quadruplex DNA: Determination and Analysis of Mutation Rates

Biological System: Certain DNA sequences containing runs of guanines (G) have the ability to adopt 4-stranded quadruplex DNAs. Sequences that can form quadruplex DNA are widely found associated with oncogenes that cause cancer. Presumably, the ability to form an alternative or unusual DNA structure in the human genome can lead to mutations, including chromosome rearrangements that are often associated with cancer cells. To study the genetic instability of quadruplex-forming DNA we have taken sequences that have been shown to form quadruplex structures (Risitano and Fox, 2003; Kumar et al., 2008) and cloned them into the chloramphenicol acetyltransferase gene in plasmid pBR325. These sequences include: $(G_3T)_4$, $(G_4T)_4$, $(G_3T_2)_4$, $(G_4T_2)_4$, and $(G_3T)_8$. This system allows the measurement of the rate of deletion of the quadruplex sequence from the DNA. We have also reversed the orientation of the unidirectional origin of replication in these plasmids, creating pBR235 plasmids. Thus, in plasmids pBR325 and pBR235 the G-tracts are on either the leading or lagging strand of DNA replication. These plasmids were then transformed into *Escherichia coli* strains BW25113 and JW0784-1 to study the possible effects of the DinG protein in the unwinding of such quadruplex structures. The DinG protein is a helicase that can reportedly unwind unusual DNA structures. Some of the quadruplex-forming sequences are genetically very unstable in cells, and initial data show a 40-fold ratio comparing sequences in pBR325 and pBR235. The results suggest that quadruplexes are forming *in vivo* in the *E. coli* cells in a leading or lagging strand specific fashion. Future analysis will determine if the DinG helicase is involved in removing quadruplexes.

Mathematical Analysis: Mutations are permanent changes in an organism's DNA. Observable changes that occur in the DNA can be measured and a mutation rate at which these changes occur can be established by performing experiments such as the fluctuation assay (Luria and Delbrück, 1943). The question of how to best determine rates from the widely variable distributions of mutants obtained by these fluctuation assays has been addressed several times during the past fifty years with varying degrees of success (Rosche and Foster, 2000). Our mathematical goal is to improve this understanding and calculation of mutation rate. Kumar,N., Sahoo,B., Varun,K.A., Maiti,S., and Maiti,S. (2008). Effect of loop length variation on quadruplex-Watson Crick duplex competition. Nucleic Acids Res. 36, 4433-4442.

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Pawelec, Kendall, Michigan State University, "Mathematical Modeling of Stem Cell Response to Polyelectrolyte Multilayer Films."

Kendell Pawelec, Linxia Zhang, Sumit Mehotra, Chris Hunley, Seungik Baek, Christina ChanChemical Engineering & Materials Science, Depart of Biochemistry and Molecular Biology,Michigan State University, East Lansing, MI.

Polyelectrolyte multilayers (PEMs), thin films consisting of electrostatically deposited polyelectrolyte layers, have enormous biotechnological potential. PEM's intrinsic characteristics, such as structural rigidity, swelling, thickness and surface morphology, are known to affect cell adhesion. One of the most profound factors affecting these parameters is the number of polyelectrolyte layers deposited. The mechanics of the cell attachment onto a surface are therefore expected to vary with respect to film thickness, and may also be dependent on the cell type. A mechanistic knowledge of the inter-play between stiffness, swelling, thickness and cytophobicity/cytophilicity of these films can help in understanding the varying responses of cells to these biologically relevant substrates. Based on this information, a mathematical model was constructed which seeks to understand mesenchymal stem cell response to PEMs as a function of PEM thickness. Strong polyelectrolytes, which are known to exhibit linear growth and little swelling, were used to construct PEMs, varying the thickness by changing the number of layers assembled onto the substrate. Mathematical modeling suggests that cell interactions with PEM films are influenced primarily by changes in the stiffness of the film experienced by the cell. As film stiffness decreases, cell spreading decreases, which serves to keep the total energy expenditure of the cell within a narrow range. Gaining insight into cell interactions via modeling will allow cellular response to be fine tuned in biotechnological applications by varying only one PEM parameter.

Rodriguez, Grayson, Northern Kentucky University, "Florida's Cicada Killer Wasps Cast Doubt on Current Dogma." Cicada killer wasps reputedly hunt cicadas opportunistically, but analysis of two communities in Florida indicate that the wasps hunt selectively by size (hunting the largest cicada they can handle). While both locations support similar cicada populations, whose sizes can be grouped as small, medium, and large, there is a curious difference between the two sites: one has significantly larger wasps. Furthermore, both sites are striking because their wasp populations are normally distributed in size, whereas the dogma is that individual cicadas are converted into individual male wasps. Why, then, do we not see three distinct sizes of male wasps? The talk will explore these mysteries.

Thomason, Sarah, Murray State University, "Evaluation of Microsatellites in *Ambystoma tigrinum nebulosum*"

Phenotypic plasticity is the ability of a trait to change in response to an environmental cue. Salamanders are known to exhibit phenotypic plasticity in the form of facultative paedomorphosis, producing a paedomorphic (aquatic) or a metamorphic (terrestrial) body morphology, which provides a unique vertebrate model for understanding the evolution of phenotypic plasticity. Previous research has revealed the mechanisms that produce this polymorphism (i.e. larval body size as an indicator of success); however, little is known about the evolutionary mechanisms that maintain it. As a first step to addressing this question, we are using nuclear markers to assign parentage within a closed population of tiger salamanders located at the Mexican Cut Nature Preserve in Gothic, Colorado. Microsatellites are a tandemly repeated nuclear marker that are ideal for addressing parentage and relatedness because they are highly variable between individuals within the same population and band sharing is conserved between parent-offspring pairs. We optimized a variety of microsatellite primers designed for ambystomatids using PCR and are currently focusing on optimizing *Ambystoma* tigrinum specific microsatellites. Once variable primers have been successfully optimized and scored, relatedness and paternity statistics will be used to design a pedigree. This pedigree will help us better understand the evolution of facultative paedomorphosis, the fitness consequences associated with each morphology, and tiger salamander life history.

Tracht, Samantha, Capital Univeristy, "Mathematical Modeling of the Effectiveness of Facemasks in Reducing the Spread of Novel Influenza A (H1N1)."
On June 11, 2009, the World Health Organization declared the outbreak of novel influenza A (H1N1) a pandemic. With limited supplies of vaccines and antivirals, countries and individuals are looking at other ways to reduce the spread of novel H1N1, particularly options that are cost effective and relatively easy to implement. Recent experiences with the SARS and 2009 H1N1 epidemics show that people would wear facemasks to protect themselves against infection; however, little research has been done to quantify the impact of the use of facemasks in reducing the spread of disease. We construct and analyze a mathematical model in which a portion of the population wears a facemask during the pandemic. We look at two scenarios, one in which N95 respirators are worn and one in which surgical masks are worn. To estimate the parameter values used for the effectiveness of facemasks, we used available data from studies done on N95 respirators and surgical masks. If N95 respirators are 20% effective in reducing susceptibility and infectivity only 10% of the population would have to wear them to significantly reduce the number of novel H1N1 cases. We conclude from our model that, if worn properly, facemasks are an effective intervention strategy in reducing the spread of novel H1N1.

Washington, Marvin and Hyun J. Cho and D. Lu, Jackson State University, "Developement of Water Correction Algorithm for Underwater Vegetation Signals." The unique spectral characteristics of green vegetation, low reflectance in red and high reflectance in Near-Infrared (NIR), have been used to develop vegetation indices, such as Normalized Difference Vegetation Index (NDVI). Our preliminary studies suggest that NDVI was not a useful indicator for submerged aquatic vegetation (SAV), even in clear water, due to energy absorption by water in the NIR region. In order to improve the use of the vegetation indices, we modeled the depth-variant water absorption and scattering through a controlled indoor experiment. We used a GER 1500 spectroradiometer to collect spectral data over an experimental water tank (70cm tall, 50cm wide) that was deployed with a black panel or a white panel at a time; the panels were cut to fit the bottom of the tank. Our assumptions were: (1) the black bottom panel absorbs 100% incoming light; (2) the white bottom panel reflects 100% incoming light; and (3) the water volume scattering and absorption remains the same for the two conditions (black and white bottoms) at a given depth. The measured upwelling radiance was converted to % reflectance. After conducting our experiments, we found that the addition of water significantly affected the vegetation signal, especially in the NIR region. After finding the contribution of

water absorption and volumetric reflectance, we removed the partial water effects from the measured data. The application of the algorithm significantly improved the vegetation signals in the NIR region. Our results suggest the conventional NDVI: (1) is not a good indicator for submerged plants even at shallow waters (<0.5 m); and (2) the index values can significantly improve once the water effects are modeled and removed. The applied the correction algorithm to image data. Although the visualization of the image itself did not show much improvement in distinguishing vegetated bottom from the bare sediment, the spectral profile of an area with submerged plant beds showed the NIR reflectance was increased and the red reflectance was decreased. Our next step is to extend the correction algorithm to account for different levels of turbidity.
Keywords: SAV, reflectance, vegetation indices, absorption, volume scattering

Zingarelli, Erin, FIT, “Artificial Neural Net Model of PLCg-dependent Calcium Release and Growth after Fertilization in the Starfish *Asterina miniata*.”

Cristina Mazzone[1], Erin Zingarelli[1], and Adam Hernandez[1]
Supervisors: D. Carroll[1] and S. Koksal[2]
[1]Department of Biological Sciences and [2]Department of Mathematical Sciences
Florida Institute of Technology, Melbourne FL 32901

During fertilization in all plants and animals, there is an increase in the concentration of intracellular free calcium due to the production of inositol 1,4,5-trisphospate (IP3) by a member of the phospholipase C (PLC) enzyme family. In several animal phyla, including echinoderms, PLCg is the isoform responsible for calcium release. Furthermore, inhibition of PLCg activity inhibits both the calcium increase and the initiation of embryonic growth. However, the relationships between these molecules at fertilization has never been tested in a rigorous quantitative manner. To address this issue, an artificial neural net (ANN) was developed to model fertilization, focusing on the contribution of PLCg, its products (IP3 and diacylglycerol), and downstream effectors (protein kinase C and calcium) to embryonic growth. This is a multilayer hybrid ANN that combines both the perceptron and back-propagation training algorithms. The ANN is currently being tested in the laboratory by inhibition of PLCg enzyme activity in living eggs via microinjection of a competitive PLCg-inhibitor followed by microscopic imaging of intracellular free calcium at fertilization. Thus far, only 1/11 eggs injected with between 4.75 – 19 mM PLCg-inhibitor exhibited any calcium release, compared to 5/5 control-injected eggs. This suggests that there is a threshold level of PLCg activity that is required to initiate the fertilization-induced calcium increase. Future experiments will focus on testing lower concentrations of the PLCg-inhibitor to determine if a threshold exists for calcium release and/or for cell growth.