Speakers & Abstracts of Second UBM South Regional Conference
(Ordered by Scheduled Time)
University of Houston-Downtown, Houston, Texas
Friday & Saturday, October 28-29, 2011 (All talks in Academic Building A300)

Friday 1:45-2:25   Keynote Speaker
A Leader's Edge – How to Become a Successful PhD Student!

Mesias Pedroza, University of Texas Health Science Center

Abstract

One of the major challenges of an academic career is scholarly productivity. Maintaining high productivity in publishing and funding is central to a successful research career. This session will provide strategies, experiences, and advice in becoming a successful PhD student. Topics include: Becoming part of the Research Community, Balancing Life and Career, What Scholarships and Fellowships look for in PhD Candidates, Important habits for Researchers, Scientists and Social Media, and Scientists and Public Policy. The final discussion will briefly introduce the Future of Academic Medicine and the road for the MD/PhD track.

Friday 2:30-2:50
The Effects of Hurricane IKE on a Coastal Wetland Ecosystem

Glenda L. Thammavongsa & Conrad Cacho

University of Houston-Downtown

Abstract

This study utilizes two distinct taxonomic groups to study the ecological changes that occur in a natural wetland system before and after a major natural storm. Anahuac National Wildlife Refuge is a sixty year old, 64,000 acre, natural wetland located adjacent to Galveston Bay, Texas. Shoveler Pond is a pristine fresh water wetland within the ANWR that supports diverse flora and wildlife populations. The wetland was struck by Hurricane Ike in 2008 which caused severe damage to the wetland due to direct wind damage, debris from Bolivar Peninsula, and saltwater intrusion from East Bay. The salt water intrusion caused a dramatic change in the species diversity that resided in the marsh. These changes were observed at a microscopic level through the study of the death assemblages of diatoms and arcellaceans. Diatoms, unicellular algae, and Arcellaceans (thecambians), unicellular testate rhizopods, both serve as indicators of soil and water conditions over a period of time. Statistical analyses were used to study changes in alpha and beta diversity of these organisms before and after the effects of Hurricane Ike. Alpha diversity is a measure of the species richness in a particular ecosystem. Beta diversity is a measure of richness and relative abundance. The study was expected to show that stable assemblages present before hurricane Ike changed over two years as the death assemblage formed, and that the assemblages began to show recovery in the third year. Shannons index was used to exhibit the alpha diversity of diatoms and arcellaceans at the ANWR. Both Spearmans similarity and Bray-Curtis dissimilarity indices were used to study beta diversity. The use of both Spearmans and Bray-Curtis measurements allowed us to determine the impact of rare genera. Results from Shannons Index show alpha low diversity prior to Hurricane Ike, a drastic increase in alpha diversity after the hurricane, and a decrease in alpha diversity in year three. Spearmans index showed a similar pattern, though it was not possible to show that the amount of change was significant compared to trends in previous years. Bray-Curtis measurements were more dramatic, however, indicating that changes in beta diversity did occur and were due mostly to the introduction of rare genera.

Advisors: Dr. Brad Hoge & Dr. Ronald Barnes, University of Houston-Downtown

Quantitative Measurements Of Delay And Variability In Transcriptional Signaling

Elizabeth Van Itallie, Andrew Hirning, & Matthew R. Bennett
Department of Biochemistry and Cell Biology, Rice University

Abstract

Transcriptional regulation is the basis of genetic networks and is especially important in prokaryotic systems. There are many steps involved in the maturation of proteins from mRNA to active complexes. Thus there is a delay time between the transcription of the gene by the polymerase and the forming of the active protein. Variation among the length of the intermediate steps such as translation and folding results in a distribution of the delay times. We are building a simple synthetic network that will allow us to determine the mean and variance in the time between transcription of the $araC$ gene and maturation of the active AraC protein. We will use micro-fluidic devices and live imaging fluorescence microscopy. We will use fluorescent proteins to report on the state of the network and thus determine the delay time in individual cells. The resulting mean and distribution will not only inform us about protein maturation delay times in prokaryotic systems but will also give us parameters that can be used to test the accuracy of a new mathematical model of transcriptional regulation in prokaryotes.

Variability of Cell Growth and its Effects on Population Dynamics

Priya Rao, Jatin Narula, & Oleg Igoshin
Department of Bioengineering, Rice University

Abstract

The inherent stochasticity of biochemical reactions leads to population variability in cellular gene expression profiles. Due to the coupling between the expression of essential metabolic enzymes and cell growth, this variability can lead to population variability in growth rates. In this study we investigate the effects of growth rate variability on bacterial population dynamics. Our simulations show that when fluctuations in protein levels are heritable, the population adapts, and the mean growth rate increases due to faster growth of cells at the edge of the gene expression distribution. However, when the fluctuations in gene expression are not heritable, there is no change in the mean population growth rate. We also found that heritable variability in cell growth can also provide a selective advantage when two populations compete. When population growth is constrained, the probability of fixation is higher for the mutant with greater variance of growth rates, even without differences in mean growth rate. The selective advantage of growth variability decreases as the probability of growth inheritance decreases. When inheritance is unlikely, our simulations agree with the classical result where growth variability reduces the chances of fixation. This relationship between gene expression variability and population growth dynamics might influence the selection of regulatory network architecture. We compare the response of a gene regulated by activators or repressors and show that coupling with cell growth can indeed lead to differences in the expression variability and selection of these otherwise equivalent regulatory circuits.

Friday 3:30-3:50 Coffee Break

A Genome-wide Assessment of Insertion and Deletion Variation in African-Americans

Lilian Antunes, University of Houston-Downtown

Abstract

Background: The sequence of human DNA is variable among individuals. There are two main types of DNA variation: variation in the sequence itself and variation in the length of the sequence because of insertions or deletions. When small insertions or deletions (InDels) occur in a protein-encoding gene they may lead to a dysfunction protein or a premature stop codon. Previous research on InDels has focused primarily on InDels in only select targeted genes. As a result of advances in sequencing technology, it is now possible to measure InDels on the entire human genome. Understanding the frequency, characteristics and distribution of InDels is a first step in understanding their contribution to human physiology and disease.

Case study: Genome sequence data from fifty-four African-Americans having abnormal blood pressure measurements have been surveyed to identify common InDel variations. On average each individual has approximately eleven thousands InDel variations distributed across their exome and nearby flanking DNA (i.e. the protein encoding portion of the genome), where seventy percent of these InDels were deletions. The size of the InDels ranged from one up to ten nucleotide base pairs for insertions and up to twenty nucleotide base pairs for the deletions. In order to preliminarily investigate the relationship of these InDels with blood pressure, we identified seventeen genes previously identified to be hypertension-susceptibility genes, and then investigated the distribution of the InDels in these hypertension genes. A simple summary will be given, but these analyses are ongoing. These data are the first survey of insertion and deletion variation across the genome of African-Americans, and they are a first step toward understanding the role of such variation in human disease.

Advisors: Dr. Eric Boerwinkle, Department of Epidemiology, Human Genetics and Environments Sciences (UTHSC), The University of Texas Health Science Center at Houston (UTHealth)

Analysis of Diatoms and Arcellacean Death Assemblages to Determine Inclusion or Exclusion of Rare Event Data in Comparison with Various Missing Data Analyses Techniques

Edgar Aquino, Cory Ali, & Ilian Rojas, University of Houston-Downtown

Abstract

In this project, diatom and arcellacean death assemblages were studied to determine if trends exist in the succession of a mitigation wetland ecosystem in Greens Bayou Wetland Mitigation Bank compared to a stable wetland ecosystem in the Anahuac National Wildlife Refuge. The statistical package EstimateS (Statistical Estimation of Species Richness and Shared Species from Samples) was used to calculate the various statistical indices used to determine alpha and beta diversity between GBWMB and ANWR. EstimateS was used to analyze the raw data and alternatively, the rare species in the diatom and arcellacean assemblage were removed using the theory of listwise deletion and then analyzed by EstimateS. The comparison of traditional missing data analyses such as listwise deletion, partial listwise deletion, imputation, and partial imputation via SAS to the inclusion and exclusion of rare genera results used by EstimateS were compared to analyze the impact of the rare genera of the diatom and arcellacean death assemblage. This missing data analysis shows that the inclusion of rare genera is important to the succession signal in the mitigation wetland.

Advisors: Dr. Brad Hoge & Dr. Ronald Barnes, University of Houston-Downtown

Friday 4:30-4:50

Mathematical Modeling of the BMP-4 and FGF Signaling Pathways during Neural Induction in *Xenopus laevis*

Amie Albanese, Jose Trejo, & Robert Nguyen, University of Houston-Downtown

Abstract

How does undifferentiated embryonic tissue become committed to develop into the central nervous system? The hypothesis: neural development is established by a quantifiable imbalance in the cross-regulation of the BMP and FGF signaling pathways. To study this, embryos of the frog *Xenopus laevis*, are used because 1) they share similar embryonic development characteristics with human embryos, and 2) they are much easier to study than mammalian embryos. During embryonic development, ectodermal cell fate in *Xenopus laevis* is determined by interaction of the mitogen-activated protein (MAP) kinase and bone morphogenetic protein-4 (BMP-4) signaling pathways. To further understand the quantitative features of the interactions between these two pathways, a mathematical model consisting of coupled, nonlinear ordinary differential equations (ODE) was developed consisting of five key proteins, including MAP kinase, FGF, BMP-4, SMAD, and TAK. Previous research has shown these proteins to be critical players in cell fate decision in the ectoderm at the time of gastrulation. This mathematical model was created to generate testable predictions of the hypothesis. Simulations using the ODE solvers of MATLAB were then conducted to test the biological validity and reliability of the model. These simulations used some parameter values suggested from previous research literature. A reduced form of this extensive model, which includes the proteins from the epidermal pathway, is also studied. Steady states of the reduced model are analytically derived and numerical computations are carried out to elucidate the interaction between the two signaling pathways. Future work will involve increasing and decreasing the MAP kinase and SMAD parameters in the original model to observe if simulations in MATLAB can produce the change that occurs biologically when MAP kinase activity is increased four to six fold.
Advisors: Dr. Edwin Tecarro & Dr. Akif Uzman, University of Houston-Downtown

Friday 4:50-5:30   Keynote Speaker

What Can We Learn About Pathogens from Mathematical Models?

Claudia Neuhauser, University of Minnesota Rochester

Abstract

Pathogens are ubiquitous. They range from viruses to bacteria and fungi, and are implicated in numerous diseases across all organisms. We will explore mathematical models to understand the role of pathogens in shaping the evolution of populations, maintaining biodiversity, and curing cancer. The explorations range from the theoretical approach using paper and pencil to high-performance computing and high-throughput technologies, demonstrating the synergy of old and new ways of gaining new knowledge.

Dinner Banquet, Friday 6:30—8:00

Breakfast Networking, Saturday 8:30—9:30

Matrix Analysis of Lone Star Tick Populations

Adam Kley, Department of Mathematics, Texas A&M University, College Station

Abstract

Lone Star ticks are important to model because they carry harmful bacteria. In this project we implemented the 1987 matrix model of Haile and Mount, which accounts for the affects of changes in relative humidity, daylength, and temperature on survival, reproduction, and growth rates. Our results show that certain life stages are more sensitive to climatic changes than others, and that the most sensitive life stages are not constant year round.

Advisors: Dr. William Grant, Dr. Rose Wang, Dr. Masami Fujiwara (Wildlife and Fisheries Sciences), & Dr. May Bogges (Math), Texas A&M University, College Station

Fast-start Swimming Performance in Hybrid Male Swordtail Fish

Danielle Macedo, Department of Biology, Texas A&M University, College Station

Abstract

Individuals subject to sexual selection may display traits that allow for higher mating success while being costly to performance. These traits may also be affected by hybridization. The hybrid system of Xiphophorus birchmanni and X. malinche was used in this study since male X. malinche display a sword, or an extension of the caudal fin, X. birchmanni do not, and hybrids are polymorphic. Fast-starts are a common anti-predator behavior used by fish which may be impacted by morphological traits, such as the sword. The purpose of this project was to discern the link between morphology and fast-start swimming performance in this hybrid system. Overall, we found that hybrids generally performed better than the parental species, possibly due to hybrid vigor and that there is no correlation between morphology and performance. Our results were surprising, since previous work had found such correlations, though this may have been due to a larger number of hybrid individuals analyzed, relative to parental species.

Advisors: Dr. Gil Rosnethal (Biology)& Dr. Jay Walton (Math), Texas A&M University, College Station

Modeling the Rate of Formation of cAMP in Preformed Signaling Complex of G-Proteins and Adenylyl Cyclase

Layne Held & Jeongsook Larson, University of Houston-Downtown

Abstract

In reference to cellular signal transduction, it is the accepted doctrine that heterotrimeric G-Protein complexes are activated by the binding of a ligand to a receptor. Exchange of GDP for GTP on alpha subunit of $G\alpha\beta$? causes the separation of $G\alpha$ from $G\beta$?, and these subunits then diffuse to their respective effector. GTP-$G\alpha$ activates the effector, adenylyl cyclase (AC), which catalyzes the production of the cyclic AMP (cAMP), the second messenger in the cell. However, recent data shows that Inactive G-proteins (GDP-$G\alpha\beta\gamma$) exist as a complex with adenylyl cyclase. G-proteins interact with adenylyl cyclase at two distinct sites; the inactive G-proteins are scaffolded at N-terminus of AC while active G-proteins(GTP-$G\alpha\beta\gamma$) interact at the catalytic domain of AC. This supports the existence of preformed signaling complexe of adenylyl cyclase 5 (AC5) and heterotrimeric G-proteins ($Gs\alpha\beta$?). We hypothesize that the existence of preformed signaling complexes play role in fast activation and inactivation of the signaling pathway and will be mathematically modeled in terms of rate of formation of cAMP.

Advisors: Dr. Rachna Sadana (Biology) & Dr. Steve London (Math)

Saturday 10:30-10:50 Coffee Break

Saturday 10:50-11:10

Optimal Movement Strategies for Thermoregulating Snakes and Lizards within a Habitat

Curtis Balusek, Casey Hartnett, & Kristen Pelo, Sam Houston State University

Abstract

Reptiles are poikilotherms whose body temperatures are governed by ambient environ- mental temperature. Some species of reptiles use behavioral thermoregulation to maintain a preferred body temperature while others simply thermoconform to the thermal environment. Movement and thermoregulatory behaviors are often in uenced by sit-and-wait or active for- aging strategies. Huey and Slatkin present a qualitative analysis of optimal thermoregulatory strategy that we examined quantitatively with algebraic equations. We used a piecewise lin- ear function, a differential equation and a computer simulation to mathematically investigate Huey and Slatkins' theoretical model of thermoregulation. This research allowed for evaluating the cost and benefits associated with thermoregulatory strategy of a snake species, the timber rattlesnake, Crotalus horridus.

Advisor: Dr. John G. Alford (Math).

Saturday 11:10-11:30

Ray sensory neuron control of the *C. elegans nematode* Worm Mating Behavior

Laura Caflish, Department of Mathematics, Texas A&M University, College Station

Abstract

Many evolutionarily significant behaviors, such as mating, involve dynamic interactions with animate targets. This raises the question of what features of neural circuit design are essential to support these complex types of behavior. The C. elegans male uses 18 ray sensilla of the tail to induce and coordinate a systematic search for the hermaphrodite vulva, but precisely how ray neuron types, A and B, endow the male with a high degree of spatial and temporal precision is unknown. We have quantified the postures produced by measuring the angles of various points along the males body axis. Calculation and comparison of angles produced by A- and B-neuron populations shows that, although the postures produced are superficially similar, there are statistically significant differences between them. Together these data reveal that the robustness of the search, stem from considerable functional overlap between ray neuron populations and precision is due to the subtle differences in their output.

Advisors: Dr. Robyn Lints (Biology)& Dr. May Boggess (Math)

Saturday 11:30-11:50

Mathematical Modeling of *Pseudomonas aeruginosa* Biofilm Growth

Amber Burkett, Mayra Sanchez, & Kimberly Walker, University of Houston-Downtown

Abstract

The focus of this research is to mathematically model the growth of bacteria as a biofilm. Biofilms are a collection of microorganisms that adhere to each other and to a moist surface. This is in contrast to planktonic growth where bacteria grow as individual organisms. There are many different factors that influence this mode of bacterial growth. Bacteria under stressful conditions generally form biofilms more readily. In addition, a moist surface and a critical number of bacteria are necessary for biofilm growth. In this project, *Pseudomonas aeruginosa* bacteria are used to model bacterial growth as a biofilm. In addition mathematical equations are being developed to model the growth of the biofilms. First, planktonic growth of *Pseudomonas aeruginosa* was replicated by us. The data was plotted and fit K where R = bacteria growth rate and $N(t)$ = population as a function of time. Biofilm growth is being studied using three assays: scrape and plate, dry weight, and live/dead. The data collected from the three assays agree qualitatively. Most of the data modeled an oscillating growth pattern. It is predicted that the oscillations will dampen as the nutrients run out. Based on these new findings a nonlinear differential equation is proposed to model the population growth.

Advisors: Dr. Poonam Gulati (Biology) & Dr. Youn-Sha Chan (Math)