

Speakers & Abstracts of Third UBM South Regional Conference

University of Houston-Downtown, Houston, Texas

Friday, October 12, 2012 (All talks in Academic Building A300)

— 1:00–1:15 pm Opening remarks

§—————§ Break (1:15–1:20 pm) §—————§

— 1:20–2:20 pm Keynote Speaker

Role of Topology Optimization in Reconstructive Surgery

Alok Sutradhar, Ohio State University

Abstract

Restoring normal function and appearance after massive facial injuries with bone loss is an important unsolved problem in surgery. Current methods are limited to heuristic ad hoc design of bone replacements by the operating surgeon at the time of surgery. This problem might be addressed by incorporating a computational method known as topology optimization into routine surgical planning. Topology optimization is a structural optimization method that combines a numerical solution method e.g., the finite element method (FEM), with an optimization algorithm to find the optimal material distribution inside a given domain. It determines which portions will have material and which will have voids. This technique has the potential to guide and clarify in which places skeletal materials are necessary to withstand the expected loads (e.g., for mastication) and support soft tissue structures, specialized organs (e.g., orbital contents), and prosthetic devices. We performed a three-dimensional topology optimization to design bone replacements. The final solution to meet functional requirements may be shaped differently than the natural human bone but be optimized for functional needs sufficient to support full restoration using a combination of soft tissue repair and synthetic prosthetics. Topological optimization for designing facial bone tissue replacements has the potential to improve current clinical methods and provide essential enabling technology to translate generic bone tissue engineering methods into patient-specific solutions.

— 2:20–2:40 pm

Discrete Modeling of Chemostat Population Dynamics of Escherichia coli strain B and Bacteriophage T4

Molly Zumbro and Rob Bierman
Trinity University

Abstract

The interactions between predator and prey in a microbial system serve as a controllable and informative model that can be used to better understand complex ecological systems. This work focused on the microbial community consisting of T4 bacteriophage, T4 sensitive E. coli B, and T4 resistant E. coli B in a glucose (carbon) limited,

steady-state environment. The chemostat was aseptically maintained for several weeks with *E. coli* culture in the absence of T4 bacteriophage to establish steady state levels of phage resistant and sensitive bacteria in medium containing 20 mM glucose. Prior to the introduction of phage, the chemostat contained a mixed population consisting of approximately 109 sensitive bacteria and 106 resistant bacteria. Bacteriophage T4 (with latent period of 30 minutes) was used to infect this population at a multiplicity of infection of 0.1. After phage addition, aliquots of the bacteria/phage populations were removed and preserved every thirty minutes for the first twelve hours; every three hours for the next twelve hours, and finally every twelve hours over the subsequent four days, resulting in the collection of thirty-seven time points. Phage titers, numbers of sensitive and resistant bacteria, as well as complexes formed by sensitive bacteria and phage were determined in triplicate from each of these time points. The collected data will be scrutinized using nonlinear regression and the mathematical computer software R to estimate the parameters for the mathematical model that was generated by the discretization of the coupled differential equations described by Bohannon and Lenski (*Ecol. Lett.* 3:362-377). After the estimation of parameters, the model and the initial conditions for the systems will be used to produce a hypothetical data set. The data recorded from the chemostat will then be statistically tested against the generated data set to determine the strength of our model.

Advisors: Drs. Saber Elaydi (Mathematics), Frank Healy (Biology) & Hoa Nguyen (Mathematics).

— 2:40–3:00 pm

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

Jungsook 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 $G\alpha\beta\gamma$ causes the separation of $G\alpha$ from $G\beta\gamma$, 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 complex of adenylyl cyclase 5 (AC5) and heterotrimeric G-proteins ($G\alpha\beta\gamma$). 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.

Advisor: Dr. Rachna Sadana and Dr. Steven London.

— 3:00–3:20 pm

Diversity and Homogeneity Revealed in SSR Analyses of NCGR Cultivars

Abstract

The popularity of the well-known home remedy ingredient cranberry (*Vaccinium macrocarpon* Aiton) has been growing in the past few decades. Previous crosses of cranberry cultivars have produced advantageous offspring therefore the objective of this study was to determine the genetic fingerprinting and identify the true parents from the pedigrees of cultivars in order to assist in the process of developing new and desirable cultivars. A set of 12 simple sequence repeat (SSR) markers was used to characterize 280 accessions across 54 cultivars from the National Clonal Germplasm Repository (NCGR) by using fluorescent primers in polymerase chain reaction (PCR). Amplified fragments were separated by size and the resultant alleles were scored. We expected that within a cultivar, the alleles of each accession would be identical, and across cultivars, alleles of different accessions would differ. Many discrepancies were found therefore not all of the pedigrees could be established. However, comparison to previously defined consensus genotypes showed that accessions of the same cultivar were often grouped together near the consensus genotype, suggesting that some *V. macrocarpon* cultivars are gene pools rather than pure genotypes. This finding suggests a need to change the approach used to determine pedigrees.

Advisors: Dr. David Andrews, University of Dallas and Juan Zalapa, Ph.D. - USDA-ARS, Department of Horticulture, University of Wisconsin-Madison.

§—————§ Coffee Break (3:20–3:40 pm) §—————§

— 3:40–4:00 pm

Mathematical Modeling of Glassy-Winged Sharpshooter Population

Wei Yang Kevin Wang & Sara Wilder, University of Houston-Downtown

Abstract

Pierces disease (PD) is the result of *Xylella fastidiosa*, a bacterium found in the xylem of plants and is a serious threat to California and Texas wine industries. The Glassy-winged Sharpshooter (GWSS) is considered to be the main xylem feeding insect vectoring PD in Texas vineyards. An extensive database has been compiled consisting of the GWSS population frequencies within 25 participating vineyards in Edward Plateau in central Texas. We consider a model to investigate the effects of pest management campaigns on the dynamics of the insects population within the region. The model is a delay Gompertz differential equation with harvesting and immigration terms, and we use the data to estimate the model parameters.

Advisor: Drs. Jeong- Mi Yoon, Volodymyr Hrynkiv & Lisa Morano.

— 4:00–4:20 pm

Development of Dispersive Nutria Population Model and Comparison of Control Techniques

Grant Cavalier, Chris Meaux & Logan Perry
University of Louisiana at Lafayette

Abstract

Myocastor coypus, or the nutria rat, are an invasive species which is currently thriving in the wetlands of southern Louisiana. Nutria are particularly damaging because of their diet of marshland plants. The nutria remove the roots of these plants and thereby destabilize the fragile marshland soil, after the vegetation of a marshland patch is lost it becomes subject to erosion. This research investigates the behavior of the nutria population subject to two control techniques. The first technique models the system currently implemented by the Louisiana Department of Wildlife and Fisheries, wherein the trapper population varies based on monetary incentive, but is assumed to be spatially homogenous. The second technique models a strategy implemented by Great Britain from 1953-1956 to rid itself of a wild rabbit infestation. This technique utilizes a constant trapper population that continually seeks out the area of highest nutria population density. A mathematical model is created to describe the migration of nutria between localized patches in an arbitrary arrangement. Lotka-Volterra type predator-prey difference equations are used to describe the nutria population dynamics at each patch. This research could provide insight to the continued development of nutria population control paradigms in Louisiana.

— 4:20–4:40 pm

Mathematical Modeling of *Pseudomonas* species Biofilm Growth and Inhibition

Kimberly Walker, Caroline Barbosa & Antonio Mendoza
University of Houston-Downtown

Abstract

The focus of the research is to mathematically model the growth of bacteria as a biofilm. Biofilms are a community of microorganisms that adhere to each other and to a moist surface. This is in contrast to planktonic growth where bacteria grow as free floating individual organisms. There are many different factors that influence the biofilm mode of 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 formation. The biofilm mode of living offers bacteria many advantages such as increased resistance to antibiotics, additional evasion strategies from the host immune system responses and higher resistance to nature's insults. This is more common growth mode in nature. In this project, *Pseudomonas* species are being used to mathematically model bacterial growth as a biofilm. Whereas planktonic bacteria have been extensively studied and their growth has been modeled using the logistic model, biofilm growth has not been well studied. Our studies indicate a dampening oscillating growth curve for the bacteria within biofilms. We have developed a preliminary mathematical model using the Bessel equation which strongly resembles our data. Inhibition studies of the bacterial biofilms versus planktonic cells are also being conducted and the results will be modeled.

Advisors: Drs. Youn-Sha Chan & Poonam Gulati.

— 4:40–5:00 pm

Chaos in Two Stage Ecological Model

Logan S. Perry
University of Louisiana at Lafayette

Abstract

We develop a non-autonomous discrete juvenile-adult population model with non-linear Ricker-type survivorship rates. We begin the examination of our model's dynamics by showing that the extinction equilibrium, or trivial equilibrium, is globally asymptotically stable and then confirm these results numerically. Given the inherent complexity of our system, we make use of several numerical methods to convey the rich chaotic behavior it exhibits. First we vary the birthrate and examine the resulting bifurcation diagrams in order to gain insight into which regions are chaotic. We then make use of Lyapunov Exponents to show that our system possess sensitivity to initial conditions for certain birthrates. Finally we examine the attractor of our system by looking at the long term behavior of single initial condition. We continue by breaking our domain R_+^2 into quadrants and then inspecting where numerous initial conditions from these respective quadrants are mapped to after successive iterations.

— 5:00–5:20 pm

Mathematical Modeling of SMAD-1 and Noggin in the Epidermal Signaling Pathway during Neural Induction in *Xenopus laevis*

Jose Trejo & Bruno Toledo
University of Houston-Downtown

Abstract

How does undifferentiated embryonic tissue become committed to develop into either the central nervous system or the epidermis in *Xenopus laevis*? It starts when an embryo is in its Gastrula phase, when it is 10,000 cells old. Several proteins come into play in its development but in this study we focus on 5 interacting proteins: MAP kinase, fibroblast growth factor (FGF), morphogenetic protein-4 (BMP-4), Noggin and TAK-1. These proteins are key players of two pathways that inhibit each other in order to decide the cell's final fate, whether epidermal or neural. To further comprehend this biological model, systems of ordinary differential equations have been developed to mimic the activity rates of these proteins in their pathways. The first model consists of five equations that attempt to describe the activity rates of each of the five proteins. Then a reduced two-equation model is studied as an initial step to further understand the five-equation model in sections. MATLAB and XPPAUT ODE solvers are used to generate graphs and bifurcation diagrams that attempt to describe experimental results, such as the sudden drop in SMAD-1's activity rate as Noggin's activity rate is increased.

Advisor: Dr. Edwin Tecarro, Department of Computer and Mathematical Sciences, Dr. Akif Uzman, Department of Natural Sciences.

— 5:20–5:40 pm

Need to take a Physiology Exam? Get your iPad!

Ashik Khatri
University of Houston

Abstract

The Computational Physiology Lab at University of Houston main campus would like to analyze and compare in detail how a student performs on examinations on electronic devices like an iPad vs. a pen and paper testing environment. I was tasked to develop an app which would record activity of the student to later use to study stress patterns.

\$—————\$ **Dinner Party (6:00–8:00 pm)** \$—————\$