Texas A&M University: Department of Mathematics
REU/MCTP/UBM/KAUST
Summer Research Mini-Conference: Wednesday July 28, 2010
Abstracts

Session 1 – Moderator: May Boggess

Modeling the epidemic of multidrug-resistant tuberculosis in Russia
> Shelby Lee – Texas A&M University UBM

Russia is experiencing an epidemic of tuberculosis that caused over 150,000 active cases in 2008. An alarming 21% of tuberculosis cases in this country are multidrug-resistant, resistant to the two most effective drugs and requiring years of expensive, painful treatments. A system of ordinary differential equations is used to model two-strains of tuberculosis and to determine if the recommendations in the Stop TB Partnership's Global Plan to Stop TB, 2006-2015 will be effective in halting Russia's multidrug-resistant tuberculosis epidemic.

Epidemic Models for Human Swine Influenza in Hong Kong
> Ka Ying Lam – KAUST

Human Swine Influenza is caused by the novel Influenza A (H1N1) virus. Since its discovery in North America in April 2009, the disease has led to epidemics in many parts of the world. A traveler who arrived in Hong Kong by air on May 1 2009 from Mexico was diagnosed with the disease and was Asia's first confirmed case of the new flu. In this paper, we apply various deterministic models to the H1N1 epidemic of 2009 in Hong Kong. We then consider a modified logistic curve and a Double Epidemic Susceptible-Exposed-Infected-Removed-Protect model.

Mathematical Models for Analyzing the Effect of Transmission-Blocking Vaccines on the Spread of Malaria
> Gabe Davis-Carleton College

We introduce a new ODE model for the spread of malaria which assumes birth and death of both humans and mosquitoes as well as a latency period in the host population. This model is used to assess current malaria-control techniques and then further generalized to assess the effect of novel transmission-blocking vaccines (TBVs). We find that TBVs are not significantly more effective on short timescales (1-3 years) but may have potential to help eradicate the disease over generational time if enough newborn children are vaccinated. Stochastic models based on the ODE models are introduced, and they confirm the results of the deterministic models.

The Origin of AIDS: Iatrogenic Transfer?
> Anne Wiley – Texas A&M University UBM

Researchers have proposed several theories to explain the transfer of a simian immunodeficiency virus from chimpanzees to humans, where the virus became HIV-1 group M, the cause of most AIDS cases worldwide. One of these theories is that the CHAT oral polio vaccine administered in the Belgian Congo in the late 1950's was contaminated with SIV chimpanzee, and thus the researchers testing the vaccine inadvertently sparked the AIDS epidemic. A correlation between early AIDS cases and CHAT vaccination sites has been proposed, but not previously analyzed statistically. This paper presents data on early AIDS cases due to HIV-1 group M, data on the CHAT vaccination campaign, and a score test for evidence of clustering of cases around each of the vaccination sites. Of the fifteen verified vaccination sites, only Kinshasa, the largest city in the country both then and now, was found to have evidence of clustering. However, this clustering may be due to social and economic factors, and not the administration of CHAT.

Session 2 – Moderator: Jay Walton

Extremal Fewnomial Systems
> Abel Chan – Stanford University

This presentation is about multivariate systems of polynomial equations. As part of a much larger effort to develop bounds on the maximum number of real roots such systems can have, I will be discussing computational techniques to study and search for sparse systems with many roots (extremal examples). Key concepts covered will include A-discriminants and the Horn Kapranov Uniformization.

Modeling the Effects of Cannibalistic Behavior in Zebra Mussel Populations
> Patrick Davis – Eastern Michigan University

The threat of invasive species has increased with the expansion of global transportation. In the United States, zebra mussels became a problem by the early 1990's when they were introduced by ballast water into Lake St. Clair in 1988. In 2007, a new deterministic discrete-time model for zebra mussel populations was proposed by Casagrandi. We show how this model produces periodic, stable, and chaotic population patterns. In addition, a parametric analysis corrects some results of Casagrandi concerning the effect of changes in the adult cannibalistic behavior through filter-feeding. Finally, a new stochastic continuous-time model is proposed, abstracted from the Casagrandi model and implemented via the Gillespie algorithm.

Extinction Equilibria of Stage Structured Populations
> Georgia Pfeiffer – The College of William & Mary

Invasive species have disrupted ecosystems worldwide threatening native populations that are often ill equipped to out compete them. The interaction between invasive and native populations can be complicated by varying intensities of competition at different life stages. Pressures from resource availability increase as populations grow causing heightened competition between invasive and native species. The parameter analysis through matrix modeling in this study accounts for staged life cycles and density dependence yielding criteria dependent on competition strength and intrinsic growth rates to determine the stability of total and partial extinction equilibria.

Session 3 – Moderator: Sue Geller

Sequence Alignment Using the Needleman-Wunsch Algorithm and the Polytope Propagation Algorithm
> Alex Gendreau – Wellesley College
> Maya Bam – Gordon College
> Tiara Henry – Prairie View A&M University

The process of sequence alignment arranges strands of DNA, RNA, or proteins to determine similarities that may result from their biological relationships. The problem of aligning two sequences leads to connections with graph theory in the form of the shortest path problem. The Needleman-Wunsch Algorithm can be used to find the shortest path in a weighted graph and thus the optimal alignment of two sequences. Using similar ideas, the Polytope Propagation Algorithm extracts optimal alignments from the vertices of polytopes. We will discuss the relationships between sequence alignment, the Needleman-Wunsch Algorithm, and the Polytope Propagation Algorithm. We assume no background in biology or convex geometry.

A Mathematical Model of the Effects of Antioxidants on Atherosclerotic Lesion Growth
> Hayley Belli – University of Oregon

Atherosclerosis is a form of cardiovascular disease characterized by an accumulation of cellular debris and inflammation in the innermost layer of the arterial wall. Currently, statin drugs have been the primary method for treating atherosclerotic lesions; however, recent research suggests that lifestyle changes, in particular consuming a diet rich in antioxidants, may be equally effective at preventing and potentially reversing the process of

atherosclerotic lesion growth. In this paper, two mathematical models are developed. The first is a system of six ordinary differential equations, and the second is a one-dimensional spatial model composed of six partial differential equations, both of which model the reaction diffusion process of atherogenesis at the biological level. The purpose of the ordinary differential equation model is to define a healthy state through the computation of equilibrium values over a spatially uniform domain. Meanwhile, the system of partial differential equations uses a discrete Taylor series approximation to incorporate unique boundary conditions and to model athlerosclerotic lesion growth and supplementary regression through the application of distinct parameters. To avoid a numerical instability, a finite difference scheme for parabolic equations is used to develop a diffusion coefficient for the model. Through the use of these equations, applied mathematicians can supply cardiologists with means for simulating and numerically analyzing various lesion regression scenarios.

Modeling Therapeutic Strategies of Tumors Using the Mass Balance Equation
   Junsong Zhao – KAUST

Currently the most threatening diseases are undoubtedly cancers most of which are malignant tumors, because of the high occurring rate and the high death rate . Therefore, a lot of research has been done on modeling tumor growth in order to facilitate basic cancer research and clinical treatment. In the first part of this paper, we reviewed a previously established model based on the mass balance equation and the advection diffusion equation. After the tumor reached its maximum size, some consequential treatments such as size-dependent therapy, constant dose therapy, logarithmic intensification therapy and linearly increasing tensity therapy were added to this model to see the effect of different therapeutic strategies on the evolution of the tumor size. We found that the logarithmic intensification therapy should be one of the best choices among those treatments.

Solution Behavior of a Parabolic-Hyperbolic PDE System
   Mark Houston – KAUST

Population models that account for size and structure within the population often do so by introducing a structure parameter which obeys its own evolution law. While this approach is logical, it often comes with a drastic increase in computational cost because introducing a structure parameter translates to increasing the number of independent variables. As an alternative approach I will discuss a method for continuous population modeling where size is taken into account but is instead viewed as a dependent variable. The resulting model consists of a system of two partial differential equations, one parabolic and the other hyperbolic. Solutions of this system are determined by the competition between diffusive and wave-like behavior that stem from the parabolic and hyperbolic PDEs, respectively. Focus will be on numerical analysis of the solutions in one and two spatial dimensions.

A Categorization of Mexican Free-Tailed Bat 'Tadarida brasiliensis' Chirps
   Gregory Backus – Bard College

Male Mexican Free-tailed Bats *Tadarida brasiliensis* attract mates and defend territory using multi-phrase songs with a structured set of rules. A subjective view of their spectrograms shows similarity and dissimilarity between the chirps (a syllable within the song) of different males. We developed a rigorous algorithm to characterize the shapes of these chirps. The discrete Fourier transform allowed us to focus on frequency information while a four level Daubechies 2 wavelet decomposition allowed us to focus on time. For comparison, we compressed large data vectors into a single data point using multidimensional scaling. Segmenting chirps, to further emphasize ranges of time and frequency, gave categorizations that most closely resemble the subjective groupings.

Texas A&M University: Department of Mathematics
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Summary Research Mini-Conference: Thursday July 29, 2010
Abstracts

Session 1 – Moderator: Jay Walton

Signature Recognition using Wavelet Decomposition
        Sylvia Charchut, Joel Coppadge, Kristen Moore, Runqi Song, and Mary Spuches

We attempt to differentiate between real and fake signatures using algorithms involving Wavelet decomposition, Fourier transformation, and the comparison of unedited signatures. We discuss the performance of the 3 methods.

Developing Algorithms for Automated Spoken Word Recognition Utilizing Wavelet Analysis
        Laura Booton, Suren Jayasuriya, Kristen May, Katie McKeon, and Erika Meza

We use signal analysis techniques in order to recognize spoken words. We compare the word identification performance of different wavelet families and the Discrete Fourier Transform. We will discuss the algorithms developed as well as our results.

Chord Recognition Through Wavelet Decomposition
        Jason Bathke, Elisabeth Berg, Heather Johnston, Ashley Moore, and Nicholas Spear

Many factories use signal analysis as a warning system for machine malfunctions. This is related to the problem of identifying different notes and chords. We will discuss this signal analysis problem and how it can be treated through wavelet decomposition. We will present an algorithm that identifies guitar chords

Continuously Moving Parseval Frames on Smooth Manifolds
        Ryan Hotovy – University of Nebraska-Lincoln
        Eileen Martin – The University of Texas at Austin

Moving bases on manifolds are important in the study of differential geometry and are applied in mathematical physics, but moving bases do not exist on all manifolds, for instance, the sphere. An alternative to a moving basis is a Parseval frame of unit-length vectors. We examine the existence of such frames on the Möbius strip, the Klein bottle, and n-dimensional spheres. We prove the existence of a continuously moving, unit-length Parseval frame on S^n when n is an odd integer. In particular, we investigate the relationship between the existence of a nowhere zero vector field and that of a continuously moving Parseval frame of unit length. One potentially useful tool in studying this relationship is the frame force associated with the frame potential. To better understand this possible method, we are led to a study of the dynamical properties of the frame force.

Session 2 – Moderator: Maurice Rojas

Unitary Equivalence to Matrices with Constant Main Diagonal
        John Myers – South Dakota School of Mines & Technology

Two iterative algorithms are developed to transform a given matrix to a unitarily equivalent matrix with constant main diagonal: one if the matrix has elements in $\mathbb{R}$ and one for elements in $\mathbb{C}$. In both cases, the algorithm will

converge in finitely many iterations if the dimension of the matrix is a power of 2. Neither algorithm is globally continuous and for $\mathbb{R}$ a characterization of points of discontinuity is given. For $\mathbb{C}$, computer experiments reveal suspected points of discontinuity. Then – despite the algorithms' failure to be globally continuous – it is shown that in special cases there exist paths of matrices along which the algorithm is continuous. The results of further computer experiments are given that indicate such paths may exist in more general cases as well.

On the Roots of Univariate Trinomials
        Kenny Ascher – Stony Brook University

Currently, there is no known formula to solve for the roots of polynomials of degree 5 or more using simple arithmetic operations. We show how to compute the number of roots of $f(x) = a + bx^\alpha + cx^\gamma$, where $a, b, c \in \mathbb{R}^*$ and $0 < \alpha < \gamma$ are integers, by simply analyzing the parity of α and γ. Using the log uniform distributions for coefficients we prove that we will expect $\frac{3}{2}$ roots in $\mathbb{R}^*$ on average. We show that the number of roots of $f(x)$ can also be obtained by simple analysis of the Archimedian-Newton Polygon and we finish by giving an algorithm to approximate the roots of $f(x)$.

Symbol Recognition Through Wavelet Analysis
        Kara Grier, Reed Jordan, Katherine Shoemaker, Chelsea Yost, and David Wen

To distinguish various handwritten cursive letters using direct methods, Fourier Analysis and Haar Wavelets and to compare the performance of each method.

Session 3 – Moderator: May Boggess

Orthogonal and Maximal sets for Bernoulli Measures
        Patrick Orchard – University of Oklahoma

We consider orthogonal and maximal sets on $L^2(X_\lambda, \mu_\lambda)$, where μ_λ is the canonical measure associated with the Bernoulli Iterated Function system for $\lambda \in (0,1)$ and X_λ is the support of the measure. We look at orthogonality and maximality of a constant multiplied by previously obtained maximal families for $\frac{1}{2n}$ (we denote these $\Gamma_{\frac{1}{2n}}$) and our constant is dependent on $2n$. We have proved that the set $3\Gamma_{\frac{1}{4}} \cup \left\{ -4^n(1 + \sum_{j=n+1}^{p} a_j 4^j) : p < \infty, a_j \in \{0,3\} \right\}$ is an orthogonal and maximal set for the space $L^2(X_{\frac{1}{4}}, \mu_{\frac{1}{4}})$.

Unitary Equivalence of Vector Spaces over the Binary Field
        Ryan Hotovy – University of Nebraska-Lincoln
        Sam Scholze – University of Wisconsin-Platteville

Vector spaces over the binary field $\mathbb{Z}_2$ share certain properties with familiar vector spaces over $\mathbb{R}$ such as the existence of bases for spaces. There are, however, many differences. For example, when equipped with the dot product ,a vector space over $\mathbb{Z}_2$ becomes an indefinite inner product space where non-zero vectors may have zero length. We continue previous work on these spaces by investigating subspaces of $\mathbb{Z}_2^n$ and ask when two vector spaces are unitarily equivalent. In particular we consider embeddings of subspaces into $\mathbb{Z}_2^n$ for some *n*. An algorithm is given showing that every vector space over $\mathbb{Z}_2$ can be embedded in this manner. We also investigate the existence of both Parseval frame sand dual frames for vector spaces over $\mathbb{Z}_2$ and their relation to the Grammian operator. Finally we show that, unlike vector spaces over $\mathbb{R}$, the existence of a dual frame pair does not necessarily imply the existence of a Parseval frame of the same length for a space.