WimSoCal Symposium
6^{th} Annual Women in Southern California Symposium
May 4, 2014
University of San Diego
Titles and Abstracts

Plenary Speakers

Joanna Bieri, University of Redlands
Mathematical models of edge-flames: using asymptotic and numerical approaches to understand flame dynamics

Edge-flames in micro-channels extinguish, reignite, and spontaneously oscillate. These dynamics are not well understood, so applied mathematicians seek to predict conditions for which these behaviors will occur. There are a variety of ways to go about gaining mathematical information about a complicated system and we will discuss some of the common approaches. First, we will develop a mathematical flame model and discuss the implications of the simplifying assumptions made. Next, an asymptotic prediction will be given for very narrow channels. Finally, a numerical scheme will be discussed and results from numerical simulations presented.

Jocelyne Bruand, Illumina
Short tandem repeats analysis in sequencing data

Sets of polymorphic, repetitive DNA elements are useful for many genetic applications including paternity testing, human identification (forensic DNA analysis), chimera monitoring (tissue transplantation monitoring), as well as many other uses in plant and animal genomics. One class of these repetitive elements comprises of the short tandem repeats (STRs). The allele of an STR locus is defined by its length, or number of repeat units, and by its sequence variation. While capillary electrophoresis systems can show the length of the allele, sequencing technologies have the additional differentiation power of discovering sequence variation, such as SNPs. In order to take advantage of NGS data, it is crucial to be able to accurately and efficiently assign reads to the correct STR locus and STR allele. Previous techniques have focused on creating a ?reference genome? by building a ladder of all known STR alleles and aligning the reads to this reference, as typically done with NGS whole genome sequence data or targeted sequencing of non-repetitive DNA regions. There are shortcomings to this method: 1) known information about the STR sequence, such as primer sequence or conserved flanking regions, is ignored; 2) the ladder is incomplete as the sequence for many polymorphic repetitive regions is currently unknown; 3) due the highly variable nature of these genomic regions, new alleles may be discovered in the future; 4) changes to the sequence of one allele in the reference may have global effects to the reads alignment due to homology between the sequences. We propose a new method, which uses the conserved flanks of repetitive polymorphic loci to effectively determine the sequence of the repetitive DNA element. First, we align the beginning of the read sequence to the possible primer sequences to establish the locus and strand to which the read corresponds. We then align sections of the appropriate flanking sequences on each side of the repetitive locus to the read in order to pull the exact length and sequence from the read. These alignments are seeded using a k-mer strategy in a pre-chosen high-complexity region of the flanking sequence, close to the repeat region, but avoiding low-complexity sequence with homology to the target locus. This avoids misalignment of low-complexity flanking sequences close to the repeat region of interest.

Careers in Mathematics Panel Discussion

Karen Acquista, Center for Communications Research
Jocelyne Bruand, Illumina
Kristin Lauter, Microsoft Research
Ruth J. Williams, University of California, San Diego

Special Sessions

Nausheen Ahmed, Calfornia State University Channel Islands
Impact of story-telling on students' learning of mathematics

The two different language based projects were designed to introduce the concepts of parabolas and integration. Integration was introduced to college students, and eighth grade students worked with parabolas. We incorporated the use of a story and acting exercises to help students be active participants in the learning process. To make it interesting to children the story was illustrated with colorful pictures in the eighth grade activities. The goals for this research were to evaluate if there was a significant difference in the overall performance of the test groups versus the control groups, and if there was a significant improvement in learning on the conceptual problems. Our data shows that the project was successful and students involved in the story based activities performed better.

Alina Bucur, University of California, San Diego
TBD

Theresa Chadwick, University of San Diego
Analyzing SIDS data with piecewise linear functions

Sudden Infant Death Syndrome (SIDS) is a phenomenon in which an infant under the age of one dies from unknown causes, even after a thorough autopsy. In fact, it is the largest cause of infant deaths in the United States of America. Consequently, it is of great concern for countries around the world. The Back-To-Sleep campaign in the USA, which started in 1992, has attempted to lower SIDS death rates by encouraging parents to place their children to sleep on their backs rather than on their stomachs to allow for smoother air flow and decrease body temperature.

Our project aims to provide a mathematical approach to model and analyze data using piecewise linear models. We used regression analysis and various re-sampling methods to determine the number of linear functions used to model the data. This method is grounded upon the balance between the complexities of the model with the goodness of fit of the model, which are both increased by adding functions. As a result, change points are detected. Change points are simply defined as an instance in time where the statistical properties before and after this time point differ. Naturally, these are the spots in the data between each function in the piecewise linear models. Also, both the linearity of the functions and the change points themselves can tell information about the effect of outside events on data.

Overall, we created automated method to model data as a piecewise linear function. Then using this method we modeled SIDS data and analyzed the effects of the Back-To-Sleep campaign in various countries.

Ameera Chowdhury, Carnegie Mellon University
The Manickam-Miklós-Singhi conjectures for sets and vector spaces

More than twenty-five years ago, Manickam, Miklós, and Singhi conjectured that for positive integers n, k with $n >= 4k$, every set of n real numbers with nonnegative sum has at least $\binom{n-1}{k-1}$ k-element subsets whose sum is also nonnegative. We verify this conjecture when $n \geq 8k^2$, which simultaneously improves and simplifies a bound of Alon, Huang, and Sudakov and also a bound of Pokrovskiy when $k < 10^{45}$. Moreover, our arguments resolve the vector space analogue of this conjecture.
Joint work with Ghassan Sarkis (Pomona College) and Shahriar Shahriari (Pomona College).

Sorina Ionica, Microsoft Research USA
Elliptic curves, endomorphisms rings and cryptography

In elliptic curve cryptography, the basic multiplication used in most protocols is computing the multiple of a point on the curve, by some large number. This can be done efficiently by using a double-and-add-algorithm. We will explain how to use efficiently computable endomorphisms on the curve to speed up this algorithm and present recently found families of elliptic curves with fast endomorphisms.
This is joint work with Aurore Guillevic.

Alona Kryshchenko, Children's Hospital Los Angeles
NPEST: a nonparametric method and a database for transcription start site prediction

In this talk we present NPEST, a novel tool for the analysis of expressed sequence tags (EST) distributions and transcription start site (TSS) prediction. This method estimates an unknown probability distribution of ESTs using a maximum likelihood (ML) approach, which is then used to predict positions of TSS. Accurate identification of TSS is an important genomics task, since the position of regulatory elements with respect to the TSS can have large effects on gene regulation, and performance of promoter motif-finding methods depends on correct identification of TSSs. Our probabilistic approach expands recognition capabilities to multiple TSS per locus that may be a useful tool to enhance the understanding of alternative splicing mechanisms. We will presents analysis of simulated data as well as statistical analysis of promoter regions of a model dicot plant Arabidopsis thaliana. Using our statistical tool we analyzed 16520 loci and developed a database of TSS, which is now publicly available at www.glacombio.net/NPEST.

Kristin Lauter, Microsoft Research
Cryptography on genus 3 curves: news and directions

This talk will survey progress in several recent projects investigating the status of algorithms for genus 3 curves in cryptography, both attacks and constructions. This is joint work with a long list of collaborators on these projects.

Perla Myers, University of San Diego
Smile... it's mathematics! Engaging teachers and students in mathematics through origami

How do people react when they hear the word ?mathematics?? Imagine if they smiled! I will describe Project Mathigami, a pilot program that provides positive experiential education opportunities for future teachers and other college students to engage children in mathematics and deepen their mathematical understanding.

Manizheh Nafari, DePaul University
AS regular graded skew clifford algebras that are twists of AS regular graded clifford algebras

M. Artin, W. Schelter, J. Tate, and M. Van den Bergh introduced the notion of non-commutative regular algebras, , and classified regular algebras of global dimension 3 on degree-one generators by using geometry (i.e., point schemes) in the late 1980s. They also defined twists by automorphisms and they proved that the regularity of algebras and GK-dimension are preserved under this twisting in the late 1980s. In 2010, T. Cassidy and M. Vancliff generalized the notion of a graded Clifford algebra and called it a graded skew Clifford algebra. In this talk, We prove that if A is a regular graded skew Clifford algebra and is a twist of a regular graded Clifford algebra B by an automorphism, then the subalgebra of A generated by a certain normalizing sequence of homogeneous degree-two elements is a twist of a polynomial ring by an automorphism, and is a skew polynomial ring. We also present an example that demonstrates that this can fail when A is not a twist of B.

Amber Puha, Calfornia State University San Marcos
Shortest remaining processing time queues

Stochastic processing networks are probabilistic models that arise naturally in a variety of areas including communications, transportation, biological systems, and health care. Such models feature complex interactions that result in wide range of interesting mathematical challenges. One such challenge is that they are often infinite dimensional. My work has focused on using measure-valued processes to track system dynamics and analyze performance. In this talk, I will discuss work on shortest-remaining processing time queues as an illustrative example.

Orit Raz, Tel Aviv University
Expanding polynomials over the reals and applications to Erdős type problems

In a recent work (joint with M. Sharir and J. Solymosi) we characterize real bivariate polynomials which have a small range over large Cartesian products. We show that for every constant-degree bivariate real polynomial f, either $|f(A, B)| = \Omega(n^{4/3})$, for every pair of finite sets $A, B \subset \mathbb{R}$, with $|A| = |B| = n$, or else f must be of one of the special forms $f(x, y) = r(p(x) + q(y))$, or $f(x, y) = r(p(x)q(y))$, for some univariate polynomials p, q, r over $\mathbb{R}$. This improves a result of Elekes and Rónyai (2000). The result provides a unified tool for improving bounds in various Erdős-type problems. In the talk I will discuss this result and introduce several applications of this kind.

Blerta Shtylla, Pomona College
Mathematical modeling of cellular nano-machines

At the micron-scale inside our cells force generation and transport requires the rectification of diffusive motion. Such a task is no small feat particularly as several mechanical events in our cells need to be highly precise in their action. In response to these needs, cells have evolved exotic nano-machines that can harness diffusion to complete their tasks. In this talk, I will develop mathematical models of the mechanisms driving cell division nano-machines, called kinetochores. These highly specialized structures assemble on chromosomes during mitosis and mediate the equal partitioning of our genetic material. Using modeling, we will show that diffusion and specialized binding architectures can be used to generate directed kinetochore movement. However, internal protein compliance can have a surprising role, which we show can be rather similar to the muscle contraction paradigm.

Athena Sparks, California State University, Northridge
The cylindrical crossing number of the complete bipartite graph

A cylindrical drawing of a complete bipartite graph $K_{m,n}$ consists of a set of m vertices placed on the top rim of a cylinder and a set of n vertices placed on the bottom rim of the cylinder where every vertex at the top is connected to every vertex at the bottom by an edge on the lateral surface of the cylinder. When projected onto the plane these drawings have the sets of vertices placed on concentric circles, or boundaries, and the edges do not intersect these circles. The cylindrical crossing number is defined as the minimum number of crossings among all cylindrical drawings of a graph. A formula is derived for the cylindrical crossing number of $K_{m,n}$ as well as an algorithm for creating a drawing that achieves that number. With this result, we show that among all cylindrical drawings of the complete graph K_n where the edges between two vertices on the inner (or outer) boundary are contained inside (or outside) the boundary, the drawing with half (or nearly half) of the vertices on each boundary has the fewest crossings.

Tatiana V Tatarinova, University of Southern California
Lengths of orthologous prokaryotic proteins are affected by evolutionary factors

Genes of the same functional family (for example, kinases) may have significantly different lengths. It is an open question whether such variation in length is random or it appears as a response to some unknown evolutionary driving factors. The main purpose of this paper is to demonstrate existence of factors affecting gene lengths. We believe that the ordering of genomes according to lengths of their genes, followed by the calculation of coefficients of association between genome rank and genome property, is a reasonable approach in revealing such evolutionary driving factors. We examine four ranking methods and demonstrate that one approach, Bubble-sort, combines stability, accuracy and computational efficiency as compared to other ordering methods. Application of Bubble Sort to the set of 1390 prokaryotic genomes confirmed that genes of Archaeal species are generally shorter than Bacterial ones. We observed that gene lengths are not random: within each domain, different phyla have preferences for short or long genes. We demonstrated that thermophiles tend to have shorter genes than the soil-dwellers. We also found that species with high GC3 genic content tend to have longer genes than species with low GC3 content.

Ani Velo, University of San Diego
Modeling stress wave propagation in one-dimensional Goupillaud-type layered elastic media

Using characteristic-line invariants, we model the stress and velocity in impact problems through a system of recursive relations. Further analysis of the system allows us to predict analytically the stress and velocity time history as well as the long term behavior of the system. An important aspect of this work is that it provides exact solutions and analytical results for verification of computational codes used to solve large scale problems. One of the impact problems considered is a semi-infinite linear elastic impactor that welds to a layered target. The one-dimensional layered medium is assumed to be Goupillaud-type (equal wave travel time for each layer).

Ruth J. Williams, University of California, San Diego
On slowly oscillating periodic solutions for delay differential equations with non-negatively constraints

Dynamical system models with delayed feedback, state constraints and small noise arise in a variety of applications in science and engineering. Under certain conditions oscillatory behavior has been observed. Here we consider a prototypical fluid model approximation for such a system — a one-dimensional delay differential equation with non-negativity constraints. We give sufficient conditions for the existence, uniqueness and stability of slowly oscillating periodic solutions of such equations. We illustrate our results with a simple examples from gene regulation.
This talk is based on joint work with David Lipshutz.
