Julie Bergner (UC Riverside)

Diagrams of spaces and algebraic structure

There are often many different ways to define an algebraic structure on a topological space. One way is to take a collection of many spaces, together with specified maps between them, satisfying some relations which impose the desired algebraic structure on one (or more) of the spaces. For many algebraic structures, there is a known way to find such a collection, but with an unwieldy number of maps involved. The goal is then to find a simpler collection with fewer maps. In this talk we'll consider solutions to this problem for algebraic structures such as monoids, groups, categories, and operads.

Alina Bucur (UCSD)

Statistics for points on curves over finite fields

A curve is a one dimensional space cut out by polynomial equations. In particular, one can consider curves over finite fields, which means the polynomial equations should have coefficients in some finite field and that points on the curve are given by values of the variables in the finite field that satisfy the given polynomials. A basic question is how many points such a curve has, and for a family of curves one can study the distribution of this statistic. We will give concrete examples of families in which this distribution is known or predicted, and give a sense of the different kinds of mathematics that are used to study different families.

Man-Wai Cheung (UCSD)

Ricci flow on Wallach flag varieties

"Wallach flag varieties" are manifolds of flags in 2 dimensional projective space over the complexes, the quaternions and the octonions. We study the effect of Ricci flow on the Sectional and Ricci curvature. This is joint work with Nolan Wallach.

Man-Wai Cheung (UCSD)

The Tropical Vertex

Tropical Vertex are developed by Gross, Pandharipande and Siebert. It is one of the key ingredients to construct mirrors to rational surfaces along with a choice of an anti-canonical cycle of rational curves in the context of tropical geometry and Gromov-Witten theory. I will discuss this construction and its connection with quiver representations and cluster varieties.

Cynthia Flores (UCSB)

Decay properties of solutions to the Benjamin-Ono equation

I will introduce the IVP for the Benjamin-Ono equation, a nonlinear dispersive PDE modeling gravity waves. My motivation will be a unique continuation property that may be deduced by some decay properties of solutions to the Benjamin-Ono equation when considered in weighted Sobolev spaces.

Jane Friedman (University of San Diego)

Fitting continuous piecewise linear models to Data

A method will be presented which uses simulation to fit continuous piecewise linear models to data. The method can be used with either a ordinary least squares or a reduced major axis approach to regression.

Cymra Haskell (University of Southern California)

Integrating Data from a Battery of In Vitro Assays to Determine the Effects of Xenobiotic Chemicals on the Estrogen Receptor Pathway

A signal molecule, such as a hormone, interacts with receptor molecules triggering a cascade of downstream events which we call its pathway. Xenobiotic chemicals can alter normal biological functions by interacting with receptors in ways that mimic natural signaling molecules. A new way to test xenobiotic chemicals for interference along these pathways is to use simple cell-based assays. These tests are considerably cheaper and far less time-consuming than traditional animal-based tests (a very important consideration when we think of the tens of thousands of chemicals to which we are exposed). However, the assays are themselves complex biological processes that can respond to chemical perturbations in multiple ways, so determining the levels of interference of the chemicals from the data is non-trivial. In this talk we discuss a mathematical model that can be used to integrate data from a large number of assays and derive a measure of the probability that activity in the assay is due to activity in the intended pathway or due to activity in a number of assay interference pathways. The approach is employed to analyze data from a battery of 20 estrogen receptor assays in which 1800 chemicals were tested. The results are compared with expected data from a set of reference chemicals.

The work was initiated at a 1-week workshop title "Modeling Problems Related to our Environment," at the American Institute of Mathematics.

Johanna Henning (UCSD)

A Generalization of Lie's Theorem

Lie's theorem is a basic result in the classical theory of finite dimensional Lie algebras. We prove an infinite dimensional version of Lie's theorem: namely, that every Borel subalgebra of a locally finite Lie algebra is the stabilizer of a maximal, generalized flag in a certain type of infinite dimensional module.

Silvia Heubach (California State University Los Angeles)

Building Nim

The game of Nim, with its simple rules, its elegant solution and its historical importance is the quintessence of a combinatorial game, which is why it led to so many generalizations and modifications. We present a modification with a new spin: "Building Nim". With n tokens and s stacks, this two-player game is played in two phases: first, the building phase, where players alternate to put one token on one of the s (initially empty) stacks until all n tokens have been used. Then, the players (beginning with the player who started the building phase) simply play Nim. Of course, because the solution for the game of Nim is known, the goal of the first player is a placement of the tokens so that the digital sum of the s stack heights at the end of the first phase is different from 0, while the goal of the second player is to make this sum equal to 0.

This game is a trivial win for the first player if n is odd as the digital sum could never be 0, and a win for the second player if both n and s are even; the second player simply copies Player 1's move on another stack, resulting in a digital sum of 0 after each of the second player's moves, and therefore, at the end of the first phase. We present the solution for this game for the non-trivial cases, namely when n is even and s is odd. This is joint work with Eric Duchene (Claude Bernard University of Lyon 1, France), Matthieu Dufour (University of Quebec at Montreal, Canada) and Urban Larsson (University of Gothenburg, Sweden).

Juhi Jang (UC Riverside)

Decay rates to equilibrium of some kinetic equations

We discuss the rate of convergence to the equilibrium of solutions of Fokker-Planck type equations. Two different strategies are introduced. One is based on the explicit representation formula and the other is based on the construction of energy inequalities.

Lily Khadjavi (Loyola Marymount University)

On the ABC Conjecture

The ABC Conjecture has been labeled by some as a "holy grail" of number theory. Last August came an exciting announcement from Shin Mochizuki of a proof, but the details of his work are still being verified. To better understand number theorists' interest, we will discuss what the ABC Conjecture is, along with its surprising number of implications. Work of Noam Elkies (referenced by Mochizuki) using elliptic curves and Belyi maps gives us a concrete approach to generating examples of interest. Time permitting, we will discuss a computational approach to attacking the ABC Conjecture and an obstruction which arises involving Wieferich primes; this is joint work with Victor Scharaschkin.

Kristin Lauter (Microsoft)

$2 > 1$

In this work we show how to do fast cryptography on Jacobians of genus 2 curves, faster than on genus 1 curves for the same security level!
This is joint work with Joppe Bos, Craig Costello, and Huseyin Hisil.
http://eprint.iacr.org/2012/670.pdf

Kuei-Nuan Lin (UC Riverside)

Hypergraphs and regularity of square-free monomial ideals

This is joint work with Jason McCullough. We define a new combinatorial object, which we call a labeled hypergraph, uniquely associated to any square-free monomial ideal. We provide a general upper bound on the regularity of a square-free monomial ideal in terms of simple combinatorial properties of its labeled hypergraph. We also give specific formulas for the regularity of square-free monomial ideals with certain labeled hypergraphs.

Janine LoBue (UCSD)

A Murnaghan-Nakayama Rule for Generalized Demazure Atoms

Haglund, Mason, and Remmel introduced a family of polynomials $\widehat{E}_\gamma^\sigma(x_1, \ldots, x_n)$ indexed by weak compositions γ of n and permutations σ in the symmetric group S_n. These polynomials, which they called generalized Demazure atoms, decompose the Schur functions, a well-known basis of the ring of symmetric functions. In this talk, I will show how the classical Murnaghan-Nakayama rule for expressing the product of a power symmetric function and a Schur function as a sum of Schur functions can be extended to generalized Demazure atoms. That is, I will give a combinatorial rule for expressing the product of a power symmetric function and a generalized Demazure atom $\widehat{E}_\gamma^\sigma(x_1, \ldots, x_n)$ as a sum of generalized Demazure atoms $\widehat{E}_\delta^\sigma(x_1, \ldots, x_n)$.
This talk is based on joint work with Jeffrey Remmel.

Elena Mantovan (Caltech)

Shimura varieties, Galois representation and Automorphic forms

Langlands' conjectures predict the existence of an interlacing network of correspondences between Galois representations and automorphic forms. The pursue of such correspondences has been at the heart of some of the most important progress in Number Theory of the past decade. My talk will offer an overview of current knowledge and recent developments. I will focus in particular on two important aspects of the theory: the role played by the geometry of Shimura varieties and local-global compatibility.

Mia Minnes (UCSD)

Randomness and computation

What do most random elements look like? What does it mean for a single mathematical object to be random? How can we exploit randomness in computation? Algorithmic randomness attempts to answer some of these questions. This active area of computability theory has many connections with other areas of math and computer science, including measure theory, probability theory, Kolmogorov complexity, coding theory, and others. We will introduce some of the main ideas and talk about new characterizations of algorithmic randomness using probabilistic algorithms also studied in complexity theory.

Perla Myers (University of San Diego)

A Taste of Singapore: A bridge from the concrete to the abstract

I will talk about the most recent mathematics result of TIMSS (Trends in International Mathematics and Science Study) and about one strategy used in Singapore to help students transition to algebra.

Cynthia Northrup (UC Irvine)

Axioms, Independence, and Models of Set Theory

This talk will introduce some of the basic motivations for set theory, some open problems, and the more familiar example of the Continuum Hypothesis. The Continuum Hypothesis asserts that there is no set whose cardinality is strictly between that of the integers and that of the real numbers. For years mathematicians wondered if this was true or false. The answer was more complicated than they first thought and was proven in two parts, by two mathematicians, twenty-five years apart!

Helen Parks (UCSD)

Computational geometric mechanics: A short introduction and some current research problems

What if your numerical integration scheme weren't just an approximation of something continuous? Could the numerics be a discrete system in their own right? Would the geometric structure of the discrete system reflect that of the continuous system? And what advantages might this point of view have? These questions drive recent and current research in the field of computational geometric mechanics - the development of geometric structure-preserving numerical integrators for mechanical systems. I will give a brief, broad introduction to the field and mention a few specific topics of current research.

Ami Radunskaya (Pomona College)

How much and how often? Using mathematics to design cancer vaccines

"How much?", "How often?", "Where?" The answers to these three questions are crucial in the design of cancer vaccines: treatments designed to trigger an improved immune response to an existing tumor. Mathematical models that describe tumor growth in tissue, the immune response, and the administration of different therapies can suggest treatment strategies that optimize treatment efficacy and minimize negative side-effects. However, the inherent complexity of the immune system and the spatial heterogeneity of human tissue gives rise to mathematical models that pose unique challenges for the mathematician. In this talk I will describe some of these mathematical challenges as well as our approaches to overcoming them.

Jacquelyn Rische (UC Irvine)

Mathematical Modeling of Language

In this talk, we will look at mathematical modeling of language using computer simulations. Using these models, we study how individuals with language spread through a population of individuals without language. We consider a population without language on one- and two-dimensional grids. Language will appear in the population through a genetic mutation. To study how the language group will grow, we focus on the

effects of talking and movement. If two individuals with language are next to each other on the grid, they can communicate. We consider their ability to talk to be advantageous, giving them a higher reproduction rate. Individuals are also able to move around on the grid and reproduce within a certain radius, called the jump radius. We are looking at how these affect the time it takes for the individuals with language to invade the population. We find that, for a two-dimensional grid, a jump radius that is too small or too large will increase the time it takes to invade. For a one-dimensional grid, we do not see the same effect. The time to invasion decreases as the jump radius increases.

Jinsun Sohn (UCLA)

Dynamics of Multicomponent Vesicles in a Viscous Fluid

Multicomponent vesicles are hollow, closed biomembranes with a lipid bilayer membrane containing different types of lipids and cholesterol. Recent experiments on giant unilamellar vesicles demonstrate that there exists a variety of behavior of multicomponent vesicles. Under this understanding, we develop and investigate numerically a thermodynamically consistent model of two dimensional and three dimensional axisymmetric multicomponent vesicles in an incompressible viscous fluid. The model is derived using an energy variation approach that accounts for different lipid surface phases, the excess energy (line energy) associated with surface phase domain boundaries, bending energy, spontaneous curvature, Gaussian bending energy, local inextensibility and fluid flow via the Stokes equations. The equations are high-order (fourth order) nonlinear and nonlocal due to incompressibility of the fluid and the local inextensibility of the vesicle membrane. To solve the equations numerically, we develop a nonstiff, pseudo-spectral boundary integral method that relies on an analysis of the equations at small scales. We present simulations of multicomponent vesicles in a quiescent fluid and investigate the effect of varying the average surface concentration of an initially unstable mixture of lipid phases. The phases then redistribute and alter the morphology of the vesicle and its dynamics. The observation of experimental vesicle geometries by T. Baumgart, et. al. give new assurance of the validity of our numerical simulations of multicomponent vesicles.

Mary E. Spilker (Pfizer)

Mathematical Modeling Opportunities Within the Pharmaceutical Industry

Mathematical modeling and simulation efforts within the pharmaceutical industry is quite varied, ranging from Systems Pharmacology support during early drug discovery to Pharmacokinetic/Pharmacodynamic modeling at the transition from pre-clinical to clinical studies, followed by population and disease modeling to support clinical development. This talk will highlight the range of models used in the industry and emphasize the cross-disciplinary nature of the work required to develop new drugs for patients.

Audrey Terras (UCSD)

A finite analog of the Poincaré upper half plane and the functions that live there

The Poincaré upper half plane has been of interest to artists, complex analysts, geometers, number theorists, and physicists for many reasons. It is just the ordinary upper half plane with a new Poincare distance (using (x, y) coordinates, the Euclidean arc length differential squared being $ds^2 = dx^2 + dy^2$ and the Poincaré ds^2 being the Euclidean one divided by y^2). In the Poincaré case, Euclid's 5th postulate fails. But the geometry is still a perfectly reasonable one. Escher's circle limit pictures give a taste of how that geometry looks to the Euclidean eye. Wiles' proof of the Fermat conjecture shows the importance for number theory of the functions that live on this space and are periodic under fractional linear transformation by the modular group of 2×2 matrices with integer entries and determinant 1. These functions are called "modular forms." In the first part of this talk, I will summarize the basics about the Poincaré upper half plane and modular forms. Then I will consider what happens if you replace the field of real numbers with a finite field.

Anna Varvak (Soka University of America)

Bootstrap methods for testing hypotheses of one mean

The general philosophy for bootstrap or permutation methods for testing hypotheses is to simulate the variation of the test statistic by generating the sampling distribution which assumes both that the null hypothesis is true, and that the data in the sample is somehow representative of the population. This philosophy is inapplicable for testing hypotheses for a single parameter like the population mean, since the two assumptions are contradictory (e.g., how can we assume both that the mean of the population is μ_0, and that the individuals in the sample with a mean $M \neq \mu_0$ are representative of the population?). The Mirror Bootstrap resolves that conundrum. The philosophy of the Mirror Bootstrap method for testing hypotheses regarding one population parameter is that we assume both that the null hypothesis is true, and that the individuals in our sample are as representative as they could be without assuming more extreme cases than observed. For example, the Mirror Bootstrap method for testing hypotheses of one mean uses a generated symmetric distribution constructed by reflecting the original sample around the hypothesized population mean μ_0. Simulations of the performance of the Mirror Bootstrap for testing hypotheses of one mean show that, while the method is slightly on the conservative side for very small samples, its validity and power quickly approach that of the widely used t-test. The philosophy of the Mirror Bootstrap is sufficiently general to be adapted for testing hypotheses about other parameters; this exploration is left for future research.

Katie Walsh (UCSD)

Patterns in the Coefficients of the Colored Jones Polynomial

The colored Jones polynomial assigns to each knot a sequence of Laurent polynomials. We will discuss the various ways of defining and calculating the colored Jones polynomial. These formulas allow us to look at patterns in the coefficients. A few conjectures relating these coefficients to the hyperbolic volume conjecture will be discussed as well as recent work by others studying the head and tail of the polynomials.

Kristin Webster (California State University, Los Angeles)

Semi-Invariants of Quivers

Let KQ/I be the path algebra of the quiver $Q = (Q_0, Q_1)$ with the ideal I of admissible relations. There is a theorem of Derksen and Weman stating that the semi-invariants for quivers with relations are also generated by the determinantal semi-invariants of Schoeld. Using this theorem, we can describe the rings of semi-invariants of tubular algebras. In particular, we are interested in the semi-invariants $SI(Q/I, \beta)$ where β is a dimension vector of a regular KQ/I-module.

Ruth J Williams (UCSD)

Queueing up for enzymatic processing: correlations through coupled degradation

A major challenge for systems biology is to deduce the molecular interactions that underlie correlations observed between concentrations of different intracellular molecules. Although direct explanations such as coupled transcription or direct protein-protein interactions are often considered, potential indirect sources of coupling have received much less attention. Here we show how correlations can arise generically from a posttranslational coupling mechanism involving the processing of multiple protein species by a limited number of copies of a common enzyme. By observing a connection between a stochastic model and multiclass queue, we obtain a closed form expression for the steady-state distribution of the numbers of molecules of each protein species. From analytic expressions for the moments and correlations associated with this distribution, we observe a striking phenomenon that we call correlation resonance: for small dilution rate, correlations peak near the balance point where the total rate of influx of proteins into the system is equal to the maximum processing capacity of the enzymes.

Based on joint work with Natalie Cookson, Tal Danino, Jeff Hasty, William Mather, Octavio Mondragon-Palomino, Lev Tsimring.