MIT PRIMES

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2014 PRIMES Conference abstracts

May 17
Mathematics

Session 1

Kavish Gandhi

Geodesics in the hypercube

Mentor Yufei Zhao

Project suggested by Yufei Zhao

A geodesic in the hypercube is the shortest possible path between two vertices. Leader and Long (2013) conjectured that, in every antipodal 2-coloring of the edges of the hypercube, there exists a monochromatic geodesic between antipodal vertices. For this and an equivalent conjecture, we prove the cases $n = 2, 3, 4, 5, 6$. We also examine the *maximum* number of monochromatic geodesics in an antipodal 2-coloring and find it to be $2^{n-1}n!$. In this case, we classify all colorings in which this maximum occurs. Finally, we explore the maximum number of antipodal geodesics in a subgraph of the hypercube with a fixed proportion of edges, providing a conjectured optimal configuration which, interestingly, contains a constant proportion of geodesics with respect to n. We also find a nontrivial upper bound in this scenario.

Noah Golowich

Removing cycles from dense digraphs

Mentor László Miklós Lovász

Project suggested by László Miklós Lovász

Given a digraph G without parallel edges, let $\beta(G)$ be the size of the smallest subset $X \subset E(G)$ such that $G \backslash X$ has no directed cycles. Let $\gamma(G)$ be the number of unordered pairs of vertices of G which are nonadjacent. We show that if r is a positive integer such that no directed cycle in G has length less than or equal to r, then $\beta(G) \leq 229\gamma(G)/(r-2)^2$, which improves a result of Fox, Keevash, and Sudakov. In order to prove this theorem, we prove a strengthened bound on the edge expansion of r-free digraphs. In the case where G is 3-free, we also prove an even stronger bound on the edge expansion of G. Finally, we show that $\beta(G) \leq .4\gamma(G)$ for certain types of 3-free Cayley graphs with additive generators.

Eric Nie and Alok Puranik

Cellular automata on a hexagonal grid

Mentor Dr. Tanya Khovanova

Project suggested by Prof. Richard Stanley (MIT)

We examine a cellular automaton on a two-dimensional hexagonal grid in which each cell has six neighbors. A cell is born if it has exactly one live neighbor, and a live cell never dies. The automata has an intricate fractal structure, and we have discovered a

connection to the Sierpinski sieve. We derived a recursive formula for determining which cells are born and the generation in which they are born.

Session 2

Arjun Khandelwal

Compact dot representations in permutation avoidance

Mentor Rik Sengupta

Project suggested by Prof. Jacob Fox (MIT)

First suggested by Arratia, the problem of the smallest permutation which contains all patterns of a given length remains unsolved. We give a sharp bound on the size of the compact dot representation introduced by Eriksson et. al and give the permutation which achieves it in the hopes of improving the currently standing bound for the size of the smallest super-pattern.

Joseph Zurier

Generalizations of the joints problem

Mentor Ben Yang

Project suggested by Prof. Larry Guth (MIT)

In this paper we explore generalizations of the joints problem introduced by B. Chazelle et al. A joint is formed when three noncoplanar lines intersect in $\mathbb{R}^3$, and other authors have proved an $O(n^{\frac{3}{2}})$ bound on the number of joints formed by n lines. We narrow the constant in this bound to between $\frac{\sqrt{2}}{3}$ and $\frac{4}{3}$, and explore the problem when the dimension of the space, the dimension of the intersecting hyperplanes, and the dimension of their mutual intersection is changed. We also consider cases where the intersecting hyperplanes do not all have the same dimension; in particular, we solve the problem of bounding the number of intersections of two lines and one plane in a single point in $\mathbb{R}^4$ in terms of the number of lines and planes. This result is used to give a new proof of the joints theorem.

Session 3: PRIMES-IGL

Jessica Li

On the geometry and mathematical modelling of snowflakes and viruses

Mentor Prof. Laura Schaposnik, University of Illinois at Urbana-Champaign

Project suggested by Prof. Laura Schaposnik

The goal of this project is to study symmetries appearing in nature, particularly in the formation of snowflakes and viruses. So far the project has revolved around three main themes: the study of the basic geometric properties of regular snowflakes and icosahedral viruses, the mathematical modeling that has been developed to visualize snowflakes, and the production of 3D printed samples of snowflake puzzles. We have summarized snowflake geometric properties via classification and icosahedral capsid construction rules, summarized mathematical models for computer modeling of snowflake

2

growth, implemented Reiter's model and generated snowflake images, and finished snow-flake puzzle design and produced samples by 3D printing.

We have begun the study of further questions in the following three areas. First, while the computer models generate snowflakes images resembling real ones, there has not been much analysis of the models in the literature; we will examine the geometric properties of the main and side branches of snowflake images. Second, the existing algorithms of snowflake growth are mostly based on diffusion models and do not take into account local geometry. We are thus trying to improve these algorithms to include, for example, the curvature effect and surface free energy minimization. Third, icosahedral viruses have an invariant, its triangulation number, and only for some of its values the viruses have been described in the past. We are now looking at mathematical reasons why viruses for other values would not exist, and in collaboration with some biologists, we are studying more subtle geometrical properties of viruses.

Yilun Du

Tiling harmonic functions

Mentor Prof. Sergiy Merenkov, University of Illinois at Urbana-Champaign

Project suggested by Prof. Sergiy Merenkov

We define the tiling harmonic function, and develop a computer efficient algorithm to calculate tiling harmonic functions given boundary conditions. We also develop a computer algorithm to calculate graph harmonic functions.

We compare different values of interior vertices from tiling harmonic and graph harmonic functions. The main method used in our algorithm was the method of relaxation.

Session 4: PRIMES-USA

Eric Neyman

Cylindric Young tableaux and their properties

Mentor Darij Grinberg

Project suggested by Prof. Alexander Postnikov (MIT)

The cylindric Young tableau was developed in the 1990s as a generalization of the semistandard Young tableau. In this presentation, we will look at the fundamentals of tableau theory, including regular, skew, and cylindric tableaux and partitions. We will then define Schur polynomials and prove their symmetry for all three types of partitions. Finally, we will look at the commutativity of operators that add or take away horizontal or vertical strips to or from partitions.

Andrew He, Suzy Lou, and Max Murin

On the existence of srg(99, 14, 1, 2)

Mentor Dr. Peter Csikvari

Project suggested by Prof. Jacob Fox (MIT)

Strongly regular graphs form an important and very useful type of graphs. These graphs are defined by a constant degree, a constant number of common neighbors for each pair of connected vertices and a constant number of common neighbors for each pair of non-adjacent vertices. We will examine the existence of a particular strongly regular graph, namely $\text{srg}(99, 14, 1, 2)$. We have used several approaches in the quest for a construction, including a basic labeling of 15 vertices, a labeling using Fano-planes, an examination of the structure of the triangles in the graph, and an examination of the largest independent set in the graph.

Session 5: PRIMES-USA

Shyam Narayanan

Improving the accuracy of primality tests by enhancing the Miller-Rabin theorem

Mentor David Corwin

Project suggested by Dr. Ben Hinkle and Dr. Stefan Wehmeier (MathWorks)

Currently, even the fastest deterministic primality tests still run too slowly, with the Agrawal-Kayal-Saxena (AKS) primality test runtime being $(log^6(n))$, and probabilistic primality tests are still highly inaccurate.

In this paper, we discuss the accuracy of the Miller-Rabin Primality Test and the number of Non-witnesses for a general composite odd integer n.

We also extend the Miller-Rabin Theorem by determining when the number of nonwitnesses $N(n)$ equals $\frac{\varphi(n)}{4}$ and by proving that $\forall n$, if $N(n) > \frac{5}{32} \cdot \varphi(n)$ then n must be of one of the following 3 forms: $n = (2x+1)(4x+1)$, where x is an integer, $n = (2x+1)(6x+1)$, where x is an integer, n is a Carmichael number of the form pqr, where p, q, r are distinct primes congruent to $3 \pmod 4$.

Finally, we present open questions about how to determine if n is one of these three forms, and whether the Miller-Rabin Primality test can become a fast deterministic primality test.

Kyle Gettig

Linear extensions of directed acyclic graphs

Mentor Benjamin Iriarte

Project suggested by Benjamin Iriarte

Given a graph, an acyclic orientation of the edges determines a partial ordering of the vertices. This partial ordering has a number of linear extensions total orderings of the vertices that agree with the partial ordering. The purpose of this paper is twofold. Firstly, properties of the orientation that induces the maximum number of linear extensions are investigated. Due to similarities between the optimal orientation in simple cases and solution to the Max-Cut Problem, the possibility of a correlation is explored, though with minimal success. Correlations are then explored between the optimal orientation of a graph G and the comparability graphs with the minimum number of edges that contain G as a subgraph, as well as to certain graphical colorings induced by the orientation. Specifically, small cases of non-comparability graphs are investigated and compared to

the known results for comparability graphs. In the second part of this paper, the above concepts are extended to random graphs, that is, graphs with probabilities associated with each edge. New definitions and theorems are introduced to create a more intuitive system that agrees with the discrete case when all probabilities are 0 or 1, though complete results for this new system would be much more difficult to prove.

Brice Huang

G-parking functions and monotone monomial ideals

Mentor Wuttisak Trongsiriwat

Project suggested by Prof. Alexander Postnikov (MIT)

It is known that for all graphs G on $\{0, \ldots, n\}$, the number of G-parking functions equals the number of oriented spanning trees of G rooted at 0. Also, when $G = K_{n+1}$ is a complete graph, it is known that the number of almost parking functions of size n equals the number of (unoriented) spanning forests of G. We define an almost-G-parking function and claim that the number of almost-G-parking functions equals the number of spanning forests of G whose connected components are rooted at their smallest vertices. We give a bijective proof of this fact. We also generalize the monomial ideal associated with the almost parking functions of size n.

Session 6: PRIMES-USA

Alexandria Yu

Classification of unital 7-dimensional commutative algebras

Mentor Sherry Gong

Project suggested by Prof. Bjorn Poonen (MIT)

In this talk, I will discuss the classification of finite dimensional unital commutative algebras. I will construct a family of 7-dimensional unital commutative algebras using Jordan forms and establish a classification result for this family of algebras. I will give a complete classification of a family of 7-dimensional unital commutative algebras discovered by Professor Poonen.

Peter Tian

On the extremal functions of multi-dimensional forbidden matrices

Mentor Jesse Geneson

Project suggested by Jesse Geneson

We say that a 2 dimensional matrix A contains P if we can delete rows or columns or change 1's to 0's in A to form a copy of P in A. Otherwise we say A avoids P. We let ex(n, P) be the maximum number of ones in a nxn matrix A that avoids the matrix P. We extend previous results about ex(n,P) for permutation matrices in 2 dimensions to d-dimensional matrices.

Shashwat Kishore

Decomposition of tensor products of Verma modules

Mentor Gus Lonergan

Project suggested by Prof. Pavel Etingof (MIT)

The Lie algebra $sl(2)$, the space of 2×2 matrices with zero trace, is an important object in representation theory. One commonly studied class of infinite dimensional representations of $sl(2)$ is the class of Verma modules. Every Verma module is indexed by a unique complex highest weight, and every complex highest weight corresponds to a unique Verma module. Representations composed of direct sums and tensor products of Verma modules can be constructed with the usual Lie algebra representation rules.

It is known that every real highest weight Verma module over $sl(2)$ can be equipped with a signature character, which is an element of $\mathbb{Z}[s]/(s^2 - 1)$. The signature character encodes the dimensions of the weight spaces of the Verma module along with the signature of the module's nondegenerate Hermitian form. The signature character obeys the usual rules for direct sums and tensor products. Moreover, every tensor product of real Verma modules over $sl(2)$ can be uniquely decomposed as a direct sum of infinitely many real Verma modules, each tensored with its own multiplicity space.

Here we investigate the decomposition of an arbitrary tensor product of real Verma modules by computing the signature characters of the multiplicity spaces. We explicitly compute these signature characters for tensor products of two Verma modules and tensor products of negative highest weight Verma modules. We describe the general form of two polynomials that govern the signature characters of the multiplicity spaces in an arbitrary tensor product, and explicitly determine the leading coefficients of the polynomials. Thus, given an arbitrary tensor product, we have accurate approximations for the signature characters of all but finitely many multiplicity spaces, leading to a fairly explicit description of the tensor product decomposition.

Session 7: Reading groups

Cameron Derwin and Margalit Glasgow

The probabilistic method

Mentor Chiheon Kim

The probabilistic method is a field largely explored by Erdös in the mid-20th century. We read a book by Noga Alon and Joel Spencer and learned how to use a probabilistic approach to prove the existence of specific structures from graph theory to geometry and number theory. This method emphasized combinatorics and used asymptotic analysis to optimize probabilities. In this presentation, we will explain several methods used in the probabilistic method including expected value and the second moment, or Chebyshev inequality. We will then demonstrate these approaches to solve problems in graph theory, geometry, and number theory.

Rohil Prasad, William Kuszmaul, and Isaac Xia

Proving the trefoil is knotted

Mentor Umut Varolgunes

Take a tied shoe. Glue the ends of its shoelaces together. Is it possible to now untangle

the shoelace(s) so that it looks like you took an untied shoe and glued the ends of its shoelaces together? It turns out it's not. We give two classic proofs that the trefoil knot cannot be untangled into the unknot.

Ravi Jagadeesan and Luke Sciarappa

Simplicial homology

Mentor Akhil Mathew

We describe several theories of the cohomology of topological spaces, including simplicial cohomology and the cohomology of sheaves. We give several applications, including to Brouwers Fixed Point Theorem and the Jordan Separation Theorem.

May 18
Computer Science
Physical and Computational Biology

Session 8

William Wu and Nicolaas Kaashoek

How to teach a class to grade itself

Mentors Christos Tzamos and Matt Weinberg

Project suggested by Prof. Costis Daskalakis (MIT)

An efficient peer grading mechanism is proposed for grading the multitude of assignments in online courses. This novel approach is based on game theory and mechanism design. A set of assumptions and a mathematical model is ratified to simulate the dominant strategy behavior of students in a given mechanism. A benchmark function accounting for grade accuracy and workload is established to quantitatively compare effectiveness and scalability of various mechanisms. After iteration of mechanisms under increasingly realistic assumptions, three are proposed: Calibration, Improved Calibration, and Deduction. The Calibration mechanism performs as predicted by game theory when tested in an online crowdsourced experiment. The Deduction mechanism performs relatively well in the benchmark, outperforming traditional automated and peer grading systems. The mathematical model and benchmark opens the way for future derivative works to be performed and compared.

Amy Chou and Justin Kaashoek

Automatically generating puzzle problems of different complexity levels

Mentor Rishabh Singh

Project suggested by Prof. Armando Solar Lezama (MIT)

Students learn by practicing over lots of problems, but generating fresh problems that have specific characteristics such as using a certain set of concepts or being of a given difficulty level are a tedious task for a teacher. In this paper, we present an iterative constraint-based technique for automatically generating problems which is general

enough for many domains. Our technique takes as parameters the problem definition, the complexity function, and domain-specific semantics-preserving transformations. We present an instantiation of our technique over automated generation of sudoku puzzles, and are currently extending our technique to generate Python programming problems. Since defining complexity of a sudoku puzzle is still an open research question, we use machine learning to learn a function that predicts the hardness of a sudoku puzzle using lots of labelled sudoku puzzles from various online sources. Our technique was able to efficiently generate more than 200,000 interesting sudoku puzzles of different sizes (9x9, 16x16, 25x25) and of different complexity levels.

Istvan Chung and Oron Propp

Inferring the structure of probabilistic graphical models
for efficient natural language understanding

Mentor Dr. Thomas Howard

Project suggested by Prof. Nicholas Roy (MIT)

Natural language interfaces for robots transform unstructured text to a machine-interpretable symbolic language. Contemporary approaches construct probabilistic graphical models using all objects and relationships in an observed environment. The computational complexity of this approach, however, increases rapidly as each possible symbol grounding must be evaluated. To address this problem, we are investigating a hierarchical approach to symbol grounding, in which we infer a set of rules to eliminate symbols irrelevant to the current expression. In this presentation we describe our progress toward this goal, discussing log-linear models, parsing algorithms, and probabilistic inference.

Session 9

Nathan Wolfe and Ethan Zou

Protecting private data in the cloud: A path oblivious RAM protocol

Mentors Ling Ren and Xiangyao Yu

Project suggested by Prof. Srini Devadas (MIT)

We live in a world where our personal data is extremely valuable. However, Dropbox, a popular cloud storage tool, has certain security flaws, one of which being that a user's access pattern is unprotected. We have thus created an implementation of Path Oblivious RAM (Path ORAM) for Dropbox users in order to provide increased security. This implementation differs significantly from how Path ORAM is normally used, in that we have been able to include several innovations, including a dynamically growing and shrinking tree, as well as the possibility for multi-client use.

Lalita Devadas

Modelling changes in gene expression in neurodegeneration in mice

Mentor Angela Yen

Project suggested by Prof. Manolis Kellis (MIT)

Previous work has shown that gene expression can be correlated with chromatin marks.

We used random forest and linear models to determine the relationship between certain chromatin features and the change in gene expression between a healthy mouse and a neurodegenerative mouse. The two-step approach that we used first classified the data into groups and then predicted the expression value based on the grouping and on histone modification data. Our results did not show a clear correlation; however we plan to reprocess the data to improve our predictive power in the future.

Michael Colavita

Network motifs of pathogenic genes in human regulatory network

Mentor Soheil Feizi

Project suggested by Prof. Manolis Kellis (MIT)

Regulation of gene expression is a vital component of a cell's internal function and responses to stimuli in its environment. Gene regulation, in which one gene enhances or reduces the expression of another gene, controls which gene products a cell is producing at any given time. Regulatory networks serve as a concise and computationally friendly means of storing and processing regulatory relationships between genes in the form of a graph.

Applying calculations and measures from graph theory to genetic information stored in this format allows us to examine gene interactions on a structural and mathematical level. Combining information from the human regulatory network with a database of genes associated with various genetic diseases, we search for statistically significant patterns known as network motifs by examining the enrichment of various network metrics within the pathogenic portions of the graph. From these results, we then locate clusters of pathogenic genes using the spectral clustering algorithm to examine the structure of genetic diseases on a regulatory level.

Session 10: Medical Informatics

Yishen (Tom) Chen

SMART Genomics API

Mentor Dr. Gil Alterovitz

Project suggested by Dr. Gil Alterovitz

Human genome sequencing has seen rapid growth in the past several years. What has previously been an expensive technique reserved only to academic researchers has become accessible to nearly anyone with the development of new sequencing technologies. However, genomic data is very large and hard to manage. In addition, each supplier of genomics data has developed their own methods for data retrieval and use. As a result, despite the advances in genomics, very little clinical applications have arisen from this data mostly due to a lack of standardization. Here we introduce a standardized API for the access and utilization of genomics data in the clinic. Through integrating this standard with emerging clinical standards like FHIR and interoperable models designed by Global Alliance for Genomics and Health, the new SMART Genomics API would enable a successful integration of genomics data into clinical care.

Xi (Steve) Chen

Genomics development library for Android

Mentor Dr. Gil Alterovitz

Project suggested by Dr. Gil Alterovitz

In the past years, a growing number of people are getting their genome sequenced at companies like 23andme. In turn, analysis of their genome yields valuable data such as a users disease risk. Through the database API, developers can access users genomic data, and use it to develop serious clinical or just plain entertaining applications. The Genomics Development Library extends the development scope from solely web to mobile, implementing whole process of authentication, data parsing and storage for SMART Genomics and 23andme API.

John Zhang

Integrating genomic, clinical, and patient questionnaire information for breast cancer diagnosis and treatment

Mentor Dr. Gil Alterovitz

Project suggested by Dr. Gil Alterovitz

Clinical applications such as Hughes riskApps use genomic and patient questionnaire information to assess a patient's risk for certain diseases. The Geneinsight Variant web service is a online web API that was developed to return patient variant information. The FHIR Genomics format is a specification for interacting with genomic data. The goal of this project was to integrate these three components to improve treatment and diagnosis of breast cancer. The variant information from Geneinsight was exposed to the FHIR Genomics format and stored on a SMART Genomics server, which was then called by a .NET framework class library to serve the data to Hughes riskApps.

Andrew Li and Arul Prasad

Exploration of disordered proteins related to drug resistance in Hepatitis B virus and lung cancer

Mentor Dr. Gil Alterovitz

Project suggested by Dr. Gil Alterovitz

Hepatitis B virus and lung cancer are two prevalent epidemics that have affected humans throughout the world in the liver and lungs, respectively. Common treatments for HBV include lamivudine and entecavir, two drugs that inhibit the reverse transcriptase (RT) of HBV. For lung cancer, chemotherapy and/or radiation therapy are often used to kill the cancerous cells. However, these drug treatments are met with resistance by the virus and cancer, as both HBV and lung cancer undergo mutations, or single nucleotide polymorphisms (SNPs). Previous research has found that the areas that most affect drug resistance in these diseases are the disordered proteins, or proteins that lack a rigid tertiary structure, that are coded by the various genes that contain these SNPs. Disordered proteins are easier to bind to since they have a more flexible structure than a normal protein, thus making them relevant for drug targeting. Two major goals of this study were

to show that disordered proteins had an effect on drug resistance and that SNPs had an effect on disordering proteins in HBV and lung cancer. Through statistical analysis with a Fisher exact test on thousands of protein sequences it was shown that for proteins with predicted disordered residue lengths between 1 and 25 there was statistical difference in drug resistance. Additionally, using a 3D protein modeling software called Python Molecule Viewer and a Python script that we wrote, we showed that SNPs are on average closer to disordered regions than ordered regions of the protein. This means that SNPs have a large impact on disorder, making them relevant to study for drug targeting in both HBV and lung cancer.

Session 11: Physical and Computational Biology

Andrew Luo

The impact of protein aggregates on the sub-diffusion of a DNA locus

Mentors Geoffrey Fudenberg and Maxim Imakaev

Project suggested by Prof. Leonid Mirny (MIT)

Investigations of DNA diffusion in living cells are critical to understanding gene expression and chromatin organization. Tracking of specific loci is usually implemented via engineering a fluorescent probe that binds specifically to that locus. Since these probes are of insignificant mass compared to that of the DNA as a whole, it is assumed that they do not affect the subdiffusion of the tracked region. In our studies, we attached masses representative of these probes to a long polymer, and used GPU accelerated libraries to simulate the process of diffusion. Remarkably, we found that the masses and positions of probes have a noticeable effect on the observed subdiffusion in our simulations.

Carolyn Lu

Loop extruding enzymes in interphase: Dynamic folding of chromatin domains

Mentors Geoffrey Fudenberg and Maxim Imakaev

Project suggested by Prof. Leonid Mirny (MIT)

Chromosome organization crucially impacts genomic functions, including gene expression, genomic stability, and faithful transmission of genetic information to the next generation. The recently developed Hi-C method provides insight into chromosome organization by measuring spatial contacts between loci on a genome-wide scale. In interphase, at genomic distances smaller than 1Mb, chromatin fiber has been shown to be compartmentalized into Topologically Associated Domains, or TADs. While TADs have been extensively studied, and have been shown to correlate with multiple genomic features, mechanisms which could form TADs, or their boundaries, are unknown.

Previously, we explored possible models for TAD boundaries which either: locally changed fiber thickness or fiber flexibility, or attached RNAs to DNA at highly transcribed genes. These models failed to produce TADs with biologically relevant parameters. Here we consider whether Structural Maintenance of Chromosomes (SMC) proteins could lead to formation of TADs. We explore a recently proposed ability of SMC complexes to extrude chromatin loops, and thus bring distal genomic loci into direct spatial contact. We additionally hypothesized that boundaries of TADs possess genomic elements which can

halt SMC complexes, preventing the formation of chromatin loops between neighboring TADs.

Since the exact mechanisms of SMC loop extrusion are unknown, we studied an extensive range of kinetic models of SMC loop extrusion, varying both assumptions about SMC loop extrusion and parameters for each model. We integrated these models with polymer simulations, and compared resulting interaction maps with Hi-C and contact probability scalings with experimental data. We find that SMC-mediated loop extrusion could locally re-organize chromatin and, in conjunction with halting at boundaries, could reconstruct experimentally observed features of Hi-C maps around TAD boundaries.

Session 12: Mathematics

Yonah Borns-Weil and Junho Won

Discrete and continuous dynamical systems: Applications and examples

Mentor Dr. Aaron Welters

In this talk, we examine two types of dynamical systems: iterative maps and differential equations. We demonstrate the concept of stable periodic points of an iterative map, then consider the orbit diagram of a particular map, the logistic map. This map has the property of period-doubling bifurcation at a certain rate, which in fact is universal for many different maps. We present the precise theorem of the universality, and examine its implications.

We then consider differential equation systems, and look at their fixed points and bifurcations, which are often analogous to the discrete case. These systems can sometimes be linearized to determine their local behavior, and we use the techniques of linearization to examine an application to chemical kinetics. Finally, we invoke the Poincaré-Bendixson to explain why a certain chemical reaction produces periodic behavior.

Joshua Xiong

On the winning positions in generalizations of Nim

Mentor Dr. Tanya Khovanova

Project suggested by Dr. Tanya Khovanova

In this paper, we study impartial combinatorial games, the most basic of which is the game of Nim. In Nim, there are several piles of counters, and two players take turns removing counters from a single pile until all of the counters are gone.

We generalize Nim by expanding the rule-set such that players can also remove the same number of counters from a specified subset of the piles; we call these variants *rectangular games*. In this paper, we prove several bounds and properties of P-positions and also formulate several conjectures related to these P-positions. In addition, we explore several unexpected relationships between these games and other areas of mathematics, including Lie algebras and cellular automata.

Niket Gowravaram and Uma Roy

A diagrammatic approach to the $K(\pi, 1)$ conjecture

Mentor Alisa Knizel

Project suggested by Dr. Benjamin Elias (MIT)

We investigate a novel approach to the $K(\pi, 1)$ conjecture for Coxeter groups using diagrammatics. In particular the $K(\pi, 1)$ conjecture deals with the second homotopy group of the dual Coxeter complex – a topological space associated with a particular Coxeter group. To each possible element of the second homotopy group, we associate a planar graph with vertices that correspond to pairs of generators and relations of the particular Coxeter group. Proving the $K(\pi, 1)$ conjecture for a Coxeter group is equivalent to the statement that every possible planar graph corresponding to the Coxeter group is equivalent to the empty graph through a series of allowable transformations. We present proofs of the triviality of all possible planar graphs corresponding to a variety of Coxeter groups including A_2, $I_2(m)$, A_3 and B_3. In addition, we provide a proof that if all possible planar graphs are trivial for groups G and H, then the group $G \times H$ also has all trivial graphs. Finally, we investigate the notion of oriented graphs, discussing a basic case and also providing avenues for further research.