



**SPRING 2021 PI MU EPSILON CONFERENCE PROGRAM**

All presentations will be held via Zoom. Below is the schedule of talks, with Zoom links provided, followed by the abstracts for each talk. The Zoom information has also been posted to the conference webpage (see here).

**SCHEDULE FOR SATURDAY, APRIL 17.**

**Keynote Address:** Dr. Jesús De Loera

**Time:** 11:00am-12:15pm

**Zoom meeting:** [join here](#)

**Undergraduate Speakers**

Time	Zoom 1 <a href="#">join here</a>	Zoom 2 <a href="#">join here</a>
1:00-1:25pm	Hennen	Moran
1:30-1:55pm	Hill and Krueger	Whalen
2:00-2:25pm	Swenson	McCurdy
2:30-2:55pm	Wilson	Austin and Diby
3:00-3:25pm	Savoy	Weatherspoon

**PRESENTATION ABSTRACTS.**

**11:00AM - 12:15PM (Keynote Address).**

**Speaker:** Dr. Jesús De Loera (University of California, Davis)

*Geometry in the Age of Artificial Intelligence and Big Data* - Geometry and Topology are often (mis)taken as pure unapplied parts of Mathematics. With the data science artificial intelligence revolution this false assumption has been shattered once more. In this talk I present two examples of how a geometer can contribute to the growing field of data science, I show how discrete geometry of finite sets of points can be used to understand statistical inference methods such as logistic regression and how basic homology of simplicial complexes plays a role in clustering data and image processing. But perhaps even more surprising, I will show with one example that data science and artificial intelligence may also help mathematical areas such as algebra. The new results I will discuss are joint work I wrote with my Ph.D students Lily Silverstein, Zhenyang Zhang, Tommy Hogan, and Edgar Jaramillo-Rodriguez.

**1:00PM - Zoom 1.**

**Speaker:** Max Hennen (College of St. Benedict and St. John's University)

*Probability of Generating a Group* - Generating a group depends heavily on the elements that are given. Determining the probability of generating certain groups if we are given two elements has already been done by two previous researchers, Fru Nde, and Travis Spillum. The former determined the probability of generating cyclic groups and dihedral groups given two elements, while the latter generalized the probability of generating the direct product of two cyclic groups. Building on the previous work by these researchers, we will find the probability of generating two different semi-direct products of cyclic groups, given two elements.

**1:00PM - Zoom 2.**

**Speaker:** Jack Moran (Carleton College)

*The Lineup Protocol: Using Simulation to Improve Visual Diagnostics* - What does a "good" diagnostic plot look like? When we look at a residual or QQ-plot, we are implicitly comparing it to what we view as a "good" plot in our mind. It turns out that we as humans are exceptional at picking patterns out of randomness and hence tend to over-interpret visual diagnostics. We attempt to remedy this problem by simulating "good" diagnostic plots for a viewer to use as references when they evaluate a visual display. In this talk, we look at a variety of simulation-based diagnostics in the context of binary logistic regression (regression where the response variable is a success/failure). We explore how to simulate data according to a fitted model and discuss how simulation can help us detect model violations. In particular, we look at the results of a simulation study for a specific type of simulation-based diagnostic, the lineup protocol. The study provides evidence that the lineup protocol is more powerful than classical diagnostics (the Goodness-of-fit test) when data violate the independence assumption of logistic regression, but less powerful when data violate the log-odds linearity assumption.

**1:30PM - Zoom 1.**

**Speakers:** Drake Hill and Jake Krueger (Concordia University, St. Paul)

*RSA Encryption Decrypted* - In this talk presenters will explain the number theory behind RSA encryption and the theory of how RSA encryption protects your data. They will also hopefully demonstrate how to implement RSA encryption in Java. No programming experience required to understand this presentation.

**1:30PM - Zoom 2.**

**Speaker:** Elizabeth Whalen (University of St. Thomas)

*Classifying Petaluma Knots* - Better understanding random knots can lead to better understanding knotting in biology, such as in DNA and other proteins. The Petaluma model allows us to study these random knots by modeling the configurations in the shapes of daisies. For each permutation on  $1, \dots, 2n + 1$ , there is a corresponding Petaluma knot whose strand heights through the central crossing point are the sequential values of the permutation. We studied the relationship between these permutations and the corresponding knots that resulted, with emphasis on characteristics such as crossing number, knot type, and data trends that result as crossing number increases.

**2:00PM - Zoom 1.**

**Speaker:** Jessica Swenson (University of Wisconsin, River Falls)

*Solving Sudoku Puzzles with the Magic of Groebner Bases* - Sudoku puzzles are fun logic puzzles played around the world. Solving a Sudoku puzzle can be done by finding a solution to a system of (possibly nonlinear) equations. An example of one such equation is that the product of all squares

in a row should equal the product of integers from 1 to 9. This project explores the use of Groebner bases, an important tool in computational commutative algebra, in order to solve Sudoku puzzles.

**2:00PM - Zoom 2.**

**Speaker:** Addie McCurdy (University of St. Thomas)

*Finding Knots in Proteins* - Recent studies have found knotting in the backbones of select protein chains; for example, the UCH-L1 enzyme makes up about 1-2% of material in the human brain, and has been shown to contain knotting. It is thought that the location of the knotting in such proteins could be linked to protein function, but more research is needed to determine the relationship. Traditional knot theory, which deals strictly with closed curves, fails to locate this knotting as proteins are open chains (i.e. they have two loose ends). There are multiple ways to define knotting in open chains, but none have been universally accepted. We propose a new definition of knotting in open chains, and use it to determine location and type of knotting found in proteins.

**2:30PM - Zoom 1.**

**Speaker:** Ally Wilson (College of St. Benedict and St. John's University)

*Minimal Base Sizes of Symmetric Groups* - This research explores how symmetric groups interact with different sets including: 2-sets, 3-sets, and 4-sets. More specifically, it seeks to find the minimal base size of symmetric groups acting on 2-sets, 3-sets, and 4-sets. To achieve this goal, the project focuses on the number of elements necessary to form a base for each set. Using this idea lower bound formulas were created. Looking at the arrangements of elements within the set allowed for the creation of upper bound formulas. Manipulating these formulas led to the development of the greatest lower bounds and least upper bounds. Through the use of these formulas minimal base sizes for 2-sets, 3-sets, and 4-sets were found.

**2:30PM - Zoom 2.**

**Speakers:** Mya Austin and N'Dri Diby (Winona State University)

*An Integrodifference Equation Model of Metapopulations in Point-Patch Habitats: Climate Change Impacts on the Mexican Free-Tailed Bat* - The Mexican free-tailed bat (*Tadarida brasiliensis mexicana*; Tbm) is a migratory mammal whose range includes parts of Mexico and Texas. It plays an important role in managing the insect population by foraging nightly. Due to climate change, southern states are expected to become hotter and drier, possibly creating a sparser insect population that will require Tbm to travel longer distances for sufficient sustenance. In this talk, we analyze how the spatial distribution, dispersal rates, and carrying capacities of caves affect equilibrium populations by constructing an integrodifference equation (IDE) model of their metapopulation in a point-patch habitat (caves in Texas). Population demographics within a cave are modeled by a logistic difference equation where population growth rates and carrying capacities are climate dependent. We assume Tbm forage and disperse (on a 1-dimensional landscape) according to a probability distribution (dispersal kernel) with dispersal rates that depend on climate conditions near each cave. Subsequently, Tbm use olfactory gradients in finding caves to return to upon dispersing. Simulations give good qualitative insight into the spatiotemporal dynamics of metapopulations in point-patch habitats. In particular, interior caves have lower equilibrium populations than outer caves due to long-distance dispersal. As the distance between the caves increases, equilibrium populations approach respective cave carrying capacities. Finally, equilibriums for caves with higher dispersal rates (due to climate-driven food shortages) are generally lower than other caves.

**3:00PM - Zoom 1.**

**Speaker:** Thomas Savoy (Winona State University)

*3D modeling mathematics* - Blender, a free and open-sourced 3D modeling program, can be used

to demonstrate and visualize mathematics. Blender is easily accessible so that anyone can use the program. Blender could be a powerful tool in the classroom for students to interact, create, and understand the concepts they are studying. We will discuss the Lindenmayer systems or L-system for short during this talk and demonstrate how to use blender to model them. Afterwards, we'll show how to generate the Mandelbrot set and Julia sets, along with samples of visualizations from geometry, topology, and differential equations.

**3:00PM - Zoom 2.**

**Speaker:** Kaylee Weatherspoon (University of South Carolina, Columbia)

*Hadwiger-Nelson Restricted to a Disk* - With the recent development of a non-four-colorable unit distance graph by biomedical gerontologist Aubrey de Grey, there has been a resurgence of work on the venerable Chromatic Number of the Plane problem (Hadwiger-Nelson Problem). Proposing that there is some sufficiently large disk such that the chromatic number of the disk is in fact the chromatic number of the plane, I present results identifying the intervals of disk radii within which the transition from chromatic number  $k$  to chromatic number  $k + 1$  for  $k = \{1, 2, 3, 4, 5, 6, 7\}$ .

I also discuss results on a classification of all maximal unit distance graphs, including concepts of cogonality and rational-gons. The few possible non-rigid maximal unit distance graphs are beautiful and highly symmetric. One example even involves the golden ratio.

While our classification of maximal unit distance graphs is interesting in its own right, we also hope that our classification will lead to the discovery of more small-circumradius/high chromatic number unit distance graphs. We could use these graphs to more narrowly identify the radii at which the transition from chromatic number  $k$  to chromatic number  $k + 1$  occurs. This work represents a collaboration with Prof. Joshua Cooper (University of South Carolina) and Prof. Michael Filaseta (University of South Carolina).