

ABSTRACTS

(in alphabetical order)

1. **Applying Topological Data Analysis to Plant Veins**

Kelsi Anderson*, *St. Mary's College of Maryland*

Alyson Jones*, *Morgan State University*

We all know that plants absorb nutrients through their roots. However, what we often do not know is the name of the vein in which these nutrients are transported. Xylem is the structure within plants that helps both give them their form and deliver nutrients to the rest of the plant. Here we are developing tools to automate and mathematically quantify mutant patterns within this xylem tissue. We are using image-processing tools within Matlab and topological data analysis libraries within Python in order to characterize the shape of our image data. Topological data analysis is the name of a broader set of tools that we use to determine the shape of data. The main tool that we use in topological data analysis is persistent homology. In computing persistent homology, we start with a set of points and slowly increase their radius. When increasing their radius, these points will eventually touch one another and form connected components (clusters) and possibly holes or loops. These connected components and holes are significant due to persistent homology's roots within topology. Topology is the study of shapes in an abstract way. Within this field of study we focus on how many holes and pieces (connected components) a shape can have. This abstract way of looking at objects is very helpful when giving data, such as a grid of pixels or photo, a shape. Persistent homology allows us to look at images of xylem structure and mathematically determine the impact of mutations on the xylem patterns.

*Research Institution: Purdue University
Research Advisor: Dr. Alexandria Volkening

2. **Graph and Group Theoretic Properties of the SOMA Cube and SOMAP**

Kyle Asbury*, *Rose-Hulman Institute of Technology*

Ben Glancy*, *Rose-Hulman Institute of Technology*

The SOMA Cube is a puzzle toy in which seven irregularly shaped blocks must be fit together to build a cube. There are 240 distinct solutions to the SOMA Cube. One rainy afternoon, Conway and Guy created a graph of all the solutions by manually building each solution. They called their graph the SOMAP. We are studying how the geometric structure of the SOMA Cube pieces informs the graph theoretic properties of the SOMAP, such as subgraphs that can or cannot appear and vertex centrality. We have also used permutation group theory to decipher notation used by Knuth in previous work on the SOMAP.

*Research Institution: Rose-Hulman Institute of Technology
Research Advisor: Dr. Josh Holden

3. Cubulated Holonomy

Stephanie Atherton*, *Otis College of Art & Design*

Josue Molina*, *Texas Tech University*

Holonomy is well-known in the continuous context in studying parallel transport maps, yet here we explore its discrete analogue in "rolling" polyhedra in loops over combinatorial symmetrical surfaces. Extending previous research conducted at Duke University which introduced the notion of "combinatorial holonomy" in terms of the tetrahedron rolled on triangulated surfaces, we apply their approach to the holonomy of the cube on cubulated surfaces. Our generalizations then allow us to formally categorize families of cubulated annuli and further, families of cubulated tori as having holonomy isomorphic to either A_4 or S_4 .

*Research Institution: Indiana University Bloomington

Research Advisor: Dr. Seppo Niemi-Colvin

4. Modeling the Impact of Venous Collapsibility on Retinal Blood Flow

Schuyler Brennan*, *University of Delaware*

Charlotte Weiss*, *McGill University*

Glaucoma is the second leading cause of blindness worldwide and is characterized by irreversible vision loss. Elevated intraocular pressure (IOP) is a primary risk factor for glaucoma and is currently the sole target for glaucoma treatment. However, various other risk factors exist for glaucoma, including impaired blood flow and oxygenation in the retina. Several mathematical models have been developed to understand the vascular mechanisms which contribute to glaucoma. This study will expand upon an electrical circuit compartmental model of the retinal vasculature to represent the venules as Starling resistors (instead of fixed resistors) to allow for venous collapse when external pressure is higher than internal vascular pressure. Autoregulation of blood flow is the phenomenon in which blood vessels constrict or dilate to maintain a relatively constant level of blood flow for a wide range of pressure levels. At elevated levels of IOP, the autoregulation plateau is predicted by the model to be shifted to a higher incoming pressure range, indicating that the capacity for autoregulation is lost in the range of physiological pressures. Correspondingly, resistance in the venules increases at elevated levels of IOP, and near venous collapse is predicted at low input arterial pressures when IOP is increased above its baseline value. This suggests that elevated IOP may lead to detrimental hemodynamic effects in addition to its established structural effects on retinal ganglion cells.

*Research Institution: Indiana University Indianapolis

Research Advisor: Dr. Julia Arciero

5. Simulation of Elementary Cellular Automata with Stranded Cellular Automata

Nathan Chen*, *Rose-Hulman Institute of Technology*

Elementary Cellular Automata (ECA) are one-dimensional cellular automata over a possibly infinite grid of squares where each square has two possible states, and its state combined with its neighbors' states determine its state in the next iteration based on a given rule. One such ECA rule, Rule 110, is capable of universal computation, meaning that an ECA using Rule 110 could theoretically compute

anything that is computable. Stranded Cellular Automata (SCA) are motivated by ECAs but each cell is a rectangle containing two possible strands moving vertically that can either remain parallel, or cross over each other, governed by the turning rule. There is an additional crossing rule to determine how exactly the strands cross over each other. We show that two steps of an SCA can simulate certain ECA rules, and that relaxing some constraints of an SCA can simulate additional ECA rules. We also present some additional ideas for SCAs simulating ECAs that could potentially simulate Rule 110, which would show that SCAs are also capable of universal computation.

*Research Institution: Rose-Hulman Institute of Technology
Research Advisor: Dr. Josh Holden

6. Forecasting the 2024 U.S. elections

Joseph Crompton*, *Purdue University*
Thanmaya Pattanashetty*, *Purdue University*

Forecasting elections is an exciting, yet complicated, endeavor that is often scrutinized by the public. Many organizations have created their own forecasting approaches, however they are often not fully transparent about their methods. Our research aims to accurately forecast the 2024 U.S. presidential, senatorial, and gubernatorial elections and share our methods and code with the public. We use a compartmental model, a framework which is often used to describe disease transmission in epidemiology, to track interactions between Democratic, Republican, and undecided voters through differential equations. We use polling data to determine our model parameters and simulate ten thousand election night scenarios. In past election cycles, this method performed as well as major forecasters such as Sabato's Crystal Ball and FiveThirtyEight. Our baseline method treats all polls equally, and we are working to give more weight to polls with larger sample sizes, and to shift polls based on their pollsters' typical partisan lean to improve forecast accuracy. Additionally, we are analyzing the quality of pollsters by comparing their error in each state to the average error in the state across all pollsters. Lastly, sharing our forecasts includes creating engaging visualizations to provide a deeper understanding of our model's results and the uncertainty of election forecasting. Our forecasts and visualizations for this year's election will be posted on <https://c-r-u-d.gitlab.io/2024/> throughout this election season.

*Research Institution: Purdue University
Research Advisor: Dr. Alexandria Volkening

7. Sum-Product Theorems using Geometric Techniques

Adam Cushman*, *Indiana University Bloomington*

Informally, the Sum-Product conjecture states that for any finite set of real numbers, either the sum set or the product set must be of nearly maximum cardinality. A related conjecture states that for finite convex sets of real numbers, the sum set must be of nearly maximum cardinality. In this talk, I will explain both conjectures as well as the methods which have been used to make progress on them.

*Research Institution: Indiana University Bloomington
Research Advisor: Dr. Shukun Wu

8. Translation Surfaces and Kontsevich-Zorich Monodromy Groups, Part I

Felix Filozov*, *City University of New York, Brooklyn College*

A translation surface is a collection of polygons in \mathbb{R}^2 with an even number of sides where we identify pairs of parallel edges of equal length. A square-tiled surface is a special case of a translation surface that arises as a collection of unit squares. Our focus is on a particular square-tiled surface called Eierlegende Wollmilchsau (EW). As a surface in \mathbb{R}^2 , a certain subgroup of $SL(2, \mathbb{R})$ maps EW to itself. We investigate how this group acts on the curves on EW. The representation of this group is called the Kontsevich-Zorich monodromy group, which is used to study the dynamics of surfaces in the space of translation surfaces. In the second part of this talk, we will consider coverings of EW and their properties.

*Research Institution: Indiana University Bloomington
Research Advisor: Dr. Joshua Wayne Southerland and Dami Lee

9. Cahn-Hilliard Model on Two-Dimensional Lattices: Center Manifold and Dynamical Transition Theory

Jared Grossman*, *Boston University*

The Cahn-Hilliard Model is used to model a phase transition of a thermodynamic system consisting of two species of particles. The model is written as a partial differential equation, with both a linear and nonlinear component with periodic boundary conditions. The spatial domain has a lattice structure spanned by two linearly independent vectors. The question that arises is how the geometry of the lattice affects the type of phase transitions and patterns of solutions that occur? To analyze this, we found the eigenvalues and eigenstates of the linear part of the equation and found the first set of modes that go unstable as the bifurcation parameter gets increased. We used center manifold theory to write the stable component as a function of the unstable component. We were then able to write the reduced equations for the coefficients of the unstable component. Behavior of the amplitude along straight lines was used to determine the transition type. The different geometry of the domain will affect whether solutions will stay near the origin or tend away from the origin at the critical value of the bifurcation parameter. Additionally, steady states were computed as well as their stability. This analysis leads to detailed characterizations of how different patterns can form from the system depending on the geometry of the lattice and the physical parameters. Such patterns can include rolls and hexagons.

*Research Institution: Indiana University Bloomington
Research Advisor: Dr. Shouhong Wang

10. Cahn-Hilliard on Two-Dimensional Lattices: Pattern Formation

Evan Halloran*, *Indiana University Bloomington*

This talk examines the dynamic phase transitions and pattern formations attributed to binary systems modeled by the Cahn-Hilliard equation. In particular, we consider a two-dimensional lattice structure and determine how different choices of the spanning vectors influence the resulting stability and pattern structures. As the trivial steady-state loses its linear stability, the binary system undergoes a dynamic transition which is shown to be characterized by both the geometry of the

domain and the physical parameters of the model. Unlike rectangular domains, we are able to observe the emergence of hexagonally–packed circles, as well as the familiar rolls and square structures associated with the Cahn-Hilliard model. In analyzing the reduced equations, we consider the different multiplicities that the critical eigenvalue can have, which is shown to be dependent on the geometry of the lattice. We briefly consider the long-range interaction model and derive similar results.

*Research Institution: Indiana University Bloomington
Research Advisor: Dr. Shouhong Wang

11. Modeling Neurocircuitry in Binge Drinking

Nicholas Hayek*, *McGill University*
Amy Rude*, *University of Washington*

Binge drinking occurs when a person vigorously seeks alcohol intoxication. It is characterized by two distinct phases: a period of high-rate consumption, called “front-loading,” followed by a period of lower-rate “maintenance” drinking. Frequent binge drinkers exhibit increased levels of depression, stress, violent behavior, and impaired judgment when sober. They are also at an increased risk for alcohol use disorders and dependence. Understanding and simulating front-loading and maintenance during a binge session may shed light on the role of biological factors on excessive alcohol use and possible pharmacological solutions. The involvement of striatal networks in binge drinking has been well-documented, but the exact connections that govern the transition between front-loading and maintenance are unclear. We devise a computational model, terminating in the striatum, that integrates glutamatergic projections from the insula and medial prefrontal cortex (mPFC), as well as dopaminergic projections from the midbrain. We propose that the striatum relays information about the rate and vigor with which one drinks to the motor cortex. Neuron groups in the mPFC track the agent’s consumption, ultimately inhibiting downstream activity once an internal tolerance is reached. Conditioned stimulus reinforces seeking behavior and mediates dopamine release, which then modulates firing characteristics of the striatum. Our model uses a system of differential equations to encode the excitatory and inhibitory connections between neuron populations. A neuron group’s excitability, drive, synaptic weights, and time constants are parameterized within physiologically relevant bounds. Using data components supplied by rodent models, we replicate front-loading and maintenance phases, as well as population-specific activity. By tuning parameters, we mimic brain irregularities and observe resulting changes in drinking behavior. Novel patterns in our model may help motivate future research on the networks involved in binge drinking.

*Research Institution: Indiana University Indianapolis
Research Advisor: Dr. Alexey Kuznetsov

12. Analysis of Fibonacci Numbers in Phyllotaxis

Allan Newman*, *Indiana State University*

Fibonacci numbers occur naturally in the number of clockwise and anticlockwise spirals present in the formations of leaves and seeds of many plants. The physical structure of these natural arrangements can be modelled by deformable unit area cylindrical lattices with a generating helix where lattice points represent the location of the plants’ leaves or seeds. The number of clockwise

and anticlockwise spirals (m, n) are called the parastichy pair of this lattice. All possible lattices can be generated by two parameters, x and y , which are dependent on the divergence angle of generating helix, circumference of the cylinder and chosen height intervals. We thus have a moduli space of all possible lattices which is tessellated by the parastichy pairs. The energy function of lattices is a function on this moduli space, and we can analyze local minimum trajectories of this function to indicate lattices which are naturally occurring. In this talk, we further discuss the mechanics of this model and present potential future steps to further understand the natural phenomenon driving these pattern formations.

*Research Institution: Indiana University Bloomington
Research Advisor: Dr. Sanjana Agarwal

13. Quantification of the Cell Spheroid Morphology in Glucose and Lipid Bilayer Dynamics

Daniel Nykamp*, *Carleton College*

Ronan Tiu*, *Stony Brook University*

The availability of glucose is relevant to biological function. We quantify the effect of glucose as a parameter that affects the morphology of cell spheroids which model tumor biology and bioprinting. We utilize CompuCell3D, an open-source software designed for Monte Carlo-based simulations of the cellular Potts model, to simulate cell spheroids, each beginning as 33 cells, on a 500x500 lattice representing 4 mm². We supplement qualitative visual analyses with quantifying spatial distributions by using inertia tensor components and radial distribution functions. Our findings lay the groundwork for a more nuanced understanding of spatial distributions, offering potential applications in bioprinting and in vitro tumor simulations. On the molecular level, we used CHARMM-GUI, a molecular dynamics input generator, to construct simulations of various lipid bilayer mixtures, with each leaflet of the bilayer containing 100 lipids. By examining which parameters will enable the simulations to equilibrate and run in a physiologically accurate manner, we produced several successful simulation setups. These setups are the starting points for a quantitative approach to examining the spatial distribution of lipid bilayers in the future, which will provide insight into mechanisms such as the diffusion of nutrients and signaling molecules through the cell membrane.

*Research Institution: Indiana University Indianapolis
Research Advisor: Dr. Horia Petrache

14. Modeling Subcellular Structures Involved in Cell Migration

Addison Powell*, *Brigham Young University*

Laura Schoenzeit*, *University of Minnesota, Twin Cities*

Our group's general goal is to create a model of mesenchymal cell migration by adding new subcellular structures including focal adhesions and actomyosin fibers to an existing model of a cell membrane. Such models will allow insights into how focal adhesions and actomyosin fibers mechanically interact with other cellular components. In this project, the cell membrane is represented by a damped spring network. The resulting dynamics of the network are governed by a system of first order ordinary differential equations (ODEs) derived from balancing elastic forces (Hooke's law) and viscous or damping forces. Additional forces are included that help the model mimic physiologically realistic behaviors such as conserved cell volume and membrane surface

area. In our contribution, we add focal adhesions, modeled as stiff springs, to connect the exterior of the membrane to the flat extracellular matrix (ECM). The focal adhesions are assumed to attach and detach to the ECM in a probabilistically biased manner that encourages cell motion and deformation. For instance, such additions cause an initially spheroidal cell to flatten out on the ECM. Additionally, biasing the connections to be denser in the direction of chemical gradients encourages cell movement in that direction, reproducing cellular chemotaxis. In the future, also including actomyosin fibers will allow us to better match the model with experimental data that includes measurements of forces in the modeled subcellular components. This calibrated model can then be used to estimate forces during cell migration and consider how subcellular components and their associated forces direct cell migration.

*Research Institution: Indiana University Indianapolis

Research Advisor: Dr. Jared Barber

15. Translation Surfaces and Kontsevich-Zorich Monodromy Groups, Part II

Jaedon Rich*, *University of Washington*

This is the second part of a two-part talk. After introducing translation surfaces and KZ monodromy groups in the first part, we now carry out computations on a particular countable family of square-tiled surfaces, showing their KZ monodromy groups to be small in a suitable sense, namely that they are non-arithmetic. We work out examples of full KZ monodromy groups in the cases where this is computationally feasible, and for the general case we use properties of ramified covers to obtain results for the entire family of translation surfaces.

*Research Institution: Indiana University Bloomington

Research Advisor: Dr. Joshua Wayne Southerland and Dami Lee

16. Concatenation methods in phylogenetic reconstruction

Daniel Rickert*, *Indiana University Bloomington*

One of the major goals of phylogenetics is to describe the evolutionary relationship among species. This relationship is often summarized by a rooted or unrooted binary tree referred to as the *species tree*. Ideally, we hope to recover properties of the species tree using DNA sequence data available from genes (loci) in the tip species. However, the genetic relationships among sampled loci may be incongruent with each other and the species tree. *Concatenation methods* ignore this complication, estimating parameters under the incorrect assumption that all loci have evolved among the same tree. The hope is that such estimators nonetheless converge on the correct answer as more loci are sampled. Here, we explore the *statistical (in)consistency* of common concatenation methods, determining where in tree space consistency holds using a new technique of computing expected branch lengths in gene trees. We also present a novel *pseudo-maximum-likelihood* estimator that holds the potential for consistent joint inference of the species tree's topology and internal branch lengths.

*Research Institution: Indiana University Bloomington

Research Advisor: Dr. Matthew W. Hahn and Dr. Wai-Tong (Louis) Fan

17. Continuous-Time Binary Branching Processes for Virus Evolution in Serial Passages

Allison Yusim^{*}, *University of Wisconsin-Madison*

Serial passages experiments provide valuable insights on the dynamics of a virus's evolution over time but are often costly and require materials that can be difficult to obtain. We created a stochastic model for such experiments to account for the probabilistic nature of virus evolution. We gathered information from previous experiments to develop realistic assumptions and used a binary branching process where the branching rate is inversely proportional to the length of the virus to build a simulation for virus replication in host cells. We then modeled the process for two special cases, one of which is a simple birth-death process modeled by a continuous-time Markov chain that converges to an ordinary differential equation. We modeled the second case with a more complex stochastic equation and simulation statistics suggest that it will converge to a partial differential equation.

^{*}Research Institution: Indiana University Bloomington
Research Advisor: Dr. Wai-Tong (Louis) Fan

18. Reconstructing population histories through the conditional genealogy under a multiple merger coalescent model

Alicia Zhang^{*}, *Massachusetts Institute of Technology*

An important goal in population genetics is to infer the history of populations using present-day genetic data. Here, we examine the effect of highly reproductive events (HREs) within a diploid population-genetic model, where occasionally a single pair of individuals has some number of offspring on the order of the population size. Specifically, we study the case where the population size tends to infinity. The gene genealogy of a sample of the population is characterized by a standard Kingman coalescent interrupted by HREs whose times are determined by a Poisson point process. First, we present an algorithm for simulating this model. Next, we examine specifically the expected height of the coalescent tree conditioned on the first few HRE time points, as opposed to the whole process. Building upon previous literature, we compute the expected pairwise coalescence time conditioned on the first few time points. By combining (1) our knowledge of the number of time points necessary to determine the expected height up to some small error and (2) our computation of this height in terms of these time points, we hope to recover HREs from real-life genomic data.

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