

Student Talk Abstracts

Gordon Bogardus, Hamilton College

Baseball, Percentages, and Regression

Abstract: Baseballers love percentages and statisticians love regression, but the two don't always play nice. One problem is that percentages ignore the sample size, but sample size is crucial in determining the uncertainty inherent in the percentages. Ordinary least squares regression treats each percentage equally regardless of the sample size used to determine the percentage, and therefore ignores the uncertainty associated with each data point. In reality, percentages resulting from a large sample should be given greater weight than percentages from a small sample because the larger sample has less variability associated with it. An approach that allows sample size to be taken into consideration is weighted least squares regression, with weights chosen to be the sample standard deviations. My talk will start with an introduction to weighted least squares regression, explain why weighting by the sample standard deviation is appropriate, and illustrate the technique with examples from the 2016 Major League Baseball season.

Pheobe Cai, Hobart and William Smith Colleges

Constructing the Species Tree from the Gene Tree

Abstract: Constructing gene trees from DNA data and then building the species tree from the gene trees is traditionally how species trees are estimated. The traditional way of estimate species trees from gene tree are either too slow or not accurate. We introduced a quartet based species tree structure algorithm, which is more efficient and statistically consistent assuming evolution occurs under the coalescent model.

Sterling Campbell, Alfred University

Discrete Morse Theory for Medial Subdivision

Abstract: Let F represent a discrete Morse function on a simplicial complex L . If we subdivide L using medial subdivision, will F be conserved? Is there a bijection between the critical simplexes? Do the internal and external paths remain non-cyclic? We will answer these questions by presenting a method of construction that maintains the properties of the discrete Morse function when a simplicial complex is subdivided. This talk is on research completed during the SAM REU 2016 at Sam Houston State University under Dr. Brian Loft.

Ashley Case, SUNY Brockport

Extending the Applicability of the Lagrange Multipliers Method

Abstract: We will discuss how to use Lagrange Multipliers in the case of constraints given by inequalities.

Luke Ciminelli, Niagara University

Markov Chain Methods to Produce a Walking Bassline in Jazz Music

Abstract: Improvisation is essential to jazz music, and modeling aspects of improvisation has long been an interesting question in mathematics. Most of the literature on this topic focuses on analyzing or producing jazz solos, but there is another improvised element of jazz music that has garnered less attention: walking basslines. This talk will discuss the use of a probabilistic method (Markov chains) to produce a walking bassline. This is joint work with Dr. Chad Mangum.

Mark Curiel and Jacqueline Kane, Hobart and William Smith Colleges*Analysis of Phylogenetic Trees Used in Quantitative Trait Mapping*

Abstract: Determining the specific genes that cause genetic diseases and traits is a difficult process. Phylogenetic trees are used to inform statistical tests about the association between a particular trait and a single gene or multiple genes. Many genes among different species are identical. Thus, to associate a disease with a particular gene, genes that differ from others become essential. Genes where this event occurs are called SNPs (Single Nucleotide Polymorphism). Certain genetic factors may be discovered by looking into phylogenetic trees that correspond to the evolution of nucleotides. However, constructing accurate trees is challenging since there is limited local data, but a very large number of genes under consideration. We examine the accuracy of the tree reconstruction for each SNP data. Our goal is to determine any weakness in this current approach that would lead to a better algorithm for building local trees. We analyze models of these phylogenetic trees to establish their accuracy to real evolutionary data. Improved construction of local trees would dramatically improve our ability to identify SNPs, which may be the cause of a particular disease or trait.

Hui Duan, University at Buffalo, SUNY*A Comparison of Three Fractional Derivatives in Finite Difference Approximations to Fractional Differential Equations*

Abstract: In recent years, a number of numerical methods for solving fractional differential equations has been proposed. In this talk, we compare three different types of fractional derivatives, namely Riemann-Liouville, Caputo and Grünwald-Letnikov fractional derivatives and their low order finite difference approximations. In particular, a numerical study for the errors and oscillations by the three different fractional derivatives and a comparison of their performances will be presented. Numerical results illustrate that the Caputo and Grünwald-Letnikov derivatives will yield better approximations than the Riemann-Liouville derivative. For the impulsive fractional differential equation, we found and will present that the finite difference solution with the Riemann-Liouville derivative is oscillatory if the fractional order is small.

Emily Hedison, Hamilton College*Extensions of Rock-Paper-Scissors*

Abstract: The classic game Rock-Paper-Scissors is an example of a balanced tournament of three “weapons” in which each weapon beats exactly one other weapon and loses to exactly one other weapon. But what happens when we consider balanced tournaments of more than 3 weapons? Through the use of automorphism and permutation groups, recent work by Marc Chamberland and Eugene Herman have shown it is possible to determine the number of distinct, isomorphic and non-isomorphic balanced tournaments for larger number extensions of rock-paper-scissors. Further, we look at the use of Borromean rings to visually describe this phenomenon.

Shoshanna Longo and Hunter Collin, RIT*Comparison study of Adomian's Decomposition Method and Homotopy Perturbation Method for the Non-Linear Differential Equations*

Abstract: In this work, we compare the series solution obtained from the Adomian's Decomposition Method with the Homotopy Perturbation Method for the linear and non-linear differential equations originated from the engineering discipline. We are in the process of implementing the Picard's method in order to gage the efficiency and accuracy of both semi-analytical techniques. It is expected that the speed to convergence for the Adomian's Decomposition Method can be improved by appropriate modification into the standard algorithm.

Sean Lyons, Le Moyne College*Exploring NHL Team Styles and What Determines Success*

Abstract: I examine the effect of play style on how a team performs in the NHL. To classify team styles, I used general linear models, linear regressions, and principal components to create mathematical models that were able to classify a team's style. Using the results of the classification models, I found that a team's style does not strongly affect a team's success.

Jesse Maltese, Hobart and William Smith Colleges*Species Tree Estimation Under the Coalescent Model*

Abstract: Traditionally, gene trees created from DNA sequence data are used to estimate species trees. Under the coalescent model, we construct species trees with branch lengths directly from the DNA data itself, bypassing the step involving gene trees. We then estimate distances on the species tree between two taxa and use these distances to build species trees. Contradicting common intuition, we find that the distance between two taxa on a species tree could depend on more than the two taxa themselves.

Michael McDermott, Brendan O'Braitis, and Thomas Maurer, SUNY Oneonta*A History of the Mathematics Department at SUNY Oneonta*

Abstract: As part of a class project, we have produced a small documentary about the history of the mathematics department at SUNY Oneonta. The documentary consists of interviews conducted with four current mathematics professors within the department. The interviews were concentrated on the integration of new technologies and new courses to the department, as well as instructional methods that are found to be the easiest and most beneficial for the students at a collegiate level math class. The professors being interviewed are indicative of the changes over the years since they graduated from graduate school and were hired as professors. Reforms in the educational system and developments in educational technology that have impacted classrooms around the country are discussed in the film. This short film provides insight into the path of progress of educating the future mathematicians of today and tomorrow.

Hector Miranda, RIT*Domain of Possible Configurations for Planar 3 Body Problem*

Abstract: This work focuses on the planar three body problem (P3BP): consider 3 points in a plane M_1, M_2, M_3 with masses m_1, m_2, m_3 , moving under the mutual Newtonian attraction. To study this motion we use Jacobi's coordinates $(r_1, r_2, \phi_1, \phi_2)$ given by:

r_1 = distance between M_1 and M_2

r_2 = distance between the center of mass G_{12} (of masses m_1 and m_2) and M_3

ϕ_1 = angle between M_1M_2 and the x -axis

ϕ_2 = angle between $G_{12}M_3$ and the x -axis.

In these coordinates we write the moment of inertia I , the kinetic energy T , the force function U and the angular momentum c . We consider the following inequality, recently published, on the domain of configurations of the P3BP:

$$2I(U + h) - c^2 \geq \mu_1 \mu_2 r_1^2 r_2^2 \dot{\phi}$$

where μ_1, μ_2 depend on m_1, m_2, m_3 and $\phi = \phi_2 - \phi_1$.

We study the case when this inequality becomes an equality and we explore regions of possible motion for different values of the total energy, $h = T + U$, ($h > 0, h = 0, h < 0$). Moreover we use Mathematica to describe some qualitative features of the problem.

Dakota Morano, Niagara University*Predictions and Outcomes in the MLB*

Abstract: Predicting baseball statistics, mainly hits, runs, and wins, is the main purpose of this study. The research used R-stat, Sports Illustrated, and Baseball Reference to determine how many hits a team will get in a season and what their win percentage will be based on the total hits in that season and hits in each game. The results from this study had some large error but were able to predict some win percentages accurately. Team's total runs scored versus total hits was brought into consideration if the study is repeated to create a better model.

Erin Nannen, Ithaca College*Mathematical Symmetry in Poe's Work*

Abstract: Symmetry is an interesting mathematical concept for many reasons, particularly its unique ability to present itself throughout different realms. Different forms of symmetry can be found within nature, such as the symmetry of a snowflake or the petals of a flower or the spirals on a pine cone. Symmetry can be observed in the Fibonacci spiral which is used as a measure of proportionality and human beauty. Thus, it is no surprise that symmetry can be found in literature as well. Symmetrical objects are seen as a standard of beauty and thus for an author to employ symmetry throughout his or her work is no surprise. Some authors, however, are explicit in their use of such instruments of beauty, as evidence by their collections of work and even their statements about composition. Edgar Allan Poe is one notable author who uses different types of symmetry to impose a greater meaning on his literature.

Binh Nguyen, Hamilton College*What is the Hidden Markov Model? And How Does it Help Advance Our Understanding of Biology?*

Abstract: The Hidden Markov Model is a probabilistic model underlying the development of pattern-seeking applications, such as speech recognition. It is also gaining ground in the application to biological problems, such as the construction of genetic linkage maps, differentiation between coding and non-coding regions of DNA, and scoring sequence alignments. This talk will discuss the basic concepts behind the Hidden Markov Model, and how it is used in a particular example of multiple sequence alignments. In this particular application, a training set is first created by the assembly of a group of sequences that are known to be structurally or functional related. Second, the model size (i.e.: the number of acceptable states), preliminary probability value of each state transition, and preliminary probability value of each outcome given a particular state, are determined. Third, "training" of the model is performed by optimizing these probabilities so that a random output from the model is most likely a member of the original training set. Finally, this trained model is used to align test sequences to examine whether the structure underlying the training set is also present in these test sequences. The Hidden Markov Model provides a robust foundation to analysis studies concerning evolutionary relationship between different sequences.

Brandon Payne, Elmira College*The Similarities of Open and Closed Primaries through Fairness Criteria*

Abstract: This talk explores the theoretical and practical similarities between open and closed primary elections using "fairness criteria." We discovered that both election systems satisfied unanimity and near-decisiveness, were neither imposed nor dictatorships, and neither system satisfied the Condorcet and Independence of Irrelevant Alternatives criteria. We discuss the proofs of a selection of these results and their implications.

Michelle Persaud, SUNY Fredonia*Discovering Parallels Between Euclidean Constructions and Origami Constructions*

Abstract: What can we construct using origami? This is similar to the question “What can we construct using a straight edge and compass?” Euclid made the first attempt to axiomatize compass and straight edge constructions approximately 2500 years ago in his series of works, The Elements. 19th Century mathematicians used algebra to provide a framework for determining what is and is not constructible. Recently, mathematicians have used an isomorphic axiomatic and algebraic approach to determine what is foldable using origami. The goal of this presentation is to demonstrate how origami constructions can be axiomatized, and to determine what restrictions someone would face when creating an origami construction.

Michelle Piwonski, SUNY Brockport*The Probability that a Cubic Equation has Only Real Roots - The Special Cases*

Abstract: I will look at the probability that a cubic equation with one coefficient equal to 0 has all roots real.

Rachel Schank, SUNY Fredonia*Mathematical Group Theory and Triadic Harmony*

Abstract: Mathematical Group Theory allows us to talk about the cyclic structure of musical harmony by performing group actions on musical chords, which we limit to the major and minor triads. We will discuss two different group actions on the set of triads. In the end, when we embed them both in a larger group, we see how they are related.

John Steiner, SUNY Brockport*Approximation of Fractals*

Abstract: I will look discuss the approximate construction of fractals with an irrational self similarity factor.

Emmerson Zhaimé, Hamilton College*Using Cronbach's Alpha to Assess the Reliability of Alcohol Survey Questions*

Abstract: Cronbach's alpha is a measure used to assess the reliability, or internal consistency, of a set of scale or test items. It is most commonly used when you have multiple questions in a survey/questionnaire where the responses are on a Likert-type scale (such as Strongly Disagree to Strongly Agree), and you wish to determine if the responses are internally consistent. It is used in survey research in fields ranging from psychological research to medical studies, and may not be well known in the general statistics community. My study focuses on using Cronbach's alpha to explore the reliability of a set of questions asked of Hamilton College students in an Alcohol Survey Questionnaire administered to NESCAC schools in 2015.

Jenna Zomback, SUNY Geneseo*Colored Unlinking*

Abstract: In links with two components there are three different types of crossings: self crossings in the first component, self crossings in the second component, and crossings between components. Previous work by Peter Kohn has mostly not made this distinction between the different types of crossings. In this talk we examine the minimum number of crossing changes needed to unlink without changing the crossings between components. For this, we restrict our attention to unlinking two component links with linking number zero and both components unknotted. After observing how to unlink linking number zero links, we move on to changing links of nonzero linking number to designated base links.