AARMS-CMS Student Poster Session

SHOHEL AHMED, University of Alberta
Behaviorally Structured Consumer-Resource Dynamics

Animals adjust their behavior in response to physiological states to optimize the trade-off between energy acquisition and survival. Consistent individual differences in behavior, often referred to as animal personality, play a crucial role in shaping ecological and evolutionary dynamics, particularly in foraging behavior. Traditional approaches in behavioral and evolutionary ecology typically focus on average behavior, neglecting the significance of individual variability. This study examines the impact of consumer behavior on ecological dynamics, focusing on how variations in food availability influence behavioral strategies and ecosystem functioning. The diverse expression of behavioural changes in a population has the potential to influence the whole population. This phenomenon has been modeled using a variety of methods, including population compartment models. Rather than make use of discrete levels of expression, we propose a novel model that treats the behavioural phenotype as a continuous distribution. The result is a coupled system composed of an ordinary differential equation and a partial differential equation, with the dynamics associated with behavioural phenotypes modeled as a diffusion process. The resulting analysis avoids some of the difficulties of scaling to larger systems of equations and opens up the possibility of using other techniques available for the qualitative analysis of partial differential equations.

GRACE D'AGOSTINO, University of Guelph
Uncertainty Analysis of a River Quality Model

Uncertainty analyses were performed on a simple river quality model, the Streeter-Phelps equations, using parameter estimates, comparison theorems, and differential inequalities.

Model parameters in environmental systems are often non-constant and may only be known with some uncertainty. When parameters are not known exactly, the solution of the model cannot be obtained analytically or numerically.

The Streeter-Phelps equations are two partial differential equations describing the transport of pollutants, also called the biological oxygen demand (BOD), and dissolved oxygen in a river. In their original formulation, the model permits negative dissolved oxygen concentrations due to the lack of dependence of BOD degradation on available oxygen, marking a breakdown of the model. To remedy this, a dependence was imposed using the Monod function, creating a situation-adaptive transition of solutions between when oxygen is abundant and when oxygen is limited.

To satisfy the quasi-monotonicity condition of the Comparison Theorem for Quasimonotone Increasing Systems, the system was redefined in terms of the oxygen deficit, which is the difference in the saturation concentration and the dissolved oxygen concentration. Possibilistic regions in which the solution of the model with unknown parameters exist were constructed.

Parameter estimates were chosen arbitrarily based on data reported by the Grand River Conservation Authority for illustrative purposes. Plots were produced and limitations were discussed.

AMAURY DE BURGOS, University of Calgary
The length of cyclic algebras

Cyclic algebras, introduced by Leonard Eugene Dickson in 1906, were one of the earliest examples of non-commutative division algebras over a field. A notable numerical invariant of any algebra over a field is its length, defined as the length of its longest chain of linear subspaces. In 2016, the length of 4-dimensional cyclic algebras was proven to be 2 (Guterman & Kudryavtsev). More recently, in 2021, the length of cyclic algebras of dimension 9, 16, and 25 was stated to be 4, 6, and 8 respectively (Miguel). Through the use of two counterexamples, we show these latter values are ill-derived, meaning the length of cyclic algebras of dimension greater than 4 is still an open problem. In pursuit of solving this open problem, we construct an infinite family of cyclic division algebras and give a lower bound on the length of its members.

XINWEN DING, University of Toronto
Walk-on-Interfaces: A Monte Carlo Estimator for Elliptic Interface Problem

Elliptic interface problems arise in many areas of science and engineering, modeling heterogeneous materials whose physical properties change abruptly across internal boundaries. Computing solutions to these problems efficiently and accurately remains challenging, especially in domains with multiple irregular interfaces. In this poster, we present Walk-on-Interfaces (WoI), a grid-free Monte Carlo estimator for Neumann elliptic interface problems with general flux jump conditions. Unlike many numerical schemes, WoI maintains uniform accuracy throughout the domain and avoids near-interface singularities. Moreover, gradients of the solution can be estimated at almost no additional cost by differentiating the Green's function within WoI. Taking a scientific machine learning approach, we train a deep neural network to filter out high-frequency sampling noise, yielding a smooth and continuous representation of the solution. The resulting method is highly parallelizable, scales naturally to high dimensions, and can solve problems that are intractable for traditional numerical solvers. Numerical experiments demonstrate the effectiveness of the approach and highlight its potential for real-world applications.

TAN PHUONG DONG LE, Department of Applied Mathematics, University of Waterloo
Stable Mesh-Free Variational Radial Basis Function Approximation for Elliptic PDEs and Obstacle Problems

We present a comprehensive study of radial basis function (RBF) network approximations for elliptic and obstacle-typed boundary value problems under a variational formulation. Our focus is on practical accuracy, robustness and efficiency across a range of partial differential equations. To address ill-conditioning in dense systems, we apply truncated singular value decomposition (TSVD) in the linear regime and quantify its effect on stability and accuracy trade-offs. Numerical experiments on benchmark problems demonstrate fast error decay and high accuracy. We map the trade-off between approximation and truncation errors for practical settings for number of basis functions N, oversampling ratio ζ and truncation threshold τ. Compared with other numerical methods, RBF variational approach would deliver competitive accuracy for boundary value problems.

ANTUN NIKOLA DVORSKI, University of Toronto
A new proof of Baernstein's convolution inequality on the unit circle using geometric flow

The well-known Riesz-Sobolev inequality (or Riesz rearrangement inequality) asserts that for non-negative measurable functions f, g, and h on $\mathbb{R}^n$, the quantity $f * g * h(0)$ does not decrease when f, g, and h are replaced with their symmetric decreasing rearrangements. There is an analogous convolution inequality for non-negative measurable functions on S^1 due to Albert Baernstein, for which we provide a novel proof using a flow of measurable subsets of S^1.

JOEY FINGOLD, University of Guelph
Latent Gaussian Importance Sampling for Thinned Poisson Autoregressions

Count time series have gained popularity in infectious disease modelling due to their connection to traditional mechanistic transmission models and their straightforward implementation using both maximum likelihood and Bayesian paradigms. However, observed data corresponding to daily infections is subject to under-reporting, where fewer than the true number of infected individuals are reported as sick. Thus, for each time series of data, Y, we have an associated time series of unknown true counts, X.

Conducting inference on these unknown counts is challenging as the X's are serially correlated integer-valued unknowns. State-of-the-art methods like Hamiltonian Monte Carlo utilize gradient-based optimization and thus do not apply due to the count-valued unknowns. We consider an approximate model defined by a latent Gaussian time series that imposes continuity in the parameter space and a non-bijective mapping that recovers the intended discrete marginal distributions of the target model whilst preserving the autocorrelation structure in the approximate model. We further introduce a self-normalized importance sampling approach to weight these observations to improve the estimation of expectations under the target posterior distribution.

SHAN GAO, University of Alberta
Outbreak or Not? A Framework for Detecting Infectious Disease Outbreaks

Forecasting the occurrence and absence of novel disease outbreaks is essential for disease management, yet existing methods are often context-specific, require a long preparation time, and non-outbreak prediction remains understudied. To address this gap, we propose a novel framework using a feature-based time series classification (TSC) method to forecast outbreaks and non-outbreaks. We tested our methods on synthetic data from a Susceptible–Infected–Recovered (SIR) model for slowly changing, noisy disease dynamics. Outbreak sequences give a transcritical bifurcation within a specified future time window, whereas non-outbreak (null bifurcation) sequences do not. We identified incipient differences, reflected in 22 statistical features and 5 early warning signal indicators, in time series of infectives leading to future outbreaks and non-outbreaks. Classifier performance, given by the area under the receiver-operating curve (AUC), ranged from 0.99 for large expanding windows of training data to 0.7 for small rolling windows. The framework is further evaluated on four empirical datasets: COVID-19 incidence data from Singapore, 18 other countries, and Edmonton, Canada, as well as SARS data from Hong Kong, with two classifiers exhibiting consistently high accuracy. Our results highlight detectable statistical features distinguishing outbreak and non-outbreak sequences well before potential occurrence, in both synthetic and real-world datasets presented in this study.

CAMERON JAKUB, University of Guelph
Depth Degeneracy in Neural Networks: Vanishing Angles in Fully Connected ReLU Networks on Initialization

Despite remarkable performance on a variety of tasks, many properties of deep neural networks are not yet theoretically understood. One such mystery is the depth degeneracy phenomenon: the deeper you make your network, the closer your network is to a constant function on initialization. In this paper, we examine the evolution of the angle between two inputs to a ReLU neural network as a function of the number of layers. By using combinatorial expansions, we find precise formulas for how fast this angle goes to zero as depth increases. These formulas capture microscopic fluctuations that are not visible in the popular framework of infinite width limits, and leads to qualitatively different predictions. We validate our theoretical results with Monte Carlo experiments and show that our results accurately approximate finite network behaviour. We also empirically investigate how the depth degeneracy phenomenon can negatively impact training of real networks. The formulas are given in terms of the mixed moments of correlated Gaussians passed through the ReLU function. We also find a surprising combinatorial connection between these mixed moments and the Bessel numbers that allows us to explicitly evaluate these moments.

VINAY JOSHY, University of Guelph
Sparse Group Lasso for Variable Selection in Finite Gaussian Mixture Regression Models

When analyzing heterogeneous data with latent subpopulations, finite mixture regression (FMR) models are effective as they allow for variations in regression coefficients across mixture components. Variable selection is important at two levels: (1) at the group level by removing completely irrelevant covariates across all subpopulations and (2) at the individual level by removing irrelevant covariates within each subpopulation. However, existing variable selection methods for FMR focus solely on individual-level selection using the least absolute shrinkage and selection operator (LASSO), providing no mechanism for group-level variable elimination. We introduce a sparse group LASSO regularization method that performs efficient variable selection at both levels simultaneously in finite Gaussian mixture regression models. We developed a novel optimization procedure through a Majorization-Minimization algorithm. Simulation studies demonstrate our proposed method's effectiveness in retaining relevant covariates and accuracy in clustering observations into subpopulations. We apply our proposed method to a Chiroptera (bat) dataset exhibiting morphological heterogeneity for identifying relevant environmental and morphological covariates that influence bat forearm development.

LEXY LAWRYSHYN, University of Guelph
A Nonlinear ODE Model of Butyrate-Tumour-Immune Cell Dynamics in Colorectal Cancer

Colorectal cancer progression is strongly influenced by metabolic signals from the gut microbiome, yet the underlying mechanisms remain poorly understood. In particular, the short-chain fatty acid butyrate - produced by fiber-fermenting gut bacteria - has been shown to inhibit cancer cell proliferation while supporting the growth and function of healthy colonocytes and immune cells. We formulate a system of non-linear ordinary differential equations to describe key metabolic and immunological interactions between butyrate, colorectal cancer cells and host cell populations. The parameter space is explored through steady-state and sensitivity analyses, and preliminary simulations illustrate the emergence of varying dynamical behaviour driven by butyrate availability.

ERICA LIU, University of Waterloo

Toric Compactifications and Critical Points at Infinity in Analytic Combinatorics

The field of Analytic Combinatorics in Several Variables (ACSV) provides powerful tools for deriving asymptotic information from multivariate generating functions. A key challenge arises when standard saddle-point techniques fail due to the presence of critical points at infinity (CPAI), obstructing local analyses near singularities. Recent work has shown that Morse-theoretic decompositions remain valid under the absence of CPAI, traditionally verified using projective compactifications. We present a toric approach to compactification that leverages the Newton polytope of a generating function to construct a toric variety tailored to the function's combinatorial structure. This refinement not only tightens classification of CPAI but also enhances computational efficiency. Through concrete examples and an introduction to tropical and toric techniques, we will demonstrate how these methods clarify the asymptotic landscape of ACSV problems, especially in combinatorially meaningful settings. This poster draws on joint work studying toric compactifications as a bridge between algebraic geometry and analytic combinatorics.

RACHANA MANDAL, University of Guelph

Modelling and Simulation Experiments on Directed Movement of Bacteria in Aqueous Medium with Counter-Diffusive Substrate Uptakes

Particulate Organic Matter(POM), sediment grains, microplastics serve as substrates for various microorganisms, including planktonic bacteria, which are suspended in aqueous medium. Planktonic bacteria colonize particles' surfaces by forming a bacterial biozone and consume released nutrients to stimulate growth. For sinking particle plume in marine ecosystems, this bacterial activity and reshaping of the carbon plume affect marine carbon pump and thus carbon sequestration in deep sea. The nutrient gradient drives accumulation of bacteria as a response to directed movement. We develop a mathematical model that describes the planktonic bacterial growth and lysis, movement of cells by diffusion and a chemotaxis-like directed movement and perform simulation experiments. We assume that the biomass growth depends on the concentration of substrates, such as carbon, an electron donor, and oxygen, an electron acceptor. Carbon, sourced from a particle surface wall, diffuses into domain from one boundary, while oxygen enters from opposite boundary, a distant source, establishing a counter-diffusion system. These two growth-limiting substrates control direction of transport of cells and bacterial colony accumulates in regions with favorable growth conditions. The Keller-Segel-Patlak type one-dimensional model with two stimuli consists of three non-linear PDEs. The transport terms in bacterial concentration equation are discretized in space using a flux-conservative-finite-volume method and substrate equations are discretized using library 'ReacTran' from 'R'. Then three discretized one-dimensional equations are solved numerically using a time-adaptive method from 'R'. The energy estimate method is applied to linearised system around uniform steady state to explore the long and short time behaviour of bacterial concentration.

ARION OKUBO, University of Toronto

Explicit Estimates for the Size of the Markoff mod p Cage

The Markoff equation is given by $X^2+Y^2+Z^2 = 3XYZ$ and the positive integer solutions to this equation are called Markoff triples. Involutions can be defined on the set of Markoff triples by fixing two coordinates and finding the other root of the resulting quadratic. The group generated by these involutions and coordinate permutations, called the Vieta group, acts on the set of Markoff triples, and the graph defined by this action is known to be connected. In 1991, Baragar conjectured that the same holds modulo any prime p. Since the action of the Vieta group commutes with reduction mod p, this would imply that every mod p solution to the Markoff equation has an integer lift. In 2015, Bourgain, Gamburd, and Sarnak made progress toward this conjecture by proving that a subgraph called the cage is always connected. Computations suggest that roughly 80% of triples lie in the cage, but explicit bounds have been difficult to find. We provide an explicit lower bound for the size of the cage for primes p where $p+1$ has sufficiently large valuation. We also estimate the size of the cage for all primes in terms of the Euler totient function under a reasonable heuristic assumption. Our work also yields practical conditions for a Markoff triple to lie in the cage.

KENNETH SHEN, Carleton University Math Enrichment Centre
Families of rational-sided triangles with the same area and perimeter

Can two non-congruent triangles share the same area and perimeter? While it may seem impossible at first, we soon find that for any non-equilateral triangle with *real*-valued sides, there exist infinitely many other triangles with the same area and perimeter. This raises the following question: what would an analogous result look like for *rational*-sided triangles?

We introduce the idea of *confined* triangles: rational-sided triangles for which only finitely many other non-congruent rational-sided triangles share the same area and perimeter. A triangle is *isolated* if no such companions exist. We prove that confined *scalene* triangles must be isolated, and completely characterize the structure of confined triangles, showing that only three configurations are possible: a single isolated isosceles triangle, exactly two isosceles triangles, or a single isolated scalene triangle.

Finally, we prove that the asymptotic proportion of confined triangles that are scalene tends to zero.

JOHN HUNN SMITH, University of Waterloo
Explicit Diagonal Asymptotics of Symmetric Multi-Affine Rational Functions via ACSV

Multivariate sequences are often best studied via their generating functions, which are multivariate power series whose coefficients are the terms of the sequence. Analytic combinatorics in several variables (ACSV) provides a framework for deriving asymptotics for certain "diagonal" univariate subsequences using these generating functions and tools from topology, complex analysis, and algebraic geometry. In this work we show how to use ACSV to derive explicit asymptotics for diagonals of multivariate rational functions whose denominators are symmetric (invariant under permutations of the variables) and multi-affine (linear in each variable). By "explicit" we mean that all quantities involved in the asymptotic formula are effectively computable, and we give our asymptotic not in terms of a Big-O term, but instead in terms of explicit constants which bound the error between our asymptotic and the true sequence of interest. Applications will be discussed, including coefficient positivity problems which are concerned with detecting whether a sequence, univariate or multivariate, has all positive terms.

AIDEN WILLIAM JAMES TAYLOR, University of Calgary
Multiresolution Analysis and Machine Learning Methods for the Classification of Auroral Images

The Aurora Borealis (or Northern Lights) is a natural phenomena regularly observed in North America which has fascinated humans for thousands of years. Even today, this phenomena gains a great deal of attention from the general public, media outlets, tourists, and scientists, where the latter have been collecting data on auroral behaviour for many years, most notably in the form of *all-sky images* (ASI). In recent years, there has been a push to label ASI data with the specific classifications that an aurora can take, e.g. arc, diffuse, discrete, etc..., which gives rise to a particularly interesting interdisciplinary *image classification problem* that many believe would greatly benefit from the usefulness of *machine learning* (ML). For our purposes, we intend to use this classification problem as an avenue to highlight the compression possibilities that *wavelet transforms* offer in the preprocessing stage of ML by implementing a proposed *discrete projection algorithm* (DPA) that can calculate the coefficients of a particular wavelet basis efficiently and accurately. The resulting wavelet coefficients can then be used as input to a *convolution neural network* (CNN), which in our case will be trained and validated on the Oslo aurora THEMIS (OATH) dataset. We hypothesize that the combination of this DPA with even a simple CNN will result in classification accuracies $>$ 80% and have tangible improvements in the efficiency of the preprocessing stage.

XUEMENG WANG, Simon Fraser University

Christoffel Adaptive Sampling for Sparse Random Feature Expansions

Random feature models are powerful tools for approximating high-dimensional functions and solving PDEs. Sparse random feature expansion (SRFE) enhances these methods by incorporating sparsity and compressive sensing, which is especially beneficial in data-scarce settings. We integrate active learning with SRFE by using the Christoffel function to guide an adaptive sampling process, dynamically selecting informative samples. Drawing random samples via the Christoffel function allows a weighted least-squares approximation with near-optimal sample complexity. Numerical experiments show that Christoffel adaptive sampling maintains high accuracy, demonstrating strong potential for scientific computing.