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14th Americas Conference on

Differential Equations and Nonlinear Analysis

PROGRAM

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Conference Schedule

Registration and all talks will be in Middlesex College Building (MC)

Monday, August 3

08:30–08:50	**Registration in the lobby of MC**	
08:50–09:00	**Opening Ceremony in Room MC110**	
09:00–10:00	**Sell Memorial Lecture I by Michael Jolly** — chaired by Yingfei Yi	
10:00–10:30	**Coffee break**	
	S1-1 in Room MC110 Chair: Yuming Chen	S1-2 in Room MC105 Chair: Wenying Feng
10:30–11:00	Jacques Belair :	Stephen Anco
11:00–11:30	Zhisheng Shuai	Junping Shi
11:30–12:00	Connell McCluskey	Jose R. Quintero
12:00–12:30	Yuan Yuan	Yixiang Wu
12:30–14:00	**Lunch Break**	
14:00–15:00	**Plenary talk by Andrea Ceretani** –chaired by rene Fonseca	
15:00–15:10	**Photo**	
15:10–15:40	**Coffee break**	
	S1-3 in Room MC110 Chair: Jacques Belair	S1-4 in Room MC105 Chair: Junping Shi
15:40–16:10	Irene Fonseca	Bei Hu
16:10–16:40	Wenying Feng	Russell Milne
16:40–17:10	Aidan Backus	Yuanwei Qi
17:10–17:40	Kunquan Lan	Yuming Chen
17:40–19:00	Reception	

Tuesday, August 4

08:40–09:00	**Registration in the lobby of MC**	
09:00–10:00	**Plenary Lecture by Jianhong Wu**—chaired by Jose Quintero	
10:00–10:30	**Coffee break**	
	S2-1 in Room MC110 Chair: Xiaoqiang Zhao	S2-2 in Room MC105 Chair: Adrian Lam
10:30–11:00	Rachidi Salako	Zhongwei Shen
11:00–11:30	Xinzhi Liu	Yingfei Yi
11:30–12:00	Ke Zhang	Chengzhang Fu
12:00–12:30	Qingwen Hu	Fanze Kong
12:30–14:00	**Lunch Break**	
14:00–15:00	**Sell Memorial Lecture II by Michael Jolly** —chaired by Jianhong Wu	
15:00–15:30	**Coffee break**	
	S2-3 in Room MC110 Chair: Xinzhi Liu	S2-4 in Room MC105 Chair: Zhongwei Shen
15:30–16:00	Sue Ann Campbell	Adrian Lam
16:00–16:30	Xiaoqiang Zhao	Kyung-Han Choi
16:30–17:00	Felicia Magpantay	Yu Jin
17:00–17:30	Xueying Wang	Lin Wang
17:30–18:30	**transport to banquet restaurant**	
18:30–20:30	**Banquet**	

Wednesday, August 5

08:50–9:00	**Welcome from the dean and the chair**	
09:00–10:00	**Plenary talk by Rustum Choksi**—chaired by by Olga Trictchenko	
10:00–10:30	**Coffee break**	
	S3-1 in Room MC110 Chair: Falicia Magpantay	S3-2 in Room MC105 Chair: Kunquan Lan
10:30–11:00	Yao Li	Jack Hughes
11:00–11:30	Na Yu	Chunyi Gai
11:30–12:00	Felix Ye	Carlos Roman
12:00–12:30	Sirou Wang	Zhaosheng Feng
12:30–14:00	**Lunch Break**	
Aferternoon	**Free for networking, collaboration and excursion etc.**	

Thursday, August 6(talks marked with * are contributed talks with 20 minutes duration)

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10:00–10:30	**Coffee break**	
	S4-1 in Room MC110 Chair: Rachidi Salako	S4-2 in Room MC105 Chair: Wenjing Zhang
10:30–11:00	Jocirei Dias	Michael Y. Li
11:00–11:30	Wilten Nicola	Rongsong Liu
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16:00–16:30	William Barker	Marco Tosato
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Modelling the effect of social distancing on spreading and controlling infectious disease with Point Pattern Process

Sayeda Irin Akter
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This work explores the spatial dynamics of disease transmission using Point Pattern Processes (PPPs) and distance-dependent infection rate within a Susceptible-Infectious-Removed-Susceptible (SIRS) framework. By modeling individuals as points in a continuous space, we examine how social distancing and spatial separation influence the spread of the virus. The infection rate is not uniform but varies with the distance between individuals, simulating the real-world effects of reduced contact through interventions like social distancing. We use mathematical models and point pattern analysis to investigate different spatial configurations, from clustered (high transmission risk) to dispersed (reflecting effective social distancing). The pair correlation function g(r) is employed to capture spatial clustering, while pair approximation simplifies the modeling of spatial interactions by considering the effect of pairwise interactions. Prior to social distancing, high P_I probability of infection values are observed due to frequent close contacts, leading to clustered transmission patterns. After implementing social distancing, P_I decreases as individuals are more dispersed, reducing the likelihood of infection. This approach allows us to quantify the impact of public health measures on transmission dynamics, providing insights for optimizing interventions to control the spread of disease.

Dynamics of cell cycle models with quiescence and time delay due to interphase

Shaza Alsibaai
Queen's University, Canada
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The cell cycle is a tightly regulated biological process that governs cell growth and division. In this talk, I will present two mathematical models of cell cycle dynamics incorporating cell quiescence and a time delay associated with interphase. We consider both a constant-delay model, in which the interphase duration is fixed, and a state-dependent delay model, in which the interphase duration increases with the number of mitotic cells due to competition for limited resources. For the constant-delay model, we show that when the death rate of mitotic cells exceeds twice their proliferation rate ($\mu_1 > 2b_1$), the trivial equilibrium is the only biologically feasible steady state and is asymptotically stable. When $\mu_1 < 2b_1$, a critical interphase duration, τ^*, separates extinction from unbounded growth, and a one-parameter family of equilibria emerges at the critical value. These analytical results are further supported by numerical bifurcation analysis using DDE-Biftool in MATLAB. We then investigate the corresponding state-dependent delay model, in which the interphase duration depends on the total number of mitotic cells, $\tau = \tau(U)$. Numerical simulations and bifurcation analysis indicate that, for a range of parameter values, the system admits a positive bounded equilibrium that is absent in the constant-delay model, demonstrating that state dependence fundamentally alters the system dynamics. Establishing the non-negativity of solutions for

the state-dependent model presents additional analytical challenges. I will conclude by discussing the current results and the remaining open problems.

Weak compactons of nonlinearly dispersive KdV and KP equations

Stephen Anco
Brock University, Canada
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The gKdV and gKP equations provide models of physical phenomena exhibiting nonlinearity and dispersion, such as shallow water waves, matter-wave pulses in Bose-Einstein condensates, ion-acoustic waves in plasmas, and ferromagnets. In this talk, a weak formulation is presented for a nonlinearly dispersive generalization of the gKdV equation having compacton solutions. With this formulation, explicit weak compacton solutions are derived, including ones that do not exist as classical (strong) solutions. Similar results are obtained for a nonlinearly dispersive generalization of the gKP equation in two dimensions, which possesses line compacton solutions.

Optimal transport and the nonsmooth Plateau problem in split signature

Aidan Backus
University of Toronto, Canada
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A theorem of Kim, McCann, and Warren (2010) and McCann, Pass, and Warren (2012) asserts that the graph of an optimal transport map is a volume-maximizing spacelike rectifiable current for a certain natural split-signature pseudo-Riemannian metric. We generalize this theorem to various situations in which the cost function is not assumed C^2, including the square-distance cost on $C^{1,1}$ Riemannian surfaces, and certain "translucent" obstacle costs. This is joint work with Mitchell Gaudet and Robert McCann.

Traveling waves in Lotka–Volterra systems with delayed diffusion

William Barker
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This talk examines traveling wave solutions for Lotka–Volterra-type reaction–diffusion systems in which the diffusion terms depend on past states. The traveling-wave reduction produces a coupled system containing delayed second derivatives and nonlinearities that do not satisfy standard quasimonotonicity conditions. By introducing partial quasimonotonicity and constructing suitable upper and lower solutions, an iterative framework is developed to establish the existence of traveling waves. The analysis also identifies conditions on the wave speed and model parameters that ensure convergence of the wave profiles to the prescribed equilibria.

Compliance and awareness in an infectious disease model

Jacques Bélair
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Management of the COVID-19 pandemic required in its early stages the deployment of non pharmaceutical interventions (NPIs) [social isolation, physical distancing, mask-wearing, hand-washing]. We consider a compartmental model of disease propagation in which information is the infection: knowledge of, and compliance with, measures limiting the propagation of an infectious disease (such as non-pharmaceutical interventions (NPIs)) are modeled as dynamic parameters. Conditions for the existence of multiple stable equilibria will be discussed as well as the consequences for the control of the infection.

A New Approximate Greedy Best Response Dynamics for Generalized Nash Equilibrium Problems

Benjamin Benteke
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Generalized Nash Equilibrium Problems (GNEPs) provide a framework for modeling strategic interactions among multiple decision-makers with coupled constraints. Solving GNEPs is challenging due to nonconvexity, equilibrium existence issues, and the possible infeasibility of players' strategy sets. This paper proposes a simple and practical local search method for solving GNEPs, termed Adaptive Greedy Local Search (AGLS). The proposed method combines local search with adaptive player updates guided by a Gauss-Southwell selection rule. AGLS is evaluated on a diverse collection of benchmark problems, including jointly-convex and general GNEPs, as well as parameterized GNEPs. The method is further validated on real-world GNEPs, including autonomous racing, network switching, oligopoly models, and electricity markets. Computational results show that AGLS successfully identifies generalized Nash equilibria (GNEs) across a broad range of instances, including challenging cases where classical approaches such as best-response dynamics and Gauss–Seidel methods exhibit cyclic behavior or fail to converge. In addition, we compare two variants of AGLS: AGLS with random actions and AGLS with best-response directions, using the success rate (SR) and percentage of distinct points (PDP) as performance metrics. The results indicate that AGLS with random actions generally outperforms AGLS with best-response directions in terms of SR, which reflects convergence success, and PDP, which measures diversity, in most cases. The only exception is Example 2 for jointly-convex GNEPs, where AGLS with random actions achieves a lower SR. For GNEPs with non-shared constraints, AGLS with random actions consistently achieves higher SR and PDP than AGLS with best-response directions, indicating superior convergence and diversity performance. For real-world GNEPs, both variants successfully identify solutions, with AGLS random actions recovering multiple equilibria when they exist. Overall, AGLS offers a flexible framework for solving GNEPs with different constraint structures and solution characteristics.

Lipschitz equivalence of linear flows

Arno Berger
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Two flows on a finite-dimensional normed space X are Lipschitz equivalent if some homeomorphism h of X that is bi-Lipschitz near the origin preserves all orbits, i.e., h maps orbits onto orbits. This talk outlines a new approach to the complete Lipschitz classification of all linear flows on X. Though requiring only elementary analytic tools, this approach crucially draws on several properties of linear flows that are rather subtle and not shared by any wider class of flows on X. (Joint work with A. Wynne.)

An investigation of the interaction between atmospheric internal gravity waves and surface water waves

Mingyao Cai
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We examine a coupled model that describes atmospheric internal gravity waves and surface water waves. The model is based on an anelastic approximation for internal gravity waves in an upper layer and shallow water equations for surface water waves which give a lower boundary condition for the internal waves. This configuration is relevant for situations such as the generation of atmospheric waves by tsunami or other ocean surface waves and for situations where there are coupled atmosphere-ocean interactions. We consider different configurations including cases where multiple surface waves collide, interact and generate gravity wave modes, which in turn interact with each other and with the background atmospheric flow. We present a weakly-nonlinear analysis which gives asymptotic approximations that are compared with our numerical solutions. Our results include the effects of the nonlinear wave interactions on the background atmospheric wind and temperature. Joint work with L. J. Campbell.

A delay differential model for antiviral treatment and rebound dynamics

Wenben Cai
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Viral rebound - when SARS-CoV-2 viral load rises again after treatment to levels that can make patients infectious—has become an important concern during the use of antivirals such as Paxlovid. To understand how rebound affects transmission after treatment, we built a delay-differential model that incorporates key features of COVID-19 infection, including when treatment begins relative to symptom onset and how long treatment lasts.

Our simulations explore different assumptions about how infectious people are during a rebound period. We find that rebound makes up only a small fraction of treated cases when treatment delayed after symptom onset or when treatment is extended beyond the standard five-day course. However, as more symptomatic individuals receive treatment, the infectiousness of rebound cases becomes a crucial driver of overall spread. A short, five-day course can unintentionally increase total infections if rebound cases are highly transmissible, whereas extending treatment to eight days sharply reduces the contribution of rebounds to community transmission.

Overall, both delaying treatment initiation and lengthening treatment duration reduce the likelihood of rebound, revealing a trade-off between suppressing early infectiousness and preventing post-treatment viral resurgence. These results emphasize the need to consider rebound risk when designing antiviral treatment strategies to protect individuals and improve population-level control of COVID-19.

The eigenvalue spectrum of distributed delay differential equations with large mean delay

Sue Ann Campbell
University of Waterloo, Canada
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In this work we study the eigenvalue spectrum of linear delay differential equations with a uniformly distributed delay kernel. We carry out asymptotic analysis in the limit of large mean delay to show that the spectrum splits into (i) a strong critical spectrum referring to a finite set of isolated, pure imaginary eigenvalues that are unaffected by delay, (ii) an asymptotic strong spectrum consisting of a finite set of eigenvalues with limits that are determined by non-delayed terms in the model, and (iii) a pseudo-continuous spectrum consisting of infinitely many eigenvalues that limit on the imaginary axis, with real parts that scale linearly with the delay. This behaviour is similar to the fixed delay case, but the distributed delay introduces additional spectral features, including a countably infinite number of horizontal asymptotes in the pseudo-continuous spectrum at frequencies inversely proportional to the width of the distribution. We validate our theoretical results through numerical studies of several examples and compare our findings with fixed-delay results from the literature. Finally, we apply the results to study the stability and bifurcations of a Wilson-Cowan model with a delayed self-coupling, large mean delay, and homeostatic plasticity. This is joint work with Isam Al-Darabsah and Bootan Rahman.

Plenary talk—Fractional Laplacians beyond constant order: What happens when the order varies in space?

Andrea Ceretani
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The fractional Laplacian is a nonlocal counterpart of the classical Laplace operator and has become a fundamental tool in the mathematical modeling of diffusion phenomena, image reconstruction, geophysical processes, among many others. Models based on a constant fractional order have been remarkably successful both from the modeling and analytical viewpoints. However, several applications naturally lead to situations in which the appropriate fractional order may vary across the domain. A natural question is therefore: what happens when the fractional order is allowed to vary in space?

Motivated by this question, we introduce a fractional Laplacian with spatially variable order on bounded domains. The construction is inspired by the extension framework of Caffarelli–Silvestre and Stinga–Torrea, where the fractional Laplacian is realized as a Dirichlet-to-Neumann operator associated with a degenerate elliptic problem in one additional dimension. The analysis of the extended problem naturally leads to weighted Sobolev spaces whose weights may fail to belong to the Muckenhoupt class. This prevents the direct use of many classical results and raises new challenges in the analysis of trace spaces and Poincaré-type inequalities.

Despite these difficulties, the extension approach still provides a natural path toward defining and analyzing a variable-order fractional Laplacian on bounded domains. In this talk, we describe the main ideas behind this construction, including the study of the associated Poisson problem, trace regularity, and Poincaré-type inequalities under suitable assumptions on the variable order.

The results presented in this talk were obtained in collaboration with Carlos N. Rautenberg (George Mason University, USA).

Propagation Dynamics of Asymptotically Smooth Monotone Systems

Jing Chen
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This talk concerns with monotone systems on spaces of vector-valued functions, which are defined on group bundles. Under the assumption of asymptotic smoothness, we develop theory on their asymptotic propagation. By refining geometrical features of the propagation region and extending the dynamical method of Weinberger, we obtain the asymptotic annihilation, asymptotic persistence, and upward convergence for discrete-time monotone systems with pointwise asymptotic smoothness. Then we provide a continuous-discrete orthogonal decomposition of the additive group. We also introduce conditions of interval uniform asymptotic smoothness(along continuous directions) and pointwise uniform asymptotic smoothness condition (along discrete directions). Under these conditions, we establish the existence of traveling waves for discrete-time monotone systems. The obtained results are applied to a lattice-diffusion-impulse system on a cylinder with the Neumann boundary condition.

Impact of tumor anti-immunity: Dynamics of a simple tumor-immune model with two-stage lymphocytes

Yuming Chen
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To investigate the impact of tumor anti-immunity on tumor development, we develop a simple tumor-immune model which incorporates the two-stage development of T lymphocytes (naive and effector cells). With qualitative analysis, we derive threshold conditions for the existence and stability of the tumor-free and tumor-present equilibria. Combining these results with quantitative analysis, we find that tumor anti-immunity significantly enriches the dynamical behaviors which are absent in models without tumor anti-immunity. These behaviors include up to two positive equilibria, stability switching phenomena, Hopf bifurcations (both supercritical and subcritical),

homoclinic bifurcations, and saddle-node bifurcations of periodic solutions. Quantitative bifurcation analysis with the intensities of tumor anti-immunity and anti-tumor immunity as bifurcation parameters not only uncover complex dynamic behaviors of the model but also demonstrate discontinuous transitions in asymptotic states, such as transitions from the tumor-free equilibrium to a tumor-present equilibrium and from an equilibrium to a periodic oscillation. The results obtained highlight the significance of incorporating tumor anti-immunity response in comprehensively capturing the tumor-immune dynamics. They also provide new theoretical insights into tumor heterogeneity, immune escape, and potential therapeutic strategies targeting tumor immunosuppression.

Global continuation of a periodic solution to a coupled delayed algebraic-differential equation

Tianyu Cheng
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We consider a hybrid system of delay-algebraic equations motivated by an epidemic model involving both disease transmission and behavior adaptation, and we show how the $S1$-degree theoretic approach towards global bifurcations of nonlinear systems with two parameters can be adopted to develop a global Hopf bifurcation theory for such a hybrid system. We use the epidemic models, previously developed to explore mechanisms of multiple waves during the acute phase and post-pandemic phase of an emerging disease, to illustrate the effectiveness and challenges of applying the global Hopf bifurcation theory to examine the global continuation of local Hopf bifurcations when the critical parameter moves away from the critical value for the onset of the oscillation. We also show how a 3-dimensional ordinary differential competitive system with built-in cyclic symmetry and embedded negative loops arises naturally from our global Hopf bifurcation study.

The lingering phenomenon and pattern formation in a nonlocal population model with a cognitive map

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The rates at which individuals memorize and forget environmental information strongly influence their movement paths and long-term space use. To understand how these cognitive time scales shape population-level patterns, we propose and analyze a nonlocal population model with a cognitive map. The population density moves by a Fokker-Planck type diffusion driven by a cognitive map that stores habitat quality information nonlocally. The map is updated through local presence with learning and forgetting rates, and we consider both truncated and normalized perception kernels.

We first study the movement-only system without growth. We show that finite perceptual range generates spatial heterogeneity in the cognitive map even in nearly homogeneous habitats, and we prove a lingering phenomenon on unimodal landscapes: for the fixed high learning rate, the peak density near the best location is maximized at an intermediate forgetting rate.

We then couple cognitive diffusion to logistic growth. We establish local well-posedness and persistence by proving instability of the extinction equilibrium and the existence of a positive steady

state, with uniqueness under an explicit condition on the motility function. Numerical simulations show that lingering persists under logistic growth and reveal a trade-off between the lingering and total population size, since near the strongest lingering regime, the total mass can fall below the total resource, in contrast to classical random diffusive-logistic models.

Plenary talk— Data-driven maximum entropy on the mean method for linear inverse problems

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Linear inverse problems arise throughout data science, including image deblurring and denoising. Machine-learning methods—especially neural networks trained on large datasets—have transformed the practical solution of such problems. Yet many of these approaches lack a mathematical framework that permits rigorous assessment of their performance. This motivates the development of models that are both data-driven and analytically tractable. In this talk, I will present one such approach, based on the principle of maximum entropy on the mean. I will develop its theoretical foundations through variational analysis and stochastic optimization, and illustrate its performance on standard benchmark datasets, including MNIST.

This is joint work with Tim Hoheisel (McGill University), Matthew King-Roskamp (McGill University), and Gabriel Rioux (Imperial College London).

The effect of time delay on the global stability of infectious disease models and other dynamical systems

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When studying mathematical models of infectious disease, one characteristic of great interest is the long term persistence of the disease: given an initial infection rate, will it become endemic? or die out? Mathematically this is a question about the stability of an endemic equilibrium. Since the initial conditions of an outbreak are not under our control, local stability results are often insufficient: one would like to know whether the conditions present in a specific outbreak would lead the system to the endemic equilibrium, or to disease extinction. For this reason, global stability results play an important role in the analysis of epidemic models. In this talk we examine the effect of delayed variables on the global stability of systems of ordinary differential equations. This problem arises naturally in mathematical models of infectious disease, where delays may represent vector-borne transmission, incubation periods, temporary immunity, or other biological processes that prevent instantaneous responses in the system. Our approach is based on Lyapunov's Direct Method. Specifically, we construct Lyapunov functionals for the delayed system by modifying the Lyapunov functions used for the corresponding ODE model. This approach allows us to extend stability results from the non-delayed system to the delayed system, and provides a framework for analyzing the effect of delays in a broad class of dynamic models.

Plenary talk— Stackelberg strategies in the control of PDEs

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At this talk, I will present some game-theoretic strategies for the control of PDEs. I will illustrate the strategies with a heat equation. In this equation, we will act with two or more

controls, with one as the leader and the rest as followers. The objectives of these controls will be a null controllability objective (driving the solution to zero) and the other objective or objectives, a minimization one.

Analysis of a general vector transmission model for infectious disease spread

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As an extension of the framework developed by Earn and McCluskey (PNAS 2025 Vol. 122 No. 49), we consider a very general vector transmission model for the spread of an infectious disease. The human and vector populations each contain a single susceptible class and an arbitrary number of post-infection compartments, allowing for general stage structure (e.g., exposed, infectious, treated or quarantined classes). The model is based on three key assumptions. First, there is no transition from the infected classes back to the susceptible classes in either the human or vector populations. Second, each infected class is assumed to be directly reachable from its corresponding susceptible class. Third, disease transmission follows a mass-action incidence function with a criss-cross transmission structure, whereby infected vectors transmit the disease to susceptible humans, and infected humans transmit the disease to susceptible vectors. For the resulting system of ordinary differential equations, we explicitly determine the disease-free and endemic equilibria and derive a closed-form expression for the basic reproduction number. Using techniques similar to those developed by McCluskey and Earn, we study the global stability of the disease-free equilibrium when $\mathcal{R} \leq 1$ and of the endemic equilibrium when $\mathcal{R} > 1$.

Nonlinear analysis of differential equations systems describing real world phenomena

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This talk presents an analysis of nonlinear systems of differential equations modeling predator-prey interactions, with particular emphasis on the local and global behavior of solutions. The analysis begins with a three-dimensional system of ordinary differential equations incorporating a Holling type-II functional response in the predator equation. When the threshold prey quantities at which the predator growth rate becomes positive (the break-even concentrations) are distinct, the system admits four boundary equilibria. Restricted to invariant quadrants, the ODE system becomes two-dimensional, and a classical Hopf bifurcation occurs at two of the boundary equilibria. When these thresholds coincide, however, the system possesses a continuum of equilibria, leading to the so-called zip bifurcation. The continuum of equilibria loses normal hyperbolicity at an elliptic Hopf point and undergoes a Poincaré-Andronov-Hopf bifurcation without parameters. Motivated by the natural occurrence of time delays in biological processes, a delayed version of the ordinary differential equation system, obtained by incorporating a time delay into the prey equation, is analyzed. It is interesting to note that the qualitative properties described above persist in this setting. Furthermore, the analysis is extended to a modified version of the system modeling the spatial segregation of competing species, and the qualitative properties established previously are likewise preserved. The talk is concluded with ongoing work on a two-dimensional predator-prey reaction-diffusion system involving a Holling type-II functional response in the predator equation and an additive Allee effect in the prey equation. The system is posed on a bounded square domain with Neumann boundary conditions. The analysis addresses the local and global behavior of solutions, including codimension-one homogeneous and non-homogeneous classical Hopf bifurcations.

Stability and Dynamics of Delayed Population Models with Nicholson-Type Nonlinearity

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This series of studies focuses on the Nicholson's blowflies equation and its generalized models, systematically investigating the effects of delays, periodic and almost-periodic environments, neutral structures, and spatial diffusion on the stability and dynamical behavior of population systems. For non-autonomous systems involving multiple time-varying delays and periodic or almost-periodic coefficients, some criteria for the global attractivity and exponential stability of positive equilibria or periodic solutions are established. The results are further extended to neutral-type equations, for which sharp criteria are derived for the global asymptotic stability of both the zero equilibrium and the positive equilibrium, fully covering the non-neutral cases; furthermore, the existence of periodic solutions is also established. In diffusive models, the existence of traveling wave fronts is proven and the long-time dynamical behavior is characterized. Collectively, this series of studies constructs a comprehensive theoretical framework spanning ordinary differential equations, functional differential equations, neutral and diffusive equations, as well as autonomous and non-autonomous systems, and provides systematic analytical tools for theoretical population ecology.

Complex dynamics of HIV infection models incorporating T-cell homeostatic proliferation

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Recent clinical studies have displayed that the homeostatic proliferation of CD4+ T cell is one of the major drivers of HIV infection and persistence, since the replenishment of target T cells offers more chance of being infected with free HIV viruses. We propose and study several HIV infection models with T-cell homeostatic proliferation, which can induce very rich dynamics, such as saddle-node bifurcations, supercritical and subcritical Hopf bifurcations, saddle node bifurcations related to periodic orbits. Besides, we fit the dynamical model to clinical data on long-term CD4+ T cell counts before and after treatment. Our findings emphasize the critical role of T-cell homeostatic proliferation in HIV infection and persistence despite treatment, providing valuable insights for understanding disease progression and developing more effective therapies, potentially towards eradication.

From algebraic equations to abstract operators: Existence of positive solutions

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This talk presents a methodology for deriving and extending exact parameter ranges that guarantee existence and multiplicity of positive solutions. Beginning with an algebraic system, we obtain sharp eigenvalue intervals in finite-dimensional settings. These results are then extended to parameter-dependent fractional differential equations using topological degree theory and continuation techniques. Finally, the approach is generalized to nonlinear operator equations on partially ordered Banach spaces.

Parabolic system of aggregation formation in bacterial colonies

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In this work, we introduce a nonlinear parabolic system with dispersion to describe bacterial aggregation dynamics. In contrast to the corresponding model without dispersion, the inclusion of dispersion permits the propagation of bacterial clusters, indicating that dispersion can act as a regulatory mechanism for bacterial colony behavior. An analytical expression for the traveling-wave solution is derived by explicitly accounting for the dispersion coefficient. Numerical simulations further demonstrate that an initially random bacterial concentration evolves into a periodic wave pattern, which subsequently transitions into a stationary solitary wave in the absence of dispersion.

Variational models for phase separation in heterogeneous media

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Phase Separation in Heterogeneous Media: Modern technologies and biological systems, such as temperature-responsive polymers and lipid rafts, take advantage of engineered inclusions, or natural heterogeneities of the medium, to obtain novel composite materials with specific physical properties. To model such situations using a variational approach based on the gradient theory of phase transitions, the potential and the wells may have to depend on the spatial position, even in a discontinuous way, and different regimes should be considered.

In the critical case case where the scale of the small heterogeneities is of the same order of the scale governing the phase transition and the wells are fixed, the interaction between homogenization and the phase transitions process leads to an anisotropic interfacial energy. The supercritical case for fixed wells is also addressed, now leading to an isotropic interfacial energy. In the subcritical case with moving wells, where the heterogeneities of the material are of a larger scale than that of the diffuse interface between different phases, it is observed that there is no macroscopic phase separation and that thermal fluctuations play a role in the formation of nanodomains.

This analysis is hinged on tools from the Calculus of Variations, including Gamma-convergence, and homogenization theory from multi-scale convergence to unfolding techniques.

Theoretical and numerical studies of turbulence in the stochastic Navier-Stokes equations

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The two-dimensional Navier-Stokes equations provide a fundamental model for studying turbulence and the long-time dynamics of fluid flows. While deterministic forcing has been extensively investigated, the influence of stochastic forcing on turbulent scales and attractor dimension remains less understood.

In this talk, we compare deterministic and stochastic forcing mechanisms through a combination of analytical estimates and numerical simulations. Particular attention is given to Grashof numbers, the characteristic wavenumbers κ_η and κ_σ, and the Lyapunov dimension D_L, which characterize the complexity of turbulent flows. We investigate the dependence of these quantities on Grashof numbers and identify distinct scaling behaviors in the deterministic and stochastic regimes. In particular, the stochastic case exhibits faster growth rates for the characteristic wavenumbers with respect to the corresponding Grashof numbers. These numerical trends are compared with theoretical predictions.

An asymptotic analysis of spike self-replication and spike nucleation of reaction-diffusion patterns on growing 1-D domains

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Pattern formation on growing domains is one of the key issues in developmental biology, where domain growth has been shown to generate robust patterns under Turing instability. In this work, we investigate the mechanisms responsible for generating new spikes on a growing domain within the semi-strong interaction regime, focusing on three classical reaction-diffusion models: the Schnakenberg, Brusselator, and Gierer-Meinhardt (GM) systems. Our analysis identifies two distinct mechanisms of spike generation as the domain length increases. The first mechanism is spike self-replication, in which individual spikes split into two, effectively doubling the number of spikes. The second mechanism is spike nucleation, where new spikes emerge from a quiescent background via a saddle-node bifurcation of spike equilibria. Critical stability thresholds for these processes are derived, and global bifurcation diagrams are computed using the bifurcation software pde2path. These results yield a phase diagram in parameter space, outlining the distinct dynamical behaviors that can occur.

Bifurcation dynamic emergence in multiplex network modeling: coupled dynamic of individual opinion and behavior in the spreading and control of infectious diseases

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We propose a network-based model to investigate how, and to what extent, individuals' behavior and opinion toward protective measures modulate the dynamics of infectious disease transmission. We demonstrate how two concurrent spreading processes, infectious disease transmission and behavior-change contagion, interact and influence one another within the same population through a multiplex network framework. Our model quantifies behavior change as a combination of two factors. The first refers to the act of matching attitudes and the influence pressure of others, which is known as the threshold model. The second factor embodies the fear response triggered by escalating confirmed case counts, herein termed the fear effect. These two behavioral effects may occur and be disseminated via media, virtual networks, and interpersonal communications. In parallel, infectious disease transmission is modeled using an SEAIR-S dynamic. Utilizing the Microscopic Markov Chain method, we characterize the complete state space and corresponding transition probabilities. We conduct a structural comparison across common network structures: Erdős-Rényi, small-world, and scale-free network topologies. The results reveal that variations in the network's mean degree critically alter the system's dynamics, giving rise to bifurcation phenomena. Specifically, we study Neimark-Sacker bifurcation which leads to the bifurcation of periodic solutions over certain degree ranges and study the transient dynamics. To further elucidate these behaviors, we apply a mean-field approximation that reduces system dimensions and perform numerical bifurcation analysis on the system, confirming the presence of closed invariant curves. Calculation of the first Lyapunov coefficient validates that the observed bifurcation is a supercritical Neimark-Sacker. Our structural analysis further reveals three distinct dynamical regimes governed by the network's mean degree. For below approximately 11, only transient oscillations arise before the system stabilizes. In the intermediate range, persistent periodic solutions emerge, reflecting sustained epidemic-behavioral cycles. Beyond, oscillations vanish and the dynamics converge to a stable endemic equilibrium. These dynamical regimes emerge under the parameter values selected in our simulations, serving as a representative example; however, the framework is general and can be applied to a broad range of infectious diseases. The research reveals periodic solutions that indicate a reciprocal relationship between disease spread waves and behavior change. Different levels of people's adherence to protective measures exert a profound influence on disease spreading dynamics, which in turn mutually shape behavioral changes. The findings show how behavioral responses and network structure as interaction patterns jointly shape epidemic dynamics, emphasizing the intricate interplay between social influence, fear-driven behavior, and network topology in modulating the spread and control of infectious diseases.

Plenary talk— State-Dependent Delays: From Theory to Applications

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Abstract: State-dependent delay differential equations arise naturally in a wide range of applications, including biology, engineering, and control theory, where the delay depends on the current

or past state of the system. In this talk, we will present several important models involving state-dependent delays and discuss some of the main theoretical challenges associated with this class of equations. We will consider both neutral and non-neutral state-dependent delay differential equations and discuss fundamental results on existence, uniqueness, and averaging principles. We will also discuss some of the mathematical difficulties that distinguish state-dependent delays from their constant- and time-dependent counterparts. Finally, we will present several applications that illustrate the relevance of these equations in modeling real-world phenomena. This lecture is based on a series of works developed in collaboration with A. Gondim, H. Henríquez, X. Huo, B. Lani-Wayda, T. Oliveira, H. dos Reis, and S. Ruan.

Dynamics and bifurcations in biological control

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The concept of additional food suggests that providing predators with supplementary resources can improve their ability to regulate pest populations. In this study, we analyze a predator-prey model that incorporates both additional food supplementation and intraspecific competition among predators. We focus on the system's bifurcation structure and identify parameter regimes in which the interior equilibrium undergoes a higher-codimension Bogdanov-Takens bifurcation. We derive analytical conditions for the critical parameter values and show that the equilibrium corresponds to a higher-codimension cusp singularity. These results offer insight into how additional food and predator competition together influence complex population dynamics and have potential implications for sustainable pest management strategies.

Periodic solution for a free-boundary tumor model - asymptotic behavior

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A large number of free boundary models describing solid tumor growth were proposed and analyzed in recent decades; they involve mass conservation laws and reaction-diffusion processes for cell densities; nutrient concentrations are also incorporated into these models. Many models assume tumor cells are immersed in a constant supply of nutrients for simplicity. In reality, nutrient concentration varies with the intake of food. In this talk, we study the periodic solution and stability for the radially symmetric case. In particular, we shall establish the existence and uniqueness of the periodic solution in the biologically reasonable case and establish a global attractor in the class of radially symmetric initial data. Collaborators include Yaodan Huang and Jingyi Liu.

Global Hopf bifurcation of Human Respiratory System with Multiple Threshold Type State-dependent Delays

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We model the human cardiovascular-respiratory system with multiple blood transport time delays and investigate the periodic oscillations of carbon dioxide concentrations in the lung, brain, cerebrospinal fluid, and tissue compartments. We further obtain sufficient conditions for local and global asymptotically stability of the model and conduct local and Hopf bifurcation analysis when varying the commensurate scale of the multiple delays in a transformed system. Numerical simulations are presented to illustrate the general results.

Emergence and bistability of traveling waves and mesa states in a mass-conserved reaction-diffusion system

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The transition from random walk to directional motion (and back) is one of the intriguing phenomena observed in motile eukaryotic cells. However, typically, theoretical studies distinguish between the two phenomena and focus either on dissipative models or models obeying gradient flows, respectively. Using a three-variable dissipative reaction-diffusion system with mass conservation, we show how pulses, waves, and (stationary) mesas generically organize about high codimension bifurcations. Specifically, we demonstrate the novelty of mass conservation, which enters via a long-wavenumber bifurcation of a large-scale mode. Lastly, following the biological interest, we address the bistability between travelling wave and wave-pinning solution branches, which emerge from a codimension-2 bifurcation to a finite-wavenumber Hopf and a conserved large-scale mode.

Modeling, inference, and prediction in mobility-based compartmental models for epidemiology

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Classical compartmental models in epidemiology often assume a homogeneous population for simplicity, which neglects the inherent heterogeneity among individuals. This assumption frequently leads to inaccurate predictions when applied to real-world data. For example, evidence has shown that classical models overestimate the final pandemic size in the H1N1-2009 and COVID-19 outbreaks. To address this issue, we introduce individual mobility as a key factor in modeling disease transmission. We characterize disease dynamics using mobility distribution functions for each compartment and propose a mobility-based compartmental model that incorporates population heterogeneity. Our results demonstrate that, for the same basic reproduction number, our mobility-based model predicts a smaller final pandemic size compared to the classical models, effectively addressing the common overestimation problem. Additionally, we infer mobility distributions from the time series of the infected population. We provide sufficient conditions of data to uniquely identify the mobility distribution and propose a machine-learning-based approach to learn mobility from both synthesized and real-world data.

Propagation dynamics for a stage-structured population model in a shifting environment

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We study an integro-difference system in an unbounded domain for a population with a stage structure. The environment shifts between a favorite habitat and an unfavorite habitat at two ends of the domain, which makes the growth and propagation dynamics of the population depend on the changing habitat conditions. Under appropriate assumptions, we established the existence of spreading speeds and forced traveling waves for such a model. Our analysis of the propagation dynamics is based on the corresponding limiting systems at the far ends of the domain and their relation to the model. It is discovered that the habitat shifting speed greatly influences the spreading speeds of the population and may even cause the extinction of the population.

Delay-induced bifurcations and complex dynamics in a host competitor parasite model

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Time delay is an important feature of many ecological interactions, yet its influence on the dynamics of multi-species systems remains incompletely understood. In this work, we investigate a delayed host-parasite-competitor model using linear stability analysis, bifurcation theory, and normal form analysis. Conditions for Hopf, generalized Hopf, and Hopf-zero bifurcations are established, demonstrating how time delay modifies the local bifurcation structure and gives rise to additional codimension-two dynamics. Representative numerical simulations complement the analytical results by investigating more complex dynamical behaviors beyond the local bifurcation analysis, including quasi-periodic oscillations. Together, these results provide insight into the role of developmental delays in shaping the stability and dynamics of ecological systems.

George Sell Memorial Lecture 1 — The Evolution of Approaches to Finite Dimensional Dynamics

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The mathematical study of finite dimensional behavior in infinite dimensional dynamical systems has undergone its own evolution over several decades. We will follow the thread connecting global attractors to determining modes to inertial manifolds to inertial forms to determining forms, and finally, to general determining parameters and their applications in control theory and data assimilation.

George Sell Memorial Lecture 2—George Sell Memorial Lecture 2: Synchronization from Mobile and Local Observations

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Data collected from commercial flights supplement those from satellite and stationary weather stations to enhance the accuracy of forecasts. In this talk we first present analysis indicating how the effectiveness of nudging the Navier–Stokes equations with data on a moving subdomain can depend on the speed of that movement. Somewhat related is the problem of having data on only a small stationary subdomain. Dense data over a small patch of the Pacific Ocean is highly effective in improving forecasts over the continental United States. In the second part of the talk we see how this can be used for a solution to a PDE that is analytic in the spatial variable.

Global well-posedness of a stochastic self-consistent chemotaxis-fluid model

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As a significant class of complex fluid models, the Keller-Segel-Navier-Stokes system has been extensively studied in recent years. In this talk, I will present a qualitative analysis of a stochastic Keller-Segel-Navier-Stokes system describing the chemotactic movement of cells in a viscous fluid subject to environmental noise. The model features a self-consistent coupling mechanism, in which the interaction force arises from the friction between the cells and the ambient fluid. Using cut-off approximations, entropy methods and stopping time arguments, we prove the global existence of a unique pathwise mild solution in two dimensions under a subcritical cellular mass condition.

Evolution of dispersal and a conjecture of Dockery et al.

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Extending an earlier result of A. Hastings (Theor. Pop. Biol. 1983), Dockery et al. (J. Math. Biol. 1998) showed that, for two competing species that are identical except for their diffusion rates, the slower diffuser can exclude its faster counterpart regardless of the initial data. It was then conjectured that the same result holds for N competing species, for any $N \geq 3$. In this talk, we will discuss recent progress of this conjecture and further developments in the theory of principal Floquet bundles. Our discussion will include the cases of autonomous, time-periodic, and aperiodic coefficients. If time permits, we will also discuss a more recent application of this approach to the study of competition among many species in a river habitat. This is joint work with Robert S. Cantrell (University of Miami) and Yuan Lou (Shanghai Jiao Tong University).

Are the mathematical biological models governed by nonlinear first order Caputo fractional differential equations solvable?

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It was claimed in some previous papers that if the nonlinearity satisfies the locally Lipschitz condition in the second variable, then the first order Caputo fractional differential equations have a unique continuous solution. This result has been widely used in the literature to obtain the existence and uniqueness of solutions of a variety of models such as disease models and predator-prey models, recently published, for example in Scientific Reports, PLoS One, Epidemics, Communications in Nonlinear Science and Numerical Simulation, etc. In this present, I'll show that the claimed result would be incorrect. Therefore, these previous results which applied the above claimed result to obtain the existence and uniqueness of solutions of the models would not be correct.

Modeling for a purpose: an influenza outbreak in a boarding school as an example

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Assessment of models should depend on the modeling objectives. Models that incorporate more realistic mechanisms are more suitable for providing insights. To produce reliable and accurate predictions and inform public health decision making, parsimonious models are more appropriate and the modeling needs to respect the data. Most of all, model calibration results should be validated by data that is independent of the calibration data, before scenario analysis is made to inform policy. As a case study, we revisit the well-known example of a 1978 influenza outbreak in a boarding school in England. We demonstrate that a parsimonious SIR model with data informed time-dependent parameters can produce both accurate fitting to the time series data and validation by the final size of the epidemic. Furthermore, modeling results also provide evidence of the likely epidemic control measures implemented at the school.

Computational methods for high dimensional stochastic dynamics

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In this talk, I will introduce some of my recent work on utilizing modern deep learning tools to partially overcome the curse of dimensionality and solve high-dimensional partial differential equations that are related to stochastic differential equations. Our results cover the Fokker-Planck equation, eigenfunction problem of the Fokker-Planck equation, the Hamilton–Jacobi equation, and the Feynman-Kac equation.

A mosquito population model with a periodic delay and pair formation

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This paper is devoted to the study of a mosquito growth model by incorporating a two-stage structure, explicit pair formation, and a periodic developmental duration in a seasonal environment. We introduce the basic reproduction ratio $\mathcal{R}_0$ based on an associated homogeneous evolution system with time delay, and then establish a threshold type result on the extinction and persistence in terms of $\mathcal{R}_0$. For this purpose, we consider a nonlinear eigenvalue problem and prove the existence of a strongly positive eigenvector, which guarantees the continuity of the spectral radius of the homogeneous operator. Further, our numerical simulations indicate that a sex ratio close to $1:1$ is most favorable for reproduction, and a constant delay versus a periodic delay suggests that the periodic developmental duration play a crucial role in shaping the dynamics of mosquitoes. This is joint work with Professor Xiaoqiang Zhao.

Within-host HIV dynamics incorporated with $CD31^+$ and $CD31^-$ in Naive $CD4^+$ T Cell

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In this talk, I report some results on the role of T-cell homeostasis in HIV infection dynamics by incorporating the biological characteristics of the $CD31$ phenotypic marker. While standard models often treat $CD4^+$ T cells as a homogeneous population, we classify naive $CD4^+$ T cells into two distinct subsets: Recent Thymic Emigrants ($CD4^+CD31^+$) and peripherally proliferated cells ($CD4^+CD31^-$). Building upon classical logistic growth frameworks, we develop a nonlinear differential equation system that accounts for the unique proliferation and differentiation kinetics of these subsets. To isolate the impact of distinct proliferative and infectious mechanisms, we systematically analyze three biologically motivated special cases. Classical single-compartment models typically establish $\mathcal{R}_0 = 1$ as an absolute threshold for viral clearance. In contrast, we demonstrate that explicitly tracking the $CD31$ subpopulations breaks this single-threshold paradigm and reveals a rich spectrum of complex dynamics. Under specific proliferative regimes, the system exhibits bistability and backward bifurcations, providing a novel theoretical framework to explain why patients with an identical $\mathcal{R}_0$ can exhibit drastically different steady-state viral loads. Furthermore, in other parameter regimes, the presence of the $CD4^+CD31^+$ compartment fundamentally shifts classical stability boundaries and modulates viral oscillations. Ultimately, this research provides a robust mathematical foundation for understanding how thymic output and T-cell subset maintenance dictate the resilience of the immune system and the clinical progression of HIV.

Graph theory identifies autistic patterns in the prefrontal circuit of a mouse model of autism

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As a well-developed branch of mathematics, graph theory provides unique tools to quantifiably assess various properties of complex networks. Applied to brain circuits, network-level analyses can illustrate disruptions to brain organization that yield both mechanistic and diagnostic insight. Previously, graph theory has been used with functional magnetic resonance imaging (fMRI) datasets to quantify connections among different brain regions, readily capturing the macroscopic-scaled differences in brain networks between healthy and Alzheimer's subjects. Here, we applied graph theory on the microscopic scale, using miniscope-based calcium imaging recordings from the freely behaving wild type and Shank3fx mice (a mouse model of autism), and compared their functional connections among individual neurons in the prefrontal cortical microcircuits during social behavior tasks. We demonstrated that Shank3fx mice displayed reduced neural activity, a less integrated network, and fewer network changes in the prefrontal microcircuits between the presence and absence of social targets. Furthermore, we employed machine learning to test whether graph-theoretic metrics extracted from the prefrontal microcircuits could be predictive of genotype and genotype-associated social behavior difference between Shank3fx and WT mice. Our results indicate a strong link between altered prefrontal microcircuits and social behavior differences in an ASD mouse model, highlighting prefrontal microcircuitry as a potential diagnostic and therapeutic target for ASD.

Hybrid impulsive cooperative control of vehicle platoons with switching communication topology

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Cooperative control in intelligent transportation systems refers to the use of wireless communication and machine-to-machine interaction to coordinate vehicles and infrastructure. It optimizes traffic flow, reduce traffic congestion, and prevents accidents through shared data and control strategies. This study investigates the cooperative control challenges within vehicle platoons using delayed hybrid impulsive protocols. These protocols involve both time-dependent and state-dependent switching in communication topology, where each mode includes potentially destabilizing continuous dynamics. Sufficient conditions for global asymptotic stability are established by employing the Lyapunov Krasovskii functional method alongside mode-dependent average dwell time and the Lyapunov Razumikhin technique. These conditions relate to impulsive strength, switching parameters, convex switching regions, and the operational time ratio between stable and unstable subsystems, ensuring global exponential stability under both switching regimes. Moreover, the research integrates gyroscopic and braking forces to address collision avoidance effectively. Numerical simulations for each switching type validate the theoretical findings, demonstrating their efficacy and applicability. Overall, this work not only advances the theoretical understanding of cooperative control in vehicle platoons but also holds capability for enhancing the efficiency, safety, and scalability of autonomous transportation systems in practical settings.

A quantification of long transient dynamics

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The stability of equilibria and asymptotic behaviors of trajectories are often the primary focuses of mathematical modeling. However, many interesting phenomena that we would like to model, such as the 'honeymoon period' of a disease after the onset of mass vaccination programs, are transient dynamics. Honeymoon periods can last for decades and can be important public health considerations. In many fields of science, especially in ecology, there is growing interest in a systematic study of transient dynamics. In this work we attempt to provide a technical definition of 'long transient dynamics' such as the honeymoon period and explain how these behaviors arise in systems of ordinary differential equations. We define a transient center, a point in state space that causes long transient behaviors, and derive some of its properties. We also define reachable transient centers, which are transient centers that can be reached from initializations that do not need to be near the transient center. This is joint work with A. Liu, K. Abdella and A. Pasion.

Antiperiodic solutions for nonlinear asymmetric equations near resonance

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In this talk, I will discuss the existence of solutions to second order scalar differential equations with asymmetric nonlinearities, subject to antiperiodic boundary conditions. Both resonance and nonresonance cases are examined, with the Landesman–Lazer conditions imposed in the resonant setting. The proofs rely on topological degree theory. This is joint work with Alessandro Fonda, Andrea Sfecci, and Wahid Ullah.

Global stability of epidemic models with uniform susceptibility

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We consider a very general framework for compartmental disease models, allowing a single susceptible class and an arbitrary number of post-infection classes (including, for example, asymptomatic, mildly infectious, highly infectious, treated and quarantined groups). Key model assumptions: only one susceptible class; no return from the infected classes to the susceptible class; each infected class can be (eventually) reached from the susceptible class; a 'reasonable' incidence function (mass action, for example). We are able to fully resolve the global dynamics for the resulting ODE systems, obtaining the common threshold behaviour: if $R_0 \leq 1$ then the disease-free equilibrium is globally asymptotically stable; if $R_0 > 1$ then the endemic equilibrium is globally asymptotically stable. Our proof involves using properties of M-matrices to construct a Lyapunov function that is a sum of Volterra functions. This result subsumes a large number of results published over the last century, strengthens many of them by establishing global rather than local stability, avoids the need for any stability analyses of these systems in the future, and settles the question of whether co-existing stable solutions or non-equilibrium attractors are possible in such models: they are not. This is joint work with David Earn, McMaster University.

Immune modulation in the tumor microenvironment: Bifurcation analysis of cancer-CTL-monocyte dynamics

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In this talk, I will present a mathematical model describing the interactions between cancer cells, cytotoxic T lymphocytes (CTLs), and monocytes within the tumour microenvironment. The model incorporates key immunological mechanisms, including tumour antigenicity, the Allee effect, and monocyte-mediated immune activation via MHCI cross-dressing. Using systems of nonlinear ordinary differential equations, we derive analytical expressions for equilibrium points, evaluate their stability, and characterize bifurcations, such as saddle-node, Hopf, Bogdanov–Takens, and Bautin. A reduced model via quasi-steady-state approximation is also proposed, preserving the core dynamic structure to facilitate bifurcation analysis. A central finding of this study is the critical role of the monocyte-mediated T cell activation rate, denoted by the parameter β, which encapsulates the immunostimulatory potential of inflammatory monocytes presenting tumour antigens via MHCI cross-dressing. Numerical continuation corroborates the existence of multiple codimension-two organizing centres, delineating parameter regimes of tumour clearance, immune-mediated control, bistability, sustained oscillations, and inevitable escape. The results from this study quantitatively characterize the critical role of the monocyte-T-cell activation rate (β) and the Allee threshold (γ) in tipping the balance between immune surveillance and tumour persistence. This framework provides actionable bifurcation-based criteria for designing combination immunotherapies that enhance antigen presentation or monocyte functionality to shift the system toward tumour-eliminating attractors. This project is joint work with Dr. Eymard Hernandez-Lopez and Dr. Xiunan Wang at the University of Tennessee at Chattanooga.

Disordered hyper-chimeras in random neural networks

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Neural systems display dynamics where synchronous and asynchronous states can coexist. However, existing oscillator-based models of these chimera dynamics, assume symmetric coupling profiles, which are difficult to reconcile with the non-symmetric coupling commonly displayed by populations of neurons. We show that high-dimensional states where asynchrony and synchrony co-exit or “hyper-chimeras” emerge in coupled populations of recurrent neural networks with randomly generated, non-symmetric weights. The asynchronous state is a classical hyperchaotic balanced-state while the synchronous state is a random projection onto the balanced state. Further, we derive an approximation for the stability of the synchronized subpopulation and demonstrate transient synchronization/intermittency near the onset of instability. Our work provides a biologically plausible instantiation of chimeras in neural circuits caused by fully random connectivity with minimal assumptions.

Hopf bifurcation and bistability induced by delayed environmental transmission in an Avian influenza model with dose-dependent infection

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Avian influenza remains one of the most significant transboundary infectious diseases affecting poultry and wild bird populations, posing substantial threats to food security, agricultural economies, and global public health. The persistence of avian influenza viruses in the environment and the dependence of infection risk on pathogen exposure dose introduce transmission pathways and epidemiological complexities that are not adequately captured by classical direct-transmission epidemic models. This study develops and analyses a delayed environmental transmission model with generalized dose-dependent infection governed by a system of nonlinear delay differential equations. The fundamental mathematical properties of the model, including positivity, boundedness, and the existence of biologically meaningful solutions, are established. The disease-free and endemic equilibria are determined, and the basic reproduction number is derived to characterize the threshold dynamics governing disease invasion and persistence. Local stability analysis is performed using the characteristic equations obtained from the linearized system, while backward bifurcation and Hopf bifurcation analyses reveal the existence of multiple endemic states and delay-induced oscillatory dynamics. For the special case corresponding to a Michaelis–Menten infection response, rigorous global stability results for both the disease-free and endemic equilibria are established using suitably constructed Lyapunov functionals. Numerical bifurcation analysis further demonstrates that increasing the delay can induce stability switches of the endemic equilibrium, leading to transitions between stable equilibria, bistability, and sustained periodic oscillations.

Dynamics and Bifurcation Analysis of a Tumor-Immune Interaction Model with Fractional-Power Nonlinearities

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In this talk, we present a tumor–immune interaction model incorporating fractional-power tumor growth and saturated immune feedback. We derive explicit conditions for the existence and stability of system equilibria. Based on center manifold theory and normal form theory, we conduct a Hopf bifurcation analysis and prove that at least three small-amplitude limit cycles exist around the positive equilibrium. Sensitivity analysis further identifies immune killing strength, immune saturation, and immune cell loss as the core parameters dominating oscillatory behaviors. Our findings reveal prominent tipping-point dynamics, in which minor parameter perturbations can trigger drastically different long-term evolutionary outcomes of tumor–immune interactions.

Long-lasting, slowly varying transient dynamics from non-equilibrium transient centers

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Analysis of mathematical models in ecology and epidemiology often emphasizes asymptotic dynamics, such as stable equilibria and periodic orbits. However, many biologically relevant trajectories exhibit long transient dynamics in which a chosen observable evolves slowly for an extended period before a comparatively rapid transition occurs. On the finite time scales relevant to data collection, management, and intervention, these transients can be more informative than the eventual asymptotic outcome. In this work, we study long-lasting and slowly varying transient dynamics in continuous-time systems through the framework of nonequilibrium transient centers. These special points provide a geometric mechanism for prolonged slow evolution without requiring the trajectory to be near an equilibrium or attractor. We describe how nonequilibrium transient centers give rise to slow regions, how trajectories are drawn into and later escape from these regions in finite time, and how this can generate transients whose duration can be made arbitrarily large. We then illustrate the theory with applications to predator-prey and epidemiological models, focusing on regimes where population densities or disease prevalence remain low for long intervals before an abrupt qualitative shift.

Joint effects of demographic and environmental noises in transient dynamics

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Transient dynamics–long-lasting but ultimately finite-time behaviors–are ubiquitous in complex stochastic systems. Understanding their underlying mechanisms remains a fundamental challenge. In this talk, we investigate stochastic processes arising in chemical reaction networks and population dynamics under both demographic and environmental noises. A distinguishable feature is that extinction is inevitable but preceded by long-lived persistence. We show that demographic and environmental noises can induce fundamentally different transient dynamics, leading to distinct persistence and extinction patterns.

Recent results on the Gatenby and Gawlinski model of cancer invasion

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In this work a reaction-diffusion system modelling tumor invasion is investigated. The model is proposed by renowned biologist and cancer expert Gatenby and his collaborator. The underlying partial differential equation system has cross-diffusion and density-dependent degenerate diffusion coefficient. We prove the existence and smoothness of the Initial-Boundary Value problem with no-flux boundary condition. More importantly, rigorous proof of existence of traveling wave solution is proved, providing valuable insight to the dynamics of cancer invasion. This is a joint work with Xinfu Chen, Xueyuan Tao and Shulin Zhou.

On the stability of solitary waves for a Boussinesq system higher order

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In this work, we study the nonlinear orbital stability of solitary-wave solutions for a class of higher-order Boussinesq systems with Hamiltonian structure,

$$\begin{cases} \left(I - d\partial_x^2 + d_2\partial_x^4\right) u_t + \eta_x + c\partial_x^3\eta + c_2\partial_x^5\eta &= \partial_x\left(G_1(\eta, \eta_x, \eta_{xx}, u, u_x, u_{xx})\right), \\ \\ \left(I - b\partial_x^2 + b_2\partial_x^4\right) \eta_t + \partial_x u + a\partial_x^3 u + a_2\partial_x^5 u &= \partial_x\left(G_2(\eta, \eta_x, \eta_{xx}, u, u_x, u_{xx})\right), \end{cases} \tag{1}$$

where $\eta = \eta(x,t)$ and $u = u(x,t)$ are real functions, and the nonlinearity $G = (G_1, G_2)^T$ has the variational structure which includes homogeneous and non homogeneous models

$$\begin{aligned} G_1(q,r,z,s,t,w) =& F_q(q,r,s,t) - rF_{qr}(q,r,s,t) - zF_{rr}(q,r,s,t) - tF_{sr}(q,r,s,t) \\ & - wF_{tr}(q,r,s,t), \\ G_2(q,r,z,s,t,w) =& F_s(q,r,s,t) - rF_{qt}(q,r,s,t) - zF_{rt}(q,r,s,t) - tF_{st}(q,r,s,t) \\ & - wF_{tt}(q,r,s,t), \end{aligned}$$

where F is a function with some properties (like homogeneity). The main result of stability is the following:

Theorem. Assume that $a + c + 2b = 0$.

a) If $0 < p < 8$ and $0 < p < q$, there exist ω arbitrarily close to 1^- such that $\mathcal{G}_\omega$ is stable.

b) Suppose that $F(q,r,s,t)$ is a homogeneous function of order $p+2$. If $0 < p < 8$. Then, there is $\omega^* \in (0,1)$ such that $\mathcal{G}_\omega$ is stable for $\omega \in (\omega^*, 1)$.

c) Suppose that $F(q,r,s,t)$ is a homogeneous function of order $p+2$ and $F(\cdot, r, \cdot, t)$ is a homogeneous function of order β. If $p + 2\beta < 8$, then there exists $\omega_0 > 0$ such that $\mathcal{G}_\omega$ is stable for $\omega \in (\omega_0, 1)$.

Here $\mathcal{G}_\omega$ denotes the set of the ground state solutions associated with the Boussinesq system.

The onset of vortex lines and their interaction in the 3D Ginzburg–Landau model

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The Ginzburg–Landau model is a phenomenological description of superconductivity. A crucial feature in type II superconductors is the occurrence of vortex lines, which appear above a critical value of the applied magnetic field, known as the first critical field. In this talk, I will present a sharp estimate of this value and discuss the onset of vortex lines and the derivation of an interaction energy for them. In particular, we show that this onset of vorticity is directly related to an isoflux problem on curves, namely finding a curve that maximizes the ratio of magnetic flux to its length.

This is joint work with Etienne Sandier and Sylvia Serfaty. This work was supported by ANID FONDECYT 1231593.

Mathematical analysis of a reaction–diffusion epidemic model with vaccination

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We present recent results on the asymptotic spatial profiles of positive steady states for a reaction–diffusion system modeling the spread of infectious diseases in the presence of vaccination, with particular emphasis on the regime of small diffusion rates. Our analysis reveals several novel mathematical and biological insights into the effects of restricting population movement as a strategy for controlling disease transmission. In particular, we show that when the diffusion rates of both susceptible and infected populations tend to zero, disease eradication is achievable provided the environment contains a nonempty low-risk region. In contrast, when only the diffusion rate of the infected population tends to zero, the disease becomes spatially localized within high-risk areas. Furthermore, vaccination can significantly reduce the region in which the disease persists when the diffusion rate of infected individuals is sufficiently small.

Doubly parametric trigonometric functions and oscillation onset in population dynamics of ticks undergoing multi-pathway diapause developments

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We consider a scalar delay differential equation that models the population dynamics of ticks undergoing diapause across three post-egg physiological stages. The boundary of the zero set of the associated characteristic equation in the complex plane leads to a class of doubly parametric trigonometric functions of the form $PC_2 = \alpha_1 \cos(\omega) + \alpha_2 \cos(2\omega) + \alpha_3 \cos(3\omega)$ and $PS_2 = \alpha_1 \sin(\omega) + \alpha_2 \sin(2\omega) + \alpha_3 \sin(3\omega)$ With $\alpha_1 + \alpha_2 + \alpha_3 = 1$.A central contribution of this work is the first systematic and rigorous analysis of the qualitative structure of such doubly parametric trigonometric functions, including sharp monotonicity properties and a complete characterization of their zero distributions. These results resolve nontrivial analytical difficulties arising from the interaction of multiple harmonics and parameter constraints, which have not been addressed in the existing literature on delay equations. Building on this foundation, we derive explicit and verifiable criteria that identify the critical delay values at which Hopf bifurcations occur. In particular, our approach provides a unified and constructive framework to determine the onset of periodic solutions, overcoming limitations of classical techniques relying on implicit transcendental conditions. This establishes, for the first time, a direct link between the fine structure of multi-frequency trigonometric functions and bifurcation thresholds in delay differential equations.

Plenary talk— On chemotaxis models with porous medium diffusion, consumption, and logistic source on $\mathbb{R}^N$

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This talk is concerned with the global existence, uniquencess, boundedness, and regularity of weak solutions to a chemotaxis system with porous medium diffusion, logistic growth, and chemical consumption. I will first give a brief introduction of porous medium equations. Next, I will introduce the chemotaxis model and the associated central problems to be considered. I will then present the global existence and boundedness of weak solutions to the chemotaxis model for general initial data without any restrictions on the space dimension and the chemotaxis sensitivity. Finally, I will discuss Hölder continuity of weak solutions and the uniqueness of Hölder continuous weak solutions.

Large deviation, nonequilibrium fluctuation theory, and stochastic stability

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This talk is devoted to the connections among nonequilibrium thermodynamics, large deviation, and stochastic stability in the framework of randomly perturbed dynamical systems. More precisely, I will present some results on the large deviation principle for stationary distributions and quasi-stationary distributions (if time permits) and its application to nonequilibrium fluctuation theory and stochastic stability of invariant measures. A special attention will be paid to the regularity of solutions to Hamilton-Jacobi equations due to dynamical structures.

Stabilizing normal cohort development delay-induced oscillations via distributed diapause development in tick populations

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Existing literature on tick diapause often employs discrete delays, which may not completely reflect the variability of the environmental conditions leading to diapause. To bridge this gap, we developed a novel delay differential equation (DDE) model that incorporates distributed delays to better mimic this variability. We conducted a complete qualitative analysis complemented by some numerical experiments of the proposed model, focusing on the equilibrium structure and Hopf bifurcations. Our analysis of the long-term behaviors of the model system indicate that the greater the proportion of ticks undergoing diapause development, the larger the critical normal development delay for Hopf bifurcations to occur, shifting from a stable equilibrium to a periodic oscillation. We also observed that in the case when normal development delay generates nonlinear oscillation in the tick population, increasing the distributed diapause delay can stabilize the oscillation, leading to convergence of the tick population to the positive equilibrium.

Spatiotemporal pattern formation in nonlocal aggregation-diffusion model driven by spatial cognitive map

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Nonlocal aggregation-diffusion models, when coupled with a spatial map, can capture cognitive and memory-based influences on animal movement and population-level patterns. A reaction-diffusion-aggregation system coupled with a separate dynamically updating map is proposed to describe the animal population movement. It is shown that (i) when a symmetric cognitive map influences the animal movement instantaneously, animal population would aggregate in multiple locations in the habitat; (ii) when an asymmetric cognitive map influences instantaneously, a rotating movement pattern emerges; and (iii) a delayed symmetric cognitive map produces time-periodic but non-rotating patterns. This is based on joint work with Di Liu, Yurij Salmaniw and Hao Wang.

Hopf bifurcation, stability switch, and relaxation oscillations in a mass-action epidemiological model

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Oscillatory disease outbreaks are frequently observed in infectious diseases, yet the mechanisms generating sustained oscillations remain incompletely understood. In this work, we investigate a mass-action epidemiological model incorporating post-infection mortality and partial immunity. We show that the model exhibits rich dynamical behavior despite possessing a unique endemic equilibrium. In particular, the endemic equilibrium undergoes a stability switch through a Hopf bifurcation, leading to sustained periodic oscillations. Numerical bifurcation analysis further reveals the emergence of large-amplitude relaxation oscillations, characterized by prolonged periods of low disease prevalence followed by rapid epidemic surges. Unlike previously identified mechanisms involving multiple endemic equilibria or nonlinear incidence functions, the oscillatory behavior in our model arises from the interplay between post-infection mortality and reinfection while the endemic equilibrium remains unique. These findings provide new insights into the mechanisms underlying recurrent epidemics and underscore the importance of incorporating post-infection processes in mathematical models of persistent infectious diseases. Joint work with Brendan Shrader (Georgia Institute of Technology), Chunhua Shan (The University of Toledo), B Sagar (University of Central Florida), and Chadi Saad-Roy (University of British Columbia).

Data-driven computation for periodic stochastic differential equations

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Many stochastic differential equations in various applications, like coupled neuronal oscillators, are driven by time-periodic forces. In this talk, I will introduce several data-driven computational tools extended from the autonomous Fokker-Planck equation to the time-periodic setting. This enables the efficient computation of the time-periodic invariant probability measure using either a grid-based method or an artificial neural network solver, and the estimation of the speed of convergence towards the time-periodic invariant probability measure. I will also show the convergence analysis and performance of the algorithms using several numerical examples.

Bifurcation analysis of a Leslie-type predator–prey model with Allee effects

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In this talk, we investigate a Leslie-type predator–prey model with Allee effects and a generalized Holling type III functional response. Bifurcation theory is adopted to explore the high-codimension Hopf and Bogdanov–Takens (BT) bifurcations of the proposed system. The model is shown to exhibit multiple types of high-codimension BT bifurcations, including codimension-2, 3, 4 and 5 cusp bifurcations, as well as codimension-3 elliptic (focus) bifurcations. Explicit analytical conditions for the occurrence of these bifurcations are established. Furthermore, we conduct a systematic Hopf bifurcation analysis and apply normal-form theory to compute sixth-order focus values. Rigorous mathematical derivation proves that the Hopf critical point can generate at least four distinct limit cycles. (Joint work with Professor Pei Yu)

Fire-driven tick-host dynamics and their impact on tick-borne disease spread

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Although controlled burns are traditionally employed to prevent wildfires, they also have important consequences for the management of tick-borne diseases. While fire suppresses tick populations immediately, empirical studies show highly conflicting results over the long term, making the overall impact on disease transmission difficult to predict. In this talk, we present an impulsive mathematical model simulating tick life cycles, rodent hosts, and periodic burns to evaluate how these fire dynamics shape both tick populations and long-term disease risk. The model tracks both standard host-to-vector transmission and co-feeding, where ticks pass the pathogen to one another while feeding on the same host. We demonstrate that while extreme fire regimes can eradicate the vector, the threshold for effective disease control under realistic management strategies depends heavily on the broader ecological context, including local rodent abundance and transmission dynamics. This is joint work with Dr. Kyeongah Nah.

Global threshold dynamics of periodically switching population models

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In this talk, I will present some of our recent work on the global threshold dynamics of periodically switching population models. We study a reaction–diffusion model with periodic environmental switching and impulsive harvesting on a bounded domain under either Dirichlet (hostile)

or Neumann (no-flux) boundary conditions. For the corresponding spatially homogeneous model, a threshold parameter $\mathcal{R}_0$ completely determines the global dynamics: the population goes extinct if $\mathcal{R}_0 \leq 1$ and persists as a unique globally attractive positive periodic solution if $\mathcal{R}_0 > 1$. For the spatial model, we show that the threshold dynamics depend critically on the boundary conditions. Under Dirichlet boundary conditions, a diffusion-dependent threshold $\mathcal{R}_0^D$ governs the dynamics, and sufficiently rapid diffusion can drive the population to extinction even when the spatially homogeneous model predicts persistence. In contrast, under Neumann boundary conditions, diffusion does not alter the threshold dynamics. These results reveal how spatial diffusion, environmental switching, impulsive harvesting, and habitat boundaries jointly shape population persistence.

Synchronization in Markov random networks

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Many complex biological and physical networks are naturally subject to both random influences, i.e., extrinsic randomness, from their surrounding environment, and uncertainties, i.e., intrinsic noise, from their individuals. Among many interesting network dynamics, of particular importance is the synchronization property which is closely related to the network reliability especially in cellular bio-networks. It has been speculated that whereas extrinsic randomness may cause noise-induced synchronization, intrinsic noises can drive synchronized individuals apart. This talk presents an appropriate framework of (discrete-state and discrete time) Markov random networks to incorporate both extrinsic randomness and intrinsic noise into the rigorous study of such synchronization and desynchronization scenario. Convergence in distribution is established via a Lyapunov spectrum analysis. A probabilistic characterizations of the alternating pattern between synchronization and desynchronization behaviors is given if the deterministic random network (i.e. absent any intrinsic noise) is fully synchronized. This talk is based on several joint works with Arno Berger, Wen Huang, Hong Qian, Felix X.-F. Ye, and Yingfei Yi.

Target reproduction numbers for time-delayed population systems

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In population dynamics, the target reproduction number is a fundamental metric that quantifies the level of control required to achieve specified prevention, intervention, or disease control objectives. In recent years, this concept has been significantly generalized. Lewis et al. (JMB, 2019) established a general framework for target reproduction numbers associated with nonnegative matrices, while Wang and Zhao (JMB, 2020) extended the theory to positive operators on ordered Banach spaces. These frameworks encompass classical quantities such as the basic reproduction number and the type reproduction number, as well as other threshold parameters in the literature, thereby providing a unified perspective on population control. In this talk, we develop the theory of target reproduction numbers for a broad class of compartmental population models with time delays, considering control strategies that target either new infection/production or internal evolution/transition processes. We show that the target reproduction number of the original time-delayed model can be interpreted as the basic reproduction number of an appropriately modified system. Finally, we illustrate the theory through three epidemic models, demonstrating how these results enhance our theoretical understanding and provide valuable insights for designing effective intervention and control strategies in population systems. This is joint work with Xiao-Qiang Zhao.

Plenary talk— A dynamic phase plane approach illustrated on a Lotka–Volterra competition model on arbitrary unbounded time scales

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A brief introduction to the calculus on arbitrary time scales is provided. Then, a two-species Lotka–Volterra (LV) competition model on arbitrary unbounded time scales is formulated that contains, as special cases, the classical LV competition model on a continuous domain, as well as its discrete analogue, the Leslie–Gower model. To derive the global dynamics, we introduce a dynamic phase plane analysis that extends the traditional phase plane analysis that is known to be a powerful tool in the analysis of planar differential equations. It is shown why this technique had mainly been ignored for recurrences, i.e., orbits jumping over nullclines. However, motivated by recent work that revisited this technique for discrete planar maps and overcame this problem, in Sabrina H. Streipert and Gail S. K. Wolkowicz, (2023) "An augmented phase plane approach for discrete planar maps: Introducing next-iterate operators," Mathematical Biosciences, vol, 355, 108924, we develop a technique that allows the analysis of planar systems on any unbounded time scale, unifying the application of phase planes to study discrete, continuous, and hybrid systems. This is joint work with Sabrina H. Streipert, Department of Mathematics, University of Pittsburgh, PA, USA. This work was partially supported by NSERC Discovery Grant RGPIN-2022-05067.

Global dynamics of semiflows which are monotone with respect to high rank cones

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Nonlinear dynamical systems arising from biological models with embedded predator–prey interactions may exhibit order-preserving monotonicity with respect to a rank-k cone with k¿1. We show that such systems have the the limit-set trichotomy property and that the semiflow restricted to the omega-limit set of any precompact semi-orbit is topologically conjugate to a Lipschitz-continuous flow on a k-dimensional Euclidean space. In the important case where k=2, we establish a generic Poincaré–Bendixson theorem, which in turn yields generic periodicity for a broad class of high-dimensional epidemic models with nonstandard nonlinear incidence functions.The talk is based on a series of joint works with Lirui Feng and Yi Wang. Some of these results have appeared in SIAM Journal on Mathematical Analysis (2017), Journal of Differential Equations (2021), SIAM Journal on Applied Mathematics (2022), and Discrete and Continuous Dynamical Systems(2025), with several further developments to be reported

Analysis of a parabolic-hyperbolic hybrid population model: an integrated semigroup approach

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We study the global dynamics of a hybrid parabolic-hyperbolic model describing populations with distinct dispersal and sedentary stages. We first establish the global well-posedness of solutions, prove a comparison principle, and demonstrate the asymptotic smoothness of the solution semiflow. Through the spectral analysis of the linearized system, we derive and characterize the net reproductive rate $\mathcal{R}_0$. Furthermore, an explicit relationship between $\mathcal{R}_0$ and the principal eigenvalue of the linearized system is analyzed. Under appropriate monotonicity assumptions, we show that $\mathcal{R}_0$ serves as a threshold parameter that completely determines the stability of steady states of the system. More precisely, when $\mathcal{R}_0 < 1$, the trivial equilibrium is globally asymptotically stable, while when $\mathcal{R}_0 > 1$, the system is uniformly persistent and there is a positive equilibrium which is unique and globally asymptotically stable.

Causal Volterra dynamics of Mamba

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Transformers admit continuum descriptions based on mean-field interactions, but selective state space models fall into a different class. We show that the many-token limit of an input-conditioned, single-head SISO Mamba-3 block is a causal Volterra equation on the sphere with an explicit exponential memory kernel. The key reason is that Mamba's causal mask is chain-dependent: the influence of one token on another is transmitted through the full sequence of intermediate gates rather than a single pairwise weight. Under a constant-horizon scaling, we prove convergence to this limit, validate it numerically, and show that the same framework covers the SISO Mamba-3 rotation, with Mamba-2 as a special case. We also characterize the resulting memory-horizon interpolation and relate the kernel scale to pretrained Mamba-2 heads.

Quasi-stationary distributions

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Quasi-stationary distributions (QSDs) are those almost invariant to a diffusion process over exponentially long time. Representing important transient stochastic dynamics, they arise frequently in applications, especially in chemical reactions and population systems admitting extinction states. This talk will present some rigorous results on the existence, uniqueness, concentration, and convergence of QSDs along with their connections to the spectrum of the Fokker-Planck operator.

Modeling and analysis of a bulk–surface PDE system for the actin turnover cycle

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The continuous turnover of actin is essential for maintaining the structure and function of the cell cortex and plays an important role in cell migration. In this work, we introduce a bulk–surface partial differential equation model for the intracellular actin turnover cycle, describing the interaction between cytoplasmic and membrane-associated actin dynamics. The model consists of three interacting components: bulk G-actin monomers, free filament tips in the bulk, and membrane-attached actin on the cell surface. These variables are coupled through nucleation, polymerization, depolymerization, capping, severing, capture, and detachment mechanisms. The proposed model provides a framework for analyzing the dynamical behavior of the system through bifurcation analysis and numerical simulations on coupled bulk-surface domains. Bulk–surface finite element simulations complement the analysis and reveal the dynamical behaviors, including oscillatory regimes, spatially heterogeneous states for actin dynamics. This framework provides a first step toward coupling intracellular actin regulation with cell motion.

Stochastic dynamics in motif-based neuronal networks

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Neuronal networks exhibit complex dynamics shaped by their connectivity and stochastic inputs. Empirical studies reveal that these networks contain recurring subgraphs, or motifs, which act as functional building blocks supporting coherent spiking activity. Yet, the collective influence of distinct motif types within large-scale, noisy networks remains poorly understood. Here, we construct a biologically inspired spiking network composed of six representative motifs and systematically examine how intrinsic noise, coupling strength, and inter-motif connectivity govern synchronization. Both motif- and network-level coherence peak at intermediate noise intensities, consistent with coherence resonance. Among motif classes, bi-coupled (M2) and type-2 recurrent feed-forward (M3c) motifs act as local hubs that enhance synchrony across the network. Motif-deletion experiments confirm that removing these motifs produces the greatest reduction in coherence, while deletion of others yields weaker or compensatory effects. Analysis of spiking statistics reveals that M2 and M3c motifs exhibit noise-induced doublet bursting that enhance temporal precision and correlate with elevated signal-to-noise ratios. Comparison with a degree- and weight-matched random network demonstrates that structured motif networks achieve stronger and more noise-efficient synchronization. Collectively, these findings highlight the central role of local structural organization, particularly recurrent connections, in shaping noise-driven coherence and provide a quantitative link between motif topology and emergent large-scale network dynamics.

Dynamical analysis in a nonlocal delayed reaction–diffusion tumor model with therapy

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In this work, we investigate the dynamical properties of a reaction-diffusion system arising from tumor–therapy modelling that features both nonlinear interactions and nonlocal delay. By applying the Lyapunov-Schmidt reduction, we establish the existence of a nontrivial steady-state solution bifurcating from the trivial solution. In particular, we derive an approximate expression for a spatially nonhomogeneous steady-state solution. Then, we provide a detailed spectral characterization of the linearized operator and explicit stability criteria and identify the delay-dependent Hopf bifurcation regimes. To illustrate the theoretical results, we include a concrete example that verifies the claims in our theorems and numerically demonstrates how changes in treatment parameters alter stability and bifurcation behaviour. This is joint work with my PhD student Hu, Dandan.

Comprehensive understanding of combination immunotherapy for cancer treatment via bifurcation theory

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Combination immunotherapy, which integrates immune checkpoint inhibition with immune stimulation, has shown great promise in cancer treatment but remains highly sensitive to patient-specific conditions. We present a mathematical model that captures the essential mechanisms of tumor–immune interactions under combination therapy. Using bifurcation analysis, we identify distinct dynamical regimes, including tumor eradication, partial control, oscillations, and immune escape, and derive analytical conditions for transitions between these regimes within a hierarchical parametric framework. Interestingly, higher-codimension Hopf and Bogdanov–Takens bifurcations emerge, revealing rich and complex dynamics. Numerical simulations further illustrate various clinical outcomes across different parameter regions. Finally, sensitivity analysis demonstrates how parameters correlate with outcomes in partially controlled and oscillatory regimes. The results agree with simulations and further reveal dual effects of key parameters: factors that promote tumor suppression in partially controlled states may destabilize immune dynamics in oscillatory regimes. Together, these findings illustrate how nonlinear dynamics and parameter sensitivity shape treatment outcomes, providing insights into the design of immunotherapy strategies. This is joint work with W. Zhang and P. Yu. W. Zhang is supported by Simons Foundation Collaboration Grants for Mathematicians (No. A21-0013-001), and P. Yu is supported by the Natural Sciences and Engineering Research Council of Canada (No. R2686A02).

Arnold diffusion for generic analytic a priori unstable systems

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In nearly integrable systems, the existence of large scale instability is usually referred to as Arnold diffusion. Arnold conjectured that in a system with more than 2 degree of freedom, instability should happen generically. While the question has seen much progress when the Hamiltonian is smooth, the real analytic case remained largely open. In this talk, we discuss progress for a specific class of analytic systems known as the a priori unstable systems. This is based on joint work with Amadeu Delshams.

Transient dynamics and bifurcations in a cancer immune checkpoint blockade model

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We investigate the various responses in cancer immunotherapy through bifurcation theory. Our results characterise the influence of key parameters on different treatment responses and illustrate the response regions through bifurcation diagrams using parameters tuned by therapy. We examine a clinically intriguing periodic outcome featuring an extended apparent non-response, a rapid immune-driven tumour decline, and an eventual cancer relapse. The repetitive pattern in this periodic solution is formed by two quasi-steady cancer states connected by two fast transitions. Our results suggest that the transient behaviour of the delayed response, which is the fast transition after the cancer progression state, is induced by a periodic solution exhibiting an exploding period near a saddle-node bifurcation. Another transient behaviour, which shows as a fast relapse after a long period of dormancy state, is caused by the slow change near a saddle-type equilibrium. Our findings have the potential to guide and inform future therapeutic research.

Threshold dynamics of an ODE-PDE coupled model for tick population mediated by the deer population dynamics and heterogeneity

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In this talk, I report some results on the global dynamics of an ODE-PDE coupled model for tick population dynamics that extends the model in [Gourley eta. 2018] by incorporating (i) the deer population dynamics, location-dependence of the attachment rate of questing adults which reflects the spatial heterogeneity of the habitat. We first establish the well-posedness of the model, including global existence, positivity, and ultimate boundedness of solutions, and prove that the solution semiflow admits a compact global attractor. We then identify the basic reproduction number $\mathcal{R}_0$ of the model and establish the existence of a principal eigenvalue accompanied by a positive eigenfunction. Finally, we establish the threshold dynamics in terms of $\mathcal{R}_0$: when $\mathcal{R}_0 < 1$, the extinction equilibrium of the system is globally asymptotically stable; when $\mathcal{R}_0 > 1$, the system admits a unique positive equilibrium which is globally asymptotically stable. We also numerically explore the impact of the spatial heterogeneity on the spatial distribution of the tick population.

Propagation dynamics of reaction and diffusion equations in a time-heterogeneous shifting environment

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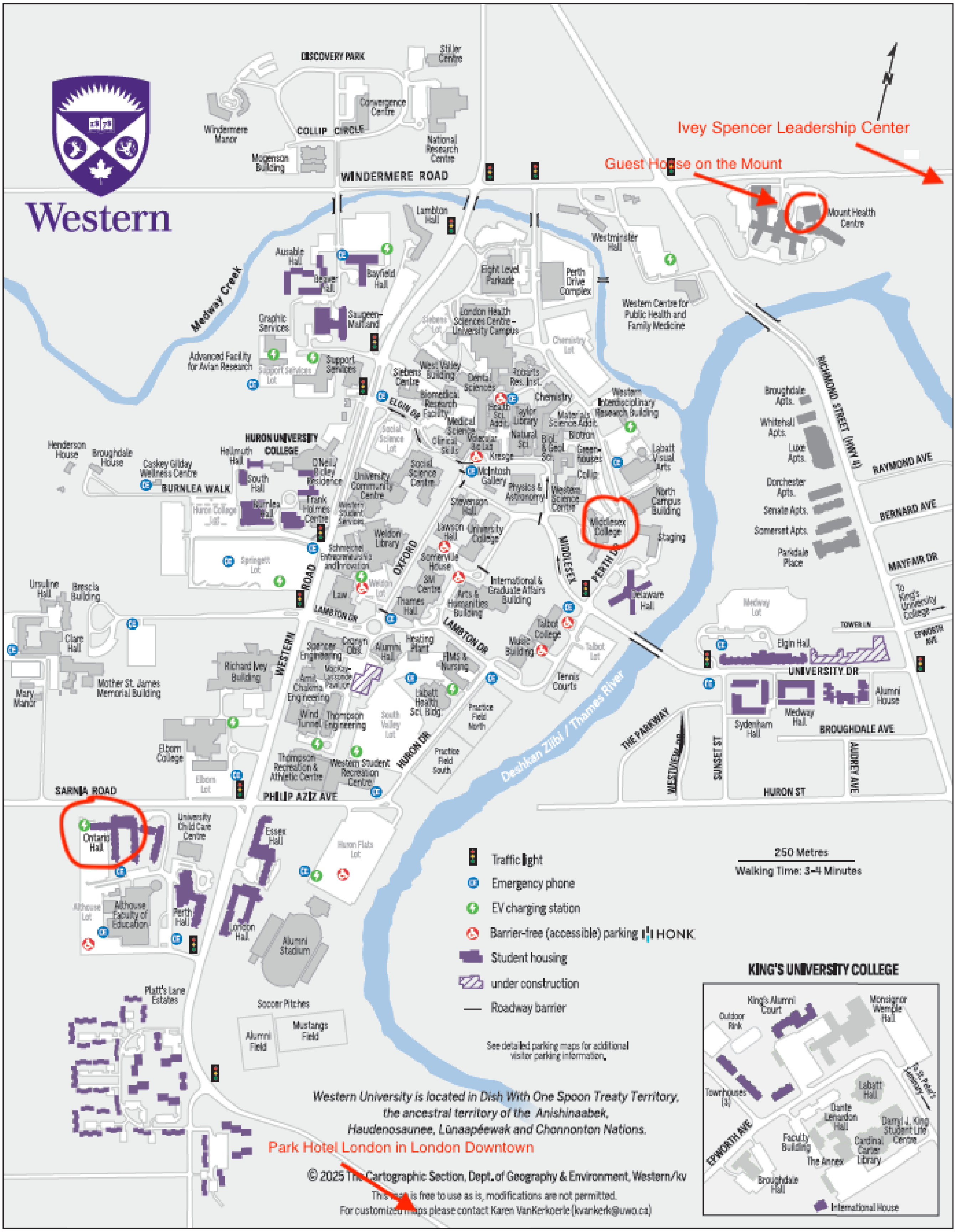
In this talk, I will first give a brief review of the propagation dynamics of evolution equations in a shifting environment. Then I will report our recent research on a large class of time and space heterogeneous reaction-diffusion equations. We obtain the leftward and rightward spreading speeds in terms of the shifting speed and the spreading speed of an associated limiting equation. We also establish the existence, uniqueness and nonexistence of the forced traveling wave, and further apply this result to obtain the existence of almost periodic traveling waves for nonautonomous SIS epidemic models. This talk is based on a joint work with Dr. L. Zhang.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Guest House on the Mount
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Western
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Stiller Centre
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National Research Centre
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South Hall
O'Neil Ridley Residence
Burnlea Hall
Frank Holmes Centre
Social Science Centre
University Community Centre
Western Student Services
Weldon Library
Stevenson Hall
Lawson Hall
University College
Somerville House
Schmeichel Entrepreneurship and Innovation
Springett Lot
Ursuline Hall
Brescia Building
Clare Hall
Mary Manor
Mother St. James Memorial Building
Law
3M Centre
Thames Hall
Arts & Humanities Building
International & Graduate Affairs Building
Delaware Hall
Talbot College
Music Building
Richard Ivey Building
Spencer Engineering
Claudette MacKay-Lassonde Pavilion
Amit Chakma Engineering
Alumni Hall
Heating Plant
FIMS & Nursing
Labatt Health Sci. Bldg.
Tennis Courts
Wind Tunnel
Thompson Engineering
South Valley Lot
Practice Field North
Practice Field South
Elborn College
Thompson Recreation & Athletic Centre
Western Student Recreation Centre
SARNIA ROAD
PHILIP AZIZ AVE
WESTERN ROAD
OXFORD
LAMBTON DR
HURON DR
ELGIN DR
MIDDLESEX
PERTH DR
Deshkan Ziibi / Thames River
THE PARKWAY
WESTVIEW DR
SUNSET ST
HURON ST
AUDREY AVE
BROUGHDALE AVE
UNIVERSITY DR
RICHMOND STREET (HWY 4)
RAYMOND AVE
BERNARD AVE
MAYFAIR DR
EPWORTH AVE
TOWER LN
Broughdale Apts.
Whitehall Apts.
Luxe Apts.
Dorchester Apts.
Senate Apts.
Somerset Apts.
Parkdale Place
Medway Lot
Elgin Hall
Sydenham Hall
Medway Hall
Alumni House
To King's University College
Ontario Hall
University Child Care Centre
Essex Hall
Huron Flats Lot
Althouse Faculty of Education
Perth Hall
London Hall
Alumni Stadium
Platt's Lane Estates
Soccer Pitches
Alumni Field
Mustangs Field
Traffic light
Emergency phone
EV charging station
Barrier-free (accessible) parking HONK
Student housing
under construction
Roadway barrier
250 Metres
Walking Time: 3-4 Minutes
See detailed parking maps for additional visitor parking information.
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Townhouses (4)
Labatt Hall
Dante Lenardon Hall
Darryl J. King Student Life Centre
Faculty Building
Cardinal Carter Library
The Annex
Broughdale Hall
EPWORTH AVE
To St. Peter's Seminary
International House