Applied Dynamical Systems and Mathematical Biology
Systèmes dynamiques appliqués et biologie mathématique
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COURTNEY ALLEN, University of New Brunswick
Modelling the dynamics of diatoms on New Brunswick's mudflats

At low tide in the upper Bay of Fundy, over a kilometre of intertidal mudflats are exposed. The microalgal biofilms that grow on these mudflats are a carbon sink, but their potential for carbon sequestration is still being understood. One hurdle is that the primary component of the microalgal biofilm, diatoms, migrate vertically within the mud. Diatoms rise to the surface when the sun comes out, but recede when the light becomes too intense and when the tide comes in. Therefore, surface measurements of diatom populations made by remote sensing technologies, such as drones and satellites, need to be corrected. To that end, we propose a one-dimensional advection-diffusion-reaction equation to describe how the diatom population changes with depth and time. The model is implemented in Julia, and some sensitivity analyses are presented to show how the surface behaviour is influenced by parameters such as temperature and light intensity.

JULIAN CHRISTOPHER, Wilfrid Laurier University
The effect of time delay on the global stability of infectious disease models and other dynamical systems

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.

KAYLEE DEVRIES, Wilfrid Laurier University
Analysis of a General Vector Transmission Model for Infectious Disease Spread

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 main assumptions of the model are as follows: there is no return from infected classes to the susceptible classes in either population; each infected class can be reached from the respective susceptible class; and transmission follows a mass action incidence function with a criss-cross structure, whereby infected vectors infect susceptible humans, and infected humans infect 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 $\mathcal{R}_0 \leq 1$ and of the endemic equilibrium when $\mathcal{R}_0 > 1$.

SHIHENG FAN, Memorial University of Newfoundland
Global dynamics of two-species competition reaction-diffusion systems in a time-varying domain

In this talk, we investigate the global dynamics of a two-species competition reaction-diffusion model in a time-varying domain under the homogeneous Dirichlet and Neumann boundary conditions. Under appropriate conditions, we establish the competitive exclusion principle for asymptotically bounded and periodic domains, respectively. By the method of upper and lower solutions and comparison arguments, we prove that one species will exclude the other in an asymptotically unbounded domain. We further apply the analytic results to a Lotka-Volterra competition model for its global dynamics and conduct numerical simulations to illustrate our findings.

OLIVIER GRIMARD, University of New Brunswick
Modelling clonal structure of saltmarsh Spartina grasses

For *Spartina* spp., clonal spread via extension of rhizomes represents a major means of colonization within saltmarsh restoration sites. Both dominant halotolerant grass species *Spartina alterniflora* and *Spartina patens* have remarkably different rhizomal structures, which affect both their rate of spread and their competitive ability. The rhizomal three-dimensional structure of both species is only superficially understood despite its apparent importance. The present work offers a detailed quantification of the rhizomal structure for both plant species and defines a set of growth rules from which this structure could arise. Quantification of rhizomal structure includes internode length, branching angles, short internode numbers and length, and node counts within functional rhizome sections, among other measurements. The rules include branching potential per node, apical bud activity variability between zones, and the sequence of functional sections. Rules hold regardless of the position within the plant while quantities change. To test whether these quantifications and rules are truly able to produce the observed structure, we implement them in a deterministic node-based three-dimensional model using Julia. As of now, the simulations capture the difference in forms characterizing each species quite well, although the details of these forms need further refinements. The results outline the need to understand both plant developmental processes and plant structures' geometric properties to obtain a set of rules that lead to a biologically realistic structure.

DANDAN HU, Memorial University of Newfoundland
Dynamical analysis in a nonlocal delayed reaction–diffusion tumor model with therapy

In this talk, we study a nonlocal delayed reaction-diffusion model for tumor growth under therapy. The model includes nonlinear tumor-therapy interactions, spatial diffusion, and a nonlocal delayed response. Using the Lyapunov-Schmidt reduction, we establish the existence of a nontrivial steady-state solution bifurcating from the trivial solution and obtain an approximate expression for a spatially inhomogeneous steady state. We then analyze the spectrum of the linearized operator, derive explicit stability criteria, and identify delay-induced Hopf bifurcation regimes. Numerical simulations are presented to support the theoretical results and to illustrate how treatment parameters affect stability and oscillatory behavior.

FATIMA ISLAM, University of New Brunswick
Impact of Dispersal on Total Equilibrium Biomass in Patch-Structured Logistic Models.

Understanding how dispersal asymmetry influences total equilibrium biomass in spatially structured populations remains a key challenge in mathematical ecology. This study extends classical two-patch logistic models by incorporating a mixed dispersal strategy that combines random and density-dependent movement. The dispersal rate from each patch is governed by a fitness function parameterized by dispersal strength and asymmetry ratio. Using geometric phase-plane analysis, specifically the intersection of an ellipse and a hyperbola derived from the equilibrium conditions, we characterize the unique positive equilibrium and prove its global asymptotic stability via Dulac's criterion and the Poincaré–Bendixson theorem. Our results reveal four distinct dispersal regimes based on the position of a limiting hyperbola relative to three critical points on the ellipse. These regimes determine whether total equilibrium biomass increases, decreases, peaks at an intermediate dispersal strength, or crosses the isolated baseline. The framework resolves the so-called Perfect-Mixing Paradox by showing that asymmetry fundamentally alters the relationship between connectivity and total biomass, offering a more complete picture than previous symmetric or purely nonlinear models.

YUCEN JIN, Western University
Delay-induced Hopf-zero bifurcation in a Host-parasite model

Host–parasite interactions play a central role in ecological and evolutionary dynamics, shaping population persistence and ecosystem stability. When these interactions are coupled with interspecific competition, they can generate highly nonlinear and often counterintuitive behaviors. In this study, we develop a delayed differential equation model describing host–competitor–parasite dynamics, incorporating a latency period in parasite reproduction. This delay represents the developmental time of infection and introduces memory effects that can significantly alter system stability. Using bifurcation analysis, we investigate codimension-two phenomena, with particular focus on the Hopf–zero bifurcation as an organizing center for complex oscillatory and mixed-mode dynamics. Our results demonstrate how the interplay between temporal delays and multi-species interactions drives the emergence of rich and intricate dynamical patterns in ecological systems.

EMMANUEL LORIN, Carleton University
Recent Advances in Neural Network-based Methods for Partial Differential Equations and Eigenvalue Problems

In this talk, I will provide an overview of recent algorithms and mathematical advances in scientific machine learning, focusing on the computation of eigenvalues and eigenfunctions of operators, as well as on the solution of partial differential equations. I will illustrate these methods with examples and highlight current research challenges in this rapidly evolving field. While the presentation will emphasize general mathematical frameworks, many of the techniques discussed have direct applications to problems arising in mathematical biology.

CONNELL MCCLUSKEY, Wilfrid Laurier University
Global Stability of Epidemic Models with Uniform Susceptibility

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: (1) only one susceptible class, (2) no return from the infected classes to the susceptible class, (3) each infected class can (eventually) be reached from the susceptible class, (4) a "reasonable" incidence function.

We are able to fully resolve the global dynamics for the resulting ODE systems, obtaining the common threshold behaviour: If R0<1, then the disease-free equilibrium is globally asymptotically stable; if R0>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 work was done in collaboration with David Earn (McMaster University).

WENTAO MENG, Memorial
A road-field population model with climate change: forced wave patterns and stability

Recently, increasing attention is being devoted to spatial invasion and wave propagation phenomena in high-dimensional heterogeneous media (such as road-field interchange networks), due to their significance in applications to population models. The combined effects of road diffusion and climate change in an unbounded high-dimensional domain introduce further complexity and challenges. In this talk, we study the propagation dynamics of a road-field system in a shifting environment.

Our results indicated that forced traveling waves exist as long as the shifting speed is less than a critical value. For each of these kind of speeds, the forced wave profile is unique and exponentially stable. While the shifting speed is greater than that critical value, we further established propagation dynamics in connection to extinction and persistence. We found that the propagation of persistence cannot be faster than the critical speed.

ZHISHENG SHUAI, University of Central Florida
A Final Size Relation for Heterogeneous Epidemic Models

We revisit the final size relation for epidemic models with homogeneous mixing and explore the challenges of extending it to heterogeneous settings. To address these, we develop a new systematic approach to construct first integrals in heterogeneous epidemic models. This approach enables a natural extension of the final size relation and yields new biological insights into reproduction numbers, turning points and peak infection levels.

WANYUE TANG, Western University, Lanzhou University
High-Codimension Bifurcation Analysis of a Predator-Prey System with Fear Effects

In this talk, we present a predator-prey model incorporating the fear effect and apply bifurcation theory to investigate higher-codimension Bogdanov-Takens (BT) and Hopf bifurcations. We demonstrate that multiple types of higher-codimension BT bifurcations can arise, including codimension-2, -3, and -4 cusp bifurcations, codimension-3 focus (elliptic) bifurcations, and other codimension-4 bifurcation types. Explicit conditions for the onset of these bifurcations are derived. In addition, we conduct a Hopf bifurcation analysis and employ normal-form theory to compute focus values up to the sixth order. Nevertheless, an exhaustive numerical search reveals that the generalized Hopf bifurcation is of codimension three, indicating that at most three limit cycles can bifurcate from the Hopf critical point associated with an equilibrium point. [This is joint work with Dr. Pei Yu.]

JUNYUAN YANG, University of Victoria
Parameter identification of age-structured epidemic models

Parameter identifiability analysis aims to determine whether model parameters can be uniquely determined from observable outputs. This is a critical step in epidemiological forecasting and the design of effective control measures. In this talk, we systematically review the theoretical foundations and practical applications of parameter identifiability and propose a framework for analyzing structural model parameter identifiability. By integrating locally and globally identifiable techniques, we systematically construct a hierarchical structure for parameter identifiability in age-structured epidemic models. Using Monte Carlo simulations and approximate Bayesian estimation methods, we identify parameters that are actually unidentifiable in the models. This is a joint work with Ziyi Wu and Maia Martcheva.